XXVI International Congress of Entomology

HELSINKI, FINLAND, JULY 17-22, 2022

Book of Abstracts

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ICE 2022 HELSINKI®

Entomology for our planet

XXVI International
Congress of Entomology

HELSINKI, FINLAND, JULY 17–22, 2022

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THE IMPORTANCE OF ICE CONGRESSES

and the benefits that result from knowledge sharing

Welcome to the XXVI International Congress of Entomology ICE2022 in Helsinki. This congress is one in a series of over 100 years of ICE congresses. This history is reflected on the cover page of the program book. The impact of ICE congresses on the field of entomology for over a century is a strong motivation to be part of this great legacy. I am happy and proud to host you at the ICE2022Helsinki.

In the context of our contemporary world, in person meetings at congresses have become less frequent - and therefore immensely valuable. Personal meetings at congresses enhance, stimulate and create knowledge, innovation, and collaboration, which is vital to the success of our discipline. Congresses give opportunity for the further creation of knowledge and the application of that knowledge. These opportunities arise from different sources and come in many forms. They may be industrial innovations, or new scientific collaborations, new professional friendships, or perhaps the emergence of new clusters of expertise, centres of excellence, and collaboration. All of these are outcomes of successful congresses.

For organising a congress, one needs multiple skills. The congress host works with those colleagues who are willing, and in a position to influence the congress direction. To enable this, we have relied on scientists, academic leaders, political and social leaders, business leaders, as well as the trained professional staff of our congress venue and the PCOs. Organizing a congress requires a long-term commitment by the organising committee to the established program. This is no minor issue, given the long period between bidding for and, if successful, running the event. In the case of ICE2022 with two years of postponement due to restrictions caused by the covid19 pandemic, this period lasted for over seven years. The organizers need a core-group of hundreds of people distributed globally, with a long-term commitment to the ICE congresses. The colleagues all around the world helped the core organizing team in Helsinki to align our objectives with those of the key stakeholders in the area of entomology. For these reasons my sincere thanks and gratitude go out to all our section organisers, symposium organisers, sponsors, exhibitors, volunteers, and congress participants, as well as to the staff of our PCOs, the City of Helsinki, and the staff of the congress venue Messukeskus and the Finlandia Hall. In terms of practical support to the ICE2022 congress the most significant was provided by the Helsinki Region Transit Authority and the City of Helsinki Mayor`s office. All congress participants receive the ticket for public transportation system in and around Helsinki for the time of the congress. Many thanks to the HSL-HRT for giving us this environmental touch. Many thanks to the City of Helsinki Mayor for hosting the reception for our delegates.

For ICE2022Helsinki, universities and other educational institutions along with research institutes are the dynamic key elements of this event. They offered standing expertise and knowledge, but they also open paths of knowledge to be followed. These new knowledge designs attract interest in our discipline and facilitate cooperation.

Since the beginning of 2020 there have been serious public health issues around the globe, which have shown us how vulnerable we are as human beings and as societies. Measures enforced in the interest of public health have left their marks on ICE2022 Helsinki. Despite these events we carried on the planning of the congress while trying to avoid over-reactions; over-reactions can lead to wrong decisions. The fact that you now read my address in the program booklet means that we have successfully overcome these two years of restrictions on meetings and travels, thanks to the support of many groups and individuals.

My sincere thanks go to the support groups that we had nationally and internationally to make this congress happen. My personal thanks go in particular to the University of Eastern Finland, Department of Environmental and Biological Sciences, which allowed me to continue to work academically. I also want to thank the Southwest University, Chongqing, China, which adopted me during the last years as one of their staff members and gave me the opportunity to continue educating the next generations of entomologists.

The congress organising team has attended international meetings and events in entomology during the past six years. This has been rewarding, but also necessary for disseminating knowledge about the ICE2022Helsinki congress. Besides the members of the organizing committee, numerous colleagues have spread our promotional material at probably hundreds of meetings around the world.

Our sincere thanks go to the numerous sponsors, who have made this congress possible, in particular the sponsors of individual symposia. Our sponsors range from the City of Helsinki and the Helsinki Region Transit Authority to influential international organisations, companies, and professional associations. Last, but not least, my sincere thanks go to all our exhibitors, who travelled to Helsinki to meet the congress participants.

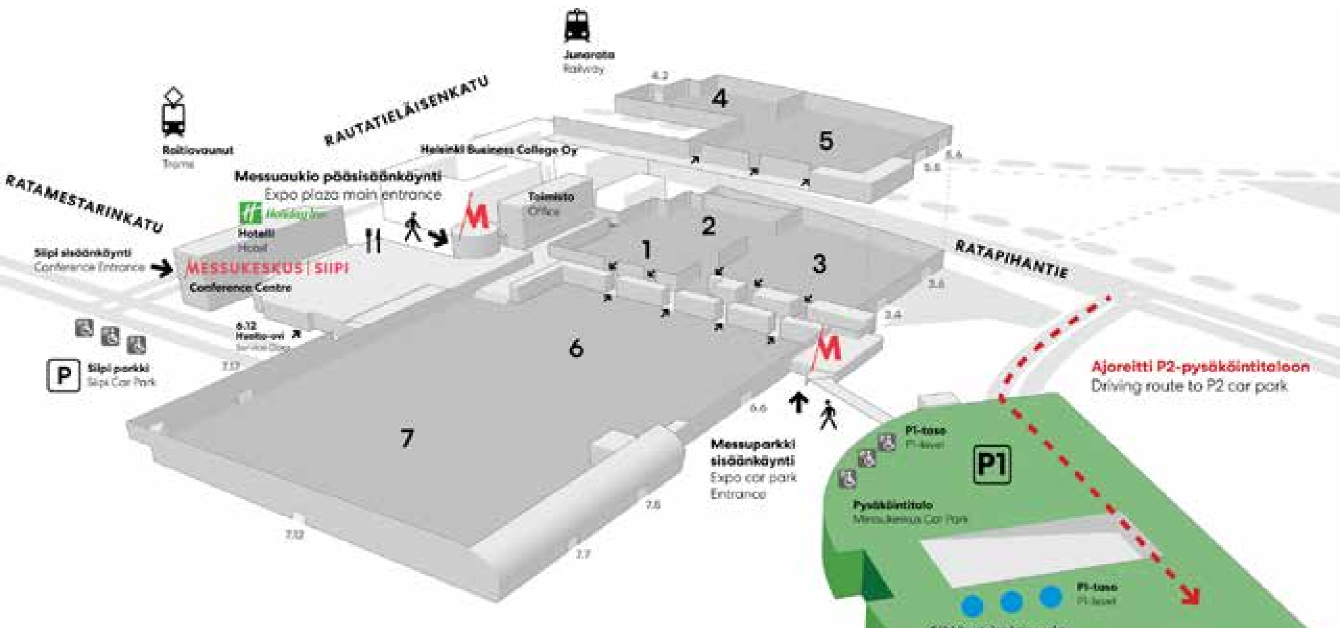
Let me close off by stating that we need nature and insects for our existence: to support our lives and our lifestyle. Insects are one of the most speciose taxa on our planet. They sustain life on Earth and fulfil many critical ecosystem functions, from pollination and biocontrol to being human food. This is the reason for us to choose as the core message on the ICE2022Helsinki congress “bear-mat”: “Insects feed the belly of nature”. This “bear-mat” every participant will find in their congress package.

Thank you all for being here, and for making ICE2022Helsinki happen. We hope the congress will contribute to a sustainable co-existence of humans and insects.

Heikki Hokkanen
President of the ICE2022Helsinki Organizing Committee

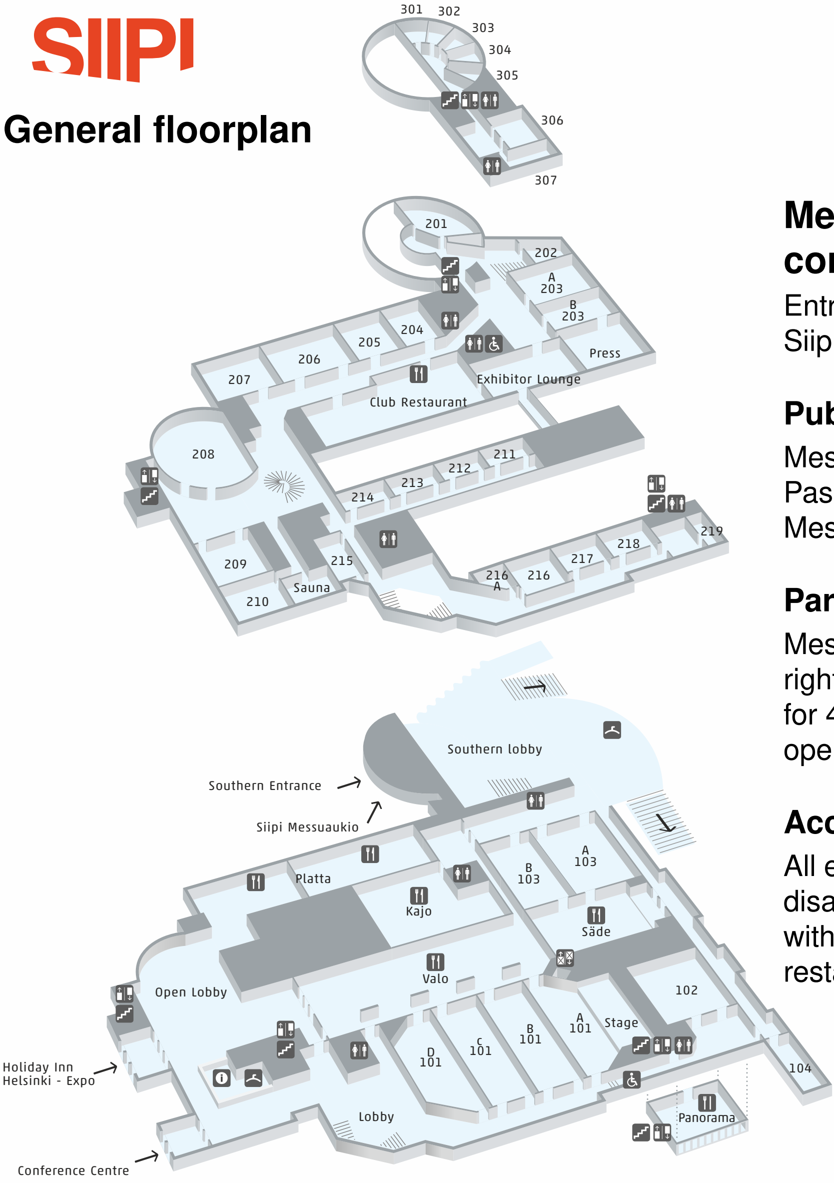
MAPS AND FLOOR PLANS

Messukeskus Siipi Entraces



SIIPI

General floorplan



Messukeskus Siipi conference centre

Entrance | Rautatieläisenkatu 3
Siipi Car Park | Ratamestarinkatu 13

Public transportation

Messukeskus is situated right next to Pasila train station. You can also reach Messukeskus easily by bus or tram.

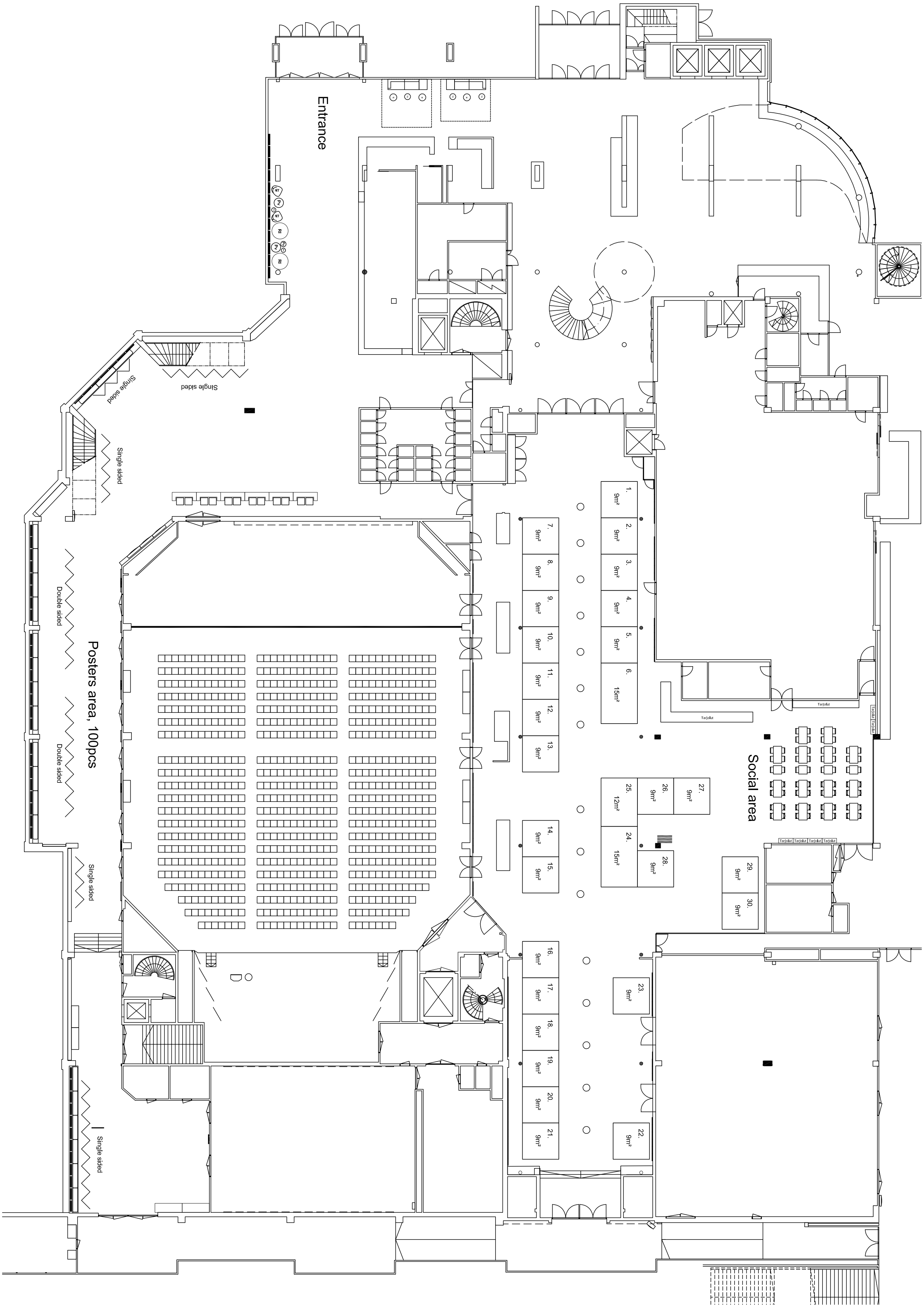
Parking

Messukeskus parking facilities are situated right next to Messukeskus and have room for 4 600 vehicles. Parking facilities are open 24/7.

Accessibility

All entrances are accessible for people with disabillities and all floors can be accessed with elevator. The majority of Messukeskus restaurants are also accessible.

1st floor exhibition stands and facilities



Congress Theme

ENTOMOLOGY FOR OUR PLANET

Insects are in many respects the backbone for Life on our Planet, being the major engineers of ecosystems and dominating organisms of the Animal Kingdom. “To a first approximation, every animal is an insect” (J. Kukalová-Peck). The biomass of insects ranges from over 2000 kg/ha in the tropics to around 1000 kg/ha in the temperate zone, while the biomass of human beings averages at only 7 kg/ha. The Theme for the ICE 2022 is “Entomology for our Planet”, in order to highlight the crucial role of insects in maintaining and shaping our lives, and overall, life on Earth. Specific emphasis includes topics such as:

Entomology for a hungry planet

Insects and mites are main competitors for humans for food, feed and fiber, requiring understanding of their properties for successful management. Progress in entomology is essential to coping with the ever-evolving race with insect pests. Insects and mites are also part of any solution to successful pest management, as more than half of all known insects are natural enemies of herbivorous insects. As the growing human population on our planet is seeking for alternative sources of animal protein to satisfy the world hunger, increasing attention is paid to the possibility to use insects as a major source of proteins for food as well as for feed.

Entomology for a diverse planet

Global biodiversity is the ecological base for sustainability of the world’s ecosystems and the ecosystem services they produce for humans, but also the resource base for and driver of bioeconomy and businesses arising from innovative uses of biomaterials, many of which originate from arthropods. Insects pay a key role in global biodiversity, as over ¾ of all known animal species are insects, and they outnumber known vascular plant species by 1-2 orders of magnitude. Furthermore, it is believed that the vast majority of all insect species have not been described yet (are unknown), and that most species will go extinct before they have been discovered.

Entomology for a healthy planet

There is a dramatic increase in vector-borne disease epidemics over the past decades, and nearly all of the most important vector-borne human diseases have exhibited dramatic changes in incidence and geographic range. These include dengue fever, malaria, Lyme disease, West Nile virus, Rift Valley fever, chikungunya, yellow fever, and most recently, zika. Overall, vector-borne infectious diseases cause a significant fraction of the global infectious disease burden, and nearly half of the world’s population is infected with at least one type of vector-borne pathogen. Vector-borne plant and animal diseases not only pose serious health hazards to humans and reduce the quality of life, but also reduce agricultural productivity and disrupt ecosystems throughout the world. At the same time, the world is facing an extreme shortage of entomologists and vector control experts, as many countries do not have any entomology programs at the undergraduate university level, and some countries have only a handful of expert entomologists.

Entomology for a changing planet

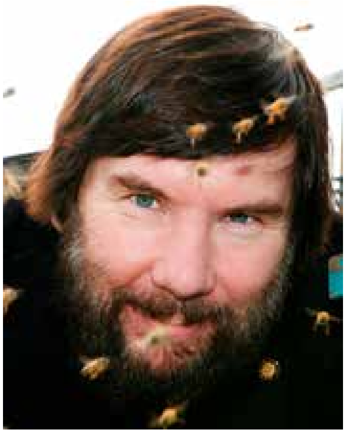
Global ecological challenges such as climate change, biodiversity loss, and invasive species all have a strong entomological component, and are usually interlinked. Thus climate change profoundly affects species distributions and abundances, exacerbates biodiversity losses, and facilitates invasions of harmful species into new geographical areas. Such drivers further disrupt critical ecosystem services such as biological control, pollination, and decomposition, in all of which insects play the determining role. Even a country like Finland records well over 100 new insect species per year, among them a recent, established invader Anoplophora glabripennis (the Asian long-horned beetle), found in 2015. In turn, we appear to be losing specialist arctic species at an accelerating pace, including some bumble bee species such as Bombus arcticus.

Entomology with latitude

Helsinki will be the northernmost ever location for the ICE Congress (at 60°10′N, equivalent to Seward, Alaska, or Nanortalink, Greenland). Thanks to the warm Gulf-stream, however, Finland enjoys (usually) warm and nice summers, and the world's northernmost agriculture (self-sufficiency in all key agricultural products). Also insect life is adapted to the white nights (i.e., practically no night in the summer), which the delegates to the ICE 2022 congress are welcome to experience and to explore.

Helsinki

President of the ICE2022Helsinki Organizing Committee Professor Heikki Hokkanen



Prof. Heikki Hokkanen is currently a visiting research professor at the Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio campus. He is professor Emeritus of agricultural zoology at the Faculty of Agriculture and Forestry, University of Helsinki. He holds a Lic. Phil. degree in ecology and natural resource management (1978. Univ. Jyväskylä. Finland), and a PhD in applied entomology (1983, Cornell University, Ithaca, NY, USA). After his PhD Heikki Hokkanen stayed for extensive periods as a visiting scholar at the Institute of Biological Control (Darmstadt, Germany), CABI Institute of Biological Control (Silwood Park, UK), University of Kiel, Germany, and at the OECD Directorate for Agriculture (Paris, France). In Finland his main work has been carried out first at the University of Kuopio (deputy professor), at the Agricultural research center of Finland (Jokioinen), and since 1990 until 2018 as a professor at the University of Helsinki. Currently he is the CEO of the SME Aasatek Oy.

His main interest and focus of work has been on all aspects of biological control, with emphasis on insect control. In recent years his interests have covered pollinators, and plant-derived bioactive compounds with an aim at plant protection applications. He has a long track record of coordinating international collaborative research, e.g., over ten years at the OECD Directorate for Agriculture (Paris). He coordinated the EU-project ERBIC (FAIR5), coordinated the FP7 project 'ForestSpeCs', and has participated in five other EU-RTD projects. Hokkanen is an active player in scientific publishing: Editor-in-Chief of BioControl (1997-2006); Founding EiC of Arthropod-Plant Interactions (2006-), editor of book series 'Progress in Biological Control', all by Springer. He recently established a new book series with CABI, called 'CABI Ecostacking Series', jointly with Dr. Ingeborg Menzler-Hokkanen (editors of the series). The first volume in this series is due to be published at the end of 2022, titled "The Concept of Ecostacking: Techniques and Applications". This book is edited by Jinjun Wang (SWU, China), Huai Liu (SWU, China), Ingeborg Menzler-Hokkanen (UEF, Finland) and Hongbo Jiang (SWU, China).

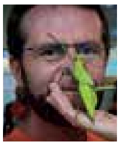
Professor Hokkanen has experience in organizing scientific meetings. He was the Chair of the Organizing Committee for the Society of Invertebrate Pathology Annual Meeting in 2004 in Helsinki. This congress gathered around 350 experts to Helsinki and has been credited as one of the most successful SIP meetings in recent times. Currently he is the President of the Local Organizing Committee for the 26th International Congress of Entomology, to be held in Helsinki in July 2022. In 2012 the International Organization for Biological Control (IOBC-Global) selected Hokkanen as its Honorary Member.

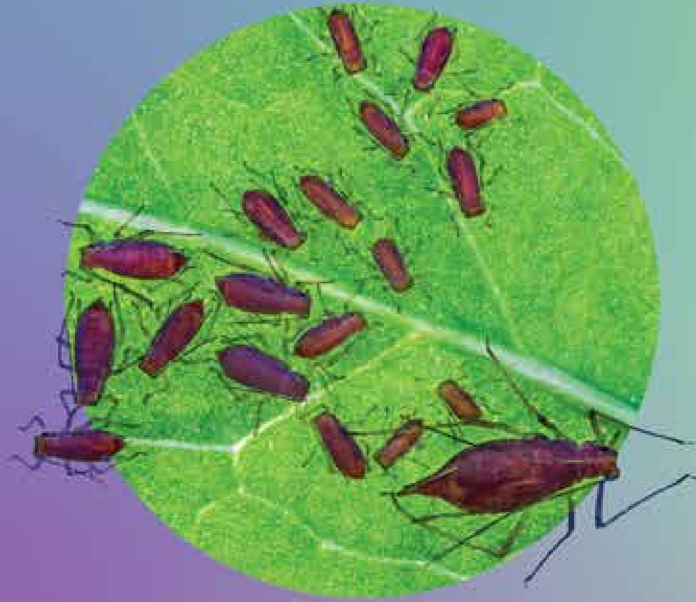
PRELUDE TO THE SCIENTIFIC PROGRAM

The daily program of the ICE2022 Helsinki congress is the result of a core group of international entomologists, who challenged the corona pandemic and other geopolitical situations to make this congress happen. The cover page of the program book lists the ICE congresses during the last over 100 years. More than 100 years of ICE congresses is a tradition which is not broken lightly.

The originally proposed symposia sometimes needed to change the speakers, and often also the symposium organizers during the past two years. After two years of modifications, and the still existing corona and travel restrictions, made it impossible for many symposium organizers to attend the ICE2022 Helsinki. Often colleagues picked up the responsibility of organization, where other scientists had to give up. Please see the current program as a platform to mend traditions after the pandemic, and to facilitate communication and knowledge exchange in-person after two years of lockdown.

The LOC (local organizing committee) had to set deadlines, and according to these deadlines this program has been compiled. The abstracts have been submitted (and peer reviewed) over a long period of time, ranging from 2019 to 2020, 2021 and 2022. Modifications of some of the abstracts submitted in 2019 could be done in time, while other abstracts and presentations are included in the original version. Some delegates, who joined research groups after 2019, might not be listed as authors. Some authors might be still listed, although they left science after 2019. LOC hopes that as delegate to ICE2022 Helsinki you have an understanding about the task which the section organizers, symposium organizers and the scientific advisory council have accomplished. Please forgive us any omissions or mistakes, which are inevitable. This is not the place to hunt for errors - this is the occasion to continue to stimulate entomological research on a global scale.





CODE OF CONDUCT

For congress participants

By attending the ICE2022 event, you agree voluntarily to abide by our ethics policy and the Code of Conduct. A code of conduct is a collection of rules and regulations that include what is and is not acceptable or expected behaviour. The ICE2022 ethics policy applies to speakers, staff, volunteers, and attendees. It defines expected behaviours, definitions of harassment, and reaffirms our support for diversity, equity, and inclusion in the field of entomology and, specifically, at our congress. Congress participants violating these rules may be sanctioned, expelled from the congress, and/or barred from future attendance at ICE events.

Expected Behaviour

- All attendees are to be treated with respect and consideration.
- Public critique should be of ideas rather than individuals.
- Avoid personal attacks directed toward other attendees, participants, ICE2022 organizers, and suppliers/vendors.
- Be mindful of your surroundings and of your fellow participants. Alert ICE2022 organizers if you notice a dangerous situation or someone in distress.
- Respect the rules and policies of the meeting venue, hotels, ICE2022 contracted facility, or any other venue.

Unacceptable Behaviour

- Harassment, intimidation, or discrimination in any form.
- Physical or verbal abuse of any participant.
- Disruption of talks at oral or poster sessions, in the exhibit hall, or at other events organized by ICE2022 at the meeting venue, hotels, or other ICE2022-contracted facilities.

Examples of unacceptable behavior include, but are not limited to, verbal comments related to gender identity, sexual orientation, disability, physical appearance, body size, race, religion, national origin; inappropriate use of nudity and/or sexual images in public spaces or in presentations; exclusion of transgender or intersex individuals; or threatening or stalking any attendee, speaker, volunteer, exhibitor, ICE2022 organizers member, service provider, or other meeting guest. ICE2022 is dedicated to providing a safe, hospitable, and productive environment for everyone attending. It is important to remember that a community where people feel uncomfortable or threatened is neither healthy nor productive. Accordingly, ICE2022 prohibits intimidating, threatening, or harassing conduct during our congress.

Authorship: All authors connected to a presentation and/or abstract must agree on all information contained in the presentation. Failure of an author to agree to the presentation format will lead to the presentation being withdrawn from the congress.

An author who submits a presentation to the congress must have intentions of attending, registering, and presenting at the meeting once the submission is accepted into the program. Repeated or consecutive last-minute cancellations by presenters may result in future submissions being denied.

Capturing, Sharing, and Posting without Permission: Presenters and attendees cannot photograph, screenshot, capture, or otherwise share images or presentation data without a presenter’s expressed written permission. Presenters are encouraged to use share/do not share icons. Presentations without “share” icons should be considered privileged and should not be shared outside the virtual platform.

Code of conduct

COVID-19 Safety: Before, During and After the Meeting

- Follow relevant guidance provided by the Centers for Disease Control and Prevention (CDC), World Health Organization (WHO), or your local health authority.
- Adhere to government issued travel restrictions and guidance issued by the region you will be traveling to and the regions you are traveling through and from.
- Evaluate your own health and that of people you are in close contact with; contact the meeting/event organizers if you have concerns.
- Stay home if you feel sick.

Onsite During the Event

- Abide by the venue's rules and requirements for onsite attendance.
- Assume all risks of attending an in-person event, including the potential risk of becoming infected with COVID-19
- Follow guidance from the local health authority, for everyday preventive actions to help prevent the spread of respiratory viruses, including:
    - Washing hands often with soap and water for at least 20 seconds, or an alcohol-based sanitizer with at least 60% alcohol.
    - Avoiding touching eyes, nose, and mouth with unwashed hands.
    - Covering your nose and mouth when coughing or sneezing. Throw used tissues in the trash.
- Agree to show proof of immunizations if required by ICE2022 or the local venue officials.
- Adhere to social distance protocols put in place by ICE2022 and respect others' personal space.
- Go to the event First Aid office (or equivalent) at any time if you feel unwell or are experiencing flu-like symptoms.
- Stay in your room and contact ICE2022 for further instructions if you wake up not feeling well during the event.

Post-event: Based on current contact tracing advice from many health authorities, if you test positive for COVID-19 up to 14 days after returning home, please contact ICE2022 to advise them.

Want to file a complaint?

Please contact ICE2022 Helsinki registration desk, or write an email to Heikki Hokkanen (heikki.hokkanen@uef.fi).

PLEARY PRESENTATION ABSTRACTS

Complex responses of herbivore insect pests to climate warming

Author: Battisti Andrea, DAFNAE, University of Padua, Italy

Abstract: Although it is well known that insects are sensitive to temperature, how they will be affected by ongoing global warming remains uncertain because these responses are multifaceted and ecologically complex. We reviewed the effects of climate warming on 31 globally important phytophagous (plant-eating) insect pests to determine whether general trends in their responses to warming were detectable. We included four response categories (range expansion, life history, population dynamics, and trophic interactions) in this assessment. For the majority of these species, we identified at least one response to warming that affects the severity of the threat they pose as pests. Among these insect species, 41% showed responses expected to lead to increased pest damage, whereas only 4% exhibited responses consistent with reduced effects; notably, most of these species (55%) demonstrated mixed responses. This means that the severity of a given insect pest may both increase and decrease with ongoing climate warming. Overall, our analysis indicated that anticipating the effects of climate warming on phytophagous insect pests is far from straightforward. Rather, efforts to mitigate the undesirable effects of warming on insect pests must include a better understanding of how individual species will respond, and the complex ecological mechanisms underlying their responses.

In relation to outbreak propensity linked to climate change, four situations are envisaged:

1. The extent of range expansion of non-outbreak insects is virtually unknown; this should come as no surprise because, by definition, these insect species occur at low density. It is quite likely, however, that such expansion has occurred but should be of minor importance from a management point of view, given that the population ecology of these putative species in the new area is similar to that in their core area.
2. A bias exists in the literature with almost all evidence of climate-change effects coming from outbreak species. In the event that outbreaks occur in the expanded range, an important question will then be whether the outbreak dynamics are similar to those in the original distribution range or show new characteristics.
3. Outbreaks in the historical area can be more, or less, frequent under climate change depending on the life history of the insect and how climate affects biotic interactions with host tree, natural enemies, insect pathogens. So far, there are no data to suggest that pest dynamics are significantly different under intensive management.
4. Plant health problems due to non-native insect species will most likely continue to increase in the future. Some non-natives will establish but with dynamics of the low-density type. The distribution of other non-natives will expand, perhaps as a consequence of climate change, and establish in areas where populations increase to outbreak level, becoming thus an invasive.

Changing the paradigm for measuring the impact of insect control interventions

Author: Hemingway Janet, Liverpool School of Tropical Medicine, Liverpool, UK

Abstract: I will describe an embedded cluster-randomised trial using Uganda's 2017-2018 campaign to distribute long-lasting insecticidal nets (LLINs) for malaria control. The largest RCT of this type ever undertaken. Clusters were assigned to PBO LLINs (PermaNet 3·0, Olyset Plus) and conventional LLINs (PermaNet 2·0, Olyset Net) using proportionate randomisation. LLINs were delivered from March 2017 to March 2018. In April–September 2019, 11 cross-sectional surveys were conducted in 50 randomly selected households per cluster; 12 households per cluster were randomly selected for entomology surveys. Due to COVID-19 13 restrictions, only 90 of the 104 clusters were surveyed. The primary outcome was parasite prevalence by microscopy in children aged 2-10 years. In the as-treated analysis, two clusters were excluded (no predominant LLIN received) and four were reassigned; LLINs with piperonyl butoxide (PBO) reduced parasite prevalence more effectively than conventional LLINs for 18 and 24 months. The underlying insect vectors and their resistance status were assessed. WHO have now made an interim recommendation on the use of these nets on the basis of this trial benefiting millions of children in malaria endemic areas.

Innovations in Insect Science for Impact

Author: Kelemu Segenet, International Centre of Insect Physiology and Ecology (icipe), Kenya

Abstract: The International Centre of Insect Physiology and Ecology (icipe) is an African Centre and a regional and global leader in research for development (R4D) through insects and related arthropods and their impacts on food and nutrition security, human health, environmental sustainability, and livelihoods. The year 2020 marked the 50th anniversary of icipe's founding. Since 1970, the Centre's achievements have reached many aspects of rural and urban life in Africa and beyond. icipe has also made a difference in science capability of the region through the significant contribution it has made to building the careers of thousands of staff and students who have worked with the Centre.

Three key elements define icipe's research strategy: (a) a focus on research domains in which insects and related arthropods have critical roles as vectors, pests or are the basis for beneficial uses (such as for food, feed, ecosystem services and value-added products); (b) innovation that can be applied to develop sustainable and safe alternatives to reliance on agri-chemicals; and (c) highly valued R4D Capacity Building and Institutional Development (CBID).

icipe and its partners have delivered science-driven, innovative, and sustainable insect-based technologies that are addressing multidisciplinary developmental challenges through an environmentally benign circular economy approach. In less than a decade, icipe's edible insects programme has generated and disseminated ground-breaking knowledge and innovations on sustainable insect farming/harvesting; recycle bio-waste into nutrient-rich organic fertilizer for improved soil fertility and crop yields; nutritional profiling and safety of insect products; integration of insect proteins in livestock and fish feeds; insect-based feed for improved gut health; and processing of insects into value-added products such as insect oils, sterols, antimicrobial target for novel drug development, chitin, chitosan among others.

icipe is a leading institution in the field of arthropod symbiosis in Africa. Microbiome research is being advanced with the aim of finding strategic entry points to reduce disease transmission. For example, the newly discovered Microsporidia MB in mosquitoes completely blocks plasmodium transmission.

icipe's innovative push-pull technology that can simultaneously address multitude of challenges such as stemborers, the fall armyworm, the parasitic weed Striga, mycotoxins, soil fertility, livestock feed, among others, that affect cereal-livestock farming systems in Africa is now effectively developed for vegetable production system.

Considering the enormous role insects play in food systems, ecosystem health, and many facets of livelihoods, this presentation would highlight and take stock of the R4D efforts in edible insects, arthropod symbiosis, and push-pull technology for vegetables.

On wings and wavelengths, or why moths fly into candle flames

Author: Pierce Naomi, Museum of Comparative Zoology, Harvard University, Cambridge, MA, USA

Abstract: The wings of butterflies are living structures that function as sensitive temperature sensors throughout the lifespan of the insect. To function properly, the wings must be maintained within a window of suitable temperatures, and these are exquisitely regulated by butterflies through multiple structural and behavioral adaptations. Despite the diverse colors and patterns of butterfly wings, regions that contain live cells, such as veins and androconial organs, are always the coolest parts of the wing. An investigation of whether butterflies and moths can also detect long wavelengths reflected by certain wing structures showed that long wavelength opsin duplication coupled with specific mutations in the protein binding pocket can result in spectral tuning shifts that may greatly extend the range of vision. The potential evolutionary significance of these results can be explored through a phylogenetically informed, multispectral survey of museum specimens.

From Me to We: Searching for the Genetic Roots of Social Life with the Honey Bee

Author: Robinson Gene, University of Illinois at Urbana-Champaign, IL, United States

Abstract: One of the most significant developments in the history of this planet has been the evolution of social life. True societies are very rare in biology, but have evolved repeatedly in a group of insects that includes the ants, bees, and wasps, with the honey bee widely considered a paragon of sociality. This lecture uses honey bees to demonstrate how sociogenomics enables researchers to understand social life in molecular terms: how it evolved, how it is governed and how it influences all aspects of genome structure, genome activity, and organismal function. Research will be discussed that illustrates that the relationship between genes and social behavior is 1) close, 2) conserved, and 3) causal.

These three principles are used, respectively, to show that:
1) shifts between cooperative and selfish behavior are subserved, at the whole transcriptome level, by surprisingly fluid and continuous changes in brain gene expression and gene regulation;
2) social behavior likely evolved using genetic toolkits present in solitary ancestors; and
3) evolutionary changes in colony aggression involve changes in brain gene regulatory networks, involving specific transcription factors in specific subsets of brain neurons. These results demonstrate how a research framework that emphasizes both the dynamic and deterministic aspects of the genome leads to new insights on the mechanisms and evolution of social life.

Insect Decline in the Anthropocene: Death by A Thousand Cuts

Author: Wagner David, University of Connecticut, United States

Abstract: The human population has grown to nearly 8 billion and anthropogenic activities are affecting marine, terrestrial and freshwater ecosystems from pole to pole. Nature is under siege. Losses in diversity, abundance, biomass, and range are well-documented for lineages across of the tree of life. Earth's plant and animal life has been plunged into crisis, with insects among the taxa at the forefront of many recent scientific reports and worldwide media attention. Population trends for insects include reports of both increasing and decreasing trends of varying magnitude that are both temporally and spatially complex, with increasing numbers of studies documenting worrisome declines. While many well-documented declines are from regions of high human settlement or activity, some studies report declines from preserves and wildlands free of obvious anthropogenic stressors such as urbanization or pesticide use. My talk will examine etiology of declines as well as studies documenting stable and increasing insect populations, briefly review annual decline rates and how we should look at these, and identify principal stressors. Special emphasis will be placed on the increasing threats of climate change to the biota of wildlands, especially changes in hydrology and climate variability. There remain many important data gaps that require study, e.g., in-situ, cross-taxon studies of pesticides effects; the spatial consequences of light pollution across different spectral bands; how agricultural practices can be changed to better protect biodiversity, locally and globally; and the impacts of tropical forest deforestation, principally for agriculture. The conclusion of the talk will address some ongoing research projects, citizen science efforts, policymaking, and solutions that can slow rates of insect decline.

Sex, conflict and selfish genes

Author: Wedell Nina, University of Exeter, Penryn, CORNWALL, United Kingdom

Abstract: Selfish Genetic Elements (SGEs) are genes, organelles or microorganisms present within the genome or cell of an organism that spread by subverting normal patterns of inheritance to increase their representation in the next generation; hence the term 'selfish'. SGEs such as endosymbionts, transposable elements, and meiotic drive genes are ubiquitous in living organisms and often associated with fitness costs to the bearer. Despite their impact on the reproduction of their host, their potential role in sexual selection and sexual conflict is largely overlooked. I will discuss some recent work examining the impact of a variety of SGEs showing they can affect the behaviour and reproduction of their host, often with sex-specific effects, and argue they are important contributors in shaping sexual selection and sexual conflict.

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NEW:
HISTORY OF ICE BOOK

This book explores the 100-plus-year history of ICE meetings, offering a glimpse into the global collaborations and scientific achievements that drove entomology to where it is today and will be tomorrow. Stop by the ESA Booth to order your copy.

ABSTRACTS OF PRESENTATIONS AT ICE2022HELSINKI

Abstracts in alphabetical order based on the first author of each abstract.

Effects of soil microbiome on phyllosphere and aphid microbiome assembly

Authors: Abdelfattah Ahmed[3], Wolfgang Adrian[2], Tack Ayco J.M.[1] and Berg Gabriele[2], [1]Department of Ecology, Environment and Plant Sciences, Stockholm University, [2]Institute of Environmental Biotechnology, Graz University of Technology, [3]Leibniz-Institut für Agrartechnik und Bioökonomie

Abstract: All multicellular organisms are now known to be associated with diverse microbial communities. Identifying the mechanisms by which these communities are assembled is crucial to understanding community dynamics. Here we aimed at identifying the effect of manipulating soil microbiome on the assembly of oak phyllosphere and aphid's microbiomes. We further evaluated the impact of aphid herbivory on the phyllosphere and soil microbiome. We used microcosms, which physically separate above- and below-ground compartments, to grow oak seedlings in three soils with different microbiomes yet the same physiochemical properties. Amplicon sequencing and RT-qPCR were used to characterize and quantify the bacterial and fungal communities in soils, leaves, and aphids. Soil microbial community composition had a significant effect on the fungal and bacterial community compositions of leaf and aphid microbiomes, indicating assembly processes, at least partially, from soil to aphids through plants. Aphid herbivory significantly decreases microbial alpha diversity in leaves. Leaf fungal community composition and soil bacterial community composition shifted upon aphid herbivory.

Efforts to use soft Pesticides for the Control of Insect Pests as contribution towards Green Chemistry

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Abstract: In the last decades during the post-war period, the agriculture has developed towards methods that are more intensive. Among these is increased use of agrochemicals. In the Sudan Gezira, as an example, cotton spraying started as early as season 1945/46 when only 1% of the cotton area was sprayed once. By 1978/79 the problem caused by the cotton insect pests, particularly the cotton whitefly (Bemisia tabaci) flared up. The number of sprays per season went up, reaching 9.25 sprays in season 1978/79, which might be attributed partly to the rapid resurgence of insects' pests as a result of the use of non-selective insecticides, which badly affected the natural enemies of these pests. The joint use of natural enemies and selective pesticides might attribute to combat this problem. Studying the side effects of pesticides is of prime importance to save natural population and encourage their role as biological control agents. This paper discuss the various methods which can be used to study the side effects on natural enemies and the results of some studies carried on the side effects of some insecticides on natural enemies both at small and large scale levels in Sudan. The study includes testing the side effects of some insecticides and their impact on bio-safety (Talstar, Polo, Metasystox, Marshal and the mixture Reldan + Endosulfan) on two Predators at small-scale level at the Gezira Research Farm, Wad medani. The Impact of Polo (diafenthiuron) on natural enemies in the cotton-based ecosystem of the Gezira Scheme (Large Scale) was tested in the Study. The results indicated that Polo was relatively safe both at small scale and large-scale level to the natural enemies observed during the study. This study can be considered as a begin of regional testing program in Africa with collaboration of international organization interested on conserving bio-agent.

Integrated Pest Management of Citrus

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Abstract: Citrus group is one of the most popular fruits in tropical regions and elsewhere. Yet, its production has significant instability and decrease since it is usually affected by several biotic and abiotic constraints. The most important abiotic constraints are edaphic factors and bad weather conditions especially during flowering and early fruit set that cause flowers and small fruits to dramatically fall. As for biotic stresses, Citrus tristeza virus, Citrus psorosis virus, Phytophthora, Fusarium and T. semipenetrans rank high in general. Although regional in scope, additional insect pests and the citrus greening disease caused by the bacteria Candidatus Liberibacter spp. should be adequately managed. Given such constraints, integrated pest management (IPM) in citrus for stabilizing high citrus yield and quality by methods that do not degrade the environment should be sought. Phytosanitary measures to prevent further infection or pest/disease transfer should also address weed control, tillage to get rid of infected residue and kill soil-dwelling insect pests, and citrus certification programs. Regulation on certifiable pathogens of citrus-propagating material may include bacteria, fungi, nematodes and graft-transmissible pathogens. Genetic resistance is considered the most desirable method to control many diseases and pests since it is more cost effective and environment friendly than the use of synthetic chemicals. Biological control may emerge as a safe alternative to chemicals, and offers economically viable and ecologically sustainable management but bio-pesticides should be integrated in ways that make them complimentary or superior to such chemicals. This is especially important where bio-pesticides can act synergistically or additively with other horticultural inputs in IPM programs. Developments in IPM of insects, weeds, main disease-causing fungi and bacteria, and nematodes on citrus trees were reviewed. This research is funded in part by Science and Technology Development Fund.

Impact of mosquito coil on the development of pyrethroid resistance in Aedes (Stegomyia) aegypti

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Abstract: In this study, we assessed the effect of pyrethroid-based mosquito coil on the development of pyrethroid resistance in Aedes aegypti. An established colony of Ae. aegypti originally from Elmina, Ghana was used for the experiment. Six generations of the colony were severally exposed to sub-lethal doses (7 min) of mosquito coil in a Peet-Grady chamber. After the sixth generation, susceptibility levels to Deltamethrin (0.05%) and mosquito coil were evaluated against the experimental colony. The colony was also genotyped for F1534C kdr mutations using an AS-PCR technique. The LT50 (95% CI) resulting from the sub-lethal dose of the coil rose from 7.8 minutes (95% CI; 6.14 – 9.41) at the beginning of the experiment (F0 generation) to 28.3 minutes (95% CI; 23.11 – 33.58) at the 6th generation. The F1534C kdr resistant allele increased from 54% in the unexposed colony (control) to 77% in the experimental colony. The data shows that exposure of Ae. aegypti to a sub-lethal dose of mosquito coil increased the tolerance of the population against the coil as well as selected for the F1534C kdr resistant mutation. This may ultimately result in the development of a pyrethroid-resistant population driven by the homozygous genotype.

A successful method of cold storing brown marmorated stink bug egg masses for the rearing of its parasitoid, Trissolcus japonicus

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Abstract: Trissolcus japonicus (Ashmead) is a candidate biological control agent that is an egg parasitoid of the brown marmorated stink bug (Halyomorpha halys Stål), a worldwide pest. As the mass rearing of T. japonicus is predicated on the availability of its host egg masses, the methods of producing and storing large quantities of H. halys egg masses is essential for future release programs. Currently, the two options for storing H. halys eggs are cold storage or freezing. However, it has been demonstrated that frozen egg masses can reduce parasitism rate by 35 - 44%. Our study demonstrates that emergence rates of T. japonicus can remain above 85% when host eggs are exposed to 8 degrees celsius storage for up to two months. T. japonicus fitness proxies such as emergence time, fecundity, activity, weight, and longevity are largely unaffected when host eggs were stored in 8 degrees celsius for 14 days.

Intraspecific variation in traits determining benefits and risks of egg parasitoids: a case study with Trissolcus japonicus

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Abstract: Egg parasitoids introduced for classical biological control have both benefits and risks that are inevitably difficult to predict. To complicate matters further, there may be intraspecific variation in egg parasitoid traits that are associated with both their potential biocontrol efficacy, and their non-target risk. Thus, the risks and benefits of an egg parasitoid introduction may depend on what strain is selected, and/or what adventively established strains are already present in introduced areas. Here, we propose using an invasion biology framework to select traits that may determine the relative efficacy and non-target risk of different strains of egg parasitoids. We use the samurai wasp (Trissolcus japonicus), a parasitoid of the brown marmorated stink bug, Halyomorpha halys, as a case study to demonstrate that there is significant intraspecific variation in egg parasitoid traits, including behaviours, symbiont infection, and life history, that are predicted to determine the risks and benefits of their introduction and spread in new geographic areas.

Non-reproductive effects of Insect Parasitoids on their hosts

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Abstract: Parasitic wasps are important components of natural communities and are used to control insect pests in biological control programs worldwide, in addition to being fruitful models in theoretical ecology. As biological control agents, their main modes of action are considered to be killing their hosts with egg laying followed by offspring development (reproductive mortality), and feeding on them directly (host feeding). However, parasitoids can also negatively affect their hosts in ways that do not contribute to current or future parasitoid reproduction (non-reproductive effects). Outcomes of non-reproductive effects for hosts can include death, altered behavior, altered reproduction, and altered development. Based on these outcomes and the variety of associated mechanisms we will first categorize non-reproductive effects into: (i) non-consumptive effects; (ii) mutilation; (iii) pseudoparasitism; (iv) immune defense costs; and (v) aborted parasitism. Since these effects are widespread in the wild, we will present some of the most representative cases of non-reproductive effects of parasitic wasps on their hosts and their implications in biological control and community ecology.

UV light environment influences host location and exploitation in egg parasitoids

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Abstract: Parasitoids respond to a variety of biotic and abiotic factors to successfully interact with their hosts in highly variable natural settings. To that effect, the influence of light environment on parasitoid behaviour and fitness could be underestimated compared to better-studied olfactory cues. Because hymenopteran parasitoids can see the ultraviolet (UV) light that can harm both their mature and immature life stages, behavioral strategies involving UV vision could not only help find hosts, but also minimise negative effects of UV exposure to both mother and progeny. To investigate if or how this type of colour vision could be involved in assessing host and microhabitat quality, we conducted a series of laboratory experiments on stink bug egg parasitoids placed under different UV intensities using UV-visible fluorescent lights as well as UV-blocking and UV-transmitting filters. First, we examined whether foraging females tend to seek or avoid UV wavelengths by evaluating the walking activity of Telenomus podisi and Trissolcus cosmopeplae (Hymenoptera: Scelionidae) in absence of hosts. Wasps spent more time in areas exposed to UV light, while individuals and species varied in the intensity of this behavioral response. We then tested the implications of this apparent attraction to UV wavelengths on patch finding ability and maternal investment intensity (i.e. oviposition and brood guarding duration), by releasing individual T. podisi parasitoids in laboratory mesocosms containing a single egg mass on top of a soybean plant under similar UV treatments and recorded it for 24 h. Results will be discussed in the context of light environment control in protected agriculture.

Creepy crawlies or beauty queens? The effect of type of insect on the evaluation of foods containing insects

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Abstract: Rich in digestible protein, insects are more and more widely considered to be “the food of the future” and a good substitute for meat. However, the willingness to ingest them depends largely on the consumers’ perception of insects. To understand the specificity of insects among other animals, their characteristics as a potential food source, and to examine what makes some insects more acceptable as food than others, we conducted two complementary studies (qualitative and experimental). The qualitative study (18 IDIs) allowed us to identify the dimensions that determine the perception of insects as potentially edible and inedible.

In the experimental study (n=437), we examined the potential of three different types of insects (larvae, ants, crickets) as food ingredients. Pictures of four versions of the same product (Bolognese sauce) were presented to the respondents – three containing insects and one without insects (control condition). The results showed that foods containing insects scored lower on each dimension. Furthermore, we observed a different impact of various insects on product evaluation: products containing crickets were evaluated higher than those with larvae. In addition, we noted some individual differences in acceptance of insects as food. Respondents with a higher level of food neophobia and a lower level of variety-seeking tendency assessed products containing insects more negatively than participants with higher levels of the latter trait.

Of insects and men - analysis of visual characteristics and labeling of a food product containing insects on its acceptance as a meal

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Abstract: Studies suggest that the appropriateness of food is more important than its sensory characteristics, such as taste. Inappropriate of insects as food seems to be linked to their appearance and texture. An image of the whole animal elicits strong objection and negative emotions to the food offered i.e. people are reluctant to eat animal heads, entire limbs, etc. Perhaps in the case of insects, the fact that they are often served whole elicits similar reactions. In addition, adding entire insects or their recognizable parts to meals may convey the impression that the food is polluted or dirty. Insects in the form of flour should reduce this strong negative response. However, data on that matter are inconclusive. Therefore, we propose a study analyzing the effects of the form of insects added to food and a description of a meal on people’s assessment of the sensory properties of food.

In our study, every participant was offered a set of three food products (a cookie, a cupcake, and a date ball). None of the dishes contain insects. However, the respondents from the two experimental groups were informed that the products contained edible insects (in the form of flour or pieces). Also, half of the products presented in the study contain an ingredient that may look like traces of added insects. Every food set had a label informing that the food contains insects in the form of flour or pieces or contains other common ingredients. For each product, the respondent was asked to fill in a short questionnaire to evaluate its taste, appearance, smell, etc. Additionally, we asked participants to fill in a set of questionnaires measuring psychological variables (such as food neophobia, disgust, sensation-seeking, etc.).

We assume that a food label indicating the insect content will lower scores for sensory properties of food. What is more, we hypothesize that meals with ingredients in the form of insects’ pieces will be scored lower than that described as containing insects’ flour. The results of the study will be presented at the conference.

No silver bullet: Multiple mechanisms are used by the wasp Cotesia congregata on its host the caterpillar Manduca sexta

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Abstract: The parasitic wasp, Cotesia congregata, uses a multi-pronged approach to control behaviour in its host Manduca sexta. During emergence from the host, the area around the exit wound is numbed by the exiting wasps. This numbness prevents the host from disturbing the wasps as they leave the host. The host also exhibits extreme quiescence. The host regains some mobility after wasp emergence. However, host feeding behaviour is suppressed. The suppression appears to be due to changes in the central brain. Both motor and chemosensory systems are normal. For example, cutting the connective to the part of the brain that controls chewing (subesophageal), restarts chewing in parasitized caterpillars. A proteomics study demonstrated a number of protein changes in the central brain that correlate with the change in host behaviour.

A proposed hypothesis of a “natural”; phylogenetic-classification for the world Blastobasidae (Lepidoptera: Gelechioidea) based on macromorphological features of the adult.

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Abstract: Previous intuitive classifications of world Blastobasidae made minimal contributions in providing a natural phylogenetic-classification for the Blastobasidae. In our study, two analyses were conducted. In the first analysis, four different phylogenetic simulations were used to hypothesize relationships between and among clades for the family. These simulations included TNT Parsimony Analysis (PA), TNT Parsimony with Bootstraps (PBA), Bayesian Analysis (BA), and Maximum Likelihood Analysis (MLA). All four simulations show high congruence in separate tree topologies at the family and subfamilial levels within the world Blastobasidae. Although PA and PBA simulations recognize different monophyletic solutions within Holcocerinae, BA and MLA recognize cause for reexamination between the cladistic relationships between Inbioxa and Hera with other Holcocerinae genera. For the Blastobasinae both PA and PBA tree topologies are nearly identical. Tree topology generated by (BA) for Blastobasinae is most similar to the tree generated by (MLA). Both show strong support at the family level. Additionally, both BA and MLA mirror values with the greatest support at the Blastobasinae node and significantly less support at the Holcocerinae node. In summary, all four simulations show high congruence in separate tree topologies at the family and subfamilial levels within the world Blastobasidae. In the Blastobasinae clade, all four simulations show high congruence levels for support of the clade containing Doscostoma, Lateantenna, Neoblastobasis + Sirindhorn. Similarly, all four simulations show strong congruence in support of the clade uniting the two sister genera Blastobasis + Hypatopa that is rooted to the clade of Pheos, Hallicis, and Barbaloba. In addition, Koleps and Pseudokoleps are also recognized in all four simulations as a clade with high support values. The cladistic relationships for the sister genera, Pigritia + Mastema remains uncertain, however, the significantly higher support value in MLA may indicate a more confident relationship with Blastobasis + Hypatopa.

In the second analysis coded data were taken from all primary types and/or authoritatively identified specimens representing species in the analysis. This approach shows that the “exemplar approach” for underestimates homoplasy within the in-group and overlooks new combinations at the generic and species levels. Contrastingly, an “all-inclusive approach” finds unrecognized genera represented from type specimens not previously dissected. Once stability is achieved in the later analysis the evolution of hosts preferences and zoographical hypotheses can be attempted for the family.

Morphological Phylogenetics of World Blastobasidae (Lepidoptera: Gelechioidea): A Comparative Approach Using Exemplar and Super-Saturated Sampling

Authors: Adamski David[2], Frandsen Paul[1], [1]Department of Plant and Wildlife Sciences, Brigham Young Univ., Provo, UT, United States, [2]Dept of Entomology, Smithsonian Institution, Washington, DC, United States

Abstract: Morphological characters and character states were taken from exemplar and super-saturated samples to construct matrices in order to generate phylogenetic trees from simulations based on cladistic methodology for the world Blastobasidae (Lepidoptera: Gelechioidea). Phylogenies generated from an exemplar data matrix using maximum parsimony analyses did not show direct evidence when taxa shared cladistic characters as part of a transformation series. Bayesian and maximum likelihood analyses were limited in diagnosing transformation series among these taxa by arranging them in unresolved polytomies. Only when a super-saturated sampling of taxa was used to construct a character matrix, and analyzed using maximum parsimony with bootstraping were these transformation series detected and arranged into fully resolved clades. Moreover, this highly resolved tree simulation, based on dense taxon sampling, shows significant advantages in detecting paraphyly at various categorical levels resulting in many nomenclatural changes at the species and generic levels, and a more “natural” phylogenetic-classification compared to those previously published.

Criticisms and recommendations on the current situation of response to invasion of the fall armyworm in Asia and Africa

Authors: Adati Taro[1], Sato Yoshiki[1], [1]Tokyo University of Agriculture, Japan

Abstract: In recent years, the fall armyworm (FAW), Spodoptera frugiperda from the Americas has invaded Africa and Asia. However, so far, there have been no reports of catastrophic crop damage due to outbreaks of the FAW in the invaded areas. In these areas, there are indigenous FAW-related species, as well as other pest species that have invaded and established themselves in the past. Whether the new invasive species will cause significantly more damage than these indigenous pests remains a matter of speculation. In fact, FAW population density in forage corn fields in south-central Kyushu, Japan, is dependent on crop height and other factors, and is not necessarily dominant in some fields among several pests, including indigenous species. In response to the invasion of the FAW into Africa and Asia, there have been calls for increased application of synthetic insecticides and the introduction of GM crops. However, the effectiveness of such measures that were implemented in the original habitat of the species is questionable due to the emergence of strains resistant to insecticide components and Bt toxin. Such measures risk increasing dependence on foreign sources of commercial crop seeds and pest control agents and fundamentally altering indigenous agricultural systems that have adapted to local environments. Therefore, from the perspective of sustainable pest management strategy and comprehensive food security, recommendations for appropriate responses to the invasion of the FAW are required.

Understanding the multi-pathway spread of agricultural pests; challenges, network models and results

Authors: Adiga Abhijin, University of Virginia, United States

Abstract: Movement of humans and their goods is widely accepted as the primary driver of invasive species invasions. But rigorous methods that account for the multiple pathways of spread are few and far between. Epidemiological models based on network dynamics can simulate the spatiotemporal spread of the pest and thereby help policy makers make informed decisions in monitoring, prevention and mitigation efforts. Unlike pest risk maps based primarily on ecological suitability, these models can provide causal explanations to the observed spread and enable counterfactual analysis. However, modelers face a number of challenges in realizing such systems: data scarcity, complexity of the phenomenon, and need for multi-domain expertise, to name a few. We have developed robust data-driven models to study the role of natural and anthropogenic drivers of invasive species spread, with application to T. absoluta. This talk will present our recent work demonstrating the role of this new modeling approach in analyzing the spread, the role of tomato trade, various intervention measures and economic impact.

Does Müllerian mimicry structure pollinators communities over time? A case study for bees and wasps in Bonifacio (France)

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Abstract: Many stinging bees and non-parasitoid wasps (Hymenoptera, Aculeata) exhibit contrasted colour patterns, which constitute an aposematic signal. Such aposematic signal enables predators to recognize and to avoid the painful experience of the sting of these potential preys. Because the efficacy of a given aposematic signal increases with its own abundance, predation pressures induce Müllerian mimicry: the convergence in aposematic colour patterns among co-occuring stinging species. Although Müllerian mimicry has already been reported for some Hymenoptera groups, to date no study has investigated this mimicry at the level of an entire community of stinging Hymenoptera. Our purpose here is to evaluate the prevalence of co-mimic species within an aculeate community sampled at a same site (Bonifacio, South Corsica) after more than a century. The mimicry rings are identified for the whole community by quantifying aposematic colour patterns using image analysis of collection specimens. Here we will show that a community of aculeates tend to be partitioned in different mimicry rings. We will also discuss how these rings are related to the size of the different species and how changes in community composition through time can affect the aposematic landscape. These data contribute to a better understanding of mimicry and its importance within pollinators communities and may help to evaluate the actual impact of predation on local extinctions and ecosystem services.

IDmyBee, a free, collaborative tool to face the current taxonomic impediment for European wild bees

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Abstract: There are more than 2000 wild bee species recorded in Europe, many of which require an expert's eye for identification due to the lack of proper identification keys. In many parts of Europe, studies and monitoring projects about wild bees rely therefore on a handful of taxonomists to identify the specimens. However, in the current state of low funding for taxonomic work, wild bee taxonomists cannot answer the high demand for bee identification, clarify taxonomic problems, educate a new generation of taxonomists, develop clear identification tools and keep them up to date, all at the same time. As a result, many pollination scientists focus on a few species, or work at a coarse taxonomic scale, which leads to under-exploitation of available pollinator diversity data. The project IDmyBee, which started in 2019, aims at developing collaborative identification tools to facilitate wild bee identification, to promote education about wild bee diversity and to centralize our knowledge on European wild bee taxonomy. Using the online platform Xper3, we are developing a set of identification tools that act as biodiversity database for the different bee genera and species. These tools have several advantages over the current identification keys: they are available freely, online, so that scientists and conservation actors can easily access this knowledge. They can be built collaboratively, so that the tedious work of key creation and improvement can be shared among taxonomists and with other actors depending on their availability. These tools can be easily updated to follow the changes in the taxonomy, so they offer an up to date vision of wild bee diversity. They are based on a matrix of characters instead of the classical dichotomic key, so they are more versatile for the user. Finally, they are not limited in terms of space or illustration. Illustrations are crucial since access to reference collections is time-consuming and difficult to many people. Despite these advantages, these tools are not aimed at replacing the taxonomic expertise. They will help identify which species require an expert's help and which can be identify by non-specialists. They will also help taxonomists to build and to keep a clear taxonomic framework that can be used by the different environment actors interested in wild bees. In the end, this project should stimulate the taxonomic work on wild bees by reducing the workload of taxonomists due to specimen identification and by providing them with a way to highlight their work through the publications linked to these tools. Once in place, this knowledge database could be linked to other identification methods such as barcoding or image analysis to facilitate wild bee identification even further.

Development of a Novel Biopesticide using an RNA Interference Approach Targeting Potassium and Fibroblast Growth Factor in Helicoverpa armigera.

Authors: Afifi Feras, Newcastle University

Abstract: This project has two main aims first, Development of a novel and sustainable form of pest control based on an RNAi approach targeting potassium ion channel and fibroblast growth factor in Helicoverpa armigera. Second, evaluation of the biosafety of the use of dsRNA on non-targeted organisms such as honeybees. The results were observed the knockdown of both target genes (potassium ion channel and fibroblast growth factor) via silencing of the expression by qPCR and measuring mortality rate after delivered dsRNA through injection and feeding. Biosafety studies will be perform by using adult honeybee to observed that there are no significant different of gene expression and mortality rate.

Current knowledge of Anagonia cf. lasiophthalma, a promising biological control agent of Gonipterus platensis

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Abstract: The Tasmanian eucalyptus snout beetle Gonipterus platensis (Marelli) is the most widely distributed Eucalyptus weevil in the world. In Portugal, this pest has been managed by classical biological control programs using the egg parasitoids Anaphes nitens (Girault) and Anaphes inexpectatus Huber & Prinsloo (Hymenoptera: Mymaridae). However, economically relevant attacks in eucalypt plantations still occur in many areas. Supplementary natural enemies of this insect pest, namely parasitoids targeting other host life stages, such as larvae, may boost the overall control of the pest.

Field surveys undertaken in Tasmania in 2017 followed by the import of Gonipterus spp. larvae allowed the establishment of larval parasitoid populations from genus Anagonia (Diptera: Tachinidae) under quarantine conditions in Portugal. Since then, a stable population of Anagonia cf. lasiophthalma is being reared and studied at RAIZ facilities.

Before A. cf. lasiophthalma can be released in the field, several aspects of its bioecology must be resolved. Furthermore, its potential efficacy as a biological control agent and the likelihood of environmental undesirable outcomes must be assessed. Here, we present the available results of the studies conducted so far on the identification, basic life cycle traits, and parasitism behaviour of A. cf. lasiophthalma.

Challenges to the use and exchange of classical biological control agents: the case of Cleruchoides noackae

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Abstract: The eucalypt bronze bug, Thaumastocoris peregrinus (Hemiptera: Thaumastocoridae) is a small sap-feeding insect native to Australia. Since the first report of this species as a pest, in 2001, it has spread and established on non-native eucalypts in many countries in the world, causing major economic losses. This insect is effectively managed by means of classical biological control using the egg parasitoid Cleruchoides noackae (Hymenoptera: Mymaridae). The first country to use C. noackae against the eucalyptus bronze bug was Chile, in 2010. Since then, Brazil, Uruguay, Argentina, South Africa, Israel, and Portugal have imported and released it in the field. All these countries are contracting parties of the IPPC and have adopted the procedures established in the ISPM3 for import and release of biological control agents. All are also members of regional plant protection organizations. However, the import and release of this biological control agent involved a variety of approaches, even between members of the same regional platform. These different approaches stemmed from particularities of each country in their national regulations or from the lack of specific legislation regarding the introduction of biological control agents. Some countries were able to introduce the parasitoid without any host-specificity tests. Other countries required results from host-specificity tests and to be included in an application for release, but even here the extent of information required differed between countries. The disparities in regulations and procedures adopted by the different countries influenced the agent's introduction promptness.

Adapt or bust? Predicting insect adaptation to new dietary challenges

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Abstract: Insects are incredibly adept at using diverse diets. Yet, it remains challenging to predict their survival and dynamics in new habitats. Which populations can adapt to sudden dietary change, and what information do we need to predict this? Among other factors, theory suggests the importance of evolutionary history and ancestral trait variation, and the position of the ancestor along the generalist-specialist continuum. We tested our ability to predict long-term adaptive dynamics in laboratory populations of a generalist pest, the red flour beetle Tribolium castaneum. We founded replicate lines using beetles collected from 10 locations in India, and allowed them to adapt to new diets for over 50 generations. Resource identity had a strong impact on population dynamics: despite substantial trait divergence across source populations, all lines adapting to the same resource showed surprisingly parallel dynamics. Although the same source populations adapted most successfully to different diets, these best-adapted populations did not always have the most "generalist" ancestors. Indeed, adaptation to each resource was associated with different ancestral traits. Thus, we suggest that predicting insect dietary shifts requires detailed understanding of ancestral trait variation, tailored to the new diet.

Influence of multifunctional flower margins on the improvement of biodiversity and production of Pisum sativum L.

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Abstract: Conventional agriculture faces three complex challenges because of climate change, high loss of biodiversity and increase demand of sustainable food production by society and markets.

As an approach to enhance pollinator biodiversity in agricultural landscapes, Syngenta had proactively introduced Operation Pollinator (OP) programme in agricultural areas which objective is to improve pollinator biodiversity in crops by mixture of flower margins.

In this presentation, we focus our experiment in three pea fields from Spain. This crop is considered as an "improvement crop" due to the ability to fix atmospheric nitrogen thanks to the bacterium Rhizobium leguminosarum, associated with its roots and the important role it plays in crop rotations. Its agronomic qualities make it a key crop in the European Common Agricultural Policy (PAC) where it is given a premium as "Area of Ecological Interest", restricting the application of phytosanitary products, so enhancing the presence of beneficial insects and pollinators can contribute to improving the profitability of the crop.

In each field a multifunctional margin was sown, and insects were sampling following a gradient of distance by sweeping net and yellow traps. The results of the pollinator biodiversity and pollinator-production correlation on pea fields are going to be presented.

Local depressions play a key role in the maintenance of ant diversity in a forested mountain landscape

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Abstract: Sinkholes (or dolines) are bowl-shaped depressions in karst surfaces. They provide a diversity of environmental factors (e.g., humidity, nutrient, soil, temperature, and water), thereby facilitating the persistence of various functional groups of species, and hence could function as local biodiversity hotspots. Here, we investigated the potential of dolines to function as safe havens by studying the distribution patterns of ants in forested and non-forested (i.e., grassland) microhabitats inside (south-facing slopes, bottoms and north-facing slopes) and outside of dolines (i.e., plateau) in the Bükk Mountains, north Hungary. We used only non-destructive sampling methods (such as baiting and hand collecting) to assess the species diversity and relative abundance of ants. We found that the fine-scale distributions of the functional groups of ants correspond to the different microhabitats and vegetation cover. The north-facing slopes and bottoms of dolines provided key habitats for ants associated with cooler and/or moister conditions (e.g., Myrmica ruginodis), while the south-facing slopes provided key habitats for ants associated with warmer and/or drier conditions (e.g., Myrmica sabuleti). The occurrence of species on the surrounding plateau indicated intermediate conditions. In addition, non-forested microhabitats had more ant species than forested ones. To our knowledge, this is the first study to illustrate that the fine-scale topography of dolines may provide microhabitats for diverse ant assemblages. We can conclude that in forested landscapes the maintenance of semi-natural grasslands may be especially important to preserve high biodiversity.

Barley varieties Stoneham and Sydney exhibit mild antibiosis and antixenosis resistance to the wheat curl mite, Aceria tosichella

Authors: Aguirre Rojas Lina[1], Michael Smith C[1] and Khalaf Luaay[2], [1]Department of Entomology, Kansas State University, United States, [23]Department of Plant Protection, University of Baghdad, Iraq

Abstract: The wheat curl mite, Aceria tosichella (Keifer), devastates cereal crops worldwide by direct feeding damage and transmission of several deadly viruses. Cereal crop varieties resistant to A. tosichella are fundamental for the integrated pest management of this pest. Barley varieties resistant to A. tosichella are not known to exist. Non-choice and choice experiments were conducted to determine if A. tosichella resistance exists in the barley varieties Sydney and Stoneham which are resistant to the Russian wheat aphid, Diuraphis noxia (Kurjumov). Sydney barley displayed mild resistance to A. tosichella biotype 1 and 2, while Stoneham barley exhibited only mild resistance to biotype 2.

Mexican Research Experiences with Genetically Modified Corn

Authors: Aguirre U Luis Alberto[1], Hernandez J Agustin[1], Flores D Mariano[1], Cerna CH Ernesto[1], Frias T Gustavo[1] and Ochoa Yisa[1], [1]Universidad Autónoma Agraria Antonio Narro, Mexico

Abstract: Genetically modified organisms (GM) is a controversial issue worldwide. In Mexico, debate is greater being the center of origin of corn. Mexico approved controlled planting in 2009-2013 for research purposes allowing testing of hybrids AgrisureTM 3000 GT, Agrisure® VipteraTM 3110 y Agrisure® VipteraTM 3111 with Bacillus thuringiensis (BT) genes which codify Cry1Ab, Vip3Aa20 and mCry3A proteins resistant to Lepidoptera and Coleoptera in the State of Sinaloa. Resistance of hybrids to foliar damage by armyworm Spodoptera frugiperda, cob damage by corn earworm Helicoverpa zea and the sugarcane borer Diatraea saccharalis and compared with their respective isohybrids and an insecticide treatment. Results proved that hybrids containing Bt genes were resistant to foliar and cob damage from above-mentioned pests. Low incidence of sugarcane borer was observed; however, damage was lower on the GM hybrid when compared with conventional hybrids. Corn pests evaluated using GM hybrids could be a strategy to be incorporated in an insect pest management system. This technology may contribute to preserve agroecosystem biodiversity compared with other management options avoiding the use of chemical insecticides if their use is approved. Evaluations in other Mexican areas are needed to better understand this technology and support regulatory decisions in the matter.

Development of a PCR-based method to discriminate between dead and living insect pest present in stored rice

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Abstract: Most of the current methods to detect the presence of insects in stored cereals are not sensitive enough to detect low pest levels or some immature stages, like the visual inspection of the grain after sieving. Once the pest is detected in the grain, the only method to determine if it is dead or alive is the grain incubation until completing the developmental period, which can last up to 40-50 days. Alternative tools to discriminate between live or dead individuals present in the grain in a shorter period are needed.

We have developed a PCR-based method to discriminate between dead and living insect pests present in stored rice by using primers that amplify long DNA fragments. Our hypothesis was that short DNA fragments are detected in both living and dead individuals, whereas long DNA fragments are only detected in living specimens, due to the degradation process after the death of the organism. For this, degenerated primers that amplify long DNA fragments have been designed within the mitochondrial regions Cytochrome Oxidase I and II. Results on some Coleoptera and Lepidoptera species that are pests in stored rice are shown and discussed depending on the time elapsed after death.

Understanding food webs in agroecosystems: the use of a universal arthropod and plant multi-primer NGS approach

Authors: Agusti Nuria[2] and Alomar Oscar[1], [1]IRTA, [2]IRTA, Spain

Abstract: The use of DNA metabarcoding is becoming an important tool to study biological control of pests in agroecosystems by revealing unknown details of the food webs. In this study, we have developed a multi-primer NGS approach to analyze the gut content of predatory arthropods present in a peach crop. This multi-primer system, which allows identifying the ingested arthropods and plants, is composed by two pairs of universal arthropod primers and two pairs of universal plant primers. The use of both arthropod universal primers was compared when used together or separately regarding the number of prey species obtained after the analysis. The resolution of both plant primers was studied to determine the assignment level to the plant resources detected. Obtained results showed that the analysed predators ingested arthropod and plant resources, including peach, other crops, and other plants present around the peach orchard. Within the arthropod resources, it was possible to detect peach pests, as well as other preys present in the peach crop and in the surrounding vegetation. This molecular tool could also be used to reveal the most important arthropod and plant resources consumed by omnivorous predators in other agroecosystems.

The diversity and spatiotemporal distribution of microbiota associated with Macrosteles leafhoppers (Hemiptera: Cicadellidae)

Authors: Ahlen Mulio Sandra[1], Lukasik Piotr[1] and Michalik Anna[1], [1]Jagiellonian University, Poland

Abstract: Microbial symbionts play important roles in insect biology, but their diversity, distribution, and dynamics over time across host populations is poorly understood.

We surveyed the spatio-temporal distribution of bacterial symbionts in several species of the broadly distributed, diverse, and economically significant leafhopper genus Macrosteles, with emphasis on Macrosteles laevis. Amplicon sequencing of the Cytochrome oxidase I (COI) gene allowed us to distinguish species, revealed lack of strong genetic differentiation across M. laevis populations combined with significant levels of heteroplasmy, and multiple cases of parasitoid infections. 16S rRNA amplicon sequencing data confirmed the omnipresence of the ancient nutritional endosymbionts Sulcia and Nasuia and a high, but variable prevalence of Arsenophonus, previously shown to colonise Sulcia cells. Other abundant symbionts included Rickettsia, Wolbachia and a previously unreported symbiont in Auchenorrhyncha, Ca. Lariskella. Further, we detected the known plant pathogen phytoplasma in 31 specimens, or 8.5% of samples. However, there was no discernable patterns in the symbiont prevalence among M. laevis populations, or associations between the presence of different symbionts. Combined, our data show how the simultaneous characterization of host and symbiont marker gene amplicons in large insect collections can reveal patterns critical for the understanding of their significance.

Influence of Macronutrients Induced Biochemical Changes in Plant as Mediator of Insect Pest Population in Okra (Abelmoschus esculentus (L.) Moench)

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Abstract: Okra is highly nutritious crop with the production rate of 303.16 tons per year from the area 232.05 ha in Pakistan with the growing contribution of 2% in the world. Insect pests of okra are one of the key factor in reducing or effecting its yield and esthetic value. Nutrition of a plant plays an important role in regulating the insect pest population and the rate of infestation. The nutrients in the plant induces the biochemical changes which act as a mediator of insects of okra. The research was conducted in the greenhouse of Institute of Agricultural Sciences during the summer season 2018-19 to evaluate that upto what extent different levels of nitrogen, phosphorus and potassium modulates the insect pest population on okra. Three levels of nitrogen and phosphorus were prepared (315, 210, 105 ppm) with two levels of potassium (117 and 234 ppm). The number of insects were counted after every 7 days of interval. The encountered sucking insects of okra include whitefly, aphid, jassid and mealybug. The results of this study were assessed through RSM (response surface methodology) which shows that the high level of nitrogen increase the rate of leaf production (RLP), and total yield of okra in contrast to nitrogen at the high level of potassium the rate of soluble sugars are reduced which suppresses the insect pest population. Conclusion from results depict that nitrogen along phosphorus enhance the primary growth of plant and soluble sugar content and potassium turns it into secondary growth. Through RSM the maximum optimum rate of yield and minimum optimum rate of insects were predicted at different recommended concentration of nutrient solution of NPK.

Assessing biodiversity value of linear farm habitats across different levels of farming intensity in agricultural grassland using Diptera as bioindicators

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Abstract: Agricultural intensification is known as one of the primary causes of rapid decline in farmland biodiversity, particularly insects. While the incorporation of linear farm habitats to counteract biodiversity decline have been proposed, much remains unknown about the specific impacts on insect diversity of different types or combinations of linear farm habitats, particularly on farmlands of different intensities. With this in mind, we investigated the value of different linear farm habitats for invertebrates using adult species of two dipteran families (Sciomyzidae and Syrphidae) as bioindicators, at three levels of land use intensity. The study was conducted on grassland farms (in the north-west of Ireland) which were grazed by sheep/cattle and categorised into extensive, intermediate and intensive farms based on stocking rates and proportional area of semi-natural vegetation/linear feature density (High Nature Value index). Five categories of linear farm habitats were selected within each farming intensity: a) Dense hedgerow; b) Open hedgerow; c) Dense hedgerow adjacent to a watercourse; d) Open hedgerow adjacent to a watercourse; and e) Watercourse only. Insect sampling was conducted from May-September 2018 using bi-directional Malaise traps which separated catches originating in the linear habitat and field respectively. In addition, the quality of the habitats was assessed using a rapid assessment method developed for both fields and linear habitat types. Our results show that hedges associated with watercourses within extensive farming systems support important habitats for the selected indicator taxa. Syrphidae species richness was significantly greater in dense hedges associated with watercourses than either open hedges or watercourses only. On the other hand, Sciomyzidae species richness was significantly greater in water courses with or without hedges than either dense or open hedges only. NMS analysis showed that the community composition of both insect families was significantly affected by habitat quality of linear habitats in intermediate and intensive farms, while in extensive farms, community structure was significantly affected by habitat quality of grasslands, soil moisture and/or organic matter. While the abundances of Syrphidae/Sciomyzidae captured were consistently greater on the linear feature side of the malaise traps across all faming intensities, proportionally more were captured on the linear feature side in intensive farms. Moreover, indicator species analysis revealed significant Sciomyzidae and Syrphidae indicators of linear farm habitats and farming intensification. Our study indicates that not only are linear farm habitat type and quality important for biodiversity but the context in which these are found i.e. farming intensity also plays a role. This needs to be taken into consideration when developing or designing new agri-environment schemes to improve biodiversity associated with linear farm habitats.

Skeletomuscular transformations in the mesosoma of ants to support forward leaping

Authors: Aibekova Lazzat[1] and Economo Evan[1], [1]Okinawa Institute of Science and Technology

Abstract: Ants, one of the most successful groups on the planet, play an essential role in almost all terrestrial ecosystems. They evolved different locomotion patterns to be able to move on different surfaces, to exploit different habitats, and also to cope with adverse conditions. Some ants are specialized in running, such as desert ants, some are specialized for gliding, swimming, and many other locomotion types. One rare specialization in the evolution of worker ant locomotion is the ability to jump. Jumping is one of the fastest terrestrial mode of locomotion. It is used to get away from predators, to move from one place to another, and for hunting prey. Forward jumping in ants convergently evolved in three subfamilies. Although, kinematics of jumping was thoroughly studied in previous contributions, no research has been done on the anatomical modifications in jumping ants. Evolution of jumping behavior often involves a combination of structural transformations, e.g., muscular volumes, skeletal elements, energy storage, and tendon. In this study, we will focus on the gross anatomy and the muscle architecture of the leg apparatus, to understand the underlying cause of the jumping ability in ants.

Developing Strategies to Use Zoophytophagus Mirid Predators to Control Pests in Open Field Tomato Crops: Preparation for the Potential Incursion of Tuta absoluta in Southern U.S.A.

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Abstract: The tomato leafminer, Tuta absoluta (Meyrick) (Lepidoptera: Gelechiidae) is expanding in the greater Caribbean region and threatens U.S. tomato production. To prepare for the potential incursion of the pest, we investigated the ability of plant-feeding mirid predators to control established leafminer (Keiferia lycopersicella Busck) (Lepidoptera: Gelechiidae) and whitefly (Bemisia tabaci) tomato pests. In cage studies, one exotic, Nesidiocoris tenuis (Reuter) (Hemiptera: Miridae), and one native, Macrolophus praeclarus (Distant) (Hemiptera: Miridae), Florida mirid species were found to significantly reduce the number of leafminers and whiteflies on tomatoes compared to tomato plants without mirids. We also investigated the ability of N. tenuis and M. praeclarus to control B. tabaci on tomato in seven open field tomato trials conducted in South Florida, U.S.A. Fewer whitefly eggs and nymphs were seen in the mirid and pesticide treatments compared to the no treatment controls. Nesidiocoris tenuis was found to establish, while M. praeclarus was observed only during the first weeks of the studies. Field trials that included sesame plants with tomato plants increased the numbers of N. tenuis when prey was scarce and allowed sustained whitefly control. U.S. native and fortuitously established mirids may prove to be immediately available biological agents for the management of Tuta absoluta should the pest reach U.S. shores.

Development of a Precision Guided SIT technology to control wild populations of D. suzukii

Authors: Akbari Omar, UCSD, United States

Abstract: Drosophila suzukii has caused significant worldwide economic losses including significant damage in the berry- and cherry-growing industries of western North America. Achieving effective control of D. suzukii has been difficult in a number of crop systems including cherries, and control measures have largely relied on prophylactic application of expensive broad spectrum insecticides, which have been expensive and problematic. Alternative, highly promising approaches that could complement existing control methods are urgently needed. To fill this void, here I will describe the development of a novel CRISPR based approach termed Precision Guided SIT technology (pgSIT) that can be used to control and eliminate wild populations of D. suzukii.

Insecticidal potential of cardamom and clove extracts on adult red palmweevilRhynchophorus ferrugineus

Authors: Al Dawsari Mona, Prince Sattam bin Abdel Aziz university, Saudi Arabia

Abstract: Toxicity of cardamom and clove seed powder and extracted compounds against the red palm weevil,Rhynchophorus ferrugineus(Coleoptera: Dryophthoridae), was assessed in laboratory exposure experi-ments. The treatments comprised different amounts of seed powder of cardamom (0.8, 1, 3, and 5 mg)and clove (1, 3, 5, 7 mg), and extract concentrations (0.2, 0.4, 0.5, 0.6, 0.7, and 0.8) for both plants usingether petroleum or chloroform. Data showed that 5 mg of cardamom powdered seed resulted in 93% mor-tality after one day and 100% mortality after two days. Whereas after two days, lower amounts (0.8, 1,and 3 mg) resulted in 26%, 40%, 46%, respectively. A similar result was obtained for clove seed powder,where 7 mg caused 53% mortality after one day and 100% mortality after three days, other amounts(1, 3, and 5 mg) resulted in 33%, 73%, and 80%, mortality respectively, after three days. We found thatall amounts of extract of both plants resulted in 100% mortality after three days. GC-MS analysis of thecardamom and clove extracts revealed the presence of a large number of terpenes of particular notewas eugenol and two novel compounds Hydroxy-alpha-Terpenyl Acetate and Labda -8(17),13(E)-Diene- 15. The current work aims at the possibility of benefiting from natural plants pesticides as beingsafer as well as on the separation of volatile oils, which was known to be important in the control pests.Ó2019 Production and hosting by Elsevier B.V. on behalf of King Saud University. This is an open accessarticle under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

The API-Tree project: Developing Apple Pest control strategies through an Integrated Agro-ecosystem approach

Authors: Alaphilippe Aude, French National Institute of Agricultural Research Experimental Unit Gotheron, France

Abstract: Apple trees account for 35% of the European orchards and apple production is questioned since it relies on a heavy use of pesticides. The objective of the API-tree project is to design and assess the efficiency and sustainability of combinations of practices alternative to chemicals to control apple pests. In this project, the whole apple pest complex has been considered, with a focus on aphids, for which chemical control solutions are missing due to regulatory pesticide withdrawal. The novelty of this project is the integrated approach that takes into account agroecosystems management, orchard design and practices, as well as economic constraints.

A range of geographic and climatic conditions is covered by API-tree thanks to the consortium, which comprises countries from Northern to Mediterranean Europe. This also permits to share various experiences and knowledge to propose innovative context-adapted solutions. API-tree will permit to design and assess new orchard systems in collaboration with end-users (mainly growers), who will participate in co-design activities and test some proposed strategies in their commercial orchards. Targeted practices will aim at building consistent and resilient systems that reduce both pest attacks and damage to attacked plants. Those practices are related to the enhancement of plant diversity (additional cultivars, cover crops, introduction of companion plants…), to soil and tree management (cultural practices) and to the design of agroecological infrastructures (e.g. habitat management to provide pest natural enemies with food resources and shelters, push-pull plant assemblages etc.).

In this presentation we will introduce a framework to combine all the levers and methods we have been working on to reach the zero insecticide in apple orchard and give an overview of the different tested levers. Following presentations will give more details on the tested levers and outcomes.

The Evolution of the Sternopriscina (Coleoptera: Dytiscidae, Hydroporinae) larval forms

Authors: Alarie Yves, Department of Biology, Laurentian University, Sudbury, Ontario, Canada P3E 2C6, Canada

Abstract: All Australian Hydroporini (Coleoptera: Dytiscidae, Hydroporiniae) have been historically regarded as strongly monophyletic and therefore put into the subtribe Sternopriscina, one of the four putative lineages within the tribe. As different expressions of the same genotype, larval characters help to complement adult characters that have been traditionally the primary basis for Holometabola classification. The fact that all Sternopriscina genera were historically regarded as strongly monophyletic raises an interesting question: what larval phylogeny tells us about the evolution of the Sternopriscina larval forms? This paper aims at comparing in a phylogenetic context the larvae of the recently described genera Chostonectes Sharp, Antiporus Sharp, 1882, Barretthydrus Lea, 1927, Megaporus Brinck, 1943, Paroster Sharp, 1882, Sternopriscus Sharp, 1880, and Necterosoma MacLeay, 187. In this provisional phylogenetic framework Paroster stands out as sister to all the other Sternopriscina studied, which are characterized by well-developed frontoclypeal lateral branches as well as by the presence of elongate natatory setae on femora, tibiae and tarsi. Such character states coupled with variably elongate urogomphi with numerous secondary setae are probably adaptations to improve the swimming ability of their larvae.

Behavioral responses of Drosophila suzukii females to odors of blackberry and bramble

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Abstract: Drosophila suzukii Matsumura (Diptera: Drosophilidae), an invasive fruit fly originated from Eastern Asia, has a wide range of crop and non-crop host plants. It infests the most valuable crops in Europe including soft fruits such as strawberries and cherries, and several non-crop plants. Similarly to polyphagous fruit pests, D. suzukii utilizes different odor cues for feeding and oviposition behaviors, involving odors emitted by host fruits and their associated microorganisms. However, D. suzukii behavioral response towards crop host fruits has been evaluated enormously, but has been rarely investigated towards non-crop host fruits. Thus, we conducted this study to assess the behavioral responses of female D. suzukii towards odors emitted by crop and non-crop host fruits of same host species. We designed a laboratory experiment using naive flies and ripen fruits of blackberry crop Rubus fruticosus along with wild blackberry fruits, commonly known as bramble. Fruits were individually treated with chemical sterilization and no sterilization then tested using dual-choice bioassays with Y-tube olfactometer. The flies showed a significant preference for non-sterilized fruits of blackberry and bramble over the sterilized fruits. Blackberry fruits showed higher attractiveness towards non-sterilized fruits more than bramble fruits. Moreover, the overall flight activity was significantly increased when both fruits were tested in sterilized treatment. The highest activity of flies was recorded in bramble fruits. Our data indicates that flies attraction can be related to volatile compounds emitted by ripen fruits and microorganisms associated with fruits' surface. The low flies' attraction towards sterilized fruits indicates that the fruits lack the active microorganisms that may attract the flies. However, crop host fruits were more attractive than non-crop host fruits due to different volatile profiles and microbial communities. These results highlight the importance of selection of key volatile compounds emitted by both crop and non-crop host fruits and their associated microorganisms to increase attractiveness of current attractive lures. Our findings present the first report of behavioral responses of D. suzukii to sterilized and non-sterilized fruits of crop and non-crop hosts, providing promising prospects for developing a new trapping system for D. suzukii management. Such system can be based on the exploitation of volatiles emission from host fruits and microbes in a selective attractant lure which enables efficient trapping of flies during the fruiting season of both crop and non-crop hosts.

Hedgehog regulation

Authors: Alenius Mattias, Department of Molecular Biology Umeå University, Sweden

Abstract: Metabolic status regulates olfaction and taste responses in insects. During starvation many insects change food preference and response to odors. Even if we start to understand the coding principles behind olfaction and taste in insects are the molecular mechanisms that connect metabolic state and chemo sensation poorly understood.

We have previously identified that Hedgehog, a key development regulator that control segmentation in most insects, is reused after development in Drosophila to regulate the olfactory sensory neurons odor response. The results revealed a non-canonical Hedgehog signaling pathway that regulate odorant receptor transport to the cilium. Our results further showed that the system is conserved in large detail from Drosophila to humans.

Here, I will present our novel results that reveal Hedgehog to be an endocrine signal. Interestingly, the endocrine signal uses a specific receptor and suppress the olfactory sensory neuron odor response. Our results show that food composition determines the level of Hedgehog in the circulation and like that link metabolic state with food detection. Finally, I will disclose how Hedgehog skews some of the odor responses and possibly change the odor perception in Drosophila.

Measuring the evolutionary potential of a diapause-avoiding parasitic wasp to climate change

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Abstract: The earth is currently experiencing rapid changes in climate. In addition to warming temperatures, an increase in the incidence of unpredictable thermal events such as heat / cold waves is also forecast. Species are differently affected by these climatic changes depending on their ability to buffer from and/or to respond to stressful thermal conditions. In areas with mild winters, an increasing number of ectothermic species have lost their diapause strategy, thus remaining active all year. As a consequence, such species are increasingly vulnerable to unpredictable cold stress events. The current study aimed to better understand the evolutionary potential of one such species by estimating heritability of cold tolerance. Using a parental half-sibling breeding design, cold tolerance, morphology and longevity of the parasitoid wasp Aphidius avenae, which has lost its diapause strategy in western France, was investigated and heritability estimates obtained. If the low heritability estimates obtained are indicative of the evolutionary potential of A. avenae cold tolerance, A. avenae may be increasingly reliant on behavioural responses and adaptive phenotypic plasticity to persist in a changing climate, with potential implications for the biological control function they provide.

Neuroendocrine control of environmental stress responses

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Abstract: Insects are exposed to a continuous multiple stressors across a range of environments. Desiccation tolerance and survival is dependent on fluid homeostasis by fluid transporting epithelia including the Malpighian tubules. Fluid transport by insect Malpighian tubules is modulated by diuretic neuropeptides which have also recently been shown to affect desiccation and cold tolerance in e.g. Drosophila melanogaster and D. suzukii.
Evidence suggests that at least three diuretic neuropeptides (capa, DH44, kinin) perform functions in environmental stress tolerance via the Malpighian tubules. Thus, Malpighian tubule function, and diuretic neuropeptides, have much wider implications for physiology and behaviour beyond osmoregulation.

Population dynamics of microbial symbionts from the common bed bug Cimex lectularius

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Abstract: The common bed bug Cimex lectularius harbours multiple symbiotic partners, at least one of which has been implicated in the supplementation of the vitamin-deficient blood diet. However, the integration of these multiple partners into the development of the insect has not been investigated in detail. In this study we monitor the population density of two cohabiting bacterial symbionts (Wolbachia and BLS) from egg to adulthood, and assess how insect gender, reproduction and availability of food impacts the bacterial populations.

Determination of Resistance Improving Potential of Cotton Whitefly Bemisia tabaci (Genn.) (Hemiptera: Aleyrodidae) Biotypes Against Cyantraniliprole

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Abstract: In this research, the resistance development potential of MEAM1 and MED genetic groups of cotton whitefly Bemisia tabaci to Cyantraniliprole was investigated. In addition, it was also determined the development of multiple resistances to different insecticides (pyriproxyfen, Spirotetramat and acetamiprid) in each biotype of B.tabaci. The obtained data will be a useful reference for future monitoring and management of insecticide resistance.

Field evaluation of natural pest control services at rice landscape

Authors: Ali MP, Entomology Division, Bangladesh Rice Research Institute (BRRI), Gazipur, Bangladesh

Abstract: Climate change induces salinity intrusion into soil and crop production land (terrestrial ecosystem) and the rate of salinity growth increases in terrestrial agricultural production landscape yearly. The impact of salinity on crop production, environment, social and food security is widely studied. However, the impact of elevated salinity on a natural pest control service system (where plant, pest and pest control providers live together) remains elusive. We tested the impact of elevated salinity on pest control service in coastal sites of Bangladesh using artificial inoculation approaches where insect pests and its eggs were released into rice field. Two gravid brown planthoppers were introduced in each place where six rice hills were covered with nylon mesh net. Three places were covered by nylon mesh net and three were exposed to natural enemies. Three locations of salinity elevated area and three locations of non-saline areas were selected for this experiment. Brown planthoppers (only 0.55) were not observed in exposed area where eggs and adult BPH were released at the mid stage of rice growth in field. On the other hand, where BPH introduced area was covered by nylon mesh cage showed significant higher number of populations developed (180.89) and feed rice plant ($P < 0.001$). Statistically similar development trends were found in three locations as saline area ($P > 0.05$). Number of natural enemies in exposed and non-exposed area were also recorded. Among the natural enemies, lady bird beetle, staphylinid beetle, carabid beetle and spiders were largely found both in exposed and non-exposed areas. These indicate that natural enemies are available to destroy insect pests in rice field. Significant number of lady bird beetles (21), spiders (13), and staphylinid beetle (30) were recorded outside the cage in rice field. Higher number of lady bird beetle (31), spiders (18) and staphylinid beetle (46) were recorded in pest exposed area. Similarly, natural enemies were observed in non-saline area both in exposed and non-exposed pest area. Significant number of lady bird beetles (12), spiders (10), and staphylinid beetle (20) were recorded outside the cage in rice field. Higher number of lady bird beetle (18), spiders (14) and staphylinid beetle (26) were recorded in pest exposed area. In non-exposed pest area, natural enemies including lady bird beetle, spiders and staphylinid beetles densely prevail closed to cage where pest remained throughout the experimental period. More importantly, we quantified the yield reduction due to pest introduced in cage. Significant lower amount of rice yield observed in non-exposed area (total 9 hills/ cage, area: 0.36 m2). Non-exposed area showed 206.52 g rice yield where as exposed area showed 238.52 g yield. This result indicates that brown planthopper can reduce 13.41% rice yield if natural enemies are absent in the field.

Establishing next generation pest control service in rice landscapes

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Abstract: Pesticides are commonly used in food crop production systems to control crop pests and diseases and ensure maximum yield with high market value. However, the accumulation of these chemical inputs in crop fields increases risks to biodiversity and human health. In addition, people are increasingly seeking foods in which pesticide residues are low or absent and that have been produced in a sustainable fashion. More than half of the world's human population is dependent on rice as a staple food and chemical pesticides to control pests is the dominant paradigm in rice production. In contrast, the use of natural enemies to suppress crop pests has the potential to reduce chemical pesticide inputs in rice production systems. Currently, predators and parasitoids often do not persist in rice production landscapes due to the absence of shelter or nutritional sources. In this study, we modified the existing rice landscape through an eco-engineering technique that aims to increase natural biocontrol agents for crop protection. In this system, planting nectar-rich flowering plants on rice bunds provides food and shelter to enhance biocontrol agent activity and reduce pest numbers, while maintaining grain yield. The abundance of predators and parasitoids and parasitism rates increased significantly in the eco-engineering plots compared to the insecticide-treated and control plots. Moreover, a significantly lower number of principal insect pests and damage symptoms were found in treatments where flowering plants were grown on bunds than in plots where such plants were not grown. This study indicates that manipulating habitat for natural enemies in rice landscapes enhances pest suppression and maintains equal yields while reducing the need for insecticide use in crop fields.

Host sex discrimination by egg parasitoids of stink bugs

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Abstract: Chemical traces deposited by herbivores walking over the plant surface may act as contact kairomones for their associated insect parasitoids during the host location process. In the several stink bug-egg parasitoid systems, these indirect host-related cues do not only provide information about the potential presence of the stink bug host in the surrounding areas but also provide information on the host sex. Particularly, egg parasitoids spend more time on the traces left by female bugs, which would normally be of higher hierarchical value, showing the fact that such female wasps have evolved strategy based on host sex discrimination to arrive in the vicinity of freshly laid host eggs. Here, we provide a comprehensive overview of host sex discrimination ability in egg parasitoids of stink bugs and discuss the role of cuticular hydrocarbons as key compounds mediating the discrimination behavior.

Release of earwigs (Forficula auricularia Linnaeus (Dermaptera: Forficulidae)) to control woolly apple aphid (Eriosoma lanigerum Hausmann (Hemiptera: Aphididae))

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Abstract: Woolly apple aphid affects apple trees and causes damage to branches, trunks and roots. Previous studies indicate that earwigs can play an important role in the control of this pest; however, even though earwigs are naturally present in apple orchards, they do not prevent outbreaks. For this reason, a trial was carried out to evaluate the effect of earwig release on the biological control of woolly apple aphid. This trial was carried out in 2017, 2018 and 2019 in an organic apple orchard located in Catalonia (NE-Spain). In 2017 and 2018 earwigs were released in June, while in 2019 they were released in May. Two treatments were evaluated: release (by means of a shelter with 30 earwigs) and control. The experimental design was completely randomized with 10 replicates. Each replicate was constituted by a tree in which an infested bud of woolly apple aphid was selected to evaluate the growth of the colony. The release carried out the first year (2017) did not affect the presence of the woolly apple aphid. However, the releases that were performed in 2018 and 2019 caused a decrease in colony size. Our results show the potential of earwigs' releases in the biological control of woolly apple aphid.

Perspectives on the potential applications of Antimicrobial Peptides

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Abstract: Antimicrobial peptides (AMPs) are small evolutionarily conserved biologically active molecules widespread in nature. These naturally occurring AMPs are considered essential protective component, thereby imparting the first-line of defense against pathogens. Currently, more than 2900 AMPs from six life Kingdoms including bacteria (335), fungi (16), archaea (4), protists (8), plants (343) and animals (2219) have been reported. Multidimensional biological characteristics such as antimicrobial, immune modulator, least toxicity and decreased resistance development make APMs versatile promising future drug candidate in pharmaceutical industries. They are mainly involved in their defense mechanism in order to protect them against invading infections agents including fungi, bacteria, yeast and viruses. In addition to antifungal, antiviral and antibacterial response through diverse mechanisms, AMPs provide the avenues for the development of novel therapeutic alternative due to their anticancer response against cancer cell lines. This presentation intents to highlight how short antimicrobial peptides can become novel therapeutic tool to tackle future resistance development challenges.

Monitoring Elaterid Beetles on Sweet Potato in the Mississippi Delta

Authors: Allen Clint[1], Johnson Chris[1] and Reddy Gadi[1], [1]USDA-ARS, United States

Abstract: Wireworms, the larvae of click beetles, are insect pests with a wide host range consisting of vegetables, grains and other crops such as peanuts, strawberries and tobacco. They are capable of inflicting economic damage to the roots and tubers during their long-life cycles. They are difficult to control due to their protected habitat below ground. In Mississippi and in the southeastern U.S. Conoderus spp are major wireworm pests. The cryptic life cycle of wireworms renders chemical control efforts unsuccessful and estimation of pest numbers difficult. The primary objective of this research was to determine the damage potential and distribution of wireworms/click beetles. The Noronha Elaterid Light Trap, or "NELT", is made with three pieces — a small solar-powered spotlight, a plastic white cup and a piece of screening. The light is set close to the ground to attract the source of the wireworms, the female click beetles that emerge from the ground in April and May. These traps will be installed at several sweet potato fields in the Mississippi Delta. The proposed survey work will help us to determine the distribution of click beetles in the Mississippi Delta and the potential need for preventative control of this important insect group.

Australian Eadya (Braconidae) as larval endoparasitoids for classical biocontrol of globally invasive paropsine leaf beetles

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Abstract: A number of countries using Eucalyptus in plantations have been the recipient of a number of invasive paropsines (Col.: Chrysomelidae: Chrysomelinae) from Australia. All species are significant defoliating pests. In a departure from the reliance upon egg parasitoids, further investigations into larval endoparasitoids began as a result of interest in locating host specific classical biological control agents. A collaboration between the University of Tasmania and Scion in New Zealand and the University of Central Florida over the last eight years has resulted in the description of four new species discovered in the field and confirmed with molecular identifications, as well as a revised key for the genus of Eadya. Eadya which are striking black and orange wasps, were found to be larval parasitoids of nine differing paropsine species, and one species studied in most detail suggest all attack any of the four larval instars during spring/early summer when they are feeding either clustered or singly on Eucalyptus leaves.
Paropsis charybdis is New Zealand's arguably most damaging eucalyptus pest, Eadya daenerys which attacks P. charybdis has now been approved for release there. The most common field host of this parasitoid in Tasmania is Paropsisterna agricola. Paropsisterna variicollis is also a pest causing concern in New Zealand and spreading rapidly. Field and laboratory host range data suggest Eadya annleckieae specialises on Pst. variicollis and Pst. selmani. With Pst. selmani being a pest of Eucalyptus plantations in Ireland, this species could become a promising biocontrol agent in both New Zealand and Ireland.

Invasive ants and virus dispersal

Authors: Allen Margaret, U.S. Department of Agriculture, Agricultural Research Service, United States

Abstract: Ants are highly effective invasive species. I have scrutinized RNA viruses in Mississippi USA populations of red imported fire ants, and have identified evidence of six viruses. Each virus present has unique implications and potential applications.

The Role of Chemical Ecology in the Management of Forest Insect Pests

Authors: Allison Jeremy, Great Lakes Forestry Centre, Canadian Forest Service, Canada

Abstract: The study of the chemistry, biochemistry and function of natural products (chemical ecology), has immense potential to inform our understanding of the biotic world. It also has the potential to provide biorational tools for integrated pest management (IPM) and the promise of this potential has been the primary impetus for the development of the discipline of chemical ecology. Examples of pest management tools based on the chemical ecology of target pests are now common but remain far more numerous for agricultural than forestry pests. In part this is a product of a larger research investment into agricultural than forest pests. It is also a reflection of the reality that trying to develop IPM for forest insect pests has challenges unique to forest settings. Primary among these are: 1) rotation periods that can mean that decades pass before a return on the investment in IPM can be realized; and 2) spatial scales and associated limited infrastructure that can make implementation of IPM difficult. While the area of planted forests is increasing globally and compartments of planted forests can be large, plantation forests are typically characterized by intensive management and consequently good infrastructure and accessibility, as well as short rotation periods. As a result, the temporal and spatial constraints that limit the application of chemical ecology to the IPM of insect pests in natural forests may be attenuated in plantation forests. This presentation will provide an overview of current applications of chemical ecology to the management of forest insect pests and discuss potential areas for increased contributions to the development of IPM tactics for insect pests in plantation forests.

Sugar feeding increases immunity in the gut and protects the female mosquito Aedes aegypti against arboviruses

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Abstract: Female mosquitoes usually drink sugars from plants and flowers for their own energy but also require a blood meal to reproduce. Due to this last strategy, they are vectors of arthropod-borne viruses (arboviruses) such as Zika (ZIKV) or chikungunya (CHIKV) viruses. Sugar sources can be rare in some arboviral endemic regions, forcing female mosquitoes to feed exclusively on blood to use it as a nutrient source and therefore, leading to a higher risk of arbovirus transmission. Mosquito immunity is an important factor influencing vector competence. The gut is the first barrier to be overcome by an arbovirus after blood meal and is the major determinant of arbovirus infection. We demonstrate that the gut immunity in females is enhanced and maintained through regular sucrose solution feeding. Our data show that sucrose, glucose and fructose (sugars naturally present in plant and flower nectar) can all maintain gut immunity in females. We next investigated the role of the intestinal microbiota in sugar-induced immunity. Antibiotic-treated mosquitoes showed a stronger sugar-induced immunity than non-treated mosquitoes. Therefore, sugars increase gut immunity independently of the microbiota. Moreover, microbiota decreases immunity, either by directly competing with the mosquito host for sugars, either by directly inhibiting immunity. Also, we found that females that fed on sucrose few hours before the intake of an arbovirus-infected blood meal are less susceptible to the virus than non-sugar-fed females. Altogether, these results showed the extreme importance of sugar on the gut immunity and on arbovirus infection in the female mosquito Aedes aegypti.

Pea leaf weevil and broad bean weevil control time in broad bean (Vicia faba)

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Abstract: Pea leaf weevil (Sitona lineatus) and broad bean weevil (Bruchus rufimanus) are destructive insect pests on broad bean (Vicia faba) worldwide. The best control time under natural field conditions of these two pests was investigated at the Institute of Agriculture, Lithuanian Research Centre for Agriculture and Forestry during 2018-2020. Contact and systemic insecticides were used. The abundance of S. lineatus and B. rufimanus was monitored from germination till full ripening. For S. lineatus, several application times were tested (at growth stage BBCH 08; when the first weevil adult was caught in the yellow water trap; when the daily air temperature for three days exceeds that of threshold for adult activity; at the local threshold (5–10 beetles m-2); at the growth stage BBCH 10–11). For B. rufimanus, several application times were tested (when the first weevil adult was caught in the yellow water trap; when the daily temperature for three days exceeds that of threshold for adult activity; at the end of flowering (BBCH 69); spray three times beginning at growth stage BBCH 69 with a one-week interval).

At low density of S. lineatus adults (3.5 beetles m-2) at early growth stages, application of insecticides according to the tested spray regimes did not show significant effect on leaf damage (notches). At high density of S. lineatus adults (18 beetles m-2), application according to the local threshold gave significantly the lowest number of notches on leaves compared to the early spray at BBCH 08 growth stage. The abundance peak of B. rufimanus adults corresponded with the full flowering stage (BBCH 65). The best control of B. rufimanus was achieved when insecticide application was done three times beginning at the end of flowering (BBCH 69) with a one-week interval. This spray regime decreased the damaged seeds by 57.7% compared to the untreated control and resulted in 38.9% yield increase.

Recent trends in stream macroinvertebrates: warm-adapted and pesticide-tolerant taxa increase in richness

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Abstract: In recent years, massive declines in insect biodiversity have been reported from many European countries.

We analysed nationwide, systematic monitoring data on aquatic insect diversity collected at 438 sites in Switzerland from 2010 to 2019. In addition to taxonomic richness, we considered functional traits such as temperature preferences and feeding guilds. Furthermore, we explored the sensitivity of aquatic insects towards pesticides. We found that insect species richness increased in the time period considered. Warm-adapted species showed the strongest increase with time while cold-adapted species richness remained stable. Generalists such as collector-gatherers displayed the highest gain in species richness, and pesticide-insensitive taxa increased most with time. Moreover, we developed a predictive model of aquatic insect richness by considering both in-stream conditions such as temperature and catchment-level factors such as land use and found that the importance of predictors depended on the functional group under consideration.

Our results suggest that recent developments in insect species richness are context-dependent and affect functional groups differently. Longer investigations are needed to confirm the positive trend and to reveal if the increase in temperature and pesticide tolerant species could lead to a decrease in specialised species and a homogenisation of biotic communities in the long term.

Effect of landscape complexity and Bt technology on phytophagous stink bugs and predatory arthropods abundance in soybean

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Abstract: In Uruguay, as in the rest of South America, agroecosystems underwent two major changes: agricultural intensification and the inclusion of Bt crops. The removal of natural habitats caused by landscape simplification and the high adoption of transgenic cultivars resistant to defoliating lepidoptera could generate side effects on phytophagous and beneficial arthropods. This research aimed to evaluate the effect of landscape complexity (percent of landscape in agriculture) and the technology used at the local scale (RR or RRBt) on the abundance of phytophagous stink bugs and predominant predatory arthropods in soybean. Sampling was completed in 32 fields (16 RR and 16 RRBt) located in the Northwest of Uruguay throughout the whole cycle of the crop during 2017-18 season. Arthropod abundance was estimated every three weeks using sweep netting conducted inside the fields and in field edges. Landscape complexity was measured as the proportion of agriculture-land use within 1km radius circle. The average values obtained in the six sampling moments were accumulated and analyzed fitting generalized linear models ($p\text{-value}<0.05$). Piezodorus guildinii was the predominant stink bug species in all sampled fields, while spiders, predatory bugs and ladybugs were the most abundant predators. Soybean fields surrounded by landscapes with more than 75% of agriculture had higher number of stink bugs, but reduced landscape complexity did not affect any group of predators. Abundance of stink bugs or predators was not significantly different between RRBt and RR soybean fields. Spontaneous vegetation at the edges of the field had a greater abundance of spiders than the crop area, while stink bugs, predatory bugs and ladybugs were more abundant inside the crop. Understanding the relative importance of agricultural practices at different scales and the interaction with stink bugs and predators dynamics will facilitate recommendations on the sustainable management of soybean pests at the local and landscape scales.

Effect of landscape composition and Bt technology on phytophagous stink bugs and predatory arthropods abundance in soybean

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Abstract: South America agroecosystems underwent two major changes: agricultural intensification and the inclusion of Bt crops. The landscape simplification and the adoption of transgenic cultivars resistant to defoliating lepidoptera could generate side effects on phytophagous and beneficial arthropods. We evaluated the effect of landscape composition (1km radius) and the technology used (RR or RRBt) on the abundance of phytophagous stink bugs and arthropods predators in soybean. Over two-year, sampling was completed in 60 soybean fields in the Northwest of Uruguay. Arthropod abundance was estimated using a sweep and a beating sheet. Piezodorus guildinii was the predominant stink bug, while spiders, predatory bugs and ladybugs were the most abundant predators. The abundance of stink bugs and predators in soybean was affected by the type of vegetation cover and did not differ between RRBt and RR soybean fields. Spontaneous vegetation at margin's fields had a greater abundance of spiders than the crop area, while stink bugs, predatory bugs and ladybugs were more abundant inside the crop. Abundance of many predators in soybean was positively associated with their abundance in the margins. Our results contribute to understand the relative importance of agricultural practices at different scales towards the sustainable management of these pests.

Priming of Beauveria bassiana spores to enhance biocontrol of the red-banded stink bug Piezodorus guildinii

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Abstract: The hydrocarbon layer of the insect epicuticle represents the first barrier to infection by entomopathogenic fungi such as Beauveria bassiana. The aim of the present research was to study the effect of hydrocarbon nutrition on virulence and gene expression of two B. bassiana strains (ILB308-high and ILB299-low virulence) towards Piezodorus guildinii, a hemipteran highly resistant to infection. Strains were grown on minimal media (MM) with n-pentadecane as sole carbon source (HC15); Piezodorus guildinii insects were inoculated by immersion and mortality was recorded daily for 12 days. The expression of genes involved in either spore viability and osmolarity, spore adhesion, hydrocarbon assimilation or oxidative stress was evaluated by qRT-PCR. Strain ILB308 showed an increase on its virulence towards P. guildinii as well as early over-expression of mostly all evaluated genes. The low virulence strain -ILB299- also showed an increase on its virulence when grown on HC15, but the overexpression of genes relevant to infection and HC degradation metabolism was low and delayed in time. In conclusion, gene induction patterns (identity, time, and level of induction) are different in both strains and correlate well with the different virulence enhancement patterns exhibited on P. guildinii.

Insect-specific virus-arbovirus interactions in mosquitoes

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Abstract: Virus discovery has long depended on outbreaks, and the research to understand their pathogenicity depended on their isolation and culture. Due to the persistent nature of their infections, the ubiquity and diversity of insect-specific viruses of mosquitoes have been only discovered following the recent advances in sequencing technologies. While the interactions of these viruses with arboviruses raised scientific interest in insect-specific viruses, these interactions are usually studied in acute infections and not in persistently infected hosts. In this study, we focus on a recently isolated insect-specific virus Agua-Salud Alphavirus (ASALV, Togaviridae). We studied the interactions of ASALV with different arboviruses and have observed differences in the interference capacity of ASALV with arboviruses depending on its infection status (acute versus persistent). ASALV was able to interfere with the replication of two different arboviruses, but only in the case of ASALV persistent infection. No difference in arbovirus replication was observed in the case of simultaneous co-infection of ASALV and the arboviruses. Further research is needed to understand the mechanisms behind these interactions.

The RNAi response in vector mosquitoes against mosquito-specific viruses versus arboviruses

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Abstract: Mosquito-specific viruses (MSVs) often share several similarities with arboviruses, but are, in contrast to arboviruses, restricted to their mosquito host. All findings support a worldwide distribution of MSVs in a variety of mosquito species, including important arbovirus vector mosquitoes.

RNA interference has been shown to be one, if not the most important antiviral response in mosquitoes against arboviruses and linked to vector competence. Although, for some MSVs it was shown that they also induce and interfere with the RNAi response, little is known about this interaction for most MSVs, especially the ones sharing strong similarities to arboviruses. Besides, it is unclear whether the interaction between MSVs and the mosquito vector could in turn have an effect on a potential co-infection with an arbovirus. Comparing the interaction of an arbovirus and a MSV, belonging to the same virus genus, with the mosquito RNAi response is important to understand potential effects on vector competence of mosquitoes for arboviruses.

Knockdown experiments of key proteins of the different RNAi pathways (siRNA, miRNA and piRNAs) in Ae. aegypti derived cells are performed followed by infection with the mosquito specific Agua Salud Alphavirus (ASALV). Effects on ASALV infection are compared to results of arbo-alphaviruses (e.g. Chikungunya virus and Semliki Forest virus). Moreover, production of virus specific small RNAs in infected cells is investigated.

Similar to arbovirus infection, the siRNA pathway is triggered by ASALV infection and has antiviral activity. Surprisingly, an antiviral effect was also observed for the miRNA pathway in case of ASALV, not seen for the arbovirus infections. Results regarding the piRNA pathway, showed an antiviral activity for Piwi4 for MSV and arboviruses; however, no ASALV-specific piRNAs could be detected.

Taken together, these results highlight important differences between the interactions of the mosquito with MSVs versus arboviruses.

Field-evolved resistance to Bt Crops in Latin America

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Abstract: Fall armyworm, Spodoptera frugiperda (J.E. Smith) is one of the most destructive maize pests in the tropical zone of the American Continent, causing significant yield losses under moderate-high infestations. Historical S. frugiperda management in South America relied on plant protection with synthetic insecticides, ranging from 1-10 applications per crop cycle, depending on pest pressure and crop system management. More recently, genetically modified maize plants expressing insecticidal Bt proteins gained significant role in managing this pest in the region due to its effectiveness. Nonetheless, local environment, landscape, and agricultural practices can create intense selection pressure favoring resistance development to chemistries and biotech traits, representing a significant challenge to effective long-term control of this pest. Short term financial and food security goals driving maximization of land productivity in large monoculture agricultural systems with potential extraction of two to three crops per year impose strong selection pressure through an environment biologically accelerated. Understanding regional landscape, pest ecology, insect-crop/trait interactions, and genetic variability is fundamental for deployment of effective, locally adapted practices. The utilization of a variety of control tactics is key for sustainable management and cropping systems. The biggest challenge is balancing economic, environmental, and social aspects of sustainability at the local level.

Crop pollination by nocturnal bees

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Abstract: Most bees are active during the day. However, approximately 1% of the bee species are nocturnal and forage in search for flowers during the low light intensities of the night, between sunset and sunrise. They account for about 250 species and are distributed among the families: Andrenidae, Apidae, Colletidae and Halictidae. We evaluate the role of nocturnal bees in the pollination of “cambuci”, Campomanesia phaea, Myrtaceae, and “guarana”, Paullinia cupana, Sapindaceae, both economically highly important plants of the Brazilian Atlantic Rainforest and Amazon, respectively. Furthermore we collected floral volatile from the host plants using dynamic headspace method and tested if these compounds were capable of attracting nocturnal bees in the field. Synthetic scent mixtures that contained various of the identified floral scent components, successfully attracted nocturnal bee pollinators. Our data show that cambuci and guarana attract their nocturnal bees by strong floral scents and suggest that the chemical communication between these plant and their pollinators is a key step in crop production of these economically important plant species.

Insect role in transmitting Dickeya dianthicola among potato plants

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Abstract: The blackleg bacterium Dickeya dianthicola Samson is an important pathogen of potato, Solanum tuberosum, in North America and Europe. Previous work has suggested that insects, particularly aphids, may be able to vector bacteria in this genus between plants. However, no empirical work was conducted to evaluate their epidemiological role in transmitting this disease on commercial potato fields. We tested vector potential of the two potato pests most common in most temperate growing areas: the Colorado potato beetle (Leptinotarsa decimlineata Say) and the green peach aphids (Myzus persicae Sulzer).

Olfactometry and recruitment experiments evaluated if either insect discriminates between infected and uninfected foliage. Infection was determined using visual symptoms and genus-level PCR primers for Dickeya. In the laboratory, beetles and aphids were fed infected plants and then transferred to uninfected plants to determine if bacteria would be transmitted between plants. In the field, insect densities were manipulated to correlate them with the incidence of the disease.

Neither Colorado potato beetles nor green peach aphids were attracted to infected foliage in either olfactometry or recruitment experiments. To the contrary, presence of butanediol, which is product of Dickeya fermentation, significantly reduced beetle attraction to the odor of potato foliage. Green peach aphids preferred uninfected foliage, but only when conspecifics were present. Neither Colorado potato beetles nor green peach aphids acquired and transmitted D. dianthicola through feeding on infected plants in the laboratory. In the field, neither insect’s abundance correlated significantly with the spread of this disease. Therefore, controlling these pests is unlikely to prevent blackleg outbreaks in potato fields. Instead, the efforts to limit spread of this disease should focus on sanitation, water management, and seed screening.

Endogenous insect resources for a more sustainable aquaculture

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Abstract: The future and the ability of the world food system to ensure food security for a growing world population are closely tied to improve the protection of natural resources, and in the delivery of alternative sustainable protein sources. The need for more sustainable feedstuffs in the aquaculture sector has determined the use of alternative food sources, and in this context, insects have been investigated as potential ingredients. However, nutritional profiles of commonly studied insects lack important nutrients for marine organisms. Here, we show how endemic costal insect species may contribute to overcome this gap and contribute to improve the nutrition of aquaculture marine species.

Hermetia illucens egg volatile signalling and its relevance for mass-scale production

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Abstract: Available data on oviposition behaviour of H. illucens, one of the most important insect species reared for food and feed, is scarce and highlights the variability associated with oviposition in this species reinforcing the need to gain additional knowledge on this topic to achieve economically feasible mass-scale production. Here we provide a first screening of the volatile organic fraction of H. illucens eggs from oviposition to hatching, shedding light over the temporal evolution of semiochemicals composition, a knowledge which can contribute to advance the state of the art on H. illucens mass-scale production.

Can insect pests be controlled using antifungal lipopeptides?

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Abstract: The development of organic agriculture and the increasing restriction on pesticide use have impulsed a growing interest to develop new strategies of weeds, pathogens and pests control. Bacteria are well identified sources of biocontrol molecules, among which lipopeptides exhibit interesting properties such as broad spectrum of activities (Ongena and Jacques, 2008) and biodegradability. Although lipopeptides produced by Bacillus subtilis show well-documented anti-bacterial and anti-fungal properties, the number of studies on their putative insecticidal effects remain scarce (Guo et al., 2015) despite a growing interest to develop ecofriendly alternatives for plants protection. Aphids are major pests causing great damages to vegetable crops and orchards either because of their direct action by sap sucking, or indirectly by the transmission of viruses. We compared the effects of three different lipopeptides families (fengycin, mycosubtilin and surfactin) produced by B. subtilis strains, on Myzus persicae (a polyphagous aphid) and Dysaphis plantaginea, the major aphid pest of apple trees. Two modes of exposure were used, either by topical application or by ingestion using artificial diet with different lipopeptide concentrations. The effects of each lipopeptide were assessed on aphid survival and fertility. The results are discussed in the context of versatile molecules combining both pests and pathogens biocontrol properties in a management program.

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Companion planting involving Amaryllidaceae (ex. Alliaceae): a strategy for aphid pest control?

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Abstract: “Companion planting” is one specific type of polyculture, under which two plant species are planted together that are known, or believed, to synergistically improve one another’s growth trait. This kind of plant association can help to control insect pests either directly, by disturbing pest settling and/or indirectly, by attracting natural enemies. Some plants belonging to the Alliaceae family (chives, garlic, onion, leek) release Volatile Organic Compounds (VOC) with strong repellent potentialities. The aim of this work was to investigate the disturbance of aphid pest colonization behavior when submitted to putative repellent plant or essential oil extracts. Plants selected in our experiments belong to species conventionally grown in the field or in greenhouses in the Hauts de France Region and Belgium. The companion plants belong to Alliaceae, whereas pepper was the target plants. The positive control consists of submitting volatils from Alliaceae extract to the pest – plant target system. EPG technique and Clip cage experiments were used to assess the effects of companion plant vs essential oil extract VOC on the feeding behavior and demographic parameters of aphids when feeding on the target plants. Results are discussed in the context of environmentally friendly and sustainable pest management strategies.

Insect decline – an issue in forensic entomology?

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Abstract: At the end of 2017, a study showed a significant decline in insect populations within the last 27 years in German nature reserves. This was a scientific validation of what many had long since subjectively perceived: a widespread reduction in insect abundance. Insects play a key role in terrestrial ecosystems and perform important ecosystem functions and services such as pollination, the formation of important linkages in food webs or the disposal and recycling of dead organisms. The latter builds the bridge to forensic entomology (FE) and its use of necrophagous insects, degrading the dead organic matter, here: human bodies. Statements in the media give the impression that insect decline threatens FE. However, no reliable data on this exist at this time. Numerous factors of insect decline are discussed, such as the intensification of agriculture with increased pesticide consumption and the establishment of large monocultures, are of questionable relevance for necrophagous insects. In addition, the main application of FE is mainly based on the analysis of an insect complex that can be described as “species-poor”, focusing on a few polyvoltin species with an extremely high reproductive potential. In accordance with these assumptions, our own studies over the last 20 years at the institute of legal medicine in Frankfurt/Germany show no significant changes in the diversity and abundance of these species on human bodies and in the field. However, it cannot be ruled out that this will change in the coming years, not least because of the challenges associated with climate change such as e.g. prolonged heat waves or the dispersal of invasive species. This could lead to a shift in phenology patterns and abundances of forensically relevant taxa.

50 shades of green – a case-based introduction to the insect infestation of the living and the dead

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Abstract: Forensic entomology uses insects to draw conclusions on legal matters. The main emphasis is on estimating the minimum post-mortem interval (PMImin) by determining the age of the juvenile insect stages developing on a corpse. It is highly useful when human remains are found more than 72 hours after death, at a point when forensic pathological approaches are no longer appropriate to determine the time of death. Forensic entomology can also help in the detection of neglect, where living people are infested with insects. Such infestation of live vertebrates (humans and/or animals) with dipterous larvae, which feed at least for a certain period of time on the host's dead or living tissue is defined as myiasis. Since 2001 the Institute of Legal Medicine Frankfurt am Main analyses insect infested bodies and research on necrophagous taxa, supports death investigations at the crime scene and during autopsies, and delivers entomological reports to answer questions of legal interests. To proof the importance of forensic entomology we evaluated insect associated cases from 2001 to 2019 (n = 852). Sex and age of the deceased, date of autopsy and discovery, place of finding (indoor or outdoor), supposed post mortem interval (PMI) (based on the time last seen or other hints such as newspapers, letters or neighbors' statements), and the cause of death were noted. Overall more dead bodies were found indoor (82 %) than outdoor (18 %) regardless of year and month and the majority were male (70 %) and in the age of 60 – 70 years. From June to August, i.e. summer months and typical blow fly season the most bodies were found, while in winter December to March only a few bodies were colonized. In more than 70 % of all cases the PMI ranged from one day to three weeks, so that in these cases it would have been possible to estimate the PMImin to the day on the basis of entomological findings. In about half of the cases the person died of natural causes (e.g. cardiac failure) but in many cases a clear cause of death was not visible due to external and internal decay of the body. Detailed information on insect species and diversity was available for about 25% cases. There were over 20 frequent insect taxa, of which the blow flies Lucilia sericata and Calliphora vicina were the most dominant species. There was a seasonal trend in the occurrence of the two species, with L. sericata being active in the summer months and C. vicina colonizing carcasses mainly in spring, autumn and winter, i.e. during the colder period of a year.

When it comes to the infestation of the living, most cases have been neglect in a domestic environment where people were overstrained with the care of their relatives. The relevant species differed according to where the living or meanwhile deceased person was found. While blowflies and here Lucilia sericata dominated the outdoor cases, mainly Muscidae colonized the bodies indoors. Musca domestica was the most common species here.

Intercepted Mosquitoes at New Zealand's Ports of Entry, 2001 to 2018: Current Status and Future Concerns

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Abstract: Mosquito vectors are extending their range via international travel and trade. Climate change makes New Zealand an increasingly suitable environment for less tropically adapted exotic mosquito vectors to become established. This shift will add a multiplier effect to existing risks of both the establishment of new species and of resident exotic species extending into new areas. We describe trends in the border interceptions of exotic mosquitoes and evaluate the role of imported goods as a pathway for these introductions. Ae. aegypti and Ae. albopictus, the two most commonly intercepted species, were only intercepted in Auckland. Used tyres and machinery were the main mode of entry for both species. The majority of Ae. albopictus were transported as larvae by sea, while most Ae. aegypti were transported as adults by air. Continuing introductions of these mosquitoes, mainly arriving via Japan or Australia, increase the risk of the local transmission of mosquito-borne diseases in New Zealand in general and in the Auckland region in particular. These findings reinforce the need for a high performing and adequately resourced national biosecurity system, particularly port surveillance and inspection. Recommended biosecurity improvements are described.

Invasions old and new: reconstructing the spread of winter moth (Operopthera brumata) in Europe and North America

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Abstract: Native to Europe, outbreaks of the invasive geometrid Operophtera brumata (winter moth) have in recent times been reported in geographically isolated populations including Northern Scandinavia (1900s), Nova Scotia (1930s), Oregon (1950s), the Pacific Northwest (1970s), Northern Africa (1970s), and New England (1990s). Using a combination of phylogenetic and population genetic techniques, we explore the evolutionary history of winter moth populations across four continents to unravel 1) the ancestral origins of this species; 2) the use of glacial refugia in Europe and Africa during the Last Glacial Maximum (LGM); and 3) the contemporary origins of invasive winter moth populations. Using coalescent species tree analyses based on DNA sequences from three nuclear loci (28S, EF1?, and Wingless) and one mitochondrial locus (COI) we find that winter moth is more closely related to Asian species in the genus Operophtera than to European or North American species, and that it likely diverged from species found in Japan and Eastern Russian between 400,000 and 1.4 million years ago suggesting that winter moth is a relatively new addition to the European ecological community. To explore the use of glacial refugia during the LGM as well as the contemporary origins of invasive species in Northern Africa, Northern Scandinavia, and North America, we amplified 24 polymorphic microsatellite loci and conducted Approximate Bayesian Computation (ABC) simulations. These simulations indicate that 1) the invasive population in Northern Africa is native to the region, and likely established in the North African refugium during the LGM; 2) that outbreaks in Northern Scandinavia are caused by a population that likely migrated along the coast of Norway from the British Isles following the retreat of glacial ice sheets after the LGM, and 3) that invasive populations in North America are the result of at least three separate introductions from geographically distinct source populations.

Real-time witness to formation of a hybrid zone between non-native winter moth and native Bruce spanworm

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Abstract: The European winter moth, Operophtera brumata (Lepidoptera: Geometridae), is an invasive species in North America which is known to hybridize with a related native species, Bruce spanworm, O. bruceata. We genotyped thousands of moths across a hybrid zone in New England using polymorphic microsatellite loci from 2007-2018. This period captured the time when the hybrid zone was settling on the landscape. This study is a unique glimpse at hybrid zone formation in nature and may provide insight into the impacts of hybridization between native and non-native species on biological invasions.

Functional characterization of odorant receptors in the spruce bark beetle Ips typographus and prediction of their ligand binding site

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Abstract: The European spruce bark beetle (Ips typographus L.) causes severe destruction of spruce (Picea abies) forests across large parts of Europe. Improved pest management is urgently needed, and one avenue towards this aim could be to target the odorant receptors (ORs), which are used by the beetles to find mates and hosts. Hence, we sequenced an antennal transcriptome, and identified 73 ORs of which 52 ORs were present as full-length sequences. Functional characterization of two of these ORs in HEK293 cells and Xenopus oocytes revealed highly selective responses to pheromone compounds that are used by several bark beetle species in chemical communication. Homology modelling and ligand docking simulations were performed to predict the ligand binding sites of these ORs. Site-directed mutagenesis targeting two of the amino acid residues that were predicted to be central for the binding, abolished the response to pheromone, demonstrating a key functional role of these residues. The characterization of the two ORs and their putative ligand binding sites is an important first step towards OR-targeted control of bark beetles because these ORs can be screened for better agonists or antagonists, or be employed in biosensors for early detection of bark beetle infestations.

Food webs associated with epigeal predators in an integrated crop-livestock-forestry system in Brazil

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Abstract: We conducted a large-scale experiment manipulating vegetational diversity and evaluate the effects on the epigeal natural enemy community. We used molecular gut content analysis to determine what the most common predator species were consuming to determine how these predators might contribute to pest suppression. We tested four hypotheses: (1) the vegetationally diverse production system has higher predator species richness at higher abundance than the other systems; (2) the predator community composition of the diverse system will overlap the community composition of all of the other production systems; (3) the predators in the diverse system will have more prey and more herbivore prey than in the other systems; (4) the prey consumed in the diverse system will overlap the prey consumed in all of the other production systems. In addition, we describe a food web associated with 15 common predators in this study. We will discuss the implications of our findings.

Integrating adverse effect analysis into environmental risk assessment for exotic generalist arthropod biological control agents: a three-tiered framework

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Abstract: Environmental risk assessments (ERAs) are required before utilizing exotic arthropods for biological control (BC). Generalist arthropod BCAs (GABCAs) have been considered inherently risky and less used in classical biological control. To safely consider exotic GABCAs, an ERA must include methods for the analysis of potential effects. A panel of 47 experts from 14 countries discussed, in six online forums over 12 months, scientific criteria for an ERA for exotic GABCAs. Using four case studies, a three-tiered ERA comprising Scoping, Screening and Definitive Assessments was developed. In the Scoping Assessment, likelihood of establishment (for augmentative BC), and potential effect(s) are qualitatively assessed. If risks are identified, the Screening Assessment is conducted, in which 19 categories of effects (adverse and beneficial) are quantified. If a risk exceeds the proposed risk threshold in any of these categories, the analysis moves to the Definitive Assessment to identify potential non-target species in the respective category(ies). When at least one potential non-target species is at significant risk, long-term and indirect ecosystem risks must be quantified with actual data or the petition for release can be dismissed or withdrawn. The proposed ERA should contribute to the development of safe pathways for the use of low risk GABCAs.

A study case of invasion of Aleurocanthus camelliae cryptic species in Japan: Identification, symbionts infection, and wasp parasitism

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Abstract: Aleurocanthus camelliae (Camellia spiny whitefly) is an invasive whitefly pest of tea and is considered a cryptic species due to its similarity with Citrus spiny whitefly, A. spiniferus. Both species originated from China and were intercepted in Japan in 2004 and the early 1920s, respectively, and they were separated by host preference. Recently, A. camelliae which is predominantly parasitized Theaceae plants has been also detected in Netherland (2018), Italy (2020), and Indonesia (2020). This cryptic species is divided at least into 3 morphospecies, i.e., A. camelliae, consisting of 3 haplotypes; A. spiniferus, consisting of 2 haplogroups; and A. woglumi. Due to morphologically indistinctive, we then characterized the detection of cryptic species by the symbionts infection. This study revealed the novel cryptic species of Japan on Eurya japonica (Theaceae) which harbor different strains of Portiera, the primary symbiont of whiteflies. Moreover, unlike A. camelliae which is highly Wolbachia infected whiteflies, whiteflies belonging to A. spiniferus morphospecies tend to be Wolbachia uninfected populations. In addition, a new record of Eretmocerus wasp in A. camelliae has been discovered. Using a multiplex PCR, the existence of parasitism was confirmed in January 2020. The bacterial symbiont-based detection of A. camelliae cryptic species and new potential parasitoid wasp are discussed.

Role of ovipositor and sensory cues in short-range host selection by Drosophila suzukii

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Abstract: Drosophila suzukii is an invasive pest native to Eastern Asia able to lay eggs on undamaged ripening fruits, rather than in fermenting substrates like most other Drosophila species. This ability is due to the exploitation of visual, olfactory, and tactile cues for the location of the best oviposition site and to the presence of an enlarged and serrated ovipositor. In a series of studies, we explored the sensory system of the ovipositor of D. suzukii, comparing it to that of closely related species, and elucidated some behavioral and chemical aspects of short-range site selection of this species. We first sequenced the ovipositor transcriptome in D. suzukii and in three Drosophila species characterised by progressive changes in oviposition behaviour and revealed a set of gustatory and ionotropic receptors conserved among the four Drosophila species. We therefore tested the occurrence of chemosensory neurons in D. suzukii ovipositor using an anti-horseradish peroxidase antibody to target presence and shape of neuronal structures: results indicate that neurons associated with D. suzukii ovipositor spines have mechanosensory function. Further analysis of morphology and ultrastructure support the hypothesis that these structures are involved in mechanoreception and are likely used to test the stiffness of substrates. We also demonstrated that D. suzukii preferred to lay eggs on already egg-infested fruits instead of artificially-pierced or intact ones. Video recordings of ovipositional behaviour evidenced the release of an anal secretion over the fruit surface near the oviposition site. Choice and non-choice tests indicated oviposition preference towards egg-infested fruits, suggesting a role of the released liquid as a marking pheromone attracting multiple ovipositions. The knowledge gained with these studies may accelerate establishment of control strategies based on the interference and disruption of the processes involved in D. suzukii egg-laying site selection.

Multifaceted sublethal effects of insecticide microdoses on the orientation of the spotted wing Drosophila

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Abstract: Exposure to sublethal doses of insecticides can result in various physiological and behavioral traits of the exposed organisms. Insect pests have evolved fine mechanisms for host detection and among these the orientation towards host-borne volatiles are of paramount importance for pest reproduction and thus for yield losses. The spotted wing drosophila (SWD), Drosophila suzukii (Matsumura) (Diptera: Drosophilidae), is a devastating invasive pest of soft-skinned fruits. In this context, we first characterized the baseline toxicity of four neurotoxic insecticides through ingestion during larval development and via adult residual exposure. Then, the estimated lethal doses 10% (LD10) for the four chemicals were used to carry out a multilevel analysis of their sublethal effects on orientation behavior. Olfactometer, electroantennographic (EAG) and olfaction gene expression experiments were carried out on insects survived to the exposure. The resulting LD10s proved to be extremely lower than insecticide label doses and, more interestingly, the exposure to these microdoses strongly impaired the host location capacity in exposed flies. The results strongly support the need to comprehensively study the potential sublethal effects of agrochemicals, even at very low doses, on key biological traits.

Exploitation of population dynamics and chemical communication for integrated management of Drosophila suzukii

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Abstract: Drosophila suzukii (Matsumura), also known as Spotted Wing Drosophila (SWD), is a vinegar fly belonging to the Diptera order and Drosophilidae family. It is native to South East Asia and it has recently invaded western countries, affecting fruit production. Because of its rapid spread, the economic impact has been huge in most of the invaded countries. SWD infestations generate direct and indirect economic impacts, through yield losses, shorter shelf life of infested fruits, extra labour and costs for monitoring, field sanitation and post-harvest handling. For all these reasons, deeper information about the biology, ecology, chemical-ecology, genetics and behavior are necessary to better manage the species. In the last four years a lot of work was developed by us to contribute towards a better understanding of these topics, in order to find a scientifically supported and effective solution. In particular, our work focused on three aspects: 1) understand the spread and therefore the capacity of movement of SWD in large and small scale, 2) study the chemical aspects of short-range ovipositional site selection within the context of D. suzukii reproductive biology and 3) manipulate the egg-laying behavior thanks to an innovative technology, which is able to attract and arrest flies on alternative substrate by therefore, reducing the egg-infestation level in the crop. Understanding seasonal and daily migrations SWD populations is fundamental, since it could help farmers and industries decide where to apply specific management techniques. We found that abiotic factors, such as temperature and humidity, as the food availability, play a fundamental role in the environmental distribution of the species. The finding of a consistent seasonal and daily movement from the crop to the surrounding vegetation and towards areas with different altitude, recorded by our works, may lead to use treatments, especially chemical, in precise periods of the year and in defined zones on the border of the crop. The dispersal movement of SWD is also highly dependent and affected by the odors emitted by conspecific individuals, by other insect species and by plants. By performing a study on the anal secretions release after oviposition by SWD females, we were able to identify some specific volatiles which attract, arrest SWD flies and stimulate the release of eggs to the already egg-infested berries. Using these knowledges, we identify specific plants which produce the same volatiles. By mixing these plant extracts with more ingredients, we developed a new technology able to arrest SWD flies on an alternative matrix substrate and reduce the infestation level on berries. This promising approach was tested in laboratory and open field condition on blueberry, cherry, strawberry, cranberry and grapes. Taken together, the results contribute to enhance our understanding of SWD biology, ecology and chemical and to expand integrated pest management options.

Innovation in solitary bees is driven by exploration, shyness and activity levels

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Abstract: Behavioural innovation is widely considered an important mechanism by which animals respond to novel environmental challenges, including those induced by human activities. Despite its functional and ecological relevance, much of our current understanding of the innovation process comes from studies in vertebrates. Understanding innovation processes in insects has lagged behind partly because they are not perceived to have the cognitive machinery required to innovate. This perception is however challenged by recent evidence demonstrating sophisticated cognitive capabilities in insects despite their small brains. Here, we study the innovation capacity of a solitary bee (Osmia cornuta) in the laboratory by exposing naïve individuals to an obstacle removal task. We also studied the underlying cognitive and non-cognitive mechanisms through a battery of experimental tests designed to measure learning, exploration, shyness and activity levels. We found that solitary bees can innovate, with 11 of 29 individuals (38%) being able to solve a new task consisting in lifting a lid to reach a reward. The propensity to innovate was uncorrelated with learning capacities, but increased with exploration, boldness and activity. These results provide solid evidence that non-social insects can innovate, and highlight the importance of interpreting innovation in the light of non-cognitive processes.

The clades of the Palaearctic Hydrobius fuscipes species group – chromosomes and morphology

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Abstract: DNA analysis of Hydrobius fuscipes (L.). sensu lato by Fossen et al. (2016) has demonstrated the existence of at least nine distinct clades, some of which have already been given names as separate species.
Chromosomally Hydrobius clades are all very similar, but with some useful distinctions. Clade 1 has a distinctly longer X chromosome than the others, Clade 3 has distinct centromeric C-bands, and H. subrotundus and Clade 7 have interstitial satellite C-bands. Hydrobius chromosomes are difficult to work with, with demonstration of the C-bands tricky. The related Limnoxenus niger has strong centromeric C-bands, but Limnohydrobius convexus has delicate C-bands like Hydrobius but an X-chromosome even longer than that of Clade 1.
Morphologically the Hydrobius taxa divide into a H. arcticus-rottenbergii group in which the aedeagus has the parameres relatively shorter and distinctly incurved apically, and the others in which the parameres are more attenuate and less incurved. Members of this group, with the exception of H. arcticus and the Chinese H. pui, usually have the large trichobothria-bearing punctures on elytral interstices 3 and 5 placed in striae 3 and 5 in the basal sections of the interstices but, as has been pointed out, this character can vary. The H. arcticus-rottenbergii group are all placed in the same (large) section of Fossen et al.'s cladograms, but the others are scattered round the edge. Apart from the aedeagal differences, there are indications that the form of the mentum, especially in males, may be helpful in recognising various clades, and the arrangement of the elytral striae apically also appears promising.
Work led by D. T. Bilton suggests that H. fuscipes and H. subrotundus have very different thermal tolerance ranges. This work proceeds slowly as it is dependant on accurately named (by DNA or in some cases chromosomes) material.

Effects of tree richness, structural variation and leaf traits on herbivory and predation in different local scales in a subtropical BEF-experiment

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Abstract: Biodiversity loss is one of the most urgent challenges in the world affecting ecosystem functions and ecosystem services. BEF-China is the world's largest BEF (Biodiversity-Ecosystem Functioning) experiment, located in subtropical China. As part of the research consortium TreeDi "Tree Diversity Interactions: The role of tree-tree interactions in local neighborhoods in Chinese subtropical forests", we focused on how tree richness, plant nutritional quality and tree structure affect the herbivory and predation pressure in different spatial-scales in close neighborhoods, going from tree with its immediate neighbors to plot level (~26 x 26 m). Understanding how forest structure and leaf quality affect trophic interactions in relation to tree diversity is important as higher trophic level interactions can strongly affect the structuring and functioning of species-rich forest ecosystems. Our results showed that forest structure and leaf quality affected herbivory and predation, but the effects varied between spatial scales and tree richness levels. Scale dependence of forest structure affected the responses between predator groups (arthropods, birds and mammals). Furthermore, the predator group responses varied in response to tree apparency and vegetation density. The results offer insight into how biodiversity loss of producers affects higher trophic levels in relation to other main features of forest stands.

Cattle intensification as a potential driver of dung beetle diversity and ecosystem services loss: a global experiment

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Abstract: Biodiversity provides ecosystem services that sustain human life. However, anthropic disturbance is affecting negatively the diversity, functioning and provisioning of these ecosystem services. One of the main drivers of this effect is land-use intensification, which is an important factor in pastures used for livestock breeding. Dung beetles are important in removing waste on these ecosystems and contributing to the cycling of nutrients. However, their action could be hampered by land-use intensification, impacting negatively their diversity, functional structure, ecosystem services they provide and causing potential local extinctions. In this study we conducted a global multi-site experiment in 24 countries to understand the effect of cattle density on dung beetle diversity and dung removal. For each sampling site selected an area with extensive and another with intensive cattle use, and in each of them we quantified dung removal through an experimental approach, sampled dung beetle's diversity, and quantified functional diversity (FD). Pairwise comparisons were used to evaluate differences in diversity and dung removal of intensive and extensive areas. Structural equation models (SEM) were performed for disentangling the relative importance of cattle intensification, climate, and diversity on dung removal rates. Cattle intensification has an overall negative effect on species richness but not on abundance, evenness, FD, and dung removal. A SEM model, using cow density as a proxy of cattle intensification, shows a direct negative effect of intensification on dung diversity and dung removal. However, in the SEM models built separately for extensive and intensive sites, the main drivers are different; for extensive sites richness and climate affects dung removal, while for intensive sites only abundance drives dung removal. These results highlight the negative impact of land-use intensification on biodiversity and ecosystem services, and the potential loss of biodiversity in a global perspective.

Evolution of diapause across space and time in the invasive mosquito, Aedes albopictus

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Abstract: Invasive species that spread rapidly across broad geographic ranges represent an outstanding opportunity to investigate the temporal dynamics and selective targets of rapid climatic adaptation. The invasive and medically important mosquito, Aedes albopictus, invaded the US in 1985 and rapidly spread across ca. 15 degrees of latitude. Comparison of critical photoperiod (CPP) among populations across latitudinal gradients in both the native (Japan) and invasive (US) ranges has been conducted across 30 years at three time points (3, 23 and 33 years post-invasion). These data are provide a unique spatial and temporal record to investigate the dynamics of rapid adaptive evolution and responses to ongoing global climate change. Additional traits related to climatic adaptation in North American Ae. albopictus, including traits expressed during diapause and traits presumably unrelated to diapause (chill coma recovery), have also been evaluated. Taken together, the results of these experiments demonstrate multiple components of rapid adaptation to climatic variation across the invasive North American range of Ae. albopictus. Mechanistic studies are being performed to determine the underlying molecular and physiological basis of these adaptive changes.

Biological Control of Tuta absoluta from a Mediterranean Prespective

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Abstract: The South American tomato moth, Tuta absoluta (Meyrick) (Lepidoptera:Gelechiidae) is a pest native to South America that produces significant damage to tomato crops and was first detected in Europe in late 2006 in the Mediterranean coastal area of Spain. Soon after the invasion, the Integrated Pest Management (IPM) programs based on biological control shown to be useful for the control of this pest. These programs were based either in the conservation or in augmentative releases of the zoophytophagous predatory mirid bugs Macrolophus pygmaeus (Rambur) and Nesidiocoris tenuis Reuter (Hemiptera: Miridae). They are voracious T. absoluta egg predators, but have low efficacy feeding on larvae. Currently, their use is a cornerstone in the IPM programs, both in greenhouse and open field crops.

More than 50 species of T. absoluta parasitoid wasps have been identified to date attacking T. absoluta in the Mediterranean basin, being by far the largest group the wasps that attack larvae followed by the ones that attack eggs. Among larval parasitoids, only few were considered as effective potential biocontrol agents. The most extensively studied has been Necremnus tutae Ribes & Bernardo (Hymenoptera: Eulophidae), first identified as N. nr. artynes (Walker). Although currently it is not commercially available, natural populations of this parasitoid effectively contribute to control T. absoluta on tomatoes crops in Spain and other Mediterranean countries. On the contrary, egg parasitoids are scarce, and only Trichogramma achaeae (Nagaraja & Nagarkatti) (Hymenoptera: Trichogrammatidae) has been considered for inoculations in greenhouse crops as a complementary tool for T. absoluta control.

In Mediterranean conditions, conservation of natural enemies seem to play an important role in T. absoluta control. Laboratory and field studies have demonstrated the positive influence of some selected insectary plants to improve the fitness of T. absoluta natural enemies and to boost their populations on the crops. Therefore, the use of ecological infrastructures such as flower margins with selected plants has been considered as a strategy to enhance predators and parasitoid populations near tomato crops.

Diversity of aphid parasitoids in East Africa and the implications for biological control

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Abstract: Aphids, particularly Aphis fabae, are a major pest of common bean (Phaseolus vulgaris) which is an important food crop and dietary protein source among East Africa smallholders. We investigated the potential of natural enemies, particularly parasitoids, to control this pest and identified interventions that could be used to conserve or augment populations of these natural enemies. Parasitoids of A. fabae were monitored using sentinel plants, sweep netting and sticky traps at small holder bean farms in Kenya, Tanzania and Malawi. They were identified using DNA barcoding and the most common primary parasitoids were selected for further study. There were found to be differences in the identity of primary and secondary parasitoids between the three countries investigated, with the most common primary parasitoids being Aphidius colemani and Lysiphlebus testaceipes, but the latter being found primarily in Malawi. Additionally, the most abundant secondary parasitoid was a Pachyneuron sp., which was primarily found in Tanzania. Fields with high plant-diversity margins yielded higher numbers of parasitoids compared to plant-depauperate margins. These results suggest that there is potential to augment the population of primary parasitoids on smallholder bean farms by encouraging plant species-rich field margins containing floral resource plants; however, management needs to be tailored to favor the key primary parasitoids in each region without disproportionately benefitting pest insects or secondary parasitoids.

Not just more plants, but the right ones: supporting ecosystem services on African smallholder farms

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Abstract: Plant-diverse field margins are commonly promoted in temperate countries to support beneficial insect communities for pollination and natural pest regulation. The benefits on tropical smallholder farms are less clear. Here we report the results of biodiversity surveys from smallholder bean farms, and the relationship between field margin richness, natural enemy abundance, pollinator activity, and ultimately, yield. Botanical surveys, pan-trapping and walked transects were carried out in Tanzania and Malawi on smallholder bean farms.

A range of natural enemies are present on smallholder farms in both countries, using various native- and non-native plant species in margins. While botanical richness was linked to beneficial insect activity, this related to particular types of plants - including trees and native species. Many plants showing high interaction rates with natural enemies had other benefits to farms, such as sources of medicines or pesticides, livestock fodder, firewood or vegetables. Fields with plant- and tree-rich margins showed significant higher yields than fields without. The findings indicate that non-crop botanical diversity can confer multiple benefits and is a valid component of an ecological intensification system for these farms.

Perspectives for using RNA interfering approach to control the invasive pest of beehives Aethina tumida

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Abstract: The small hive beetle (SHB) Aethina tumida is a parasitic beetle of Apis mellifera, native to South Africa which damages preferably commercial apiaries. Its presence impairs the production of honey and wax and undermines the integrity of the colony. This pest was included in the OIE list of bee pathogens with the goal of preventing its further spread. SHB is also among the diseases of interest of the EU (Regulation EC 2016/429) since it was found in 2014 in Calabria region (southern Italy) where it continues to be present. The RNA-interfering (RNAi) technique exploits a natural mechanism present in eukariotic organisms to lead to the loss of functionality of a gene. A first attempt to use RNAi to control SHB was made by Powell et al. (2016, doi.org/10.1002/ps.4365) who found that oral delivery of dsRNA against V-ATPase subunit A in solutions resulted in 50% larval mortality, however gene suppression could not be verified. We tested v-ATPase and ribosomial protein 13 dsRNA designed to silence essential genes of A. tumida. We amplified regions of four target genes with primers containing the T7 promoter, using PCR products for in vitro transcription. In vitro bioassays were setup to evaluate their potential as biological insecticides.

An autonomous system for the detection and counting of the malaria mosquitoes larvae in natural populations

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Abstract: Malaria is the cause of death for about half of the million people every year and Anopheles mosquitoes are the exclusive vectors of the malaria parasite. Monitoring of the natural populations of Anopheles mosquitoes provides essential data for effective malaria control. The density of malaria mosquitoes larvae is an important indicator of the possible outbreaks of diseases and the effectiveness of insecticide treatment. All traditional methods of mosquitoes density estimation are time and effort consuming, thus new autonomous and remote approaches became more attractive.

In our work, we present an autonomous system for the detection and counting of malaria mosquito larvae in natural populations. The system consists of two major components: 1) a device (Figure 1), which scans the surface of the natural water reservoir and sends the image to the remote drive and 2) a software, which recognizes larvae on the images and estimates the number of the larvae. The device is based on a 64-bit mini-computer Raspberry Pi 3b with a Raspberry v2.0 camera module. The images with 2592x1954 pixels resolution are transmitted by a high-speed modem according to UMTS-2100 (3G) standard. The resolution of the images is high enough to identify a small object within a few millimeters in size. Li-ion batteries and solar modules provide up to 2800 hours of autonomous work of this device at above zero degrees. The modules were mounted on the upper part of the aluminum framework in a truncated pyramidal shape. Cylindrical polystyrene floats were installed on the corners of the device's base to keep the device on the water. A white screen was mounted on the underwater part of the device in order to provide a contrasting background for the living objects.

The Anopheles larvae have distinguishable among the other objects patterns of swimming on the water surface, which is a useful feature for neural network training. Faster R-CNN with ResNet feature was used as a pre-trained model for malaria mosquitoes larvae differentiation. Before the model training, the images were annotated by LabelImg. TFrecord file was used as an input file for the neural network training. The model trained with Intel Core i5 9400 OEM, until the logarithmic loss became to be 0.0002. The current model recognizes mosquito larvae with 82% accuracy.

The presented system is necessary for the monitoring of mosquito populations in the remote and poorly accessible for people regions. The area of monitoring is restricted only by 3G-net coverage. The depth of the study (the number of images per time unit) can be adjusted depending on the aim. Therefore the distributed network of the devices presented here will be useful for real-time, remote and simultaneous evaluating of the mosquito population density in multiple locations where malaria control required.

Acknowledgments: This study was supported by the Tomsk State University competitiveness improvement program.

Management of Popillia japonica in Japan

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Abstract: Japanese beetle (Popillia japonica) is a serious pest of turf and ornamental plants in Japan. Japanese beetle larvae were collected in Hokkaido to discover insect pathogenic bacteria which were effective for beetle control. We isolated and identified novel Paenibacillus popilliae (Pp)strain from Japanese beetle larvae (Matsuki et al., 1997). The cry43Aa gene cloned from the isolated P. popilliae hime strain had insecticidal activity against Japanese beetle larvae. Also, we want to determine the whole genome sequence of P. popilliae strain (Iiyama et al., 2013). As a result, it was revealed that P. popilliae had no catalase gene, and that artificial culture could be performed by adding its activity. From Bacillus thuringiensis (Bt) collections in our laboratory, two Bt strains (SDS-502, BBT2-5) with insecticidal activity against Japanese beetle larvae and adults were found (Asano et al., 2003; Yamaguchi et al., 2008). The cry8Da gene has been cloned, and its insecticidal activity mechanism has been studied (Yamaguchi et al., 2013). We are promoting the development and commercialization of Bt and Pp strains as beetle pest control agents, and have developed a scarab-resistant turf grass by introducing the cry8Da gene.

An insect specific system for terrestrialization: eco-evo perspective on the occurrence of insects

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Abstract: Previously, we proposed a new hypothesis on the mechanisms by which insects adapted to terrestrial environments during their evolutionary history. This hypothesis is based on presence of a unique system for cuticle formation that is catalyzed by an insect-specific enzyme, laccase. The main function of laccase is the oxidation of catecholamines, the products of which are highly reactive and possibly mediate cross-linking between cuticular components (proteins and chitin fibers). The laccase-mediated system does not require high amounts of calcium ions, in contrast to the cuticle-hardening system of crustaceans, the closest relatives of insects. Crustaceans are dominant animals in marine environments and known to be morphologically the most diverse among any taxa. This diversity is often compared with that of insects, and both insects and crustaceans can be characterized by their high potential to adapt to various environments by diversification, although their main habitats are terrestrial and marine environments, respectively. Our idea is that the systems for cuticle hardening are one of the most important factors affecting their distributions in these habitats. In contrast to the abundance of calcium ions in sea water, calcium ion content is restricted on land or in fresh water. Such a situation can be exemplified by the behavior of crustaceans: formation of gastroliths with calcium ions from the old cuticles before molting of crayfishes, or consumption of exuviae for recycling of calcium ions in the old cuticles by isopods. Alternatively, by evolving the laccase-mediated system, insects can harden their cuticles without the high requirement of calcium ions. In the process of terrestrialization, insects may have extended their distributions far from the seashores to inland areas more freely than that by crustaceans. Noteworthy, the laccase-mediated system can be an adaptive trait to utilize molecular oxygen from the atmosphere, since this system utilizes molecular oxygen as the electron acceptor from substrates. The content of molecular oxygen in air is much higher (30 fold) than that in water due to its low solubility, and this level in the evolutionary era had already reached the current value. Cuticles that are hardened without biomineralization are less rigid although they are light-weight, which may be a contributing factor towards insects becoming the first to fly in the kingdom Animalia. With the ability of flight and the high diversification potential, insects may have extended their distributions by creating new and open niches that other animals could not easily access. Currently, insects are one of the most successful organisms with their large biomass and high impacts on eco-systems. However, it seems difficult for them to re-adapt completely to marine environments where the insect-specific cuticles are not necessarily advantageous.

The functions of a chitin-binding protein in flight and jumping of insects

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Abstract: Insects have evolved various styles of locomotions such as jumping and flying, both of which are rapid and efficient. With regard to the mechanical properties of body structures enabling insects to jump and fly, previous studies have suggested the involvement of an insect specific protein, Resilin. Resilin is a chitin-binding protein that was originally found as a component of elastic matrices in wing hinges of dragonflies or in the leg joints of grasshoppers. Resilin is composed of three regions from the N-terminus; 1) repeats of elastic motifs ((PxxxYGAP)s), 2) chitin binding motif, and 3) repeats of another elastic motifs ((GYxSGxPG)s). With the elastic and resilient properties, Resilin-matrices may adsorb mechanical resistance from high frequency of wing flapping, or may storage mechanical energy for jumping like spring. Resilin molecule has high content of tyrosine residues that are used for polymerization of Resilin molecules through formation of inter-molecular cross-links mediated by di-tyrosines or tri-tyrosines. Since the first finding, there have been many studies on Resilin. However, many of the researches were based on approaches of material science for application of Resilin molecules to produce new biomaterials. Correlations between mechanical properties of Resilin-matrices and their localizations in joint parts of insect bodies have been well explained, but in vivo functions of Resilin gene or molecular process of resilin polymerization have not yet been well examined in biological contexts. Here, we focus on the functions of the gene for Resilin in the fruit fly, Drosophila melanogaster, as an ideal model for the genetic research of Resilin. The gene (DmResilin) is expressed throughout the developmental stages, but in late pupal stages the expression is very strong, indicating that the protein is mainly used for making adult body. DmResilin knocked-down flies cannot move their wings at all and therefore they cannot fly. In addition, the jumping performance (distance and velocity) of the KD flies is worse than that of the controls. DmResilin mutant flies that were generated by CRISPR-Cas9 system show the same phenotypes as KD flies. These results indicate that DmResilin have indispensable roles in both jumping and flying, possibly with the elastic-resilient properties of matrices produced from the gene products. We also checked the sites of DmResilin expressions by reporter gene expression using Resilin promoter-Gal4 line. The GFP signals can be seen in the wing hinges at the late pupal stage, which is consistent with the previous observations of other insect species. In western analyses, the protein signal is gradually weakened after eclosion to adults, suggesting that in adult stages Resilin molecules become insoluble after polymerization via formation of di-tyrosines or tri-tyrosines.

Potential role of blood microRNAs in mosquito-virus interactions

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Abstract: microRNAs (miRNAs) are small non-coding RNAs of about 22 nt in length. They play important roles in regulation of gene expression at the post-transcriptional level in various biological processes. Blood feeding is a major event in the life cycle of mosquitoes essential for mosquitoes' egg development and reproduction with profound effects on their physiology and gene expression. Intake of blood concurrently exposes mosquitoes to a range of vertebrate-derived blood factors such as hemoglobin, complement, insulin, and pathogen-derived factors, which have roles in modifying mosquito physiology and immune responses. Studies have shown that miRNAs are present in large numbers in animal host bloods. In a recent study, we have been investigating the potential role of human miRNAs that are abundantly found in the blood meal taken by Aedes aegypti mosquitoes on replication of dengue virus. Our data analyses and experimental results suggest miRNAs present in vertebrate bloods are stable post-blood feeding, pass through the midgut barrier, and disseminate to mosquito tissues. Preliminary results also suggest that they may potentially target mosquito genes that are involved in immunity and development.

Towards the use of Wolbachia in area-wide control programs for Haematobia spp

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Abstract: Haematobia spp. are obligate haematophagous flies and major economic pests of cattle that have proven to be strongly invasive in both the northern and southern hemispheres. Horn flies (Haematobia irritans) were introduced from Europe and spread through North America in the late 1800s and more recently through most of the major cattle producing areas in South America. Buffalo flies (Haematobia exigua), very closely related to horn flies, spread from South East Asia to Oceania and are continuing to expand their range in Australia. Regulated cattle movements and compulsory chemical treatments have proven unsuccessful in preventing the spread of these flies. We are investigating the feasibility of area-wide control of H. exigua, utilising the intracellular maternally transmitted bacterium Wolbachia. We have successfully infected H. irritans cell lines with the wMel, wMelPop and wAlbB strains of Wolbachia and passaged them through more than 50 generations to adapt them to the intracellular environment of Haematobia. Investigation of different microinjection techniques indicated that pupal or adult injection is more suitable for transinfection of Haematobia spp. than more commonly used embryonic microinjection. When injected into H. exigua pupae or female flies all three strains of cell line-adapted Wolbachia established widespread somatic infections, with transmission to F1 generations in a number of instances. Wolbachia infection was associated with fitness effects including reduced adult lifespan, decreased and delayed eclosion from pupae and reduced fecundity. These outcomes suggest significant potential for the use of Wolbachia in control programs for H. exigua, which are not naturally infected with Wolbachia, as well as for H. irritans where natural infection is with a strain of Wolbachia that is genetically distinct from the strains used in our studies.

Age-stage, two-sex life history and parasitism rate of Diadegma insulare against Plutella xylostella reared on different cruciferous hosts

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Abstract: Diamondback moth, Plutella xylostella, is a serious pest of cruciferous crop in Pakistan. This study is carried out to get better knowledge related to predator-prey relationship and compare predation rates of parasitoid, Diadegma insulare on different brassica genotypes. The life history data and predation rate data of D. insulare, fed on P. xylostella reared on different brassica crop genotypes were collected at 25 °C in the laboratory. The data were analyzed based on age-stage, two-sex life table theory to take both sexes and different developmental stage into consideration. The intrinsic rate of increase for D. insulare fed on P. xylostella reared on cauliflower, broccoli, canola, cabbage, chinese cabbage and Pakchoi was 0.1971 d-1, 0.2189 d-1, 0.1868 d-1, 0.1631 d-1, 0.2024 d-1 and 0.1959 d-1, respectively. The highest net reproductive rate was observed on broccoli as 22.35 offspring while highest mean generation time for D. insulare was observed on P. xylostella reared on pak choi as 14.526 d. The net parasitism rate for D. insulare was highest on broccoli as 22.35, followed by 17.23, 16.51, 13.53, 12.42 and 9.22 P. xylostella reared on, pak choi, chinese cabbage, cauliflower, canola and cabbage, respectively. Finite predation rate was comparatively higher (0.2814) on broccoli, while it was the lowest (0.2114) on cabbage. Due to age-stage, two-sex life table studies and incorporation of finite parasitism rate, we were able to explore that although D. insulare successfully completed life cycle on P. xylostella reared on all cruciferous crops, however the parasitoid showed better fitness on the herbivore consuming broccoli leaves which is very important cash vegetable in Punjab, Pakistan.

Age-stage, two-sex life history and predation rate of Diadegma insulare fed on Plutella xylostella reared on different brassica genotypes

Authors: Asif Aziz Muhammad[1], -ul-Mohsin Ata[2], Ahmad Hafiz Ishfaq[1] and Khaliq Sobia[1], [1]Department of Entomology Faculty of Food Crop and Food sciences PMAS-AAUR, Pakistan, [2]Professor Department of Entomology Pir Mehr Ali Shah Arid Agriculture University Rawalpindi, Pakistan

Abstract: Diamondback moth, Plutella xylostella, is a serious pest of cruciferous crop in Pakistan. This study is carried out to get better knowledge related to predator-prey relationship and compare predation rates of parasitoid, Diadegma insulare on different brassica genotypes. The life history data and predation rate data of D. insulare, fed on P. xylostella reared on different brassica crop genotypes were collected at 25 °C in the laboratory. The data were analyzed based on age-stage, two-sex life table theory to take both sexes and different developmental stage into consideration. The intrinsic rate of increase for D. insulare fed on P. xylostella reared on cauliflower, broccoli, canola, cabbage, chinese cabbage and Pakchoi was 0.1792 d-1, 0.1970 d-1, 0.1698 d-1, 0.14711 d-1, 0.1864 d-1 and 0.1796 d-1, respectively. The highest net reproductive rate was observed on broccoli as 19.83 offspring while highest mean generation time for D. insulare was observed on P. xylostella reared on Pakchoi as 15.83 d. The net predation rate for D. insulare was highest on broccoli as 22.35 offsprings, followed by 17.23, 16.51, 13.53, 12.42 and 9.22 offsprings of P. xylostella reared on, pakchoi, chinese cabbage, cauliflower, canola and cabbage respectively. Finite predation rate was highest (0.2814) on broccoli, while it was lowest (0.2114) on cabbage. The results show D. insulare to be the potential biological control agent of P. xylostella in integrated pest management and the life history parameters of D. insulare can be used to predict its biological potential and develop models for the population dynamics of D. insulare.

Keywords: Life table, age-stage, two-sex, Plutella xylostella, Diadegma insulare, predation rate, intrinsic rate

Saving the wine one parasitoid at a time: analysis of Goniozus jacintae as a potential biocontrol agent for the light brown apple moth (Epiphyas postvittana)

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Abstract: Before releasing a biocontrol agent into the field, we should first understand how it interacts with its target and other environmental components, including competitors.

We conducted an array of experiments to explore the behavioural ecology of the parasitoid wasp Goniozus jacintae Farrugia (Hymenoptera: Bethylidae), to develop the understanding of the parasitoid as a potential biocontrol agent for the light brown apple moth (LBAM), Epiphyas postvittana (Walker) (Lepidoptera: Tortricidae), a pest of grapevine, Vitis vinifera L. (Vitaceae), and other crops in Australia.

How does the parasitoid find a host? A wind tunnel experiment found host-stage dependent foraging behaviour in G. jacintae: timing, frequency, and duration of foraging behaviours of G. jacintae varied among host instars.

How does the parasitoid select its host when faced with competition? We tested the host discrimination ability of G. jacintae when presented with hosts of varying quality: unparasitised or parasitised by an allospecific. Discrimination ability of G. jacintae was influenced by both the order in which different hosts types were presented and time since parasitisation.

How does the parasitoid utilise selected hosts? We observed the egg laying behaviour of G. jacintae when presented with different sized hosts. Average clutch size increased with bigger host instars.

Evaluation of a Greek diatomaceous earth and a zeolite for stored-product insect control and techniques that maximize their insecticidal efficacy

Authors: Athanassiou Christos, University of Thessaly, Greece

Abstract: In the present study, seven series of laboratory bioassays were conducted to evaluate the insecticidal efficacy and the abiotic factors that can alter the efficacy of one diatomaceous earth (DE) and one zeolite, originating from natural deposits of Greece. The DE rocks were treated in different ways (differences in grinding, sieving, diatom enrichment, powder granulometry), leading to five DE types, with different technical characteristics. In the first series, bioassays were conducted to evaluate the insecticidal efficacy of all DE types and the zeolite, when applied in organic soft wheat at different doses, against major stored-product insects, i.e. Tribolium castaneum, Tribolium confusum, Sitophilus oryzae, Rhyzopertha dominica, Cryptolestes ferrugineus and Oryzaephilus surinamensis. Then, bioassays were performed to evaluate the insecticidal properties of the DE formulations and zeolite for T. confusum, S. oryzae and R. dominica in different cereals. At the same time, the zeolite was tested also in legumes that were infested with the beetle Callosobruchus maculatus. For the two most effective DE types, the effect of temperature and relative humidity were evaluated in a third series of experiments. Separate bioassays were made in all combinations of two temperature levels and two levels of relative humidity, for S. oryzae and R. dominica. Bioassays on cement and steel surfaces also took place for these two DE types and for the zeolite, in order to evaluate their residual insecticidal activity. Finally, we examined the effect of all formulations to the bulk density of soft and durum wheat, rice and maize. Based on our results, there were significant differences in the insecticidal efficacy of the various DE types tested when applied on wheat. We consider that these differences are due to the different mechanical treatment of the DE, resulting in the presence of broken diatoms in the two most efficient DE types, as opposed to the whole diatoms found in the rest of the DE types, as well as the smaller size of the powder granules. Also, there were noticeable variations among different grains. None of the DE or zeolite formulations showed any significant insecticidal effects on maize, rice and barley compared to wheat. The increase of the relative humidity adversely affected the effectiveness of the DE formulations. On the contrary, zeolite appears to be unaffected by relative humidity fluctuations. DE formulations and zeolite appeared to be very effective for their use as insecticides on cement and steel surfaces. Surprisingly, small doses of some DE types, increased the bulk density of all the tested cereals, while the higher doses did not have any effect in it. In contrast, the most effective types of DE show an increase in bulk density with increasing dose. Overall, our data clearly indicate that these specific Greek deposits of both DE and zeolite, have considerable insecticidal properties, especially when specific techniques applied in them.

Susceptibility of insect meals to insect infestations during storage: The case of Tenebrio molitor and Alphitobius diaperinus larvae meal

Authors: Athanassiou Christos[2], Rumbos Christos[1] and Rigopoulou Marianna[1],

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Abstract: Although still in the early stages, the insect protein sector is expected to rapidly grow within the next few years. The number of companies doing business on insects as a nutrient source is increasing globally, whereas insect meal production is expected to further rise in the coming years. As with all agricultural commodities, insect meals may be vulnerable to infestations by stored-product insects during storage. However, information on the susceptibility of insect meals to infestations by storage insects is rather limited. To fill this gap, in the present study we investigated the susceptibility of substrates based on insect meals made of the yellow mealworm, Tenebrio molitor (Coleoptera: Tenebrionidae) or the lesser mealworm Alphitobius diaperinus (Coleoptera: Tenebrionidae) larvae to major stored-product insects. Both T. molitor and A. diaperinus are promising insect species for industrial utilization and commercial large-scale production. Indicatively, both species are allowed to be used for the production of insect meals as aquafeed ingredient in Europe. In laboratory bioassays, we studied the population growth of major storage insects, such as the confused flour beetle, Tribolium confusum (Coleoptera: Tenebrionidae) and the khapra beetle, Trogoderma granarium (Coleoptera: Dermestidae) on insect meals made of T. molitor or A. diaperinus larvae, as well as on substrates based on these insect meals with different percentages of wheat bran (0, 25, 50, 75, 90, 95 and 100%). Based on our results, T. molitor can infest 100% T. molitor and A. diaperinus meal and develop significant populations on these substrates. The same counts for T. confusum on 100% T. molitor meal. However, the growth and development of both species on 100% insect meal was slower in comparison to the respective growth on substrates with wheat bran. In contrast, other insect species, such as A. diaperinus and T. granarium did not manage to infest 100% T. molitor meal, whereas both species exhibited poor growth on substrates with high percentage of insect meal. To conclude, the results of our study show the susceptibility of T. molitor and A. diaperinus meals to infestations by major stored-product insects.

This work was supported by a postdoctoral scholarship program (Acronym: FISHECT, Project number: 5394.02.13) implemented by University of Thessaly and funded by Stavros Niarchos Foundation.

Digitizing phosphine to manage stored product insect resistance to phosphine: the paradox of the “sweet spot”

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Abstract: We used sensing devices to monitor spatio-temporal distribution of phosphine gas in various types of commercial facilities and commodities. Overall, more than 100 “real-world” fumigations were monitored, in facilities ranging from ships to flourmills and containers and commodities ranging from grains and flour to dried fruit and tobacco. Based on our results, distribution in large warehouses is not usually adequate for a satisfactory level of insect control and any application may not have even distribution of phosphine, which will lead to insect survival and resistance development. One of the critical factors is that some biotic and abiotic conditions may have different weight per fumigation, i.e. often temperature may have less important role in phosphine concentration and distribution of phosphine than humidity or the commodity that is to be fumigated. As a result, concentrations are either over- or underestimated, with the concomitant implications in the expected insect control. Nevertheless, longer exposure intervals, can greatly contribute to the increased mortality of the exposed insects, regardless of their resistance status. Longer exposures and, as an extent, better fumigations, can also be used to mitigate resistance of stored product insects to phosphine. In this context, best management practices in fumigation can totally control insects that are resistant to phosphine, in non-properly performed applications. In contrast with other types of insecticides, where concentration may be more important, duration of exposure to phosphine is much more critical than the concentration, and as such, longer exposures are needed, even if concentrations are not high, to control insect strains that are resistant to this gas. However, exposures at elevated concentrations are very likely to reveal the “sweet spot”, which is the increased survival with the increase of the concentration. This is particularly important as, in contrast with what was believed, resistance to phosphine can be built at high concentrations, just like the same phenomenon occurs in the low concentrations.

Population growth performance of South American tomato moth, Tuta absoluta (Meyrick) under different temperatures and CO2 concentrations

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Abstract: Understanding the effects of temperatures and increased carbon dioxide levels to the survival, development and fecundity of insects is important for pest management in future. In this context, the population growth performance of the South American Tomato moth, Tuta absoluta (Meyrick) (Lepidoptera: Gelechiidae) was evaluated at four constant temperatures (26, 28, 30 and 32°C), and in ambient and elevated CO2 concentrations (aCO2; 380 and eCO2; 550 ppm) in BOD incubation chambers providing at 75 ± 5% RH and a photoperiod of 14:10 (L: D) h. The life history raw data of the pest were analyzed based on the age-stage, two-sex life table theory which takes into account the stage differentiation, real survival, and the male population. The projected population growth potential of the pest increased as temperature increased; the highest population growth was obtained at 32°C. The population growth rates at aCO2 conditions were higher than those obtained at eCO2 conditions at all temperatures tested. The variability in population growth increased with increasing temperatures, and in general, CO2 conditions did not affect variability that is characteristic of population growth.

Role of warm blood in the reproductive output of blood feeding arthropods

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Abstract: Blood feeding arthropods experience a substantial thermal shock with each meal, which can be a 10-15?C increase within seconds depending on ambient and host temperatures. To prevent this thermal stress, a variety of mechanism exist, which includes evaporative cooling, counter-current heat exchange, and expression of heat shock proteins to prevent/repair damage. Previous studies have shown this heat response can be damaging, but the potential benefits of a warm bloodmeal remain unclear. Here, we used tsetse flies and soft ticks to evaluate if warm blood is critical for maximizing progeny output. We noted a delay in the production of eggs or larvae when vectors consumed a cool blood meal compared to those offered a warm bloodmeal. To determine the role of the warm bloodmeal, we measured transcript levels of a milk gland protein in tsetse flies following a cool, warm, or hot bloodmeal, which showed the highest expression when tsetse flies consumed warm blood. There were no differences in the size of larvae or number of eggs produced by tsetse flies or soft ticks, respectively, which suggests that bloodmeal temperature alters the timing of egg production but not overall fecundity. These studies suggest that warm bloodmeals reduce the time of each reproductive cycle and play a minor, yet critical, role in maximizing the reproductive output of blood feeding arthropods.

Tracing the post-mating molecular interactions between male and female in the viviparous Glossina morsitans

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Abstract: The identification of molecular pathways shaping short- and long-term mating-induced changes in Glossina morsitans females may reveal specific effector genes that contribute to the regulation of key reproductive processes such as ovulation and egg development in the uterus of this viviparous species.

Transcriptome analyses of the post-mating response in the reproductive tissues of Glossina females revealed dramatic changes in gene transcription. Different waves of transcriptional changes for different gene functions are specifically activated across a post mating interval of 72 hours. Ovaries, oviducts, spermathecae and uterus differentially contribute to the activation of these transcriptional waves. At 2-4 hours post mating, the upregulated genes code for functions primarily associated with biochemical binding, cell receptor/transport and cell signaling activities. The genes upregulated 72 hours post mating code for proteins primarily associated with structural and remodeling activities such as chitin binding, cuticular proteins, cell matrix components and protease activities. The association of these activities at these timepoints suggest that the 2-4 hours post-mating period is associated with reception and uptake of components of the male seminal secretions while the 72 hours post mating period is associated with developmental changes and remodeling of reproductive tract-associated tissues.

These data reveal interspecific differences with Drosophila and provide knowledge on the components of post-mating molecular targets of manipulation for the control of reproduction of this vector of trypanosomiasis in Africa.

Understanding the Post Mating Response in Tsetse – Characterization of Mating Associated Structural and Biochemical Changes in the Female Reproductive Tract

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Abstract: The post-mating response (PMR) in tsetse flies causes female flies to become refractory to mating, stimulates ovulation and results in increased host seeking behavior and blood meal size. The PMR phenomena is exploited via the Sterile Insect Technique strategy to reduce female fertility in wild populations. However, the biology underlying this response remains unknown in tsetse. Female flies were mated and subjected to microCT and metabolomic analyses to characterize the structural and biochemical changes occuring after mating. Three-dimensional structural analysis of mated female reproductive tracts reveal that the male spermatophore is shaped such that it protects the sperm, directs them into the spermathecal ducts and creates a physical barrier preventing sperm from other matings reaching the spermatheca. Metabolomic analysis of female reproductive tracts before and after mating reveal significant changes in the biochemical constitution of this tissue after mating. At 2-4 hours post mating significant changes in lipid concentrations are observed. These include the enrichment of phosphatidyl choline and ethanolamine moieties, ceramides and cholesterol esters. These observations suggest that these compounds are being transferred from the male into the female as components of the spermatophore. These compounds may function to maintain the structural integrity of the spermatophore as well as functioning as signaling molecules or acting as nuptial gifts from the male to enhance female fertility.

Current knowledge of diving beetles (Dytiscidae) of Thailand

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Abstract: Straddling two major biogeographical subregions, the Indochinese Region in the north and the Sundaic Region in the south, Thailand enjoys a high level of biodiversity, which supports an interesting mix of flora and fauna representative of both regions. This pattern is also visible in the distribution of diving beetles.

To date, 128 species of diving beetles belonging to 23 genera and 7 subfamilies are known from Thailand. Although this can be considered a moderate number, most of the records were reported over twenty years ago. Current research in water beetle taxonomy is limited, and new records are quite rare. Furthermore, a comprehensive catalogue has not yet been compiled. Here, I present some of the known species, together with photos and distribution maps. Comments are made on species that I expect to be present in Thailand, given the distribution in neighbouring countries, but have not yet been reported. The state of water beetle research in Thailand is also remarked upon, including challenges and potential solutions.

Developing a long-term insect biodiversity monitoring program for a South African semi-arid savanna ecosystem

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Abstract: There is increasing global concern that insect diversity and abundance is under severe duress from impacts such as habitat destruction, pollutants, and global warming. Most long-term studies of insect diversity and abundance have been conducted in European countries and North America, with very few in place in Africa. African ecosystems contain large conservation areas that are subject to many of the same impacts that have been identified to reduce insect biodiversity. These areas may serve as significant reservoirs of insect biodiversity and may ensure that ecological services in adjacent agricultural areas are conserved. Conservation management actions (e.g. controlled fires, artificial waterholes, installation of infrastructure), in protected areas have the potential to impact insect communities as well. Here we describe the initiation of a project intended to provide long-term data on insect biodiversity in Balule Nature Reserve, a component of the Great Kruger Park in South Africa. The area is dominated by semi-arid savanna that comprise a number of distinct plant communities, but with limited topographical variation. We are developing baseline data for long-term monitoring efforts intended to track changes in biodiversity over time which, relates to changes in vegetation quality, conservation management, and climate change. Substantial biomass and diversity of insects is supported by seasonal grass growth, and largely determines patterns of Lepidoptera collected to date. Some trees species (e.g. shepherd's tree, Boscia albitrunca) harbor a large diversity of species of Hemiptera, Coleoptera and Lepidoptera, providing a perennial resource for insects with some turnover in species composition seasonally. Further sampling will include vegetation zones at varying distances from external impacts, such as areas transformed to agricultural production lands. In addition to providing long-term biodiversity data, this project is expected to provide options for monitoring ecosystem condition more accurately than relying on large herbivores.

Genome evolution in termites

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Abstract: Structural changes to genomes can alter phenotypes and result in major ecological and evolutionary shifts. Termites provide an excellent model to study the evolutionary implications of genome structural variants, since different lineages are known to have divergent chromosome numbers and genome sizes. Despite these differences, the extent of variation and association with different feeding ecologies, developmental pathways, and social structures remain unknown. In this project, a hybrid sequencing and multiplatform assembly approach was used to integrate long-read, short-read, and long-range data to generate 50 de novo genome assemblies that span the breadth of termite diversity. Structural variants were characterized across termite genomes and differences were assessed using a comparative phylogenetic framework to provide insight into how variants evolve, how they are maintained, and how they shape termite phenotypes.

Are the damage of an invasive seed insect directly dependent of the spatial structure and genetics of the host trees in an infested seed orchard?

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Abstract: The increase of the forest seed trade with globalization is a source of introduction of exotic species of specialized seed insects. These insects generate significant economic losses in seed orchards producing seeds with added genetic value. The seed chalcid Megastigmus spermotrophus, introduced in Europe from North America at the end of the 19th century, is strictly associated with Douglas fir, its host tree, and is a good model for studying the relationship between insect attack and genetic composition of seed orchards, especially since Douglas-Fir is one of the first reforestation species currently used in Europe.

The French seed orchard of Lavercantière in the southeast of the Massif Central consists of nearly 800 plants belonging to more than 100 genetically different clones, with a random geographical distribution of the plants. The majority of the trees in this orchard, established 35 years ago, regularly grow with years of high production that alternate with years of low or no production. The cones being harvested in summer while the insect is still in the larval stage in the seed, all the insects of the orchard are in theory eliminated, and the infestation of the orchard the following year proceeds from the arrival of insects coming from the surrounding areas. Therefore, each annual infestation can be considered a replicate. The annual number of infested seeds, one larva being present per infested seed, has been estimated since the creation of the orchard on a limited number of randomly selected plants, one per line on the 70 planted lines. Moreover, in 2018, 2020 and 2021 (years of heavy cone crop) and 2019 (a year of light cone crop), all trees in the orchard were sampled with a minimum of 10 cones per tree. The number of infested, healthy and aborted seeds per cone and per tree was estimated using X-rays. The geographic coordinates and clonal identity of each plant is known, and its annual cone production has been measured.

In this study, spatial statistics allowed to study if the seed infestation per tree is linked to its clonal/ genetic identity. We tested whether the insects are distributed among the plants according to this identity, or if they are simply distributed according to the volume of cones carried by each tree regardless of the clone.

This study is expected to identify a possible clonal susceptibility to chalcid attack, and conversely to select the clones that could serve as natural traps for these insects, which is important to take into account in the establishment of new plantations in the context of climate change.

Bio-economic modelling for optimizing surveillance effort for invasive forest pests in Switzerland

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Abstract: Switzerland has joined an EU-wide effort for early detection of several priority and other quarantine forest pests (Agrilus anxius, Agrilus planipennis, Anoplophora chinensis, Anoplophora glabripennis, Bursaphelenchus xylophilus, Dendrolimus sibiricus, Fusarium circinatum and Phytophthora ramorum). To conduct these surveys as effectively and cost-efficiently as possible, we are considering relevant international trade flows, population density, climatic suitability, host availability, costs of trapping/monitoring and eradication of detected populations for Switzerland. We adapted the bio-economic surveillance model CESAT to evaluate where in Switzerland the probability is highest that the target organisms are introduced and establish. The model is also used to estimate a cost-efficient sampling effort to optimise the surveillance effort across Switzerland while ensuring engagement with all regional forest health agencies. In this presentation, we show challenges and opportunities in handling the relevant data, and discuss which data are necessary to further improve modelling the arrival and establishment of surveyed quarantine organisms. Our results demonstrate that a data-based approach can shift geographical focus of sampling, help define regions of interest, and establish a cost-efficient survey network. Furthermore, we show how model outcomes can be used in practice, and what the stumbling stones for implementations are.

Epiblema sp. in Israel no suitable biocontrol agent of Parthenium hysterophorus

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Abstract: The North-American Ambrosia confertiflora and Parthenium hysterophorus are noxious and allergenic invasive weeds in Israel. In 2008, a North-American-stem galling moth was found in Israel on A. confertiflora. It was first identified as Epiblema strenuana, which is used as a biocontrol agent of P. hysterophorus in Australia, but was rejected for introduction in South Africa after host range testing, because it feeds also on Guizotia abyssinica, an oil crop in Eastern Africa.

We assessed the risk of non-host target feeding of Epiblema in Israel, as well its potential benefits as a biocontrol agent of A. confertiflora and P. hysterophorus. For this, we performed no-choice host range tests, and field samplings to assess its present distribution. We found that the moth had recently extended its geographic range in central Israel to the West Bank up to the Jordan River. The moth did not attack P. hysterophorus and G. abyssinica, but attacked Ambrosia tenuifolia and Ambrosia artemisiifolia. Subsequent analyses showed that the moths introduced to Israel are not E. strenuana, but rather E. minutana. This taxon was treated as a synonym of E. strenuana in the past but should be elevated to species status based on molecular and morphological data.

Associational protection: protecting trees against emerald ash borer using systemic insecticide treatments

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Abstract: Emerald ash borer, Agrilus planipennis, is an invasive wood boring insect, introduced to North America in the 1990s that attacks ash trees, Fraxinus species. A major control strategy in urban environments is the use of systemic insecticide treatments. In our study, we are investigating whether treating a subset of trees in a susceptible ash population could confer benefits to untreated trees i.e. associational protection. This treatment regime could lower insecticide use and costs of treating trees. We present results of a three-year study comprising 1200 trees in cities across Minnesota, USA, where we explore how gradients of injections may create associational protection for individual high-value trees as well as effects on non-target species.

Intracontinental and intercontinental exchange of semiochemicals allows for their use as allochthonous kairomones

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Abstract: The principle of allochthonous kairomones in bark beetle management is originally described and based on exchanging kairomones between coniferous and broadleaf forests in Europe with the aim of attracting bark beetle antagonists without attracting bark beetles. In our study, we applied this principle in a wider context not only by an exchange between different local habitats but also by an exchange on a larger geographical scale. Dendroctonus frontalis is a bark beetle native to the southeastern United States. Frontalin is a pheromone component of D. frontalis. We installed frontalin and some European bark beetle lures in southern (Georgia) where D. frontalis is native and northern (Minnesota) pine forests where D. frontalis does not occur. Our results suggest among others things that frontalin worked as an allochthonous kairomone in Minnesota by attracting Thanasimus dubius, an important predator, without attracting bark beetles.

Screening of a potential predatory mite for control of tomato russet mite, Aculops lycopersici

Authors: Aussems Evelien[1], Bosmans Lien, Van Heghe Benedikte, Vervaet Lore, Van Leeuwen Thomas, De Clercq Patrick and De Vis Raf, [1]Belgium

Abstract: The tomato russet mite (TRM), Aculops lycopersici, is an important pest species in greenhouse grown tomato crops around the world. At this moment controlling of A. lycopersici relies solely on the use of sulphur and synthetic chemical acaricides. To establish a durable IPM (Integrated Pest Management) strategy for the tomato russet mite, there is a need for an efficient biological control agent. In our laboratory experiments, the predatory mite Pronematus ubiquitus showed promising results for the biological control of TRM. Small scale greenhouse experiments demonstrated that the mite can successfully colonize a tomato crop. The potential of the iolinid mite P. ubiquitus to colonize a tomato crop and suppress A. lycopersici was also tested in a high-tech tomato greenhouse in Belgium. Here, an experiment was set up to compare a tomato cultivation cycle with and without P. ubiquitus. The results showed a clear benefit of the presence of the mite. When P. ubiquitus was present, almost no damage was seen on the tomato plants. Without the beneficial the plants turned brown, started wilting and fruits became corky. Supplementation with cattail pollen caused the P. ubiquitus population to grow faster, but also slightly reduced its efficacy as a biological control agent

Origins of parasitoid diversity: integration of sensory physiology, chemical ecology, and phylogenetics to understand diversification in Platygastroidea

Authors: Austin Andy[1], Johnson Norman[4], Chen Huayan[3] and Dowton Mark[2], [1]Australian Centre for Evolutionary Biology and Biodiversity, Department of Ecology and Evolutionary Biology, the University of Adelaide, Australia, [2]Centre for Medical and Molecular Bioscience School of Biological Sciences University of Wollongong, Australia, [3]Sun Yat-Sen Univeristy, China, [4]The Ohio State University, United States

Abstract: Parasitoid wasps are an extraordinarily diverse group of insects, yet the proximate drivers of species richness are poorly known. Chemosensory speciation offers a framework for understanding the proximate mechanisms of diversification and why some groups appear to be prone to rapid speciation. The repertoire of chemoreceptors in a model species, Trissolcus basalis (Wollaston) (Hymenoptera: Scelionidae) is described including olfactory binding proteins, chemosensory proteins, olfactory receptors, gustatory receptors, and ionotropic receptors. The expression patterns of these proteins are described on the basis of transcriptomes and qPCR assays, and differences in expression profiles between the antennae and the rest of the body and between sexes is described. The evolution of these protein families is then traced on a newly developed phylogeny for the group based on whole-genome sequencing.

Unravelling the diversity of Australia's megadiverse hymenopteran fauna: current status, directions and new technologies

Authors: Austin Andy[1] and Fagan-Jeffries Erinn[1], [1]Australian Centre for Evolutionary Biology and Biodiversity, Department of Ecology and Evolutionary Biology, the University of Adelaide, Australia

Abstract: The isolation of the Australian continent, its Gondwanan origins, and unique fauna and flora have contributed to a hymenopteran fauna that is both hugely diverse and fundamentally different in many ways to that of the Northern Hemisphere. Although there has been substantial effort directed to documenting Australian Hymenoptera over the last 70 years, morphological-based taxonomic treatments are waning, in large part, due to a reduced systematics workforce and funding base. Current data on the proportional species diversity of families/superfamilies reveal the major differences between Australia and other regions, and serve to highlight its unique and archaic elements. Approximately 80% of the hymenopteran fauna is undescribed, with the parasitic superfamilies being the least known. Clearly the major challenge for the next 2-3 decades will be how to make significant headway in developing a robust understanding of the continent's hymenopteran diversity. Here we provide an overview of the Australian fauna, highlighting its uniqueness, and discuss the potential of new technologies for documenting diversity relevant to conservation, biological control and evolutionary studies.

Whole-genome sequencing, aTRAM, and the classification of Platygastroidea (Hymenoptera: Proctotrupomorpha)

Authors: Austin Andy[1], Johnson Norman[4], Chen Huayan[3] and Dowton Mark[2], [1]Australian Centre for Evolutionary Biology and Biodiversity, Department of Ecology and Evolutionary Biology, the University of Adelaide, Australia, [2]Centre for Medical and Molecular Bioscience School of Biological Sciences University of Wollongong, Australia, [3]Sun Yat-Sen Univeristy, China, [4]The Ohio State University, United States

Abstract: The field of phylogenetics is experiencing a Renaissance. Traditional Sanger sequencing strategies have been all but abandoned for phylogenetic reconstruction methods that utilize hundreds to thousands of genetic markers mined from next-generation sequencing data. The methods used most widely in hymenopteran systematics are genome reduction approaches that target genomic regions typically associated with protein-coding genes. While useful for phylogenetics, these techniques (i.e., UCE, AHE, RNA-seq) generate data that have limited application for addressing additional questions related to organismal biology. Enter aTRAM (automated Target Restricted Assembly Method), a genome reduction approach to phylogenetics that leverages whole-genome sequencing (WGS) reads to assemble large phylogenomic datasets. Here, we document the utility of WGS and aTRAM by constructing nuclear and mitochondrial phylogenies for the parasitic wasp superfamily Platygastroidea. The application of this sequence data to test hypotheses related to host shifting and diversification within Platygastroidea will be discussed and the implications of this phylogenetic reconstruction method will be highlighted.

Delivery of Lethal dsRNAs in Insect Diets by Branched Amphiphilic Peptide Nano-Capsules

Authors: Avila Flores Adriana, Auburn University, United States

Abstract: Development of new and specific insect pest management methods is critical for overcoming pesticide resistance and off-target killings. Gene silencing by feeding dsRNA to insects has promise as one of these methods. We recently described a new class of nanomaterials made of Branched Amphiphilic Peptide Capsules (BAPCs) [1]. In this study, BAPCs were employed to facilitated uptake of dsRNA by insects through feeding. The insect diets included dsRNA with and without complexation with BAPCs. The selected insect species come from two different Orders and with different feeding mechanisms: Tribolium castaneum and Acyrthosiphon pisum. The gene transcripts tested (BiP and Armet) are part of the unfolded protein response (UPR) and suppressing their translation resulted in lethality. For Acyrthosiphon pisum, ingestion of BiP-dsRNA associated with BAPCs led to the premature death of the aphids (t1/2 = 4 - 5 days) compared to ingestion of the same amounts of free BiP-dsRNA (t1/2 = 11-12 days). Tribolium castaneum was effectively killed using a combination of BiP-dsRNA and Armet-dsRNA complexed with BAPCs; most dying as larvae or during eclosion (?75%). Feeding dsRNA alone resulted in fewer deaths (?30%). The results show that complexation of dsRNA with BAPCs enhanced the oral delivery of dsRNA over just dsRNA.

A world first: What pre-emptive biocontrol might mean for BMSB?

Authors: Avila Gonzalo[2], Hoelmer Kim A.[3], MacDonald Frances[1], Charles John[1], Hunt Sophie[1] and Davis Vicky[1], [1]The New Zealand Institute for Plant & Food Research Limited, Mt Albert Research Centre, Auckland; Better Border Biosecurity, [2]The New Zealand Institute for Plant & Food Research, New Zealand, [3]U.S. Dept. of Agriculture, Agricultural Research Service, Beneficial Insect Introduction Research, Newark, Delaware, United States

Abstract: The brown marmorated stink bug (BMSB), Halyomorpha halys, is an invasive temperate/subtropical pest of many horticultural crops, and is considered to be one of the world's worst insect biosecurity threats. BMSB is regarded as a major economic and environmental threat to New Zealand, and although it is not yet known to be present in New Zealand, it has been repeatedly intercepted at the border and there remains a high risk of entry and establishment. In preparation for its possible arrival, a pro-active (or pre-emptive) classical biocontrol programme using the egg parasitoid Trissolcus japonicus has been initiated. The potential host range of the parasitoid in New Zealand was investigated by importing parasitised BMSB eggs into quarantine from Newark, DE, USA. Emerging female T. japonicus were mated and exposed to eggs of seven species and one sub-species of Pentatomidae in no-choice laboratory experiments. Results showed that egg of the predatory pentatomids C. nasalis nasalis, C. nasalis hudsoni and O. schellenbergii, and the phytophagous M. humeralis, D. caenosus, G. amyoti, and C. simplex were all confirmed as physiological hosts for T. japonicus, although not all were equally susceptible to parasitism. Eggs of the cosmopolitan pentatomid plant pest N. viridula were not attacked. In addition to laboratory host specificity testing, climatic modelling work was also conducted to estimate the potential global distribution of T. japonicus with particular reference to New Zealand. The north of New Zealand appears moderately to highly suitable for T. japonicus, while southern regions are mostly marginal. The risk posed by T. japonicus to non-target species in New Zealand is predicted to vary between different non-targets. The likely ecological consequences of releasing T. japonicus into New Zealand are discussed, as is the subsequent decision of New Zealand's Environmental Protection Authority to approve the conditional release of T. japonicus should a BMSB incursion occurs in New Zealand.

Introducing CoRoSect, an European project for technological and sustainable insect farming

Authors: Avosani Sabina[2], Vitale Maria Luisa[2], Mockel Rico[3], Lamaj Flutura[2], Papadimitriou Alex[1] and Verrastro Vincenzo[2], [1]CERTH, [2]CIHEAM-BARI, [3]Maastricht University

Abstract: Insect farming is a promising resource supporting food security, the big challenge of our century. Besides representing excellent food sources for farming animals, edible insects were recently approved as novel food for human in the EU. Even so, many rearing processes need to be improved and innovated, to scale the production, decrease production costs and labor, and mitigate the environmental impacts. Sustainable rearing substrates, standardized farming protocols, robotization and automatization are pivotal factors around which the project CoRoSect turns, and for this reason received funding from the EU's Horizon 2020 research and innovation programme under grant agreement No. 101016953.

Here, we introduce the audience of the ICE22 to CoRoSect, whose scopes include the (i) characterization of the biological, technical, and economic requirements of insect rearing, (ii) development of standardized diets based on side-streams, (iii) creation of a novel integrated cognitive robotic ecosystems. CoRoSect is expected to foster safe and technological rearing farms where humans and robot collaborate in the framework of environmentally friendly food chains. The first pilot insect farms involved in the project are placed in different European countries and are rearing three of the leading edible species. While presenting the state of the art and the current results and perspectives, we expect to encourage a fruitful discussion in the context of the symposium.

How is Aleppo pine responding to infestation by the giant pine scale Marchalina hellenica (Hemiptera, Margarodidae): Gas exchange and water status

Authors: Avtzis Dimitrios[2], Andreadi Anneliza[5], Lyrou Fani[1], Spyroglou Gavriil[3], Radoglou Kalliopi[1] and Fotelli Mariangela[4], [1]Department of Forestry and Management of the Environment and Natural Resources School of Agricultural and Forestry Sciences Democritus University of Thrace Ores, [2]Forest Research Institute - Hellenic Agricultural Organization Demeter, Greece, [3]Forest Research Institute Hellenic Agricultural Organization - Demeter Vassilika - Thessaloniki, Greece, [4]Forest Research Institute Hellenic Agricultural Organization - Demeter Vassilika, Greece, [5]Forest Research Institute Hellenic Agricultural Organization Demeter, Greece

Abstract: Aleppo pine (Pinus halepensis Mill.) is a forest species widespread in most countries of the Mediterranean. In Greece and Turkey, it is often infested by Marchalina hellenica (Gennadius) (Hemiptera: Margarodidae), an endemic honeydew-producing scale insect, that has recently invaded Croatia and Australia. To date, there is no information available about the impact of infestation on the physiology of Aleppo pine. In the present study, we assessed the seasonal variation of gas exchange (maximum photosynthesis – Amax, stomatal conductance – gs) and water status (water use efficiency – WUEi, relative water content - RWC) in healthy and infested P. halepensis stands during one year. These findings were then juxtaposed to the infestation level of each individual tree. The impact of infestation was most pronounced from April to June, when the abundance of M.hellenica nymphs increased. Then Amax and gs of infested trees declined significantly and were strongly correlated with M. hellenica nymphs' abundance. At the same time, WUEi of infested trees was increased, thus leading to a favorable RWC regardless of the infestation. In addition, both Amax and gs recovered when the abundance of M.hellenica nymphs declined (in July) and exhibited then the highest seasonal values, despite the drought conditions of mid-summer. These results indicate that although the gas exchange of Aleppo pine is impaired under moderate infestation, still this pine species has developed mechanisms to compensate and maintain a favorable carbon and water balance. Further analysis is focused on detecting which metabolites are involved in these Aleppo pine's responses to infestation.

Taxonomic and functional diversity patterns of butterflies in Olympus and Rhodopes mountains (Greece)

Authors: Avtzis Dimitrios[2], Vlachaki Despoina[3], Kaltsas Dimitrios[3], Raptis Dimitrios[1], Dede Konstantinia[3] and Franses Rolanda[3], [1]Department of Forestry and Natural Environment Management, Laboratory of Forest Management and Economics, Technical University of Kavala, Drama, Greece, [2]Forest Research Institute - Hellenic Agricultural Organization Demeter, Greece, [3]HOMEOTECH Environmental Management Company, Thessaloniki, Greece

Abstract: We explored the different aspects of diversity of butterfly communities along altitudinal gradients within the NATURA 2000 sites of Olympus and Rhodopes mountains in Greece during 2014-2015 in a total of 24 sampling sites on each mountain using the line transect technique.

Species richness and abundance declined monotonically with elevation on the much higher and steeper Olympus that also has a smaller area size, whereas there was no significant pattern on Rhodopes where average richness and abundance were highest at the extended mid-elevations with flatter landscape. Richness and diversity patterns along the altitudinal gradient were caused by the topographical peculiarities of the landscape on each mountain and specifically by the specificity of some xeromontane red-listed species to high elevations, and the preference of common butterfly species for low or intermediate altitudes.

Additive partitioning and null model analyses suggest an ecological redundancy on both mountains, as the environment is filtering species in terms of their environmental requirements (Grinnellian niche) rather than their functional position (Eltonian niche) per se. The turnover component was the primary cause of the major diversity components. Trait convergence through environmental filtering led to the dominance of generalist species which were taxonomically and functionally close.

The application of complementary networks on the two altitudinal gradients supported the importance of the conservation targeting of butterfly SPEC's (Species of European conservation Concern) which are good indicators for the maintenance of the whole butterfly fauna, especially at high elevations, where red-listed butterflies are more frequent and potentially threatened by climate change.

Resolving the identity and occurrence of Thaumetopoea pityocampa in Greece

Authors: Avtzis Dimitrios[3], Eleftheriadou Nikoleta[3], Kavallieratos Nickolas[4], Athanassiou Christos[6], Papachristos Dimitrios[5], Mihaelakis Antonios[5], Schebeck Martin[2] and Stauffer Christian[1], [1]Department of Forest and Soil Sciences, University of Natural Resources and Life, [2]Department of Forest and Soil Sciences, University of Natural Resources and Life Sciences Vienna, BOKU, Austria, [3]Forest Research Institute - Hellenic Agricultural Organization Demeter, Greece, [4]Laboratory of Agricultural Zoology and Entomology, Department of Crop Science, [5]Scientific Directorate of Entomology and Agricultural Zoology, Benaki Phytopatho, [6]University of Thessaly

Abstract: The Pine Processionary Moth, Thaumetopoea pityocampa (Lepidoptera, Notodontidae) is one of the most abundant and widely distributed forest insects of Greece. This species occurrs both in continental parts and on islands, whereas the sister species T. wilkinsoni is limited to south Aegean islands (Crete, Rhodes). Recently, individuals assigned to the East-North African (ENA) mtDNA lineage were found in the broad region of Attika (south eastern part of Greece). Repeated sampling of Greek populations revealed that the ENA lineage was gradually expanding northwards from the Attika region, occupying areas that were formerly inhabited by T. pityocampa. To get a better understanding of the mechanism underlying the expansion of the ENA lineage, populations were screened for various heritable bacterial endosymbionts that are known to manipulate the reproduction of insects and might facilitate the spread of infected hosts, including Wolbachia, Cardinium, Rickettsia and Spiroplasma. However, none of these endosymbionts was detected. Therefore, the expansion of the ENA lineage is most likely not driven by bacterial endosymbionts. Finally, the nitrogen content of larvae belonging to T. pityocampa and ENA lineage has been previously assessed, but nonetheless, did not exhibit any statistically significant differences between them.

Entomological assessment of the risk of outbreak of Aedes-borne diseases during the Covid 19 restriction period in Cape Coast, Ghana

Authors: Ayettey Joana[1], Kudom Andreas A.[1] and Mensah Benjamin A.[1], [1]University Of Cape Coast, Ghana

Abstract: The study assessed the risk of transmission of Aedes-borne arboviruses in the Duakor community in Cape Coast during the Covid-19 restriction period in 2020, using entomological indices. A household container survey was conducted in 100 randomly selected houses. All water-holding-receptacles were examined for the presence of mosquito juveniles. House index, Container index, and Breteau index were calculated from the household data. Ecological succession and prey-predator activities of household-container breeding mosquitoes were also investigated. Only the Container index marginally exceeded the WHO threshold. The risk of a potential outbreak of Aedes-borne diseases in the Covid 19 restriction period was much lower than in 2018 when a similar assessment was done. Community clean-up exercises during the period of Covid 19 restriction may have improved the sanitation condition in the community. This, in turn, may have led to the reduction of discarded items infested by mosquitoes, which was the main cause of high larval indices in the previous study. Notwithstanding, majority (86%) of the mosquitoes were collected from water storage containers. The results from this study show the need for education on good water storage practices as part of the various health promotion activities in this pandemic period.

Population dynamics and species interactions of mosquitoes in a rapidly changing Arctic

Authors: Ayres Matthew P.[1], Culler Lauren[2], [1]Department of Biological Sciences Dartmouth College Hanover, United States, [2]Environmental Studies Program, Dartmouth College Institute of Arctic Studies, Dartmouth College, United States

Abstract: Tundra arthropods are sensitive to temperature change and serve as useful indicators of rapid environmental change in Arctic ecosystems. For example, we have used natural history observations, experimental approaches, and population models to show how warming Arctic temperatures drive changes in the timing and intensity of Arctic mosquito (Aedes nigripes, Diptera: Culicidae) emergence. As mosquitoes emerge and enter the terrestrial system, they become prey for arthropod predators such as wolf spiders (Araneae: Lycosidae) and parasites of vertebrates such as caribou. Here we present results from two studies that aim to quantify impacts to these species interactions. First, we used pitfall traps to compare the densities, sizes, and fecundity of wolf spiders collected near versus far from the margins of mosquito ponds. We found approximately equal densities and sizes of wolf spiders across the landscape. However, female spiders collected near ponds, where we regularly observed spiders consuming newly emerged mosquitoes, had larger egg sacs with more 20% more eggs, indicating that emerging mosquitoes may have a role in shaping wolf spider fitness. Second, we used four years of observational data on emergence timing to build a degree day model. When we applied the model to 70 years of historical weather data, we found that mosquito emergence has advanced by about 8 days during this time period. The phenology of vertebrate hosts, however, has not changed. The degree of temporal overlap between mosquitoes and their hosts may have important consequences for the population dynamics of both parasite and host. For example, the presence of higher densities of caribou was correlated with a 150% increase in the proportion of mosquitoes that successfully got a blood meal. The ecological roles of mosquitoes and other biting insects in the Arctic are far from fully described but our results suggest that changes to biting insect populations will have consequences for the broader tundra ecosystem, mediated through terrestrial-aquatic species interactions.

Why is the southern pine beetle not so southern anymore?

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Abstract: Dendroctonus frontalis Zimmermann is among the most aggressive tree-killing insects in the world. D. frontalis is indigenous to southern North America, where it has historically been the dominant source of disturbance in extensive tracts of southern pine forests. Over the last two decades, D. frontalis has extended its distribution northward, first in the New Jersey Pinelands, then on Long Island, and now in New England at multiple points north, east, and west of Long Island. At the same time, D. frontalis has become effectively extinct in East Texas and Louisiana, which was epicenter for D. fontalis outbreaks up until only 20 years ago. Our research has addressed the following questions. Why the northward expansion of D frontalis? Has the northward expansion been facilitated by D. frontalis reaching ecosystems that were ecologically and evolutionarily naïve to this southern pest? Is the explanation for the disappearance of southerly D. frontalis symmetrical to that for the expansion of northern populations (as predicted by the Climatic Envelope concept)?

Predicting the impact of non-native forest insects prior to arrival or establishment

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Abstract: A small proportion of non-native insects cause widespread ecological and/or economic damage on a global scale, but the ability to predict their level of damage prior to arrival has eluded scientists for decades. Advancements in the study of invasion biology and fields such as computational phylogenetics provide tools that could help to quantify the drivers that influence the eventual impact of a non-native insect. Understanding these drivers can inform management decisions including risk assessments for insects not yet established but have a high likelihood of introduction given global trade pathways. Using available data pertaining to currently established non-native insects in North American forest systems, we evaluated factors that could explain why some invading insects cause high impacts while others are benign. These drivers included 1) insect traits, 2) host tree traits, especially those related to host defenses, 3) divergence time between the insect's native and novel (North American) host trees, and 4) the relationship of the invader to insects coevolved with the novel host. We quantified the relative combined contributions of these drivers to the magnitude of impact and developed composite predictor models that can be used to predict the risk of non-native insects to cause tree mortality should they successfully become established in North America. The results from our work, both the predictive models and the compiled databases, can be significant tools for regulatory and pest management efforts in North America, and represents a successful protocol that can be extended globally.

IPM package for pearl millet in the Sahel

Authors: Ba Malick, ICRISAT, Niger

Abstract: For more than 20 years, the head miner Heliocheilus albipunctella (de Joannis) (Lepidoptera: Noctuidae), has regularly devastated crops of pearl millet, a major subsistence food crop in the Sahelian region of West Africa. Currently, the development of biological control has been given priority and augmentative releases of the endogenous larval parasitoid Habrobracon hebetor Say can lead to up 80% of MHM larval mortality. Recent trials have confirmed that the release of H. hebetor can be practically applied at the village level. Commercialization of the technique has been proposed and may prove to be a profitable business for local entrepreneurs. In addition to the larval parasitoid, the egg parasitoid Trichogrammatoidea armigera Nagaraja (Hymenoptera: Trichogrammatidae) inflicts up 60% egg mortality. Host plant resistance has been found in genotypes Gamoji, LCIC9702, Souna 3, and PE08043. Effort are being taken to combine resistance genotypes with augmentative releases of egg and larval parasitoids for an integrated management of the MHM.

Phylogenomic reconstruction, evolution and biogeography of Atta leaf-cutting ants (Hymenoptera: Formicidae)

Authors: Bacci Mauricio[4], Anahí Barrera Corina[3], Sosa-Calvo Jeffrey[2], Schultz Ted[2] and Rabeling Christian[1], [1]Arizona State University, [2]National Museum of Natural History-Smithsonian Institution, [3]Sao Paulo State University, Rio Claro, SP, Brazil, [4]Sao Paulo State University, Rio Claro, SP, Brazil

Abstract: Atta is an ecologically dominant leaf-cutting ant genus, the major herbivore of the Neotropics, and an agricultural pest of great importance. We reconstructed the most comprehensive phylogenetic estimate to date of Atta by employing 2340 ultraconserved elements loci from 224 Atta specimens, which include 14 out of the 15 identifiable species from across their geographic distributions, and 49 outgroup specimens. Our results support the monophyly of Atta and of the four clades that coincide with the previously recognized subgenera. The Archeatta clade contains three species occurring in North and Central America and the Caribbean and is the sister group of the remainder of all other Atta species. The Atta s.s. clade is composed of two species occupying North, Central, and South America. The Epiatta clade contains seven entirely South American species and the two species of the Neoatta clade occur in Central and South America. The crown-group origin of Atta was around 8.5 Ma and the extant Atta species evolved in the early Pleistocene, 1.8–0.3 Ma. The range of the most recent common ancestor of Atta consisted of the combined North/Central America and NW South America bioregions and that one daughter lineage subsequently dispersed into South America.

Population and Biodiversity Trends of Ground Beetles and Butterflies in Europe - A Review of Drivers and Pressures

Authors: Baden Christian[2], Bergtold Matthias[1], Schade Michael[5], Marx Michael[3], Toschki Andreas[4], Oellers Johanna[4] and Rumohr Quintana[4], [1]BASF, [2]Bayer AG, Germany, [3]Bayer, Germany, [4]GAIAC, [5]Syngenta

Abstract: Declines of insect biodiversity and abundances have frequently been reported. Although a broad variety of potential causative factors of these declines have been proposed, the drivers of the phenomenon are not yet fully understood. One possible way of elucidating them is the systematic analysis of published historic population data. We conducted an evaluation of scientific literature reporting data on Carabidae and Lepidoptera population and biodiversity trends in Europe. From the relevant publications identified, we extracted reported trends and classified the environmental stressors discussed along with the respective trends according to the DPSIR model (drivers, pressures, state, impact, and responses). We analyzed the level of scientific verification behind the discussed stressors. The analysis of extracted trends shows that declines are more frequent than increasing trends. For both trends, our analysis confirms that changes in populations are primarily anthropogenically driven. The reported drivers are diverse, for instance agricultural intensification, climate change, conservation activities, and urbanization. Most of the reported stressors were acting on habitat level, rather than directly affecting the organisms. The scientific verification level of the indicated drivers is different between trend types. The results of our analysis contribute to a better understanding of insect decline as a complex phenomenon.

Electronic monitoring of the potato psyllid feeding behavior on susceptible and resistant tomato lines

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Abstract: The potato psyllid, Bactericera cockerelli, is a significant pest of vegetables throughout Central and North America, New Zealand, and Australia. This psyllid is the vector of “Candidatus Liberibacter solanacearum” (Lso), which is the causative agent of diseases in several solanaceous crops. Currently, five Lso haplotypes have been identified, two of which (LsoA and LsoB) are exclusively transmitted by potato psyllids in their shared geographic range within the Americas. Plant resistance as a component of a management strategy for this pathosystem presents an attractive option. Resistance factors which reduce the time psyllids spend in phloem phases, especially salivation, could play an important role in reducing pathogen transmission. Previously, several recombinant inbreed lines (RILs) were reported to carry potato psyllid resistance from a wild tomato relative, Solanum habrochaites, in the S. lycopersicum (cv. Moneymaker) background. In this study, we used the electrical penetration graph technique to elucidate the feeding behavior of potato psyllids on five tomato RILs and each parental line to better understand the underlying resistance factors. In general, potato psyllids took longer to reach the sieve elements on S. habrochaites. Furthermore, potato psyllids were unable to sustain ingestion on S. habrochaites and one RIL relative to psyllids on Moneymaker.

A new record of the genus Euderus Haliday (Hymenoptera: Chalcidoidea: Eulophidae) from Korea

Authors: Bae Jongmin[2], Youn Young Nam[1] and Jung Sunghoon[1], [1]Department of Applied Biology, Chungnam National University, [2]Department of Smart Agriculture Systems, Chungnam National University

Abstract: The genus Euderus Haliday is a cosmopolitan genus with 80 described species. Until the present, only one species of the genus has been reported from Korea. In this presentation, we report a new record of the genus Euderus from Korea, with its figures.

Winterblues: Colour Preference of overwintering flies

Authors: Baele Amber, Ghent University, Belgium

Abstract: Water towers are a popular overwintering place for several fly species (Musca autumnalis, Pollenia spp. and Thaumatomyia notata) in Europe.

During late summer, early autumn massive swarms of flies enter buildings to seek shelter against upcoming winter conditions in crevices of their refugia. In inhabited buildings, the aggregation of flies can be a big nuisance just by their numerous presence. In industry, utility buildings and more specific water towers, their presence can pose a threat to public health as flies are known vectors of pathogens. Unraveling the preferences of these hibernating flies can thus be useful in the control of the pests in places where they can cause damage.

It is striking that the same water towers get infested year after year, while others never get visited. Colour preference could be an influencing factor to determine if a place is worth visiting or not. To test this hypothesis, tarpaulins with different colours were erected on top of a tower in the four wind directions. The flies preferred to land on the sides away from prevailing wind and preferentially on the colour blue. Yellow, a colour typically used as an attractant on insect traps, was under no circumstances an attractive colour.

Rearing insects - lessons to be learned from the housefly (Musca domestica)

Authors: Bahrndorff Simon, Aalborg University, Denmark

Abstract: Insects for food and feed is an environmentally friendly and sustainable production form. Mass rearing of insects holds many advantages over traditional domestic animals in terms the requirement for energy, space, and the efficiency accumulating biomass from a given resource. However, a number of challenges related to the genetic makeup of insects should be addressed in order to optimize the production. Using next generations sequencing technologies we investigate the genetic variation and associated microbiome within and between populations of houseflies sampled across Denmark. There was evidence for sub-structuring of Danish housefly populations and with genetic structure that differed across season and sex. Large individual variations were observed in the community structure of the microbiome and it was found to be dependent on location, sex, and collection time. Furthermore, the relative prevalence of putative pathogens was highly dependent on location and collection time. These results may have implications for large scale production of insects.

A comparative RNAseq study between phases of two pest locusts

Authors: Bakkali Mohammed[1], Bakkali Noureddine[1], Saadi Somia[1] and Obispo Valencia Alejandro[1], [1]Universidad de Granada, Spain

Abstract: Recurrent locust population outbreaks harm agriculture, livestock, ecosystems, economies and, ultimately, humans in large parts of the world. At outbreaks, locusts shift from the normal, harmless, solitarious phase to the devastating, gregarious phase in response to extraordinary increase in their population size. Locusts of the two phases differ in almost every aspect of their biology; including the level of activity, tendency to aggregate, tendency to migrate (swarming), color, morphology, physiology, development… The shift from one phase to the other is due to changes in gene expression, not to mutation, as the same individual can shift from one phase to the other. Furthermore, this striking case of phenotypic plasticity (called polyphenism) is tightly linked to perception of life conditions and to behaviour. Its most obvious association is hence expected to be with changes of the nervous system.

Identifying genes that are associated with, if not responsible for, the development and/or maintenance of the gregarious state of the locusts should provide invaluable material and information for the efforts on the fight against these pest insects.

In this study we compare the levels of gene expression between the nervous systems of solitarious and gregarious Schistocerca gregaria (desert locust) and Locusta migratoria (migratory locust).

We identify genes whose change in the levels of expression between phases is consistent between these two main pest locusts and we discuss the results at the light of the current knowledge on the phenomenon in order to highlight their potential interest.

Shotgun metagenomics as a training tool in molecular biomonitoring

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Abstract: Genomic tools are increasingly relevant for the monitoring of ecological communities. It is essential that new generations of biodiversity experts are both fluent in their use, and aware of new developments and perspectives. With this in mind we developed a field course in monitoring of insects with shotgun metagenomics. Shotgun metagenomics promises to solve problems with the quantification of biomass through DNA-sequences in metabarcoding, and might become an alternative approach in the nearer future. The field course took place at a field station in a remote area of Romania, where MSc students designed a study to compare insect biodiversity on traditionally managed (grazed or mown) grassland plots. They also contrasted a morphospecies approach and shotgun metagenomics to record differences among communities. All steps of the shotgun metagenomics study were performed at the station, from sampling through DNA extraction, library preparation and DNA sequencing to bioinformatics, data analysis and interpretation. Both morphospecies identification and metagenomics recorded that grazed meadows have considerably lower insect richness than mown meadows, and differences in community composition were not statistically, partially confirming expectations about the effects of grazing-related fertilization. In our experience the metagenomics field course format provides a rather simple and straightforward opportunity to expose future experts to the strengths and challenges of emerging molecular approaches in biomonitoring.

Two high-quality de novo genomes of the gall inducing Diplolepis rosae and D. eglanteriae (Hymenoptera: Cynipidae)

Authors: Balint Miklos[4], László Zoltán[2], Schardt Leonie[5], Veres Robert[1], Dénes-Avar Lehel[2], Szabó Emerencia[3], Mátis Attila[2], [1]Babeş-Bolyai University, Romania, [2]Hungarian Department of Biology and Ecology, Babeş-Bolyai University, [3]Hungarian Department of Biology and Ecology, Babeş-Bolyai University, Romania, [4]Loewe Centre for Translational Biodiversity Genomics, Frankfurt am Main, [5]Senckenberg Biodiversity and Climate Research Centre (SBiK-F), Frankfurt am Main

Abstract: Gall wasps (Hymenoptera: Cynipidae) which specialize on wild roses (Rosa sp.) are relatively species-poor and ecologically well-studied. Gall formation can damage economically important host plants and provides habitat for numerous parasitoids, but the mechanisms of gall formation are poorly understood. For example, it is unclear whether gall formation is induced by substances produced by the wasps themselves, or by their microbiome. Biodiversity genomics is increasingly used to answer similar questions and to identify genes behind natural substances, both in prokaryotes and eukaryotes. Today we can use long-read DNA sequencing to generate high-quality (complete and contiguous) genomes for many non-genetic model species. Here we present two de novo genomes of the gall inducer Cynipidae Diplolepis rosae and D. eglanteriae. We extracted RNA and high molecular weight DNA from single individuals. We prepared ultra-low input PacBio libraries for HiFi long-read sequencing with a protocol that requires only 5 ng DNA input, followed by whole genome amplification. We also prepared Omni-C libraries for scaffolding, and RNA-Seq libraries for genome annotation, and sequenced these on Illumina. The assembled, scaffolded and annotated genomes promise insights into the genomic mechanisms of plant gall induction and provide valuable opportunities to identify potentially involved genes.

Identification of the novel antimicrobial peptides from a rice planthopper, Nilaparvata lugens

Authors: Bao Yanyuan[2], Peng Luyao[2], Song Qisheng[1], Zhou Xiang[2] and Wang Zhechao[2], [1]University of Missouri, [2]Zhejiang University, China

Abstract: In this study, two novel antibacterial peptide genes, termed lugensin A and B were identified and characterized from a rice sap-sucking hemipteran insect pest, the brown planthopper, Nilaparvata lugens. Lugensin gene expression was significantly induced by Gram-negative and Gram-positive bacterial stains under the regulation of a signal receptor, the long peptidoglycan recognition protein (PGRP-LC) in the IMD pathway. Knockdown of PGRP-LC by RNAi eliminated bacterium induced Lugensin gene expression. Lugensins had the apparent antibacterial activities against Escherichia coli K12, Bacillus subtilis and the rice bacterial brown stripe pathogen Acidovorax avenae subsp. avenae (Aaa) strain RS-1. Lugensins inhibited bacterial proliferation by disrupting the integrity of the bacterial membranes. Scanning electron microscopy revealed abnormal membrane morphology of the recombinant Lugensin-treated bacteria. Lugensins induced complete cell disruption of E. coli K12 and B. subtilis strains while formed the holes on the cell surface of Aaa RS-1 strain. Immunofluorescence showed that Lugensins localized in the cell membrane of E. coli K12 while accumulated in the cytosol of B. subtilis. Differently, Lugensins remained in both the cell membrane and the cytosol of Aaa RS-1 strain, suggesting different action modes of Lugensins to different microbes. This is the first report of the novel antibacterial peptides found in the rice sap-sucking hemipteran insect species.

First report of tussock moths (Bracharoa mixta (Lepidoptera: Erebidae)), scarring avocado fruit in KwaZulu-Natal, South Africa

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Abstract: Avocado (Persea americana) is an important export crop for South Africa contributing ZAR 1.75 billion in export revenue to the gross domestic product. As an export-oriented industry, increasing the exportable percentage of avocado fruit is a major concern. A tussock moth, Bracharoa mixta (Snellen) is reported for the first time on avocado trees, scarring fruit and defoliating leaves. Feeding damage by the larva results in corky tissue development, making the fruit unsuitable for export. The study aimed to determine the identity of the larvae (morphologically and DNA barcoding) and ascertain levels of damage. Sequencing of the barcoding region of cytochrome oxidase subunit I (COI) gene was done. In-field fruit damage assessment of infested trees showed an 11 % scarring damage level resulting in 3.67 % downgrading of fruit. This represents a potential revenue loss of up to ZAR 1,352.90 per tonne (2.26 % revenue loss). The defoliating caterpillars also caused an 18.22 % reduction in leaf area. This study documents the potential of B. mixta to cause economic loss and sporadic, isolated outbreaks.

Acoustic mimicry in myrmecophilous butterflies

Authors: Barbero Francesca, Dept Life Sciences and Systems Biology - Turin University, Italy

Abstract: The ability to communicate efficiently and coordinate the actions of up to a million specialised nestmates has enabled ants to be among the most successful animals globally, frequently dominating several terrestrial ecosystems. Their means of communication include the multifarious use of chemical signals, posturing, and tactile interactions, and the comparatively poorly studied channel of vibro-acoustical signals. Ant defences are largely based on possessing impressive weaponry, including poisons, acids and biting, and their ability to deploy them, thanks to communication, in coordinated attacks that marshal overwhelming numbers of workers.

Nevertheless, several species of invertebrates have evolved adaptations to establish associations with ants, living undisturbed in the surroundings or even within their colonies.

Myrmecophilous interactions are well known to occur in Lycaenids, a family of Lepidoptera which accounts for 30% of butterfly species. Most Lycaenids establish associations with ants that can be facultative or obligate and range from mutualism to parasitism, with loose interactions in which larvae are only occasionally visited by several species of ants, to complex obligate associations in which larvae need to be constantly tended by ants.

Myrmecophilous butterflies show morphological, behavioural, chemical or acoustical strategies for cohabiting with ants including armour, stealth and, in the case of most mutualists, the secretion of attractive food rewards. However, the most intriguing adaptations involve the subversion of the ants' honest acoustical signalling, enabling butterfly social parasites of the genus Maculinea to achieve a high social status in the host colony hierarchy. Immature Maculinea instars mimic the stridulations emitted by host queen ants to enhance their retrieval, survival and full integration into the host society. Recent data suggest that, among lycaenid butterfly larvae, convergence has generated similar sophisticated calls that are more closely associated with the strength and specificity of a species' relationship with ants than its phylogeny.

I will present examples of acoustic mimicry, and I will discuss the function of vibro-acoustic signalling in symbioses involving butterflies and ants. The study of acoustic communication in myrmecophilous systems could bring about significant insights for understanding complex mechanisms underlying the origin, evolution, and stabilisation of many multitrophic relationships.

Hell ants

Authors: Barden Phillip, Department of Biological Sciences, New Jersey Institute of Technology, Newark, NJ, Division of Invertebrate Zoology, American Museum of Natural History, United States

Abstract: Among the oldest fossil ants known, haidomyrmecine "hell ants" are highly specialized predators. Comprising nine genera, these enigmatic ants are preserved in Cretaceous amber from Canada, France, and Myanmar, and exhibit an array of cranial features not found in any modern lineages. Hell ants are characterized by dramatic scythe-like mouthparts that are dorso-ventrally expanded into a diverse array of mandibles that are specialized for prey capture. Remarkably, these unique mandibles appear to be accompanied by a novel mode of articulation; hell ant mandibles are suspected to open vertically, in an axial plane parallel to that of all living ants. This unique feature in turn has led to the development of striking "horns" which work in conjunction with the mandibles to pin, restrain, or impale prey. Here, I will survey the diversity of this unique lineage, interpret preserved instances of prey capture, and discuss hell ants in the broader context of extinct adaptive radiations.

Biological Control Genetic Resources and Access and Benefit-Sharing

Authors: Barratt Barbara I. P.[1], Mason Peter[2], [1]AgResearch, New Zealand, [2]Agriculture and Agri-Food Canada, Canada

Abstract: The third objective of the Convention on Biological Diversity, the fair and equitable sharing of benefits arising out of the utilization of genetic resources was formally implemented when The Nagoya Protocol came into effect in 2014. However, participating countries were not provided with guidance for developing legislation on access and benefit-sharing, thus interpretation on what is equitable sharing and what are benefits is likely to be wide-ranging. The implications for biological control in the future include how biological control agents will be utilized and exchanged, how biological control will benefit the global community, and how response times for implementing biological control may be affected. The free use and exchange of biological control genetic resources has provided benefits to the global community, including to both providers and recipients of biological control agents. Consideration of this principal should be a key element of Access and Benefit-Sharing measures.

Spiny snout mite 25 years on: how relevant is the Tasmanian experience of clover flea biocontrol to New Zealand?

Authors: Barratt Barbara[2], Gerard Philippa[1], Wilson Derrick[1], [1]AgResearch Ltd, New Zealand, [2]AgResearch Ltd, Nicaragua

Abstract: A French ecotype of the Bdellid mite, Neomolgus capillatus (Kramer) (spiny snout mite) was introduced into Tasmania, Australia, in 1985 to control clover flea (L.), a serious Collembolan pest of clover in dairy pastures. Its main limitation to effectiveness was its very slow dispersal which was addressed through an extensive redistribution programme over 800 sites. The success of the spiny snout mite as a biocontrol agent in Tasmania has initiated investigations into the feasibility of introducing it into New Zealand where clover flea remains a problem in localised areas in the North Island and may intensify with expansion of irrigation and climate change. While both Australia and New Zealand have markedly tightened regulations around the introduction of new species, we postulate that past and future research in Tasmania could provide adequate risk assessment data to enable the mite to be introduced from there to New Zealand. Tasmanian and New Zealand pasture and natural ecosystems in the target regions are compared and results from a survey on presence of the mite in non-target habitats are presented. Knowledge gaps are identified where additional research should be focused to meet New Zealand regulatory system standards .

Species distribution modeling to evaluate the impact of climate change on the distribution of Nysius simulans (Stål) (Hemiptera: Lygaeidae) in soybean crops in South America

Authors: Barreto Carlos[2] and S. de Paula Alexandre[1], [1]Federal University of Ouro Preto, Brazil, [2]The University of Western Ontario, Canada

Abstract: Nysius simulans (Stål) is an economically important plant pest for soybean in South America, and a suctorial, fluid feeding herbivore that can transmit toxins and spread pathogens via saliva. Currently, the distribution of N. simulans on soybean is predominantly found in Argentina, but changes in the distribution from natural dispersal and range shifts due to climate change may affect a large soybean cultivation in south of Brazil. We compared the potential distribution of N. simulans under current and future projected climatic conditions in order to identify future areas of natural occurrence with ecological niche models produced using Maxent. Current records of N. simulans show that while the species is present in Argentina, Brazil, Paraguay, Peru and Uruguay, and our models suggest that many new suitable areas will be available for N. simulans under climate change including north, central and southern Argentina, and southern Chile. Our results also predict potential future range shifts and distributions into Bolivia, but not Peru nor Brazil. In our model, seasonal trends in temperature was shown to have the greatest contribution to the potential distribution, whereas isothermality (i.e. temperature variability) was negatively correlated to potential future distribution ranges. We conclude that current populations of N. simulans may be expanding its distribution range by diffusion (i.e., range expansion over generations at the margins of populations), and regions with potential future N. simulans distribution should be closely monitored.

Insects, robots and zombies

Authors: Barron Andrew, Macquarie University, Australia

Abstract: Insects are small but they are not simple animals. They are capable of impressive cognitive feats and have complex lifestyles and life histories. The accessibility and small size of their nervous system and brain means that we have made great progress in understanding the mechanisms of insect behaviour. The mechanisms of even complex insect behaviour are often deceptively simple. Here we discuss the consequences of a mechanistic understanding of insect behaviour for our appreciation of animal consciousness. If mechanisms of insect behaviour can be described in mechanistic and deterministic terms does this make an insect a robot or a ‘zombie’ with, as Chalmers has put it, “no inner life at all”?

Plant Derived Insecticidal Proteins for Protection of Crop Plants

Authors: Barry Jennifer, Corteva Agriscience, United States

Abstract: Current commercialized insect traits in corn, soy, and cotton are based on genes discovered by mining the soil bacterium, Bacillus thuringiensis, for proteins with insecticidal activity. These traits have been an important tool utilized by farmers to maximize productivity. However, the development of resistance to these traits has generated urgency to discover new proteins with novel Sites of Action (SoA) that can complement or replace existing products. We have identified many plants that naturally produce insecticidal proteins and have mined these plants as a source of novel actives for Corteva's insect trait development pipeline. Transgenic soybean (Glycine max L. Merill) and corn (Zea mays L.) plants expressing plant derived insecticidal proteins show protection from feeding damage by insect pests. This talk will focus on novel plant derived proteins that demonstrate promise for developing new transgenic crops for pest control.

Meeting the Challenge of Training a Next Generation of Public Health Entomologists

Authors: Bartholomay Lyric, University of Wisconsin-Madison, United States

Abstract: Given the state and rate of global change and ready movement of vectors and pathogens, the need for preparing a next generation of highly trained public health professionals is particularly pressing. The outbreak of Zika in the United States revealed a profound shortfall of public health entomologists at the ready to tackle emerging vector-borne diseases, and precipitated the establishment of 5 regional Centers of Excellence supported by the Centers for Disease Control and Prevention. Each Center developed regionally responsive training approaches and delivery modalities, to include competitive grants programs, professional development workshops, a Masters Degree Program, internships and fellowships, in-person and online training offerings. After 5 years, the Centers of Excellence trained more that 600 undergraduate, graduate and professional students, and reached more than 8,000 local vector control professionals. At the same time, a major initiative from the American Mosquito Control Association was initiated to Train the Trainers to improve vector control practices across the country. Vector control, public health and academic institutions are witnessing the benefit of this new generation of trainees who are well-versed in vector biology and vector control.

Bark beetle outbreaks and meta-population dynamics of woodpeckers in Switzerland.

Authors: Basile Marco, Swiss Federal Research Institute WSL

Abstract: Resource pulses can affect animal populations in various ways. One such pulse is the increased availability of spruce bark beetle (Ips typographus), the most common forest pest in Central and Northern Europe, following disturbances such as storms and dry summers, and the subsequent increase of other wood-boring insects. Woodpeckers are considered important predators of bark beetle, but their relationship has not been studied thoroughly. Therefore, we investigated the bark beetle-woodpeckers system using a multi-decade long dataset to understand whether increases in population size of woodpeckers can be related to bark beetle outbreaks, and whether the relationship is density-dependent. We also investigated the role of standing deadwood and salvage logging as moderators of woodpecker responses to bark beetle outbreaks. We infer on the importance of deadwood for woodpecker per se, and as a pulsing resource linked to bark beetle outbreaks. We expect that bark beetle outbreaks have positive direct effects on the abundance of woodpecker species over short time periods. Our model can be used to estimate the role of bark beetle outbreaks in influencing bird population trends and whether birds contribute to stabilizing or even controlling bark beetle infestations over time.

Latitudinal patterns in herbivory and plant defense depend on leaf age and spatial scale

Authors: Baskett Carina, Institute of Science and Technology Austria, Austria

Abstract: The biotic interactions hypothesis posits that biotic interactions are more important drivers of adaptation closer to the equator, evidenced by "stronger" contemporary interactions (e.g. greater interaction rates) and/or patterns of trait evolution consistent with a history of stronger interactions. Support for the hypothesis is mixed, but few studies span tropical and temperate regions while experimentally controlling for evolutionary history. Here, we integrate field observations and common garden experiments to quantify the relative importance of herbivory in a pair of tropical-temperate congeneric perennial herbs. Phytolacca rivinoides and P. americana are pioneer species native to the Neotropics and the eastern USA, respectively. We compared plant-herbivore interactions between three tropical populations of P. rivinoides from Costa Rica and three temperate populations of P. americana from its northern range edge in Michigan and Ohio. For some metrics of interaction importance, we also included three subtropical populations of P. americana from its southern range edge in Florida. This approach confounds species and region but allows us, uniquely, to measure complementary proxies of interaction importance across a tropical-temperate range in one system. To test the prediction that lower-latitude plants experience more herbivore pressure, we quantified herbivory rates, herbivore abundance, and leaf palatability. We found evidence supporting the biotic interactions hypothesis for most comparisons between P. rivinoides and north-temperate P. americana (herbivory, herbivore abundance, and young-leaf palatability). Results for subtropical P. americana populations, however, were typically not intermediate between P. rivinoides and north-temperate P. americana, as would be predicted by a linear latitudinal gradient in interaction importance. Subtropical young-leaf palatability was intermediate, but subtropical mature leaves were the least palatable. These nonlinear patterns of interaction importance suggest future work to relate interaction importance to climatic or biotic thresholds. In sum, we found that the biotic interactions hypothesis was more consistently supported at the larger spatial scale of our study.

Investigating resistance mechanisms and fitness costs related to avermectin resistance in the diamondback moth, Plutella xylostella L. (Lep: Plutellidae)

Authors: Bass Chris[5], Oplopoiou Maria[4], Zimmer Christoph[3], M. Leroux Alicia[2], Elias Jan[2], Guest Marcus[3], Kanitz Ricardo[1] and Slater Russell[1], [1]Syngenta Crop Protection AG, Werk Rosental Schwarzwaldallee, Basel, Switzerland [2]Syngenta Crop Protection, Stein, Switzerland, [3]Syngenta, United Kingdom, [4]University of Exeter, College of Life and Environmental Sciences, UK Syngenta Crop Protection, Switzerland, [5]University of Exeter, United Kingdom

Abstract: Plutella xylostella (Lepidoptera: Plutellidae) is an oligophagous species and an abundant pest in cruciferous crops which causes a severe threat to crop production worldwide. P. xylostella is a high-risk pest concerning resistance development, having developed resistance against > 90 active ingredients, including avermectins. Emamectin-benzoate is a potent lepidoptericide, belonging to the group of avermectin. It is synthesized from the macrocyclic lactone abamectin which is derived from fermentation of the soil actinomycete Streptomyces avermitilis. Reduced field performance of emamectin-benzoate in P. xylostella has been reported in isolate localities in Japan.
This project aims to elucidate the resistance mechanisms provoking this phenomenon and to investigate any plausibly relevant fitness costs. Two field-collected resistant strains were established in the laboratory and are artificially selected with emamectin-benzoate every two generations. Dose-response leaf dip bioassays are followed every other generation to detect any susceptibility shift.

Avermectins act as allosteric modulators to the glutamate-gated chloride channels (GluCls) and target-site mutations have been described in the literature pertaining abamectin resistance in the two spotted spider mite, Tetranychus urticae, and in P. xylostella. Our results showed that those mutations are not present in our resistant strains. Ongoing analysis includes sequencing the full length of GluCl gene to screen it for novel mutations. The results may explain the observed resistance and potentially provide us with paramount information on avermectins binding site. Isolation of the resistant trait in a susceptible background achieved by back-crossings will determine the mode of inheritance and aid genetic trait mapping.

A computer model will be adopted and different scenarios i.e. different starting allele frequencies and treatment regimens (dose, application frequency, mode of action, mixtures and rotational applications) will be tested in silico. The modelling approach will allow simultaneous testing of numerous scenarios and will help to make informed decisions on which scenarios have the potential to better manage resistance. Knowledge about the mechanism, the mode of inheritance, the persistence of resistance under different treatment scenarios and the potential impact of resistance on fitness is critical for the design of a sustainable integrated pest management (IPM) program.

Revisiting an old resistance story in the genomic era, unravelling the genomic mechanisms of esterase mediated resistance in Myzus persicae.

Authors: Bass Chris[3], Troczka Bartlomiej[1], Hunt Benjamin[1], Saurabh-Singh Kumar[3] and Field Linda[2], [1]College of Life and Environmental Sciences, Biosciences, University of Exeter, Penryn Campus, Penryn, Cornwall, United Kingdom, [2]Department of Biointeractions and Crop Protection, Rothamsted Research, Harpenden, United Kingdom, [3]University of Exeter, United Kingdom

Abstract: Nearly 30 years ago it was shown that resistance to organophosphates in Myzus persicae is mediated by increased activity of two closely related carboxyesterase genes called E4 and FE4 both being able to hydrolyse and sequester insecticidal esters. Subsequent molecular characterization at the time pin-pointed the mechanism of resistance to increase in gene copy number and changes in methylation for either E4 or FE4. However, the specific mechanism(s) by which these genes were amplified was never elucidated.
With the arrival and subsequent improvement of third generation sequencing technologies it is now possible to understand the molecular mechanisms underpinning this adaptation at much greater resolution. We have analysed sequence data from a selection of susceptible and esterase resistant M. persicae clones with various amount of amplified enzymes and are using this to understand molecular evolution at the esterase gene locus.

The genomics of adaptation to natural and synthetic xenobiotics in the aphid Myzus persicae

Authors: Bass Chris, University of Exeter, United Kingdom

Abstract: The process by which genetic novelty is created and drives the evolution of key innovations required for ecological adaptation is still relatively poorly understood. In this talk I will outline recent work investigating the mutational events driving host-range expansion and xenobiotic resistance in the peach potato aphid, Myzus persicae, the most economically important aphid pest worldwide. M. persicae is globally distributed and highly polyphagous with a host range of over 400 species including many important crop plants. Relatively recently this species host-shifted to tobacco, and we have previously demonstrated that the constitutive overexpression of a cytochrome P450, CYP6CY3, allows tobacco-adapted races of M. persicae to efficiently detoxify nicotine and has preadapted them to resist neonicotinoid insecticides. Our recent work has employed a suite of genomic, transcriptomic and post-genomic functional approaches to demonstrate the role of chromosomal rearrangements and transposable elements in creating the genetic novelty required for M. persicae to resist xenobiotics and exploit a new ecological niche.

Advancing our understanding of spatial distributions of an endangered wasp at different spatial scales

Authors: Batsleer Femke[1], Maes Dirk[2] and Bonte Dries[1], [1]Ghent University, Belgium, [2]Research Institute for Nature and Forest, Belgium

Abstract: The spatial distribution of insects is typically anticipated to be driven by environmental heterogeneity. Internal mechanisms related to social attraction and competition are from a theoretical perspective as important and may lead to stable self-organisation. Such insights are elementary to predicting changes in future distributions, but as these processes act in concert, they are extremely hard to disentangle. Understanding these mechanisms is important to make well-informed conservation decisions.

We quantified spatial pattern formation of nest aggregates of the dune inhabiting digger wasp Bembix rostrata within a local, population scale and the distribution of these aggregates at a larger landscape scale. The processes leading to the local spatial distribution were investigated by the development of a microhabitat model from remote sensing drone data and a pattern-oriented Individual Based Model (IBM). Bottom-up factors and social attraction were found to be the most important drivers to explain this local spatial pattern. At the landscape scale, we used a small scale Species Distribution Model (SDM) using remote sensing aerial and LIDAR data and data on grazing management. These analyses demonstrated the importance of landscape-structure as bottom-up driver and nature management as top-down driver of the species' distribution at the landscape scale.

We critically discuss the importance of incorporating remote sensing and pattern oriented modelling for not only the detection of spatial distribution patterns but also to understand the putative mechanisms underlying these patterns. Both important for the conservation of this dune inhabiting digger wasp.

Bark and ambrosia beetles associated with imported non-coniferous wood

Authors: Battisti Andrea[1], Jactel Herve[4], Grégoire Jean-Claude[6], Hulcr Jiri[5], Orlinski Andrei[2], Benko-Beloglavec Anita[8], Hrasovec Boris[7], Inward Daegan[3], Grousset Fabienne[2] and Petter Françoise[2], [1]DAFNAE, University of Padua, Italy, [2]EPPO, France, [3]Forest Research, United Kingdom, [4]INRA, France, [5]School of Forest, Fisheries, and Geomatics Sciences, University of Florida, United States, [6]Spatial Epidemiology lab Universite libre de Bruxelles, Belgium, [7]Šumarski Fakultet, Hungary, [8]Varstvo Gozdov Slovenije, Slovenia

Abstract: Many bark and ambrosia beetle species (Coleoptera: Scolytinae and Platypodinae) are known to have spread worldwide in relation to international trade. Concerns were expressed within the European and Mediterranean Plant Protection Organization (EPPO) about recent introductions of non-indigenous species of those groups. Regulation for non-coniferous wood trade into many EPPO member countries is currently not considered sufficient to cover such risks. In 2018, an EPPO Study on the risk of bark and ambrosia beetles associated with imported non-coniferous wood was carried out. The main characteristics of bark and ambrosia beetles that contribute to the pest risk were analysed. Biological and other factors were identified and illustrated with examples from 26 representative beetle species or groups of species. The outcomes of the study as well as the measures proposed will be presented.

Following the leader: processionary behaviour of urticating caterpillars from opposite hemispheres

Authors: Battisti Andrea[1], Zalucki Myron[4], Uemura Mizuki[2] and Perkins Lynda[3], [1]DAFNAE, University of Padua, Italy, [2]Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE), University of Padova, Agripolis campus, Italy, [3]School of Biological Sciences, The University of Queensland, Brisbane, Australia, [4]The University of Queensland, Australia

Abstract: Investigating movement behaviour of organisms has economic, societal, and conservation benefits. Larval movement of insects for example, plays many significant ecological roles, and with the expansion of the human population, encounters and conflicts with insects have increased. Urticating caterpillars are a health concern to people and animals, especially when they disperse in a gregarious and synchronised manner in areas frequented by humans. Ochrogaster lunifer and Thaumetopoea pityocampa from the southern and northern hemispheres respectively, are two geographically-isolated species with similar gregarious urticating caterpillars that can outbreak causing defoliation and medical issues. Each year from March to May, O. lunifer and T. pityocampa caterpillars leave their nesting sites and form head-to-tail processions on the ground in search of pupation sites. This pre-pupation procession behaviour and its associated risk of human contact with caterpillars was studied and compared in Australia (O. lunifer) and Italy (T. pityocampa). The duration, distance, orientation and response to light of the pre-pupation processions were studied in both species to determine general patterns. In the morning, O. lunifer and T. pityocampa processions travelled on average 40 and 16 metres per day from the nest in 153 and 223 min respectively, in search for potential pupation sites. Ochrogaster lunifer pre-pupation processions travelled generally to the north or south when leaving the nest, as was their final orientation to the bivouac/pupation site. Whereas T. pityocampa processions had no preference in orientation. Ochrogaster lunifer and T. pityocampa pre-pupation processions travelled towards the darker and the lighter areas of the environment, respectively. We hypothesize that these caterpillars use polarised light to navigate through the environment; laboratory and field experiments are currently ongoing. Some 27% of O. lunifer and 44% of T. pityocampa processions had contact with humans driving, cycling or walking. Understanding the movement behaviour of O. lunifer and T. pityocampa pre-pupation processions around populated areas is crucial for predicting exposure risk and application of management strategies.

Processionary caterpillars down-under: biology, ecology and associated risks.

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Abstract: Processionary caterpillars, Ochrogaster lunifer Herrich-Schäffer (Lepidoptera: Notodontidae); also known as bag-shelter moths, bunny tail moths or itchy grubs; are a relatively common, univoltine, endemic Australian species found feeding on the foliage of a wide range of host trees and shrubs including Eucalyptus, Corymbia and Acacia.
In outbreak years severe defoliation can result from feeding. Egg masses are laid in spring and development takes place through summer and autumn. The gregarious larvae are social throughout the immature stage moving daily from a silken nest or bag-shelter to feed. The final instars disperse in processions to locate pre-pupation sites in the soil. Various nesting forms have been described and recent genetic and cuticular hydrocarbon evidence suggests a species complex. The processionary caterpillars are separated into at least three distinct forms by development periods, minor colour differences in the larvae and moths, and their nest-building habits, namely the construction of silken nests in the canopies, on the trunks, or at the base of their host trees. Like their counterparts in the northern hemisphere, caterpillars from the third instar on carry large numbers of urticating javelin-shaped and barbed true setae (modified hairs) in mirror fields which are shed into the nest with the exuviae at each moult and passively while moving. When the late-instar caterpillars leave the nest in autumn to diapause and pupate through winter and early spring in nearby soil, the nests begin to disintegrate. Nest contents, including millions of setae, exuviae and frass drop and are spread around the local environment by wind. Contact with setae causes various allergenic reactions in mammals and ingestion by pregnant mares can cause the foal to be aborted, a condition known as Equine Amnionitis & Foetal Loss. The likely risks of exposure to setae are described as well as the potential global regions at risk of establishment should the species be introduced.

Study of some aspects of ecology of cedar processionary moth, Thaumetopoea bonjeani powell (lepidoptera, notodontidae) and its egg parasitoids in Algeria

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Abstract: Background: In this study, the diversity, abundance and impact of entomophagous associated with cedar processionary moth Thaumetopoea bonjeani which is one of the most serious pests of Cedrus atlantica in north-western Africa (Algeria and Morocco) were investigated.
Materials/Methods: The study was carried out in a C. atlantica forest in the Djurdjura Park (North Algeria), in 2014 and 2015. The occurrence of the egg parasitoids was studied during spring by weekly quantitative observations of the egg masses. 223 egg batches were collected and processed. The identity of the egg predators was assessed through observations made during daytime on a total of eight ?eld visits in August and September.
Results and discussion: The average number of eggs per egg batch increased from 143 in 2014 to 171 in 2015, while the egg mortality decreased from 47.4% and 23.9%, respectively, possibly because of a dilution effect. The most important factors of egg mortality were parasitoids and predators, with hymenopteran egg parasitoids killing from 12.1% to 34.9%, and predators from 5.2% to 7.4% of the eggs. The pattern of egg parasitism was driven largely by Ooencyrtus pityocampae, accounting for about 94% of the total parasitoids, followed by Baryscapus servadeii and Trichogramma embryophagum. An hyperparasitoid Chartocerus sp. was collected for the ?rst time from eggs of Thaumetopoea species. Field observations allowed the identi?cation of three bush crickets (Tettigonia viridissima (Linnaeus), Ephippiger ephippiger (Fiebig), and Uromenus brevicollis (Chopard)) as likely predators of eggs.
The number of eggs with dead larvae was signi?cantly higher in the 2014. The proportion of eggs with dead larvae averaged 3.9% in the 2014 and 2.3% in the 2015 cohort, with no signi?cant differences among years (one-way ANOVA, F = 98.23, p = .513). Less than 2% of the eggs were infertile showing dried-up yolk, and a very small but distinct percentage of the eggs was totally empty (below 1%).
Conclusion: During the embryonic stage, the action of parasitoids and predator is significant, given the high mortality of the host during this stage. The examined parasitoids represent, together with other beneficial insects, an important component of mortality to Cedar processionary moth. Closer studies on the sequence of pupal parasitoid emergence could provide guidance on the use of these natural enemies in the Mediterranean forest areas for summer processionary moths pest control.

The eggs of T. bonjeani in Algeria appear to be more affected by mortality than those of other species included in the same clade of the summer processionary moths associated with conifers. The egg parasitoids are the main factors in egg mortality and they are the same species affecting the more common pine processionary moth in the whole Mediterranean Basin.

Vector-Borne Disease Prevention and Control Activities at the U.S. Centers for Disease Control and Prevention

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Abstract: Vector-borne diseases are an important cause of morbidity and mortality each year in the United States. Tick-borne disease cases are increasing annually, and mosquito-borne arbovirus outbreaks are occurring in an intermittent but increasing frequency. Currently, no vaccines are available for any of the vector-borne diseases that are endemic in the continental United States, and effective vector control faces many challenges. The U.S Centers for Disease Control and Prevention maintains a comprehensive program that includes conducting reference diagnostics and national disease surveillance, responding to disease outbreaks, providing prevention education and recommendations, and conducting applied research to better understand and prevent vector-borne diseases.

Snapshot of microgastrine parasitoid wasp (Hymenoptera: Braconidae) diversity in the Kaisaniemi Botanic Garden of Helsinki, Finland

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Abstract: The Kaisaniemi Botanic Garden (KBG) is located in the heart of the city of Helsinki, Finland (60.17° N, 24.94° E). It comprises an area of approximately 40,000m2 (four hectares) with a collection of over 1,300 living plant species. Its insect diversity has been scarcely studied. Microgastrine parasitoid wasps are a cosmopolitan subfamily, with almost 3,000 described species worldwide and 162 species recorded in Finland (Fernandez et al., 2020). A Malaise trap was run in the KBG from early May to mid-September 2018, comprising 19 collecting events during the season. A total of 1,445 specimens of Microgastrinae were collected. The female specimens were studied further and were found to represent 44 species within 12 genera. We identified a new species to science of Microgaster, as well as six new species records for the fauna of Finland. The most commonly collected species were Cotesia vestalis (Haliday, 1834) and Microplitis spectabilis (Haliday, 1834). Cotesia vestalis is a parasitoid of the major cruciferous pest, Plutella xylostella (diamondback moth). The most species-rich genera were Cotesia and Microplitis, with seven and eight species, respectively. A total of 17 species (39%) were represented by only one or two specimens, suggesting the actual diversity of the area to be much higher. Considering that the botanical garden is in the heart of a heavily developed urban landscape, and that the sampling only spanned one collecting season, the diversity in the area is remarkable, representing 27% of the known species and 71% of the known genus diversity in Finland.

CRISPR/Cas9 at the service of the molecular neurobiology of moth olfaction

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Abstract: Entomology is facing the new era of high-throughput sequencing, with cumulative transcriptomics and genomics data available on a diversity of model and non-model insect species. Challenges are now to develop functional tools, especially in non-model species, to translate genome research into insect physiology.

We report here the development of the Clustered regularly interspaced palindromic repeats (CRISPR)-Cas9 technology in a moth, the crop pest Spodoptera littoralis (Lepidoptera; Noctuidae), and its use as a reverse genetic tools to decipher the molecular bases of the moth chemical ecology. We present several examples of knocked-out odorant receptor (OR) genes and the effects on the insect physiology and behavior. Among these examples, we showed that the knock-out of the Orco gene induced large anosmia. The knock-out of a single pheromone receptor impaired sex pheromone detection and disrupted mating. In Lepidoptera, loss of-function studies using RNAi are generally difficult to achieve and heritable transgenesis has been developed on a very limited number of species. Thus CRISPR, because of its simplicity, opens unprecedented routes in the understanding of Lepidoptera olfaction and, more generally, in non-model insect functional genomics.

DROMYTAL: Drosophila suzukii management through yeast-based trapping lures

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Abstract: Drosophila suzukii Matsumura (Diptera: Drosophilidae) originates from South-East Asia and was first detected in Europe in 2008 as a pest insect of soft- and thin-skinned fruit crops. D. suzukii is responsible for major commercial losses in small stone fruit, berry fruit farms and viticulture in Italy and in many other countries. Female flies lay eggs in ripening fruits through a punctured hole in the skin. Larvae feed on the flesh and the punctured skin is prone to infestations by microorganisms and other insects, leaving fruits unmarketable. Integrated pest management methods are currently developed to limit the use of insecticides. One possibility to maintain a low population of D. suzukii in the field is the manipulation of insect behavior with semiochemicals. Notably, several yeast species localized on grape fruits have been associated with feeding and egg laying in D. suzukii. The interaction between yeasts and D. suzukii can be exploited in pest control strategies to protect commercial crop systems.

The present project aims to create an attract-and-kill tool with a yeast lure which can selectively attract adults D. suzukii onto insecticide-based substrates. The final goal of this system is to reduce D. suzukii infestation and reduce the use of insecticides on commercial crops. For these reasons we developed a multidisciplinary approach consisting in: 1. The selection of the most attractive yeast strains among eight yeast strains that can be used as an attractive feeding source for D. suzukii; 2. The identification of attractive yeast volatiles for D. suzukii; 3. The identification of phagostimulants from yeasts to create a feeding substrate; 4. The characterization of D. suzukii behavior towards yeasts, plants and insecticides; 5. Semi-field and field experimentation in vineyards of susceptible cultivars (e.g. Schiava) to test the efficacy and persistence of the novel attract and kill system.

Among the eight yeast strains tested, Hanseniaspora uvarum showed to be the most attractive one. Volatile compounds were collected from yeast headspace with closed loop stripping analysis (CLSA), solid-phase microextraction (SPME) and direct headspace, and then characterized by gas chromatography - mass spectrometry (GC-MS). Bioactive compounds were characterized using gas chromatography electroantennography detection (GC-EAD) on adult flies. The detection of these chemicals was characterized with EAG dose-responses on adult flies. Metabolites were analyzed using ion chromatography with pulsed amperometric detection (IC-HPAE-PAD) and a conductivity detector and liquid chromatography-electrospray ionization-triple quadrupole mass spectrometry (UHPLC-QqQ). For testing the attractiveness and adulticide efficacy of our yeast-based trapping lure laboratory and semi-field trials were performed with and without insecticides.

The project DROMYTAL is funded by “European Regional Development Fund (ERDF) 2014-2020“.

Host preference and interspecific interactions between Drosophila suzukii and Drosophila melanogaster

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Abstract: Many Drosophila species develop on overripe fruit substrate and associated microorganisms. Interestingly, the agricultural pest, Drosophila suzukii, is capable of attacking fresh soft-skinned fruit causing economic losses to the fruit industry. From early ripening, fruit gets pierced and damaged through egg-laying and larval feeding inside the pulp. Moreover, wounding facilitates secondary microbial infections and furthermore makes ripening fruit accessible for D. melanogaster infestation. Interested in the ecological interactions between D. suzukii and D. melanogaster, we first examined the olfactory preference of D. suzukii and D. melanogaster for different developmental stages of raspberry fruits. We demonstrate that in competitive choice-assays between unripe, ripe and overripe fruit, the olfactory preference of D. suzukii females is dependent on mating state. Furthermore, fruit preference differed between females of D. suzukii and D. melanogaster. Secondly, we studied how heterospecific interactions influence the flies’ oviposition behaviour. Overall, our results suggest that the specific preference for fruit in D. suzukii and D. melanogaster is not only dependent on the fruit’s developmental stage but also the flies’ mating state as well as interspecific cues. Insight into the behavioural responses to host odours and fly signals facilitates understanding of the ecological and evolutionary relations between D. melanogaster and D. suzukii.

Influence of elevated CO2 content in ambient air on emitted leaf volatiles of Vitis vinifera and Pyrus communis.

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Abstract: Climate change can threaten our food production. Because of changing temperatures and concentrations of greenhouse gases, well-established pest insect control techniques may have to be adapted to the changing requirements to stay effective. Especially temperature, elevated carbon dioxide (CO2) and ozone concentrations will have significant impacts on the environment and therefore certainly on control strategies based on chemical ecology of insects. Here we test the hypothesis that allelochemically mediated communication is influenced by the determinants of climate change. The main question posed in this study is: Does the volatilomes of grapevine (Vitis vinifera) and of pear (Pyrus communis) got altered by climate change determinants. We present the results of a two-year survey on the effects of elevated CO2 from a field study carried out in a German vineyard equipped with a FACE (free air carbon dioxide enrichment) ring system, which enables to measure the effects of elevated (500 ppm) to ambient (400 ppm) directly.

Plant nutrient supply alters the magnitude of indirect interactions between insect herbivores: From foliar chemistry to community dynamics

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Abstract: Density- and trait-mediated indirect interactions (DMIIs and TMIIs, respectively) are important drivers of community dynamics. However, it remains unclear how plant nutrient supply affects the magnitude of such interactions. A series of experiments were performed by setting up a four-species "diamond" food web, comprising a plant species (tomato), two insect herbivore species (a leaf miner and an aphid), and a shared natural enemy (a predatory bug). We found strong indirect effects of the leaf miner on the aphid. Leaf miner eggs negatively affected aphid populations due to increased predator abundance (DMIIs), while the presence of leaf miner larvae delayed aphid development and increased its risky defence behaviour (TMIIs). The latter scenario could be further explained by enhanced foliar chemical defence and decreased nutritional quality.

Will climate change affect biological control of the European grape berry moth (Eupoecilia ambiguella)? Lessons learned from a VineyardFACE facility.

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Abstract: The increasing atmospheric carbon dioxide (CO2) concentration is expected to influence trophic interactions between plants and associated insects. While the direct effect on insects may be negligible, the indirect effect, mediated by altered host plant quality, can change the herbivore's performance and, hence, can result in bottom-up effects on natural enemies. Since CO2 assimilation via photosynthesis is a fundamental process of plant metabolism, increased availability thereof can have a major impact on plant quality, both in terms of nutritional quality and level of chemical defense. Such tritophic interactions between crop plants, herbivores, and natural enemies are pivotal components of many biological control strategies.

European grape berry moth (GBM; Eupoecilia ambiguella, Tortricidae) is an important insect pest on grapevine in Europe. In the vineyard, E. ambiguella eggs are subject to parasitism by the egg-parasitoid Trichogramma cacoecia. Larval food quality can influence numerous life history traits of tortricid moths, for instance the number and size of eggs laid by adults. Larger eggs often contain more nutrients than smaller ones which makes egg size an important factor for parasitoid fitness, possibly affecting their parasitism preference and/or performance.

We used grapes cultivated in the Geisenheim VineyardFACE (Free-Air Carbon dioxide Enrichment; Vitis vinifera cv. 'Riesling') to test whether elevated CO2 indirectly affects GBM life history traits. In laboratory experiments, we reared GBM on artificial diet enriched with grapes cultivated under ambient (aCO2: 400 ppm) or elevated CO2 (eCO2: 480 ppm). On diet containing eCO2-grapes, larval survival was lower and more females hatched successfully compared to aCO2-grape diet. The eggs females laid, however, were smaller when larvae fed on eCO2- compared to aCO2-grape diet. While increased larval mortality might lead to reduced pest pressure in the future, decreased egg size might result in reduced parasitism. The respective parasitism and emergence rate as well as tibia length of T. cacoecia are being investigated and will be presented at the congress.

While elevated CO2 concentration is only one facet of climate change, our results demonstrate that its indirect effect on insects can be complex and might differ between trophic levels. In order to anticipate future success of biological pest control, comprehensive studies are crucial.

Are we able to stop the invasion of Aedes albopictus in Germany?

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Abstract: In Germany the Asian tiger mosquito Aedes albopictus was first recorded in 2007 north of Basel at highway 5 coming from Italy via Switzerland. Since that this species expanded tremendously and is found almost at each resting/service station along the highway. The main tool for introduction to Germany are vehicals e.g. returning tourists or trucks coming from the heavily infested mediterranian area. Whereas, up to 2017 in 5 communities established populations were recorded, in 2019 16 communities were infested by Aedes albopictus. Our ultimate goal is the immediate assessment of the Ae. albopictus populations, to assess the size of the infested area and abundance of tiger mosquitoes, and if necessary set up a control programme with the city authorities in close cooperation with the health departments. The public awareness (passive monitoring) is a very powerful tool to record tiger mosquitoes area-wide. Inhabitants send us suspected specimen or pictures of invasive mosquitoes. Control operations are immediately implemented if a established population is indentified. The control strategy comprises 4 colums: 1) Community participation stimulated by thorough information of the public by flyers, press releases or exhibitions in the communities which are affected. 2) and 3) the main asset to strongly reduce or even eliminate the population are „door-to-door“ inspections in a three week interval going along with the applications of Bti (Vectobac WDG) at high dosages to achieve long-term effects for at least two months in mass breeding sites as rainwater containers or small water collections. Despite all efforts in some locations we achieved only a reduction of the Aedes albopictus population for about 95% due to cryptic breeding sites or non accessability of the promises. Therefore, we implement as 4. column the SIT (Sterile Insect Technique) in close cooperation with the Centro Agricolura Ambiente (CAA) in Crevalcore (Italy). Our genotype is massed reared, sexed by sieving at CAA and finally the males are sterilized by Gamma-radiation (35 Gray). About 1500 males/ha were released at a weekly basis in the infected areas from May till October. Employing ovitraps the sterility and occurrence of Tiger mosquitoes were determined. As a result in some areas the Aedes albopictus populations were wiped out. Nonetheless, it seems that Aedes albopictus is established in South-West Germany and needs a long-tern control activity and engagements of the communities. The establishment of the Asian Tiger mosquito is favorited by climate extremes the last years such as very hot sommers which increase the likelihood of transmission of arbovirus.

Mating system, control of breeding resources, and body size predict acoustic signalling in bark and ambrosia beetles

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Abstract: Playing a significant role in sexual behaviours, such as premating recognition, courtship, and copulation, acoustic communication in beetles is diverse and often sexually dimorphic. However, the factors that determine the presence of acoustic signalling in a given species remain unclear. We examined acoustic communication in bark and ambrosia beetles, a speciose group with diverse forms of reproduction and mating systems taking place within plant tissue. For the first time, we show that, for any given species, mating system, sex that defends breeding resources, and size predict both the presence of acoustic communication and the sex that signals.

Attack of the clones

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Abstract: The green peach aphid (Myzus persicae) (Hemiptera: Aphididae), is the most economically important aphid pest worldwide. This species is highly polyphagous and is well known for its ability to become resistant against many different groups of insecticides. We aimed to gain insight into the genetic structure of M. persicae populations in both conventional (insecticides are used in addition to biological control) and organic (no insecticides are used, and only biological control is used) Dutch sweet pepper greenhouses. We sampled aphids over four consecutive years (2019-2022) and determined aphid multilocus genotypes with the use of microsatellite analysis. Our results indicate that M. persicae populations in sweet pepper greenhouses are strongly affected by pest control strategy, as well as by the usage of specific pesticides. These strong differences in population genetic structure of M. persicae between organic and conventional greenhouses mean that biocontrol agents have to deal with different types of aphid populations in greenhouses using these two types of aphid control (organic versus conventional). Furthermore, our results seem to indicate that M. persicae continues to develop resistance against the currently used insecticides, and emphasize the need for successful biocontrol practices to keep on controlling these insect pests in agricultural systems.

Aphids out of control? The role of symbiont-driven resistance to parasitoids in greenhouse biocontrol success

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Abstract: Parasitoid wasps are widely deployed in greenhouses to biologically control aphid pests. From time to time, however, the success of parasitoids aphid pests control is unsatisfactory. In 2003, it was first published that specific bacterial endosymbionts can protect their hosts against parasitoid wasps, potentially explaining the occasional failure of parasitoids to suppress greenhouse aphid populations. Nowadays we know of multiple endosymbionts of which specific strains can protect aphids against their hymenopteran enemies. Previous studies have shown that these endosymbionts are prevalent in natural aphid populations but the occurrence and effects of these protective endosymbionts in greenhouse aphids remain unstudied. This is striking since control of greenhouse aphids relies heavily on the use of parasitoid wasps, both in organic and conventional greenhouses. Protective endosymbionts are expected to greatly affect aphid-parasitoid community dynamics in greenhouses. Because of this reason, greenhouses harboring endosymbiont-infected aphids might need alternative control strategies to optimize the control of their aphids.

In our study, we investigate the occurrence and prevalence of aphids and their endosymbionts in greenhouses and field populations in the Netherlands. Our aim is to understand which aphid-symbiont combinations are present, and how they affect parasitism rates.

La Cage aux Feuilles: Physical Exclusion of Brown Marmorated Stink Bug in Tree Fruits

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Abstract: Brown marmorated stink bug is a recent invader of the tree fruit growing regions of the western US. In an effort to avoid the disruption of IPM programs that has occurred in other invaded regions, we explored a non-pesticidal method of control: physical exclusion. Using native stink bugs as a proxy, we found that damage inside a multiple-tree cage was lower than in the sprayed or unsprayed check. Additional benefits of the cage included reduced levels of sunburn and damage from a key pest, codling moth. However, there were consistently higher levels of woolly apple aphid inside the cages, associated with greatly reduced abundance of lacewings and syrphids, known aphid predators. Single wall barriers were also tested as a less expensive alternative to orchard cages. We determined that the majority (94%) of stink bugs migrated into the orchard from native shrub-steppe vegetation between 0.4 and 3.2 meters. Replicated single-wall barriers 4 m in height were constructed on orchard borders where the native vegetation was known to harbor stink bugs. The barriers included 15 cm flaps to trap stink bugs migrating upwards on the net. These were compared with flaps fitted with insecticide-infused netting, which killed more stink bugs than the net-only flaps, but also more non-target organisms.

Cacopsylla pyricola uses substrate-borne vibrations to communicate with and attract mates (Hemiptera: Psyllidae)

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Abstract: There are a number of species within the family Psyllidae that are economic pests in fruit crops. One of the most prevalent is the pear pyslla, Cacopsylla pyricola (Förster) (Hemiptera: Psyllidae). This psylla can transmit disease, inject phytotoxin, and cause fruit russetting on pear trees. In depth understanding of their mating behavior, specifically their communication system can provide a more targeted integrated pest management strategy. Here, we report one of the first evidence of substrate-borne vibrations in C. pyricola as a way to communicate with, attract, and locate mates. We also characterized and identified signal traits of male courtship songs that can be influenced by environmental stimuli such as temperature, substrate and pheromone presence, which could provide potential mating disruption mechanisms.

From pest to delicacy: entomophagy as boon for managing scarab beetle in Majuli river island of Assam, India

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Abstract: Bioecology of the white grub beetle, Lepidiota mansueta was studied in Majuli river island and Department of Entomology, Assam Agricultural University during 2005-2010. This species had appeared as a severe key pest of many field crops in Majuli, the largest mid-river deltaic island of the world. The most severely affected crops were potato, sugarcane, colocasia and green gram and the extent of damage varied from 42-48, 15-20, 35-40 and 30-35 per cent, respectively. L. mansueta is a unique biennial species, which is the first of its kind from North East India. It has the unique distinction as the first Indian phytophagous white grub species with nonfeeding adults. The species spent its entire life cycle under the ground except for a very short period (2-3 weeks) during which adults come out of the ground for mating and oviposition. Light trap was found highly effective to catch the beetles during their premating flight (6.15-7.15 pm) and thereafter scouting to pick up the mated pairs found abundantly on sheltering plants was also feasible. To combat the beetle menace, a massive mass campaigning was conducted in the island embracing social engineering approaches exploring light traps and scouting by deploying 400 farmers at 40 beetle endemic villages during 2010-2019 leading to massive collection and killing of approximately 11.33 lakhs beetles.

Efforts were made to analyze the nutritional profiling of the beetles for their further exploration as human food/animal feed. The proximate analysis of the beetles revealed a higher amount of crude protein content (76.42%) along with other proximate parameters like crude fat (4.10%), crude fibre (5.16%), total mineral (2.98%), carbohydrate (9.18%) and moisture (2.16%). The energy content was 379.29 kcal/100g of sample. Elemental analysis revealed the presence of 7 minerals viz., Na (27.76), K (14.20), Ca (33.33), Fe (1.64), Cu (6.52), Zn (15.55) and Mn (1.30) mg/100 g of sample. As antioxidant properties, the phenol and flavonoid content was found to be 4.00 mg catechol equivalent/g and 1.59 mg quercetin equivalent/g, respectively. The DPPH was registered 22.60 per cent whereas tannin (3.24 mg/g) as antinutritional compound was recorded at acceptable level. Fatty acid profiling showed maximum amount of saturated fatty acid (2.24%) followed by mono unsaturated fatty acid (0.57%) and polyunsaturated fatty acid (0.49%). Altogether 10 fatty acid were estimated, of which palmitic acid content was recorded in maximum amount (0.28%). Amino acid profiling registered 17 amino acids, of which 8 were found essential. Considering the immense nutritional value of the beetles, two dishes viz., beetle fry and roasted beetles were developed and popularized through community feast. This mass campaigning programme had tremendous impact in terms of protecting the crops, disseminating ecofriendly technologies, enhancing crop productivity as well as improving both livelihood and nutritional security.

Improving an attract and kill strategy targeting wireworms: influence of biotic and abiotic parameters

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Abstract: Wireworms, the polyphagous soil-dwelling larvae of click beetles (Coleoptera: Elateridae), are major insect pests of worldwide relevance causing tremendous yield losses in several crop production systems, like potatoes. In the projects ATTRACT and ATTRACAP, we developed novel mechanically stable beads containing CO2 emitting baker's yeast as an attract component, an isolate of M. brunneum as a kill component and a substrate as a nutrient source and drying aid. Commercialized as ATTRACAP®, the beads are produced by bioencapsulation of both the micoorganisms and the substrate in alginate and dried with a fluidized-bed drying process. The attract and kill formulation allows an application dose of 30 kg/ha with an active substance of 1,2 x 1010 conidia/ha, thus making the product cost-effective and eco-friendly. New insights into which external factors influence the efficacy of ATTRACAP® and how new adapted formulations and application technologies are able to level out these variations will be presented.

To conclude, this novel CO2-releasing bead system is not only suitable for cost-effective delivery of low doses of fungal biological control agents to the soil against wireworms, but it can also be transferred to other soil dwelling pest species.

A long non-coding RNA modulates tiger mosquito reproductive ability and points to species-specific insecticide applications

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Abstract: Long non-coding RNA (lncRNA) research has emerged as an independent scientific field in recent years. Despite their association with critical cellular and metabolic processes in plenty of organisms, lncRNAs are still a largely unexplored area in mosquito research. We propose that they could serve as exceptional tools for pest management due to their unique advantages, such as low inter-species sequence conservation and high tissue specificity. In the present study, we investigated the role of ovary-specific lncRNAs in the reproductive ability of the Asian tiger mosquito, Aedes albopictus. Through the analysis of transcriptomic data, we identified several lncRNAs that were differentially expressed upon blood feeding. Then, we applied an RNAi pipeline and observed that silencing of a lncRNA (Norma3) resulted in significant impact on its fecundity and fertility. Specifically, compared to anti-GFP control, anti-Norma3 group laid 57% eggs, while out of the laid eggs 47% hatched. Moreover, we scrutinized the expression profile of deficient ovaries and detected a significant expression drop in a cluster of mucins, indicating a potential mechanism of in cis regulation between them. Our work demonstrates the first, to our knowledge, experimental proof-of-evidence connecting lncRNAs with mosquito reproduction and opens a novel path for pest management.

Screening of biocontrol agents in Russia: long-run experience and new approaches

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Abstract: The current approach to the screening of natural enemies is mostly just a long process of “trial and error”, which is based on comparative analysis of species in relation to some traits (so-called criteria of natural enemy efficacy). However, the same traits may have different effects depending on their combination and under different conditions.

We need an approach that could bring all the information about the species together, process it mathematically, and summarize it all in one final indicator. The methodological basis for that would be the system of life strategies invented by Grime (1973), which includes three primary strategies: violents, patients, and ruderals. In their pure form, those primary life strategies are connected by trade-off relations, i.e. mutually exclusive of each other. However, different strategies may appear in the same species depending on the Spatio-temporal changes in the environment, primarily limiting factors, the fluctuation of which put at risk the species survival. We determine the position of the species in the three-dimensional space of life strategies, taking into account indicators reflecting its resistance to stress and competitive crowding out, as well as the ability to quickly realize the reproductive potential in the presence of a competitor-free food resource. We are not limiting ourselves to analyzing the life history strategies of only predators and parasitoids, but also conducting a similar analysis of their victims and host plants. It let us expand our understanding of the co-evolutionary relationships of organisms at three trophic levels in the triotroph system (plant-phytophagous-entomophagous).

The key problem of natural enemy screening is that quick adaptation to new conditions could make species effective biocontrol agents and harmful invaders as well. Despite all the external differences, biocontrol and invasion have much in common.

Thanks to the data accumulated over the last 150 years of biocontrol development, we have a unique opportunity to “have a sneaky peek at the correct answer”. The life-history strategies of successfully used and relatively safe natural enemies might be compared with those species that are not considered promising for biocontrol. An analysis of the distribution of “successful” and “unsuccessful” natural enemies within the Grime’s triangle opens up new possibilities for selecting species within certain systematic groups. This analysis helps to identify the combination of signs and environmental factors (including anthropogenic ones) that have turned some species into our indispensable helpers in pest control, while others - into dangerous invaders.

Factors driving the within-plant patterns of resource exploitation in a herbivore

Authors: Bellec Laura, University of Rennes1, France

Abstract: In herbivores, although specific within-plant patterns of resource exploitation at the intra-individual scale have been reported, such patterns remain scarcely described and their determinants poorly understood. Here, we describe and try to decipher the determinants of the foraging pattern of the pollen beetle (Brassicogethes aeneus), a pollinivorous insect that is a pest of oilseed rape (Brassica napus). This insect feeds from flowers for almost all of its life cycle, except for a couple of weeks preceding blossoming. During this period, only flower buds are available and the insect destroys them to feed from the pollen they contain, causing serious yield losses. We found that during this critical period, pollen beetles exhibit a stereotypic intra-inflorescence feeding pattern that depends on flower bud maturity. To explain this pattern, we first deciphered the selective pressures driving pollen beetles’ feeding behavior. Since flowers are the natural food source of this insect, we used the preference for flowers over flower buds to achieve that goal. Our results reveal that pollen beetles’ feeding behavior seems to be driven by a process of maximization of total macronutrient intake. We next found that the intra-inflorescence feeding pattern of pollen beetles could be well explained through this lens.

Could E93 play the adult specifier role in the embryo?

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Abstract: E93, the factor that triggers metamorphosis in insects, has an expression peak in the preadult stage of hemimetabolans and holometabolans. We observed another E93 expression peak in early embryo of the hemimetabolan Blattella germanica, whereas E93 expression is low in the embryo of the holometabolan Drosophila melanogaster. Depletion of E93 transcripts in B. germanica embryos interrupted the development. RNA-Seq analysis of these embryos revealed a number of up- and down-regulated genes compared with controls. Downregulated genes were enriched for functions involved in development. We wondered whether low and high embryonic levels could be a general trend in hemimetabolans and holometabolans, respectively. Thus, we queried publicly available RNA-seq datasets from embryos and preadult stages of insects to estimate the expression of E93. The results showed that hemimetabolan embryos tend to express E93 at high levels, comparable to those of the last nymphal instar. In contrast, E93 in holometabolan embryos tends to be very low compared to pupal expression levels. We conjecture that E93 expression in the hemimetabolan embryo could drive the development of the adult-like morphology shown by the nymphs. Also, that the reduction of embryonic expression of E93 could have been instrumental for the emergence of the larva and holometaboly.

Paleopterans join the MEKRE93 club

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Abstract: larva (divergent from the adult), pupa and adult. Hormonal control of metamorphosis is based on ecdysone, which triggers molts, including metamorphic ones, and juvenile hormone, which represses metamorphosis. At the molecular level, metamorphosis is regulated by the MEKRE93 pathway, by which the juvenile hormone, through its Met receptor, induces the expression of the transcription factor Kr-h1, which represses the expression of the E93 factor, which is the trigger of metamorphosis. The MEKRE93 pathway is conserved in Polyneoptera and Paraneoptera (hemimetabolans) and in Endopterygota (holometabolans), although in the latter it is more complex, as it incorporates the transcription factor Br-C, which determines the pupal stage. We have found that metamorphosis in Cloeon dipterum (Ephemeroptera) is also regulated through the MEKRE93 pathway, similarly to Polyneoptera. More recently, Okude, Futahashi and collaborators have shown that Ischnura senegalensis (Odonata) also regulates metamorphosis by the MEKRE93, although with some specific variations. Thus, we can conclude that this pathway regulates metamorphosis in all insects, which suggests that its origin coincides with the emergence of wings and metamorphosis, about 410 million years ago.

African parasitoid mass rearing for Coffee Berry Borer Area-Wide control in Colombia

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Abstract: The coffee berry borer, Hypothenemus hampei (Coleoptera: Curculionidae: Scolytinae), native to Africa, is the most serious insect pest of coffee globally. H. hampei has invaded many new coffee production areas without its natural enemies. Two African parasitoids, Prorops nasuta (Hymenoptera: Bethylidae) and Phymastichus coffea (Hymenoptera: Eulophidae), were mass reared for field release against H. hampei in Manizales, Colombia. On a 70-hectare coffee farm, releases of more than 2 million wasps of each species resulted in parasitism rates of up to 12% for P. nasuta and 45% for P. coffea. Parasitoid releases lead to in a 28% reduction in H. hampei populations in replicated dispersion patches (old coffee) and a 68% reduction in colonization patches (new coffee) within this farm. Results support the technical and economic feasibility of area-wide parasitoid releases in Colombian coffee for H. hampei population suppression.

Disentangling the genetic and morphometric history of the migrant butterfly Vannesa carye (Lepidoptera: Nymphalidae), An altitudinal starting point at northern Chile.

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Abstract: The cosmopolitan butterfly genus Vanessa (Lepidoptera: Nymphalidae) is well known as a migratory genus that comprises approximately 20 species, which are present on all continents except Antarctica. In South America, the species Vanessa carye occurs from Venezuela to the Chilean Patagonia and it is suspected to be a long-distance migrant. In Chile, V. carye has been reported performing active flying at extreme high levels of altitude, in areas such as the Chilean Andean Altiplano at 5200 mt altitude (Casiri Lake and Sora Pata Lake), as well as at the sea level in the Arica & Parinacota Region. Nevertheless, in insects, and particularly for Chilean butterflies, there is an absence of studies focusing on migratory patterns, let alone studies analyzing the mechanism that these species might be using as part of their life histories to survive the extreme environmental conditions of the Andes in northern of Chile.
The following research will give a good starting point to collect information on the wing morphometrics and genetic characteristics of V. carye's. All of these information will contribute to elucidate some fundamental questions regarding V. carye's migratory patterns and adaptation to the high altitudes of the Chilean Andes. Therefore, it of vital importance understand that landscape and environments where an organism lives can strongly affect dispersal and gene flow and it is essential to clarify the biotic and/or abiotic factors influencing the differentiation of the V. carye´s populations. This can help in the understanding of the underlying mechanisms that explain the observed genetic and morphological diversity of this species.

Molecular mechanisms supporting survival of ticks (Ixodidae) following environmental, physiological, and chemical stress

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Abstract: Ticks are obligate blood feeders but spend the majority of their lives off host where they must contend with a multitude of stresses that can influence distribution and population dynamics. Ticks must tolerate extended periods of thermal stress, desiccation, lack of food, and acaricide exposure; however, little is known about the mechanisms underlying survival of ticks under these stresses. To uncover specific aspects associated with stress survival in ticks, we examined the transcriptomic responses of several hard ticks (Ixodidae) in relation to thermal stress, dehydration, starvation, and chemical exposure. RNA sequencing was used to analyze transcriptional changes following stress exposure and revealed 500 to ~3,000 differentially expressed genes with the enrichment of stress-response, proteolysis, and detoxification pathways as well as shifts in expression of metabolic-related genes. Up- and down-regulated pathways were compared among treatments and species to identify common stress response genes. Follow up analyses found the accumulation of several metabolites, including amino acids, suggesting that these molecules may protect against each stress. Finally, analysis of tick energetics demonstrated that lipid and protein resources are critical for energy during extended starvation and sufficient stores of these reserves are critical to stress tolerance. Overall, our results identified specific molecules and pathways that contribute to tick stress tolerance and lay the groundwork for further studies on biotic and abiotic stress for these important disease vectors.

Dehydration of mosquitoes alters blood feeding dynamics

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Abstract: The goal of this study was to assess the effects of dehydration on the retention of a bloodmeal and the resulting effects on survival, nutritional reserves, reproduction, and overall hydration status in mosquitoes. This study focused on Culex pipiens (Culicinae), the northern house mosquito and a vector of Sindbis and West Nile viruses, and Aedes aegypti (Culicinae), the yellow fever mosquito and a vector of Zika. In this study we exposed C. pipiens and Ae. aegypti to different relative humidities, recovery conditions, and blood feeding opportunities to compare changes in hydration status and nutritional reserves derived and retained from a bloodmeal. Results indicate that dehydrated mosquitoes increase fluid acquisition, improve retention, and decrease excretion of a post-dehydration bloodmeal. These findings ultimately suggest the involvement of compensatory and/or regulatory hydration mechanisms associated with blood feeding by dehydrated mosquitoes. Although the effects of dehydration on survival appear to be curtailed by blood feeding, increased survival appears to come at the cost of reduced reproductive output. Due to obvious implications in vectorial capacity, we expect our studies to provide insight into the mechanisms that underlie bloodmeal utilization and conservation in dehydrated mosquitoes and how that may impact arbovirus transmission dynamics. Ultimately, these results become increasingly important as drought intensifies with climate change and may be utilized to improve the efficacy of control efforts.

Effects of seed beetles and their parasitoids on plant performance and defence across generations

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Abstract: For seeds of wild lima bean plants, seed damage by seed beetles is not always lethal. We investigated the wider consequences of seed herbivory on seedling performance and on plant quality and whether parasitoids that kill seed-feeding larvae can mitigate such effects. We found that pre-dispersal seed damage by seed-feeding beetle larvae strongly affects plant performance, from germination and early plant development to chemical defence and resistance to a generalist lepidopteran herbivore. Some of these effects were dramatically attenuated by parasitism, resulting in a net increase in the number of viable seeds. However, despite their strong beneficial effects on germination and plant growth, parasitoids did not affect the infested plants' reduced ability to invest in defence chemistry. Our findings show an important role of seed feeders in the long-lasting consequences of indirect plant-mediated interactions in a community-wide ecological context and the important mitigating effects of parasitoids in terms of plant fitness.

Detection of forest insects by insect borne volatiles using IMS

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Abstract: Forest insects use pheromones for inter- and intraspecific communication. These pheromones can be used to detect those insects in an early stage of infestation. Ion mobility spectrometry was used to detect specific volatiles emitted by the European spruce bark beetle (Ips typographus (L.)) during early artificial infestation in the laboratory. After only a few days of infestation, detection was possible. Detection of nun moth (Lymantria monacha (L.)) egg masses, oak processionary moth (Thaumetopoea processionea (L.)) egg masses, spruce wood engraver (Pityogenes chalcographus (L.)) adults/infestation and bore dust of European spruce bark beetle (Ips typographus (L.)) was successful. Further research is planned to transfer the laboratory achievements into practice.

The making of an olfactory specialist

Authors: Benton Richard, University of Lausanne, Center for Integrative Genomics, Switzerland

Abstract: The evolution of animal behaviour is poorly understood. Despite numerous correlations of behavioural and nervous system divergence, demonstration of the genetic and cellular basis of interspecific behavioural differences remains rare. We have developed a novel neurogenetic model, Drosophila sechellia, a close cousin of D. melanogaster that displays profound behavioural changes linked to its extreme specialisation on noni fruit. Using calcium imaging, we identify D. sechellia olfactory pathways detecting host fruit volatiles. Mutational analysis indicates roles for different olfactory receptors in long- and short-range attraction to noni. Cross-species allele transfer demonstrates that tuning of one of these receptors is important for species-specific host-seeking. We identify the molecular determinants of this functional change and characterise their evolutionary origin and behavioural significance. Through circuit visualisation, we find that these noni-sensing pathways are also distinguished by increases in olfactory sensory neuron (OSN) population size in D. sechellia; partner projection neurons (PNs) do not change in number, but some display novel wiring properties in this species. Comparative neurophysiology of odour-evoked responses of PNs in D. sechellia and D. melanogaster reveals that increased sensory pooling results in reduced post-synaptic depression at OSN:PN synapses. This phenomenon enables more persistent transmission of repeated or prolonged olfactory signals in D. sechellia, synergising with the increases in sensory sensitivity conferred by receptor tuning changes. Together, this work reveals the accumulation of molecular, physiological and anatomical traits linked to behavioural divergence, and defines a powerful model for investigating behavioural evolution and neuroecology.

Defense characteristics among Pinus and vulnerability to mountain pine beetle

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Abstract: Long-term contact and evolutionary history between specific plant and herbivorous insect species are expected to increase plant allocation to secondary metabolic defenses. In turn, insect species can evolve counter-adaptations to avoid, tolerate, and even benefit from plant defense allocations. For example, the mountain pine beetle (Dendroctonus ponderosae, Coleoptera: Curculionidae, Scolytinae), one of the most impactful native forest insects in North America, has evolved to use host tree terpene defense compounds as pheromone precursors that facilitate mass attacks. This evolutionary arms-race between insect herbivore and host tree has undoubtedly been on-going at least since community reorganization and diversification of both trees and insects during the Quaternary. Mountain pine beetle is polyphagous on multiple Pinus species, which have evolved differing defense strategies including long-term (constitutive) and short-term (induced) responses. Plant defense is costly, however, and trees with high investment in constitutive defenses are expected to invest less in induced defenses, and vice versa. Moreover, slow growing trees and trees in resource-poor environments are hypothesized to invest a greater proportion of carbon into secondary constitutive defense metabolites than into growth. How these differing Pinus defense strategies influence vulnerability to mountain pine beetle remains unclear. We measured defense traits of several high-elevation Pinus within the range of mountain pine beetle in the western United States. Included in our study are the three species in the ancient Balfouriana group, including the notoriously slow growing and long-lived Great Basin bristlecone pine (P. longaeva). In a lab study, Great Basin bristlecone pine phloem was shown to be toxic to developing mountain pine beetle brood, and in the field Great Basin bristlecone pine had high levels of constitutive defenses and was apparently less preferred by mountain pine beetle relative to co-occurring Pinus species. Comparisons of defense strategies among and within Pinus species will be presented and discussed as they relate to vulnerability to mountain pine beetle.

Distinct genes are responsible for myrosinase activity in larvae and adults of the horseradish flea beetle, Phyllotreta armoraciae

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Abstract: The horseradish flea beetle, Phyllotreta armoraciae, possesses an activated chemical defense that consists of sequestered glucosinolates and endogenous myrosinase enzymes capable of converting these glucosinolates to toxic isothiocyanates. Here, we identified three genes that encode enzymes with myrosinase activity in P. armoraciae. These myrosinase genes differ regarding their expression in larvae and adults: PaMyr1 is expressed in adults, while PaMyr2 is expressed in larvae. Compared to PaMyr1 and PaMyr2, expression of PaMyr3 was very low in all life stages. Using RNA interference, we confirmed that PaMyr1 and PaMyr2 are responsible for myrosinase activity in adults and larvae, respectively, whereas the function of PaMyr3 is currently unknown. Predation experiments with Harmonia axyridis showed that PaMyr2 expression correlates with larval survival, confirming that the glucosinolate-myrosinase system protects P. armoraciae larvae against generalist predators. Silencing PaMyr2 expression additionally resulted in higher levels of sequestered glucosinolates, and decreased the proportion of hydrolysis products of ingested glucosinolates detected in the body, suggesting that endogeneous myrosinase activity also mediates the turnover of sequestered glucosinolates in larvae. In summary, we show that different genes are responsible for myrosinase activity in P. armoraciae larvae and adults, suggesting that myrosinases have different ecological functions in these life stages.

Evolution of traits associated with the utilization of brassicaceous host plants in the genus Psylliodes

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Abstract: The flea beetle genus Psylliodes (Chrysomelidae, Galerucinae, Alticini) comprises more than 200 species that are associated with host plants belonging to at least 24 different plant families. About 50 Psylliodes species, including the cabbage stem flea beetle, Psylliodes chrysocephala, are specialized on Brassicaceae. We investigated how Psylliodes flea beetles have adapted to the characteristic chemical defense in Brassicaceae, the glucosinolate-myrosinase system. Glucosinolates and the enzyme myrosinase are stored separately in intact plant tissue, but get into contact upon tissue damage, leading to glucosinolate hydrolysis. The resulting unstable aglucone can give rise to different toxic products of which isothiocyanates are the most reactive ones. Studies on glucosinolate metabolism in P. chrysocephala revealed that the beetles convert a fraction of ingested glucosinolates to desulfo-glucosinolates, a detoxification mechanism that prevents the hydrolysis of glucosinolates by the myrosinase. We identified a family of glucosinolate sulfatases in P. chrysocephala and could show that these evolved by duplications of a conserved arylsulfatase gene. Glucosinolate sulfatases were also identified in other Psylliodes species that feed on Brassicaceae, but appear to be absent in Psylliodes species associated with other plant families. Phylogenetic studies suggested that arylsulfatase genes diversified and evolved a novel function within the genus Psylliodes following specialization on Brassicaceae. Although desulfation reduces glucosinolate breakdown in P. chrysocephala, it does not fully prevent isothiocyanate formation. To reduce the toxicity of isothiocyanates, P. chrysocephala partially detoxify them by conjugation to glutathione. We compared glutathione-S-transferase (GST) activity towards isothiocyanates in crude protein extracts of different Psylliodes species and observed a higher capacity to detoxify isothiocyanates in species that use glucosinolate-containing plants as hosts than in non-glucosinolate feeding species. The P. chrysocephala genome encodes about 27 GSTs and members of two subfamilies were active towards isothiocyanates upon heterologous expression. To understand how isothiocyanate-specific GST activity evolved, we functionally characterized the orthologous enzymes from the Solanaceae-feeding potato flea beetle, Psylliodes affinis, and from the polyphagous hop flea beetle, Psylliodes attenuata. Interestingly, these recombinant enzymes also used isothiocyanates as substrates, but differed in specific activity and substrate spectra from their P. chrysocephala counterparts. Based on the phylogenetic relationship of these Psylliodes species, our results suggest that the ability to detoxify isothiocyanates by conjugation to glutathione was already present before specialization of Psylliodes beetles on Brassicaceae. This pre-existing trait might have facilitated the adaptation of Psylliodes species to glucosinolate-containing plants.

Specialization of Psylliodes flea beetles on Brassicaceae is associated with the evolution of glucosinolate sulfatase activity

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Abstract: The leaf beetle genus Psylliodes comprises about 200 species that feed on plants in at least 24 different families. About 50 species are specialized on brassicaceous plants, which defend themselves against herbivores with glucosinolates that are hydrolyzed upon tissue damage to release toxic breakdown products. We previously demonstrated that Psylliodes chrysocephala detoxifies glucosinolate by converting them into desulfo-glucosinolates, and identified a family of glucosinolate sulfatases (GSS) that originates from duplications of the conserved arylsulfatase gene Sulf4. In this study, we inferred the evolutionary history of specialization on Brassicaceae and the origin of GSS in the genus Psylliodes. A reconstruction of the phylogenetic relationships and ancestral host use of 60 Psylliodes species associated with different plant families indicated that specialization on Brassicaceae has evolved at least twice independently from polyphagous ancestors, which in one case was followed by a species radiation. In this phylogenetic framework, we examined the diversification and function of Sulf4-like genes using comparative transcriptomic and biochemical analyses. Our results suggest that a Sulf4 gene duplication associated with the evolution of GSS activity preceded the radiation of Psylliodes species on Brassicaceae, while subsequent lineage-specific duplications of GSS may have facilitated the adaptation to plants with different glucosinolate profiles.

Redistribution of adventive Trissolcus japonicus (Hymenoptera: Scelionidae) in Virginia, USA

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Abstract: Brown marmorated stink bug (BMSB), Halyomorpha halys (Hemiptera: Pentatomidae), has been established in Virginia, USA since the late 2000's and has caused significant ongoing agricultural and nuisance issues there and elsewhere in the Mid-Atlantic region since 2010. In 2014, an adventive population of its highly effective Asian egg parasitoid, Trissolcus japonicus (Hymenoptera: Scelionidae), was discovered in Maryland, USA. In 2015, it was detected in Frederick County, Virginia, where it has established well, although surveillance elsewhere in Virginia resulted in very few or no T. japonicus detections. With approval from the Virginia Department of Agriculture and Consumer Services, efforts to promote and accelerate the establishment of adventive T. japonicus more widely the state were initiated in 2018. At ten woodland sites from northern to southwestern Virginia, all near commercial tree fruit orchards, pre-release surveillance for T. japonicus used yellow sticky traps deployed in the mid-canopy of BMSB host trees. Sampling in early June, 2018 resulted in the detection of one specimen at the site closest to Frederick County. This was followed by two sequential releases of BMSB egg masses parasitized by T. japonicus at all sites in mid-June and late July, then post-release sampling of T. japonicus and BMSB in August, 2018. Trissolcus japonicus was not detected at any site in August, but relatively large captures of BMSB adults, and most importantly of nymphs in pheromone traps at many sites indicated that BMSB eggs had been present during the second and likely during the first T. japonicus release, potentially boding well for parasitoid establishment. In 2019, sampling in June yielded 2 to 6 T. japonicus at 3 of the 10 sites and August samples resulted in detections of 1 to 6 specimens at 3 sites, including two where it had been detected in June. Native parasitoids known to attack BMSB eggs also were captured in the yellow sticky traps. Detection of T. japonicus at 4 of the 10 release sites in 2019 is encouraging. Continued sampling and potentially additional T. japonicus releases in 2020 and beyond are hoped to yield detections at additional sites and increasing detection frequency at the positive sites from 2019.

Macronutrient balance and the longevity/fecundity trade-off in ants

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Abstract: In social insects, queens ensure the reproduction while workers take over all non-reproductive tasks. Several studies have highlighted the effects of environmental factors and in particular nutrition on the development of individual traits and caste determination. However, it remains unclear how food affects fecundity, longevity and task allocation in social insect colonies. Clonal ants, such as Platythyrea punctata, are a suitable model to study direct effects of nutrition while avoiding any other confounding factors. Despite their clonality, colonies have a well-ordered reproductive division of labor based on rank orders established through fighting. Each colony contains only one, rarely several, reproductive workers, while the majority of individuals has inactive ovaries. In this study, we investigated how different diets influenced life history traits in P. punctata workers and in particular fecundity and longevity. Contrary to solitary insects, we found that ants confined to a high-protein diet lived longer but also laid more eggs than ants raised on a low-protein diet. When we induced a nutritional bias between same-aged workers, ants fed with a high-protein diet became dominant and had better developed ovaries than workers on a low-protein diet. This study shows the importance of nutrition in task allocation and highlights the mechanisms that might lead to the evolution of life history traits in social insects.

Underground cooperation helps to increase rice yield after root herbivore injury

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Abstract: Associations with arbuscular mycorrhizal fungi (AMF) have been shown to both increase or decrease resistance to herbivory in different crop systems, but the impact of AMF on plant tolerance to root herbivory remains unknown. We investigated whether AMF inoculation of rice can stimulate rice yields and/or tolerance to rice water weevil (RWW, Lissorhoptrus oryzophilus) injury. We hypothesized that rice growth and yields would be greater and yield losses from RWWs would be smaller in the presence of AMF. We used a 2x2 factorial design, using two levels of insecticide (presence or absence of NipsIt INSIDE, a neonicotinoid seed treatment) and two levels of AMF (presence or absence of an AMF seed treatment) with 10 replications each in four field experiments over three years. Our results showed that AMF treatments slightly increased population densities of RWW relative to control plants, while insecticidal seed treatments significantly reduced weevil densities. AMF inoculation increased rice biomass before and after flooding, and a clear but not always significant increase in yield was observed. Plants treated with AMF showed higher yields compared to the untreated plants; however, treatment with AMF did not reduce percent yield losses after root injury. Analyses of nutrient contents in roots and shoots revealed inconsistent effects of AMF inoculation. In conclusion, this study shows for the first time the potential for AMF seed treatments to increase rice tolerance to root herbivory, by influencing plant biomass and yields. Rice inoculated with either AMF or NipsIt+AMF may provide an effective method for weevil control and for increasing rice yields.

Attract and Kill Technology using HOOK-RPW to Control Red Palm Weevil Rhynchophorus ferrugineus (Olivier)

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Abstract: The Red Palm Weevil (RPW), Rhynchophorus ferrugineus (Olivier) is a key pest of palms worldwide that has significantly expanded its geographical range since the mid-1980s. RPW is currently being managed in area-wide Integrated Pest Management (IPM) programs that mainly rely on the use of Food Baited Pheromone (ferrugineol) Traps and insecticide applications that are inadequate to eradicate adult weevils.

Since 2011, Attract and Kill (A&K) technology using Hook-RPW TM has been extensively validated in multilocational field trials in the Kingdom of Saudi Arabia in RPW infested date palm Phoenix dactylifera L., plantations. In all the test sites, Hook-RPW TM effectively killed adult weevils for as long as five months after application as evidenced by dead weevils in the containers with A&K dollops and suppressed RPW population densities to extremely low levels as indicated by the monitoring captures in the traditional FBPTs in treated plots as compared to the control plots where weevil captures were significantly higher. Hook-RPW TM has been successfully used to eradicate RPW in Mauritania and more recently registered for use against RPW in Jordan. Eradicating the adult floating RPW population using Hook-RPW TM in the field not only breaks the life cycle of RPW, but also significantly limits the dependence of prophylactic insecticide spray applications.

This presentation gives an overview on strengthening the existing RPW-IPM strategy through Attract and Kill technology using Hook-RPW TM.

Insecticide-Treated Clothing

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Abstract: Historically, the greatest cause of casualties in military operations has come from disease rather than from combat. Since 1951, the US military combat uniforms have had chemicals added to them to protect personnel from bites of arthropods. In 1991, the pyrethroid permethrin became the standard treatment of US military combat uniforms. In 2007 the U.S. Marine Corps transitioned from treatment with permethrin in the field to factory treatment of their 50/50 nylon/cotton Marine Corps Combat Utility Uniforms (MCCUUs). The US Army transitioned to factory treatment of uniforms in 2009. Over the past few years, an increasing proportion of combat uniforms are constructed from fabric comprised of nylon, rayon and fire resistant materials such as para-aramid or meta-aramid. These uniforms cannot be treated with in the field and must therefore be treated at the factory level. In 2015, the evaluation of etofenprox-treated clothing was completed and the data were submitted to US EPA for registration. Etofenprox has an improved toxicological profile compared to permethrin and due to this, it can be impregnated into clothing at a higher concentration. The treated uniforms were highly protective out to 75 wash cycles. This chemical is being evaluated for use in additional fabrics.

Invasiveness increases commercial success in the global pet trade

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Abstract: Wildlife trade is a rapidly expanding multibillion-dollar global business. Each year, millions of individuals from thousands of species are traded legally and illegally as ornamentals and pets. This movement of species worldwide acts as a major introduction pathway for plants and animals that escape or are released into the wild. Some of these traded species are invasive alien species (IAS), impacting native biodiversity, agriculture and public health. It is of great concern that IAS are overrepresented among traded species, relative to native species. This may occur because trade has introduced species in the past, creating opportunities for them to become invasive. Alternatively, IAS could have a greater commercial success than native species. But so far, the causal link between invasiveness and commercial success remains unknown. To test if invasiveness increases commercial success, we used an emergent, but substantial, pet trade that cannot be responsible for invasions yet : the trade in ants as exotic pets. We found 520 ant species that are sold as pets worldwide. Invasive alien species were 6.6 times more likely to be traded than native species and were sold by almost twice as many sellers as native species. Greater commercial success was linked to three ecological characteristics that were also associated with greater invasiveness: larger range size, greater habitat generalism and smaller body size. By selecting species with ecological traits characteristic of IAS, the pet trade will likely contribute to the accelerating global spread of current invaders. It may also generate opportunities for future invaders, which have not yet been transported outside of their native range.

Intra- and interspecific variation in functional traits along elevational gradients in Swiss ants

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Abstract: The variation of traits within populations is central to species coexistence, biogeographical patterns, and responses to anthropogenic change. Incorporating individual-level variability has advanced our understanding of community assembly, structure, and dynamics. A trait-based approach may yield more fruitful insights into the shifts in community structure expected with a changing climate. However, intraspecific variation has often been neglected in ecological studies of broad geographic extents; basic patterns for most taxa – particularly insects – remain unknown. As eusocial organisms, ants present an additional level of biological complexity that alters predictions stemming from physiology-based and community-based theory. Here, we detail the changes in functional traits within ant communities across elevations in western Switzerland, and investigate the environmental factors driving the variation in traits. Specifically, we ask whether trait mean and variance vary predictably across elevations at the colony, species, and community scale, and if so, which climatic and vegetation variables are most strongly related. We sampled the soil for ant colonies at 1,147 plots at 44 sites between 365–2,225m during a single summer, collecting 10 workers from each detected colony, and pair this sampling with a broad citizen science effort. We focus our study on traits previously shown to be influential to the fitness and feeding ecology of ants, namely body size, relative leg length, and color. We find considerable variability in trait values within and among colonies of the same species, and elevational trends within the trait-space at the species and community level. For the majority of all taxa, including ants, across the majority of the globe the geographic patterns of traits have not yet been identified, whether at the species or community level. This study aims to help clarify biogeographic patterns in species traits and the underlying processes responsible to improve our understanding of ecological patterns, and our ability to detect and predict impacts of anthropogenic changes in species distributions.

A novel instructor signal in insect sex determination

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Abstract: Insect sex determination depends on a primary instruction during early zygotic development. This primary instruction induces (female instruction) or represses (male instruction) the production of a functional transformer (TRA) protein. Hymenopteran insects have haplodiploid sex determination; males develop from unfertilized eggs and are haploid, whereas females develop from fertilized eggs and are diploid. The allelic state of the complementary sex determiner (csd) gene in the honeybee is the only identified instructive sex determination signal thus far in hymenopterans. To identify the instructor signal of the parasitoid wasp Nasonia vitripennis, that has no csd, we compared transcriptomes of early male and female embryos. We identified a novel gene, named womanizer (wom), that is only expressed in early diploid embryos and only from the paternal, not the maternal allele. Wom is required for female development, as its knockdown led to male development of diploid embryos. Wom knockdown also significantly decreased tra transcripts, indicating that its mode of action is activation of zygotic tra expression. Wom has arisen by exon-shuffling and has homology with p53 genes and a Nasonia-specific gene (LOC100678853). It encodes a P53-like protein that may act as a transcription factor in Nasonia sex determination. This study is another demonstration of the diverse recruitment of primary instructions in insect sex determination.

Genomic localization and characterization of male determining loci in the housefly (Musca domestica)

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Abstract: In insects, sex determination is regulated by hierarchical gene-cascades that are conserved at the bottom but variable at the top. In the housefly, a male-determining (M) locus directs male development by disrupting transformer feminizing function. M loci are located on the Y–chromosome in some populations, where males are XY and females XX, but can also be present on any of the five autosomes or on the X chromosome. M loci consist of repetitive sequences that undergo extensive duplication and translocation in the genome.

M loci on Y and autosomes II-IV contain at least one functional copy of the gene Musca domestica male determiner (Mdmd), a paralog of the spliceosome factor CWC22. An unknown gene that is not Mdmd acts as a male determiner on autosome I. To better understand the genomic complexity and dynamics of M loci, we determined the chromosomal location of different M by cytogenetic mapping and re-sequenced and assembled the male housefly genome, with M locus on autosome III. The MIII locus is over 500Kb in size and contains many copies of both complete and fragmented Mdmd sequences. Transcriptomic analysis revealed that multiple copies of Mdmd are transcribed. We discuss how our findings contribute to understanding the evolution of insect sex determination and sex chromosomes.

Host-range evolution in parasitoid wasps: potential of native parasitoid, Leptopilina heterotoma, to adapt to Drosophila suzukii

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Abstract: Host-range evolution by native species in response to biological invasions augments their ability to reduce the impact of the invader and their value for biological control. We assessed the adaptation potential of the larval parasitoid, Leptopilina heterotoma, to the invasive pest Drosophila suzukii. For this native species to evolve, heritable variation is required in traits involved in the different steps of the parasitization process: (1) host selection, (2) host attack, (3) host killing and (4) offspring development (reproduction). Although this relatively virulent parasitoid has been found to attack the novel host, offspring generally fails to develop due to high resistance of D. suzukii. We did find, however, variation in the preceding steps of the parasitization process. We investigated seven European populations and found significant variation to induce host mortality. We then tested whether we could improve killing performance by crossing these populations to produce a genetically variable source population, followed by seven generations of artificial selection on ability to kill D. suzukii. Moreover, we determined how selection on killing performance influences evolution of the preceding step of parasitization, attack rate, and the sequential last step, reproduction success, as correlated responses would promote host range evolution. Our study reveals that native parasitoids can be exploited as biological control agent of D. suzukii as they significantly reduce fly survival. Moreover, selected wasps showed an increase in their ability to reduce fly survival compared to unselected wasps, indicating that killing performance can evolve. Evolution of this performance trait was also correlated with an increased attack rate and wasps with high killing performance had a higher reproductive success. These results thus demonstrate the adaptation potential of L. heterotoma to the invasive fruit fly pest. Moreover, it demonstrates that different steps of parasitization need to be considered in the evolution of host-range and that evolutionary principles can be applied to optimize performance of native species for biological control.

Microorganisms induce asexual reproduction of haplodiploid wasps by manipulating splicing and transcription of maternally provided sex determination genes

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Abstract: Sex determination in insects involves a cascade of genes leading to differential sex-specific splicing of doublesex that controls downstream sexual differentiation. The doublesex splicing regulator transformer (TRA) is present in most insect orders. Only female-specific tra mRNA (traF) yields a functional TRA protein. In haplodiploid Hymenoptera, haploid males develop from unfertilized eggs that contain insufficient traF and diploid females from fertilized eggs. Apparently, diploidy after fertilization ensures sufficient traF for female development. Nevertheless, two parasitoid species, Asobara japonica and Leptopilina clavipes, can reproduce asexually when females are infected with endosymbiotic Wolbachia bacteria. Infected females lay unfertilized eggs and provide traF to their eggs that then develop as diploid females without a paternal genome. In contrast, sexually reproducing females without Wolbachia lay unfertilized haploid and fertilized diploid eggs and provide both types with non-sex-specific tra transcripts. The fertilized eggs rely on the paternal genome to initiate female development. This suggests that Wolbachia can manipulate host reproduction by altering the splice regulation of sex determination genes, but potentially also by substituting the early zygotic transcription of the paternal genome.

Role of gene polymorphisms in circadian and seasonal behaviour of Nasonia vitripennis

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Abstract: The larger variation in daily cycles of light (photoperiod) and night with increasing latitude has led to the evolution of adaptive photoperiodic behaviour. Nasonia vitripennis is a parasitic wasp which has been used extensively as a model for studying photoperiodism response in insects because of its clear seasonal behaviour. Females can maternally induce diapause in stage L4 larvae, depending on the number of days of a critical day-length. Previous studies reported a latitudinal cline in diapause induction of natural European populations and allelic frequencies of the clock gene period correlated with this clinal variation. As the perception of the daily photoperiod (timer) and number of days with a critical day-length (counter) are essential for diapause induction, it is hypothesised that more clock genes are involved.

In this study we test the involvement of the circadian clock genes period, cryptochrome-2, clock and cycle in the timing of diapause induction. We identified non-synonymous single nucleotide polymorphisms (SNPs) in isogenic lines established from populations of three latitudes. We used sib-ship crosses between those lines to assess their effect on diapause induction timing. Additionally, we tested these polymorphisms for effect on circadian locomotor activity, to get insight in the overlap of seasonal and circadian timing regulation.

We found that the polymorphism in period was also associated with variation in free-running period. SNPs in cryptochrome-2 and clock, but not cycle, were found to be associated with both diapause inductions and free running period. Our results demonstrate the involvement of circadian clock genes in seasonal diapause induction and thus a partially overlapping genetic architecture between circadian and seasonal responses.

A new genus of Phlaeothripidae (Insecta, Thysanoptera) from a Neotropical Rainforest, Brazil

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Abstract: Brazil Conservation proposals require prior knowledge of the fauna. Despite the relevant role of thrips (Thysanoptera) in association with plants, their diversity and biology remain poorly known. Thrips can be predators of other arthropods (Arthropoda), act as pollinators, in addition to damaging plants by plant tissue feeding or pathogen vectoring. In this study, we described a new genus and species collected in the Neotropical rainforest, municipality of Santo Antonio do Pinhal, São Paulo State, Brazil, as part of "Aguas da Mantiqueira" Conservation Project. This project aims to restore 14 hectares of river basin springs around permanent preservation areas in this region. Adults of the new genus and species of Phlaeothripidae were collected in November 2017, associated with ferns. The specimens were prepared in permanente microscope slides in Canada balsam. The slides were deposited at Coleção Entomológica Adolph Hempel, Instituto Biológico, São Paulo (IBSP), Brazil, and Coleção de História Natural da Universidade Federal do Piauí (CHNUFPI), Floriano, Brazil. The new genus and species resembles Pueblothrips. This species belongs to a monotypic genus described from Mexico, probably associated with ground litter, that has been tentatively included in the Williamsiellina, based on the position of the maxillary stylets, low and wide apart in head. This classification, however, is probably artificial, as the only species of Pueblothrips that has two pairs of wing-retaining setae on abdominal tergites, three sense cones on antennal segments III and IV and fore wing with duplicated cilia and basantra absent. The new genus and species presented herein can be recognized by the following character states: pronotum distincltly sculptured with 2 circular irregular areas on anterior two thirds; anteromarginal setae short, epimeral sutures complete, anterior marginal setae as long as discal setae, epimeral and posteroangular setae fan-shaped, longer than anterior marginal setae. This new genus is distinct from Pueblothrips, specially, due to the presence of basantra, remarklable sculpture on pronotum, posteroangular setae fan-shaped and the color of legs, with fore coxa trochanter and femur brown. The discovery of this new genus with intermediate characteristics can help in clarifying Phlaeothrips-lineage classification. In future studies, phylogenetic analysis will be carried out as an attempt to trace possible relationships with this new genus and Phlaeothrips-lineage groups.

Acknowledgments:
The research conducted in M.E.'s laboratory was supported by the Conselho Nacional de Desenvolvimento Científico e Tecnológico, CNPq - Brazil (grant 400936/2016-0) and ME is supported by a CNPq research fellowship. This work was financed partly by the "Coordenação de Aperfeiçoamento de Pessoal de Nível Superior" - Brazil (CAPES) - Finance Code 001. We also thanks "Aguas da Mantiqueira" Conservation Project, that made it possible to carry out this study.

A new species of Frankliniella Karny, 1910 (Thysanoptera, Thripidae, Thripinae) from the Atlantic Rainforest in São Paulo, Brazil

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Abstract: Frankliniella is the most species-rich genus in the family Thripidae, with above 230 species. In South America there are about 74 species recorded, over a half in Brazil. In the Brazilian Frankliniella fauna, 21 species were described based on native material, and many other species remain to be identified. Only six Brazilian species are known as pests of plant production, either by vectoring Orthotospovirus or by causing feeding injuries to plant tissues. Members of this genus can be recognised especially by the postocular setae iii or iv directed posterolaterally and usually longer and stouter than the rest; antennae with eight or rarely seven segments; pronotum always with two pairs of posteroangular major setae and usually with one pair of anteroangular and one pair of anteromarginal major setae;, and between inner pair of posteroangular setae with five pairs of smaller, posteromarginal setae; ctenidia usually on abdominal tergites IV-VII and always on VIII; andspiracles on tergite VIII anterolateral to the ctenidia. In this study, we describe a new Frankliniella species collected in a remnant of Atlantic Rainforest, located in Fontes do Ipiranga State Park (PEFI), urban area in the municipality of São Paulo, São Paulo State, Brazil. Adults of Frankliniella sp. n. were collected during summer months of 2018-2019, associated with Solanum cernuum Vell. (Solanaceae) flowers. The specimens were prepared on permanente microscope slides in Canada balsam. The type material were deposited at "Coleção Entomológica Adolph Hempel", Instituto Biológico (IBSP), São Paulo, Brazil and at "Coleção de História Natural da Universidade Federal do Piauí" (CHNUFPI), Floriano, Brazil. The new species can be distinguished from other bicolored species, especially by: body yellow with antennal segments VI-VIII, wings and abdominal segments I-VIII brown; pedicel of antennal segment III simple; pronotal anteroangular and posteroangular setae longer than a half of pronotum length; posteromarginal comb on abdominal tergite VIII complete, but with short microtrichia medially.

Acknowledgments:
The research conducted in M.E.'s laboratory was supported by the Conselho Nacional de Desenvolvimento Científico e Tecnológico, CNPq - Brazil (grant 400936/2016-0) and ME is supported by a CNPq research fellowship. This work was financed partly by the "Coordenação de Aperfeiçoamento de Pessoal de Nível Superior" - Brazil (CAPES) - Finance Code 001. We also thank Botanic Garden of São Paulo state that made it possible to carry out this study, and to Dra Claudia Del Fava from Pathological Anatomy Laboratory of Instituto Biologico, São Paulo, for allowing the use of the contrast microscope. E.A.M. thanks the Instituto Federal Sudeste de Minas Gerais, campus Barbacena for allowing to carry out this study.

Exploration of white grub beetle, Lepidiota albistigma Burmeister (Coleoptera: Scarabaeidae) as human food in Assam, India

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Abstract: Lepidiota albistigma B. is a white grub species belonging to the Scarabaeidae family under the order Coleoptera. Of late, this species has appeared as an emerging pest, posing a serious threat to many field and horticultural crops in Assam, India. L. albistigma possess annual life cycle where the adult lives for a very short period of 15-23 days. The adult emergence takes place during the evening hours (6.00-6.30 pm) which started from the 1st week of April and continued up to the 1st fortnight of May. Adult beetles mostly preferred to feed on mango, guava, ramie, citrus, arecanut, betel vine and black pepper etc. Grubs remain underground for a long period of 280-314 days infesting major field crops like potato, colocassia, green gram and sugarcane.

Considering the severity of damage, an effort was made for the mass collection and destruction of the beetles at Lower Brahmaputra Valley of Assam during 2014-2019. The beetles were collected through scouting and by using light traps as the beetles showed positive phototaxis. Approximately 40000 beetles were collected and killed at the endemic pockets and majority of them were relished as culinary delight by the tribal populace. Considering the possibilities of exploring the adult beetles as human food, extensive studies were conducted to analyze the complete nutritional profile of the beetles. Collected beetles were cleaned by removing wings and legs, keeping only the edible portion, which was then sun dried and ground to fine powder for further biochemical analysis. Proximate analysis of the sample estimated considerably higher amount of crude protein (68.54%) as compared to other proximate parameters viz., carbohydrate (11.84%), crude fiber (6.73%), crude fat (5.50%), total mineral (4.83%) and moisture (2.55%). The energy content was recorded to be 371.04 kcal/100g of sample. Elemental analysis of the samples revealed the presence of 7 nutrients in appreciable amount i.e., Na (29.57), K (144.33), Ca (29.94), Fe (1.41), Cu (2.01), Zn (2.38) and Mn (1.09) mg/100g. Both antioxidant and anti nutritional properties were also assessed. The phenol and flavonoid content of L. albistigma were recorded to be 6.42 mg catechol equivalent/g and 3.71 mg quercetin equivalent/g, respectively whereas DPPH activity was estimated to be 28.20 per cent. Tannin content was quantified to be 13.30 mg/g which was under acceptable limit. Fatty acid profiling registered relatively higher amount of saturated fatty acid (3.56%) as compared to mono (3.15%) and polyunsaturated fatty acid (1.11%). Palmitic acid content was maximum (2.85%) out of the ten fatty acids recorded. Amino acid profiling of the samples quantified 17 amino acids of which 8 were essential and leucine content was found in maximum amount (6.60%). Based on the nutritional value, a concerted effort has already been embraced for the further exploration of L. albistigma beetles as an alternate source of nutrition for human as well as animal feed in this region.

First evidence of CpGV and management of Codling moth in high altitude cold arid region of Ladakh, India

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Abstract: Codling moth is menace and no solution was available in India for its management so all the fresh fruits from Ladakh is still banned due to quarantine regulations to prevent the 15000 Crore apple Industry of Jammu and Kashmir and Himachal Pradesh. The application of pheromone dispensers and two applications of insecticides throughout the year recorded less than one per fruit damage in apple orchard in Saliskoot Village. The application of pheromone dispensers alone reduced 50 % fruit damage in treated plots as compared to control plots at high density populations of codling moth.The area wide management for codling moth in Nurla/Nimoo villages, using pheromone dispensers showed promising results as compared to untreated plots. Among the treatments, SPLAT-Cydia and two applications of insecticides recorded lowest fruit damage (1.50%) as compared to other treatments and untreated plots recorded (58.75%) fruit damage. This is the first success story for the management of Codling moth in India. Therefore the ban on fresh fruits from Ladakh may not be considered as good rationale by using our management capsule. In addion to our targets, we reported codling moth Granulosis virus(CpGV), first time from India and the isolates were named as CpGV SKUAST-1 (Acc. No. MK801791) and CpGV SKUAST-2 (Acc. No.MK801792 and may be incorporated for the management of Codling moth. This native strain from India has a potential to manage the codling moth in Ladakh because toxic insecticides are neither sprayed and nor encouraged by the growers/policy makers because of socio-religious constraints. Though, major developed strains of CpGV from world, have developed resistance against codling moth and the new identified strain can be exploited globally for codling moth management.

The phylogeography of widespread Australian Cnestus (Curculionidae: Scolytinae) ambrosia beetles and their fungal symbionts

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Abstract: The comparative phylogeographic analysis of insects and their microbial symbionts can provide important information about host-symbiont interactions, transmission ecology and symbiont evolution. Previous co-phylogeographic analyses of xyleborine ambrosia beetles (Curculionidae: Scolytinae) and their fungal symbionts have shown that beetle and symbiont diversity are a manifestation of demographic processes (e.g. as a consequence of climatic change or human introduction of beetles into new environments), and higher diversity is generally found in native than invasive ranges. However, these studies were on a small number of ambrosia beetle species and their fungal associates, and were restricted to the northern hemisphere. We studied the genetic variation of the widespread Australian-endemic xyleborine ambrosia beetle genus, Cnestus Sampson 1911 and their symbiotic fungi of the genus Ambrosiella von Arx & Henneber 1965 (Ceratocystidaceae). In eastern Australia the beetles' distribution spans from Far North Queensland to Tasmania. This extensive range includes refugial habitats for mesic habitat-adapted ambrosia beetles and biogeographic barriers that may limit their dispersal. We used targeted multi-locus PCR approaches to characterise the genetic diversity of Cnestus and Ambrosiella across 2,500 km of their eastern Australian range. Cnestus is associated with at least two closely related cultivars of Ambrosiella which is indicative of either co-evolved fungal associations within this lineage, or alternatively a more recent sharing of the same fungus across different beetle lineages. More extensive characterisation of the genetic diversity of these beetle-fungus interactions will aid in deciphering their evolutionary ecology and provide taxonomic and diagnostic information for these potentially invasive ambrosia beetles and their fungi.

Evolutionary feedbacks between insect sociality and microbial management

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Abstract: Collaborative defenses against microbes have often been considered a by-product of social evolution in insects. Here, we take the view that both defense against microbial pathogens and promotion of beneficial symbionts are major drivers of social behaviours in many insect systems — ranging from aggregation to eusociality. By supporting our view with examples from a variety of taxa, we propose evolutionary feedbacks between the insect sociality and microbial communities. We identified variation in habitat stability — as determined by breeding site predictability and ephemerality — as a main ecological factor that constrains these feedbacks. To test this hypothesis we suggest following the evolution of insect social traits upon experimental manipulation of habitat stability and microbial consortia.

The chemical basis of symbiosis: Volatile interactions between conifer bark beetles and their fungal symbionts

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Abstract: Many insects exhibit symbioses with other organisms through signaling compounds which drive the evolutionary maintenance of mutualistic associations. Bark and ambrosia beetles are associated with a diverse species of symbiotic fungi which are vital for the successful colonization and development of these insects in their host trees. Fungi are able to mobilize/supplement nutrients for beetles by growing in the bark and wood, and also be able to detoxify the defense chemicals of trees which are toxic to beetles.

We investigated if volatile organic compounds emitted from different fungal symbionts could act as cues for bark beetles to recognize and distinguish their microbial community. Fungi associated with bark and ambrosia beetle emit a variety of volatiles comprised of simple aliphatic, aromatic alcohols and its esters, benzenoids, mono-, and sesquiterpenes. Using Ips typographus and its fungal symbionts as a model system, we showed that bark beetles were attracted to fungi in olfactometer assays and beetles preferred to feed on diet colonized by symbionts but not to commensals and pathogens. Testing these fungal compounds on beetle antennae using single sensillum recording revealed that beetles can detect many fungal volatiles and possess several new olfactory sensory neuron classes specialized for detecting the fungal volatiles. Additionally we showed that synthetic blend of fungal volatiles attracted bark beetles in olfactometer assays. These findings indicate that volatile compounds produced by fungi may act as recognition cues for bark beetles to maintain specific microbial communities that might have an impact on their fitness. These biologically active fungal volatiles might also have implications in pest management of bark and ambrosia beetles by deploying fungal volatiles as attractants or repellents alone or in combination with other types of semiochemicals.

New strains of predators to overcome challenges facing biocontrol in protected crops

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Abstract: Integrated pest management (IPM) based on arthropod biological control agents (BCAs) has definitely succeeded on many crops, especially crops grown under greenhouse conditions. Augmentative biological control has proven to be an efficient and robust pest control method, using generalist predators to control key pests.

However, there are serious limitations in the implementation of biological control in some crops, areas and periods of the year. There are constraints to the establishment and success of biological control protocols due to environmental conditions (low or high temperatures, low humidity), adaptation to crops (tomato, cucumber, ornamentals), compatibility with pesticides, etc. All crops, but particularly protected crops, grow under artificial conditions, sometimes very different from those in which natural enemies have evolved. BCAs must live on plants to which they are not naturally adapted, feed on new prey or hosts, thrive under extreme environments, or be exposed to pesticide residues. These stresses challenge the success and widespread adoption of biological control.

In the development of BCAs, interspecific variation has traditionally been used to select the most effective species of natural enemies. However, there is not always new species of BCAs that can perform better. Another source of selection is the variability between individuals and populations within a species. This intraspecific variability has shown potential for developing BCAs, but has barely been applied in the current commercial use of arthropod BCAs. This variation among individuals and populations within a species is what is intended to be explored and exploited through genetic improvement.

In this way, a real possibility of progress in biological control is the genetic improvement of natural enemies, responding to the challenges posed. As successfully achieved in the development of agriculture with plant varieties and animal breeds, the artificial selection of BCAs with certain traits can contribute decisively to a greater success of biological control.

In our opinion, the most important current challenges augmentative biocontrol is facing in protected crops are pesticide compatibility (synthetic or natural), continuous presence on the crop (prey-density dependence, adaptation to alternative food), non-suitable crops (plant defenses, lack of plant-provided food), and environmental conditions (extreme temperature and humidity).

Through a genetic improvement programme of omnivorous predators commonly used in horticultural protected crops, we have selected new strains to overcome these limitations in order to achieve a wider adoption of biological control and enhance its resilience.

Plant-Insect-Microbe interactions: summarizing thoughts

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Abstract: Plant food webs include a stunning diversity of arthropods and microorganisms, and recent studies show that plant-insect-microbe interactions may be a major force structuring plant-based communities. Insect-associated microbes can strongly affect the ability of their host insects to exploit host plants and mitigate insect biotic and abiotic stress. Likewise, plant-associated microbes can strongly affect the quality of their host plants for phytophagous insects and their interactions with natural enemies and mitigate plant biotic and abiotic stress. However, environmental factors strongly modulate such interactions, limiting our ability to predict and apply these microbes in biocontrol. In closing this symposium, we will summarize some recent progress in this field and our understanding of the context-dependency in the outcome of these interactions.

The unusual reproductive ecology of tsetse and why it matters for disease control

Authors: Bierman Anandi, Stellenbosch University, South Africa

Abstract: Unlike most flies, tsetse have extreme maternal investment: females give birth to single larvae that equal their own size, and they do this continuously across their relatively long lifespan. There is no self-feeding by larvae and they are thus exclusively dependent on their mothers for the reserves which will see them surviving through the pupal stage and for the teneral period before they take their first bloodmeal. This is also the point at which they seem most susceptible to infection. Hence, understanding maternal investment has ramifications for predicting tsetse populations and disease spread.

Full-term pregnant tsetse, about to deposit a larva, are difficult to trap in the field, which makes it challenging to study mother-offspring interactions under natural conditions. Moreover, laboratory studies tend not to track the reproductive output of individual flies. Here, I present laboratory and field studies on how mothers allocate resources to their young under different conditions, using innovations in tsetse sampling and housing which alleviate these constraints.

I first describe a trapping method developed by members of our team which exploits the observation that, during the hot months of the year, savannah tsetse (Glossina morsitans morsitans and G. pallidipes) often larviposit in cooler warthog burrows. Using mother-offspring pairs caught using ‘artificial burrows’ at Rekomitjie Research Station, Zimbabwe, we show that mothers produce larger offspring when in better physiological condition themselves, and produce smaller offspring when they experience hotter temperatures during pregnancy.

We also used a new method of housing flies individually, developed at the Liverpool School of Tropical Medicine, to track how reproductive investment in the laboratory depends on maternal nutrition and age. We manipulated nutrition and showed that stressed females produce smaller offspring and, regardless of condition, females exhibit a similar age-dependent pattern of reproductive investment, reaching a peak around their third offspring and declining gradually thereafter. Maternal age can thus be important for offspring condition and life history. These matters are important in population and epidemiological modelling since they affect population responses to environmental change and, potentially, offspring susceptibility to disease.

Nutritional requirements for reproduction and survival in the blowfly, Lucilia sericata

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Abstract: Insects with access to finite energy resources must allocate these between maintenance and reproduction in a way that maximises fitness. This will be influenced by a range of life-history characteristics and the environment in which any particular insect species lives. Here the allocation of resource between survival and reproduction is considered: females of the blowfly, Lucilia sericata (Diptera: Calliphoridae), were fed diets differing in protein and carbohydrate (sucrose) content, and the allocation of lipid to reproduction was quantified using a spectrophotometric method of analysis. Immediately after adult emergence, total body lipid, scaled for differences in body size, showed an initial decline as it was utilised to meet the metabolic demands of cuticle deposition, muscle maturation and then flight. When flies were denied access to sucrose, stored lipid then continued to decrease until flies died, usually within four days of emergence. However, flies given access to sucrose were able to increase body lipid content, demonstrating that carbohydrate is essential for homeostasis and that it can be used to synthesise lipid. Nevertheless, female flies fed sucrose only were unable to synthesise egg yolk. Only flies provided with protein were able to mature eggs. However, the rate of egg maturation and number and size of eggs matured were greater for female flies given liver compared to flies provided with pure whey protein powder. The results demonstrate the importance of different dietary components for different elements of the life-history of L. sericata, namely survival and reproduction.

Integrating more realistic tsetse biology into epidemiological models of human and animal African Trypanosomiases

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Abstract: Classic epidemiological models of vector-borne diseases, based on the Ross-Macdonald framework, often make simplifying assumptions about vector biology, in part due to the lack of data or the need for mathematical tractability. Such models often assume that the biting rate is constant, or that vector mortality does not change with age. However, in the context of the African trypanosomiases, we have rich field and laboratory data on tsetse-trypanosome interactions that challenge these assumptions: for example, older flies have a higher probability of dying and young flies have higher infection rates (the teneral phenomenon).

Here, we present a partial differential equation model that incorporates this biological complexity to better compute the proportion of infected tsetse and infection transmission in vertebrate populations for a fixed vertebrate infection prevalence. Rather than assuming all flies in the population have equal mortality and behaviour, our model takes into account variation according to age and the hunger stage of flies. Young and old flies have a higher chance of dying and tsetse are obligate blood feeders that may die of starvation, which also influences their motivation to bite (depending on the time since their last blood meal). In addition, young flies have higher infection rates.

Overall, our model predicts that – depending on the species - infection prevalence in tsetse decreased up to five times with more biological realism in the model compared to classic models of human African trypanosomiases. Prevalence in tsetse decreased with the teneral phenomenon, starvation, and a more realistic parasite incubation phase but increased with mortality senescence. We use this model to assess the impact on predictions of disease elimination under different control scenarios for both human and animal African trypanosomiases, especially when considering the impact of vector control.

This approach could help improve current African trypanosomiases decision-making tools and could be generalised to other vector-borne diseases, which also stresses the need for further study of vector ecology and evolution.

Ecophysiology and biogeography in water beetles

Authors: Bilton David, University of Plymouth, United Kingdom

Abstract: The factors shaping the size and position of the geographical ranges of organisms remain poorly understood.

I will briefly summarize our recent work which has explored these issues, using water beetles as a model system, studying closely related species which often differ dramatically in the extent of their geographical distributions. Within a given habitat type physiological tolerance appears to be of fundamental importance in shaping both geographical range size and position, but shifts between habitats, whilst relatively rare, may drive dramatic changes in biogeography.

Wolbachia supplement biotin and riboflavin to enhance reproduction in rice planthoppers

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Abstract: Symbiont-mediated nutritional mutualism are important in contributing host fitness of insects, especially for insects that feed exclusively on nutritionally unbalanced diets. Here, we elucidate the functional importance of two plant-sap feeding insects' association of Wolbachia, which is known for manipulating host reproduction as a facultative symbiont. We found the brown planthopper Nilaparvata lugens (Stål) and the small brown planthopper Laodelphax striatellus (Fallén) laid significantly more eggs than uninfected planthoppers, regardless of temperature. Furthermore, experimental transfer of Wolbachia into the uninfected lines rescued their fecundity deficit. Genomic analysis showed Wolbachia strains from both planthoppers encoded complete biosynthesis operons for biotin and riboflavin. And metabolic analysis revealed Wolbachia-infected planthoppers had higher titers of biotin and riboflavin. A series of ecological experiments further verified that supplementation of a mixture of biotin and riboflavin could recover the fecundity deficit of Wolbachia-uninfected planthoppers. In addition, comparative genomic analysis suggests that the riboflavin synthesis genes are conserved among Wolbachia supergroups. However, though being rare in Wolbachia, the biotin operons of all Wolbachia strains share a recent ancestor that may have been horizontally transferred from Cardinium. Our results demonstrate a type of mutualism that involves facultative Wolbachia and plant-sap feeding insects via vitamin Bs and may lead to improved strategies for integrated pest management.

What's Amata with this moth? Aposematic variation in an Australian lepidopteran

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Abstract: Aposematism is an anti-predator strategy where defended prey species advertise their defence with conspicuous warning signals. Predators learn to recognise these warning signals after an initial unpleasant experience and associate the signals with unprofitability. Aposematism incurs selective benefits to the prey, such as increased survival rates, and warning signals are thought to be honest indicators of the strength of the defence. To be effective, warning signals need to be recognisable, memorable and consistent. However, variation in warning signals has been reported in most aposematic taxa, contradicting the theoretical assumption that warning signals are under stabilising selection.

The day-flying aposematic wasp moth Amata nigriceps (Erebidae: Arctiinae) is thought to be a complex of subspecies, which is yet to be taxonomically and ecologically defined. They are conspicuous fliers and are chemically defended by pyrazines and preliminary trials with naïve predators (Blue tits) indicate that the moths are indeed distasteful to birds. The warning signal consists of conspicuous orange spots and stripes against a black background, which varies between 10-30% proportionally, in both males and females. The aim of this study is to quantify and explain the observed variation in Amata moth warning signals. We compared colour patterns of moths from museum collections and our own collections spanning 123 years and related this to climatic variables and bird predator diversity. We found an increase in the warning signal wing spots with increasing temperatures over 90 years and across populations spanning 746kms from across the Australian east coast, but no effect of predator diversity or precipitation. We also conducted a controlled full-sibling laboratory experiment with different developmental temperatures and found no evidence of temperature-driven pattern plasticity, but high heritability (70%) of the warning signal.

We also found a distinct difference in colour pattern between males and females – females are proportionally more red than males, which may reflect sexual selection or an increased need for conspicuousness. These results help us to predict how prey populations may evolve in response to future climate and diversity impacts.

Role of fruit odors in attraction and oviposition behaviors of peach fruit fly, Bactrocera zonata Saunders

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Abstract: Several tephritid species are native to South and South-east Asia, and severely affect horticulture productions. Targeting female fruit flies using techniques that rely on the olfactory sensitivity of the flies, may support direct and more selective ways to control fly populations. This study used Y-tube olfactometer to test the physiological response of economically important pest specie, Bactrocera zonata to host fruits odors and gas chromatography mass spectrometry for the detection of major compound found in whole fruit odor. Three fruit species and their varieties; Guava (Gola, Larkana Small Surahi (LSS) Larkana Large Surahi (LLS),Mango (Sufaid Chaunsa, Black Chaunsa, Fajri Kalan, Aman Dusehri, and Anwar Ratol) and orange (Kinnow, Musami and fruiter) were used to test different behavioral and fitness parameters. Female flies showed significantly higher levels of attraction to both un-infested and infested fruit odors compared to control (blank). In pairwise comparisons of guava fruit varieties, female flies were significantly attracted towards un-infested Gola compared to un-infested LSS, while in the case of intra-varietal comparisons, significantly higher number of flies were attracted to un-infested fruits compared to infested fruit in all three tested varieties of guava. In pair-wise comparisons of un-infested mango varieties, female flies showed significantly higher level of attraction towards the S. Chaunsa compared to B. Chaunsa, A. Dusehri and A. Ratol, while in case of intra-varietal comparisons, significantly more flies were attracted to un-infested fruits compared to infested fruit in all tested mango varieties. In two-choice oviposition bioassays, B. zonata females made significantly more visits, greater numbers of oviposition, spent a significantly longer time, and larger numbers of pupae and adults developed on Gola fruits compared to LSS fruits. While in case of two-choice oviposition bioassays on mango fruit, B. zonata females made significantly more visits, greater numbers of oviposition, spent a significantly longer time, and larger numbers of pupae, average pupal weight and adult emergence on S. Chaunsa variety compared to other tested varieties. In no-choice bioassays, female flies made more visits and spent a significantly longer time on LSS compared to Gola and LLS. However, in case of no-choice oviposition bioassays on mango fruit, no significant difference was observed among the tested varieties. Orange results are in progress and hopefully, will present in congress. GC-MS analysis of guava headspace revealed presence of aliphatic and aromatic esters as a dominant group of compounds in both un-infested and fruit-fly-infested fruits, with a higher quantity mostly occurring in fruit-fly-infested fruits. Role of fruit volatiles is discussed in an ecological context of attraction and oviposition behaviors of adult females and fitness of their offspring.

Key words: Headspace, GC-MS, plant volatiles, behavior,

The Search for Invertebrate Consciousness

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Abstract: There is no agreement on whether any invertebrates (e.g. insects, spiders, worms, octopuses, crabs) are conscious and no agreement on a methodology that could settle the issue. How can the debate move forward? If we rely on a specific theory of consciousness, our inferences will only be as secure as that theory - and all general theories of consciousness are speculative and controversial. If we try to do without theory all together, our inferences are unconstrained. I aim to plot a middle path between these extremes that I call the “theory-light” approach. At the core of the theory-light approach is a minimal theoretical commitment about the relation between consciousness and cognition: the hypothesis that conscious perception of a stimulus facilitates, relative to unconscious perception, a cluster of cognitive abilities in relation to that stimulus. This “facilitation hypothesis” is commitment that is compatible with many specific theories of consciousness, and it can productively guide inquiry into invertebrate consciousness. What’s needed? At this stage, not more theory, and not more undirected data gathering. What’s needed is a systematic search for consciousness-linked cognitive abilities, their relationships to each other, and their sensitivity to masking. I illustrate the “theory-light” approach using the example of bees.

Intra-species diversification using resistant “elite plants” reduces strawberry herbivory

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Abstract: Minimizing the use of harmful pesticides is a key step towards reaching sustainable food production. However, the transition towards more sustainable plant protection with less pesticide use is difficult, because no “silver bullet” exists among the available non-chemical tools. Recently, increasing genetic diversity of plantation via cultivar mixing has been shown to be a promising method to reduce pest damage. Combining cultivar mixing with functional plant traits (“elite plants”) may thus be a safer pathway to functional Integrated Pest Management (IPM). Here, using a full-factorial experiment with 60 strawberry plantations, we show that reductions in chewing herbivore damage can be achieved through increased use of resistant “elite plants” either alone, or as mixture with susceptible plants. Importantly, the lowest herbivory was found in plantations where high diversity was achieved by cultivar mixing using multiple genotypes of “elite” plants or by using elite plants alone, whereas the highest herbivory was found in plantations with low diversity consisting of susceptible genotypes. Therefore, increasing the genetic diversity and resistance of plantations via “elite plants” likely reduce pesticide dependency.

Effects of drought and invertebrate herbivore communities on plant performance along a European latitudinal gradient

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Abstract: Plant populations are often locally adapted to the particular herbivores present in the community and the particular set of local climate conditions. However, climate change is causing multiple changes in both the abiotic and biotic environment of plants. Temperatures as well as the frequency and intensity of droughts are increasing across Europe. Simultaneously, several species adapted to a southern climate are shifting their ranges northward. As dispersal abilities differ among organisms, e.g. among plants and their different herbivores, this results in novel or no-analog communities.

The success of some non-native plants is often attributed to release from specialist herbivores, enabling plants to divert resources from defenses to growth and reproduction. However, several plant species actually increase their defense levels if herbivore species are lost. A proposed explanation is that multiple herbivores often exert interfering selection pressures on defense traits, and that escape from community complexity lifts the constraints imposed by this interference, enabling the plant to optimally defend against the remaining herbivores.

So far, however, we have limited empirical understanding of how changes in herbivore communities interact with climatic changes to affect selection on plant traits including defenses. Latitudinal gradients can be used as a space-for-time approach, with southern ecosystems representing more northern systems of the future. We set up five common gardens of woodland strawberry along a continental latitudinal gradient from southern Spain to northern Finland. Each garden consists of 16 plant genotypes from across this gradient. Per garden, half of the plants of each genotype have incoming precipitation experimentally reduced by 50%. We here present the first results on how different woodland strawberry genotypes perform along the gradient, with and without drought, and how invertebrate herbivores, local climate, and drought interact to shape the evolution of plant resistance and tolerance.

Beetles disperse viable spores of a keystone wood decay species

Authors: Birkemoe Tone[1], Lunde Lisa Fagerli[1], Boddy Lynne, Sverdrup-Thygeson Anne, Jacobsen Rannveig Margrete and Kauserud Håvard, [1]Norwegian University of Life Sciences, Norway

Abstract: Wood decay fungi are considered to be dispersed by wind, but dispersal by animals may also be important, and more so in managed forests where dead wood is scarce. We investigated 1) the arthropod community visiting sporocarps of the keystone fungi Fomitopsis pinicola by use of time-laps cameras 2) whether viable spores of F. pinicola could be found in the faeces or exoskeleton of beetles collected on the sporocarps or 3) whether viable spores of F. pinicola could be found on beetles collected from newly felled spruce logs nearby, a favorable habitat for spore deposition. We found that Coleoptera was the most numerous order caught by the camera, followed by Diptera and Aranea. Coleoptera longer than 5 mm could be identified to species. Viable spores were found on the exoskeleton and in the faeces of all beetle species collected from sporulating sporocarps and nine beetle species transported viable spores to recently felled spruce logs. Our results demonstrate that beetles can provide directed dispersal of wood decay fungi and that a larger group of arthropods might have the potential to do so.

The macroecology of ant thermal traits

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Abstract: Life on Earth walks a thermal tightrope. Too hot, or too cold, and organisms cannot survive. To maintain thermal balance, organisms have evolved a range of different thermal traits. First, physiological traits set hard thermal boundaries on the functioning of animals. Different proteins and membranes can maintain their integrity at across different temperature ranges. Second, morphological and behavioural traits can act to help keep body temperatures within these physiological boundaries. Traits such as colour and body size play critical roles in the gain and loss of heat – particularly for ectotherms who largely cannot generate their own heat. Darker colours absorb heat faster than reflective, pale colours do, while larger bodies gain and lose heat at a much slower rate than small bodies. Finally, the thermal advantages offered by these traits can be maximised through behavioural regulation: consider a dark coloured butterfly basking in the sun to heat its flight muscles, or a reptile seeking shade to avoid overheating.

Do these thermal traits distribute across geography in predictable ways? The answer to this question will not only reveal how animals have evolved and spread across the planet, but will also suggest the ways in which the biosphere might change in the face of rising temperatures.

Here, I will synthesise a body of work showing how ants (Hymenoptera: Formicidae) respond to a diversity of thermal gradients via a suite of physiological, morphological and behavioural traits. We use thermal gradients ranging from seas to summits, the understory to the canopy, and from disturbed to pristine ecosystems. Together, they are helping us build a predictive picture about why different ants live where they do, and where they might be going next.

Insecticidal Properties of the Main Components of Trachyspermum ammi (L.) Fruits Against the Small Hive Beetles, Aethina tumida (Murray)

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Abstract: Small hive beetles (SHB) (Aethina tumida Murray, Coleoptera: Nitidulidae) are native to sub-Saharan Africa where they exist as scavengers in colonies of western honey bees (Apis mellifera L.). They feed on pollen, honey and larvae of honey bees. However, SHB within their native range rarely inflict severe damage on strong bee colonies. In the current study, contact, fumigant and repellent toxicities of the main constituents derived from Trachyspermum ammi (Linn.) Sprauge fruits were evaluated against the small hive beetles (SHB). Hydrodistillation of T. ammi fruits grown in Ethiopia yielded a light pale yellow essential oil (3.5% v/w) with a strong aromatic odor. Analyses by gas chromatography-mass spectrometry (GC-MS), twenty-two compounds, accounting 98.68% of the total oil were identified. The oil was dominated by monoterpenoids such as gamma-terpinene (32.72%), p-cymene (27.92%) and thymol (24.36%). The essential oil showed strong contact and fumigation toxicities against the small hive beetle adults, with LD50 value of 66.64 µg/adult and LC50 value of 89.03 mg/L Air, respectively. Among the main constituents, thymol was the most toxic component found in both contact (LD50=41.79 µg/adult) and fumigation (LC50=52.66 mg/L Air) toxicities. The other two components, gamma-terpinene and p-cymene, were less effective in both contact and fumigant toxicities testing. The results showed that T. ammi essential oil and thymol could serve as potential alternatives to synthetic insecticides for the control of SHB.

Genus Hydrovatus Motschulsky, 1853 - a pantropic enigma with focus on the taxonomy of the species in Japan (Coleoptera, Dytiscidae, Hydroporinae)

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Abstract: The genus Hydrovatus Motschulsky, 1853 is one of the most species-rich diving beetles genera with currently about 210 valid species. Together with its sister-group, the genus Queda Sharp, 1882, with only three recognized species, Hydrovatus forms a monophyletic tribe Hydrovatini, which is placed in the subfamily Hydroporinae. Monophyly of Hydrovatini is based on morphological and molecular characters. Closest relatives on tribe-level are Hyphydrini and Hygrotini. Hydrovatus is distinguished from Queda by having visible labrum (in part) and by deep metacoxal incisions (corresponding characters in Queda are labrum concealed and metacoxal incisions shallow). Hydrovatini has an extensive pantropic distribution. Distribution of Queda is restricted to northeastern part of Neotropical region while Hydrovatus is pantropical, being most diverse on both side of Equator between the Tropic of Cancer and the Tropic of Capricorn. Hydrovatus extends, however, its distribution outside the tropics, generally being less diverse there.
Japan is located north of the Tropic of Cancer. Eight species of Hydrovatus have been recorded from the country. All of them belong to four different species groups, the main distribution of which is between the tropics. Accordingly, we assume that the origin of the species recorded in Japan is also to be located between the tropics. Our studies have thus far revealed one new species, H. remotus Biström & Watanabe 2017, distributed in the southernmost islands of the Ryukyus. DNA analysis has been undertaken in critical cases of species delimitation. Moreover our studies of various material including types will contribute to a more exact and reliable species list of Hydrovatus in Japan.

Investigating how conservation measures affect pollinator communities – implications for ecosystem services and insect conservation

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Abstract: Efforts to mitigate declines in pollinators on farmland include use of field margins that are florally enhanced with wildflower seed mixes. These have mainly targeted bumblebees and honeybees, yet uncertainty remains over their effectiveness for other pollinating insects. Adult hoverflies (family Syrphidae), despite being highly abundant and important crop pollinators in temperate agricultural ecosystems and showing long-term declines, are a relatively neglected group in studies of plant-pollinator interactions and conservation effectiveness of agri-environment schemes.

The questions we aim to answer are, does floral enhancement of field margins: (i) affect dietary niche parameters of hoverflies; and (ii) influence the functional diversity of the visiting hoverfly community?

It is not known how florally enhanced field margins influence dietary niches (including breadth and specialism) in hoverflies at either the individual insect or the species level. Determining this is important for pollinator assemblages for two reasons: (i) greater individual specialism in plant species visited is thought to result in greater pollinator effectiveness; and (ii) greater average generality of pollinator species is thought to increase stability of pollinator networks, hence pollination services. Ecological generalist species are often found to consist of heterogeneous collections of specialised individuals. Optimal foraging theory predicts that an increase in resource availability will lead to an increase in dietary specialism of individuals. However, alternative mechanisms mean that net effects of floristic enhancements on specialism/generalism of individual hoverflies and species remain uncertain without dietary analysis. We measured ecological resource-use and diet using DNA metabarcoding, which has better taxonomic resolution than traditional light microscopy for the identification of pollen from key plant families such as Asteraceae.

A functional trait-based approach focused on resource use can aid our understanding of causal links between pollinator conservation interventions, pollinator diversity, and pollination services. Trait variables such as body size, tongue length and morphology influence pollinator preferences for particular floral morphologies. Species-specific functional trait values can be used to calculate multi-species functional diversity metrics for pollinator assemblages under different management regimes. Functional diversity is known to be a better predictor, hence index, of the rates and resilience of ecosystem processes and functions (e.g. pollination) than simple species richness.

Our work tests the effect of field margin floral enhancement on the functional diversity of whole hoverfly assemblages with intra-specific dietary composition and diet breadth for a subset of common hoverfly species.

Compiling and summarising the evidence for effective conservation action for butterflies & moths

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Abstract: Lepidoptera (butterflies and moths) are the second most speciose group on the planet, and play a vital role in many terrestrial ecosystems as pollinators and primary consumers. Butterflies in particular are probably the most popular and well-known group of insects, and in an era of increasing concern about global declines in insect abundance, much of the best evidence comes from butterflies and moths. Despite facing a wide-range of threats, from habitat loss and conversion, to pollution and climate change, only around 1,500 species of Lepidoptera (of ~180,000 described) have been assessed for the IUCN Red List, the majority of which are butterflies. From these assessments, around 30% of species are thought to be in decline, and 5-10% are threatened with extinction. Conservation management is required to reverse these declining population trends, and to recover species that have suffered local extinctions.

Evidence-based knowledge is key for planning successful conservation strategies and for the cost-effective allocation of scarce conservation resources. Targeted reviews may be carried out to collate evidence on the effects of a particular conservation action, but this approach is labour-intensive, expensive and ill-suited for areas where the data are scarce and patchy. The evidence for the effectiveness of conservation actions aimed at insects is scarcer than for vertebrate taxa, and accordingly, only a small number of targeted reviews on butterflies and moths exist. Assembling the existing evidence for butterfly and moth conservation actions in one place, alongside information for other taxa, facilitates easy-access for both conservation scientists and conservation practitioners.

We used a subject-wide evidence synthesis approach to simultaneously summarise the evidence for all actions dedicated to the conservation of butterflies and moths. By simultaneously targeting the entire range of potential actions, we were able to review the evidence for each action cost-effectively. The resulting synopsis can be updated periodically and efficiently to incorporate new research. I will present the theory behind the Conservation Evidence approach, and discuss the findings from our recently published synopsis. The synopsis will be freely available online and, alongside the Conservation Evidence online database, will be a valuable asset to the toolkit of practitioners and policy makers seeking sound information to support butterfly and moth conservation.

The evolutionary demise of a social interaction: social partners differ in the rate at which interacting phenotypes are lost

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Abstract: Phenotypic plasticity enables animals to flexibly adjust their behaviour to their social environment – sometimes through the expression of adaptive traits that have not been exhibited for several generations. We investigated how long social adaptations can usefully persist when they are not routinely expressed by using experimental evolution to document the loss of social traits associated with the supply and demand of parental care. Populations of burying beetles Nicrophorus vespilloides were evolved over 48 generations - in ‘Full Care’ populations traits associated with the supply and demand of care were expressed, whereas in ‘No Care’ populations we prevented expression of these traits experimentally. We then revived trait expression in the No Care populations at generations 24, 43 and 48 by allowing parents to supply post-hatching care, and compared these social traits with those expressed by the Full Care populations. We found that offspring demands for care decayed in the No Care populations more rapidly than a parent’s capacity to supply care. Furthermore, male care decayed faster than female care. We suggest that this reflects differences in the strength of selection on offspring, males and females, for the expression of alternative traits which are more likely to enhance fitness when post-hatching care is disrupted.

Evolution of Aposematic Coloration in Xylocopa: An Unsupervised Machine Learning Approach

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Abstract: Large carpenter bees (genus Xylocopa), are a species-rich, easily recognizable genus resembling bumble bees in size and appearance. Carpenter bees are found on every continent except Antarctica, and display a diverse array of color patterns. In some lineages, aposematic coloration, often consisting of brightly colored bands or patches of pubescence on the dorsum of the bee, is displayed by many species. Some species also exhibit sexual dichromatism, in most cases the female is the brightly colored sex while the male is often drab and covered in yellow or brown pubescense. As part of this study, I am imaging the dorsum of a variety of aposematic carpenter bees species from museum collections and using an unsupervised machine learning approach to cluster species with similar aposematic patterns. Each image will also be overlaid onto a standardized bee template, both the original photographs and templates will be run separately and compared. The evolution of color patterns will then be investigated by testing for the presence of phylogenetic signal based on a phylogeny of Xylocopa constructed as part of this project. In addition, color pattern clusters will be correlated with Xylocopa species distributions to test whether the ranges of members within a cluster overlap, and co-occurring species may have converged on similar color patterns to reinforce the warning signal to predators through Mullerian mimicry. This study’s ultimate goal is to identify potential drivers underlying the evolution of color patterns across Xylocopa and lay the groundwork for future studies on additional factors influencing present patterns.

Key innovations and the diversification of Hymenoptera

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Abstract: Hymenoptera (wasps, ants and bees) are one of the most diverse animal lineages, but whether specific key innovations have contributed to their diversification is still unknown. We assembled the largest phylogenomic framework for Hymenoptera to date and tested if particular morphological and behavioral innovations influenced diversification in the order: the wasp waist of apocritan wasps; the stinger of aculeate hymenopterans; parasitoidism, a specialized form of carnivory; and secondary phytophagy, a derived plant-feeding strategy. Our time-calibrated phylogenies indicate that a parasitoid regime in Hymenoptera originated in the Late Triassic and remained dominant until the Early Cretaceous. We found strong evidence that transitions to secondary phytophagy (from parasitoidism) had a major influence on hymenopteran diversification rate. Support for parasitoidism, the stinger and the wasp waist as key innovations remains equivocal, but there is indication that these traits laid the anatomical and behavioral foundations for adaptations more directly associated with diversification.

Unraveling diversity patterns and endemism in Malagasy ants: a phylogenomic approach

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Abstract: The first step in preserving biodiversity and its associated ecosystem functions is assessing and quantifying measurable units of this diversity. Two key elements of measuring biodiversity across space and time are species diversity and endemism. In the past, most survey efforts have been focused on using taxonomic species as the unit of diversity and endemism, but over the last decade it has become more common practice to assess phylogenetic (or lineage) diversity alongside taxonomic species richness. Measuring arthropod diversity based on either of these units is challenging, given that surveys are often too limited in geographic scope to capture the magnitude and breadth of arthropod species distributions and diversity, and timely identification of collected samples is difficult. Arthropods are thus often excluded from conservation planning decisions. Here we outline the goals and first results of our project MAMI (Malagasy ant microendemism), which aims at a synthesis of survey efforts for ants in Madagascar spanning two decades. We use a phylogenomic approach to investigate regional patterns of phylogenetic diversity, endemism, and community structure across more than 1,200 species of ants in Madagascar based on ~2,200 loci of ultraconserved elements. We analyze phylogenetic patterns of community structure, diversity and endemism of ants in Madagascar across several different habitat types and along climatic and primary productivity gradients. Our island-wide community analyses uncovers general patterns of species richness, lineage diversity and endemism across ant communities in Madagascar, allowing us to draw broad, widely applicable conclusions about the importance of these patterns for conservation planning.

Eradication of Ips typographus from the UK: progress 18 months from the first finding

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Abstract: Ips typographus is one of the most significant pests of spruce throughout its native range in Europe. Though the UK relies on spruce (primarily Sitka and Norway) for a large portion of its forestry industry, Ips typographus has never managed to establish here, and for over 25 years detailed surveys as part of the EU Protected Zone against invasive Ips in the UK had never found the species established and breeding here, until 2018.
Several hibernating adults were found in Kent (the most south easterly part of England, closest to France) in November 2018, and a follow up survey revealed that there was an established breeding population in a restricted woodland setting. Other surveys in spruce woodland in south east England have failed to pick up any additional Ips typographus populations, and one year on from the initial finding no other breeding populations have been located.

The woodland is now part of an eradication program, led by Forestry Commission England and Forest Research, which aims to eradicate Ips typographus from the UK and prevent any potential spread of the species further through the UK. Following significant works to reduce any breeding substrate on the woodland, work over the following seasons has attempted to trap out adults from the site, as well as monitoring other areas using pheromone traps. The success of the eradication actions will be indicated following pheromone trapping in 2020, although eradication itself won't be declared, if successful, until at least 2022. Pheromone trapping data will be presented alongside insights from molecular and host-choice experiments to indicate how such research has helped inform the decisions surrounding the management of Ips in the UK.

Successful eradications of bark beetles are rare, therefore this eradication attempt will serve as a case study highlighting areas of success (and failure) with the aim of helping inform other bark beetle eradication attempts. The on-ground work will be presented as a case study discussing what went well and what didn't, highlighting recommendations for any future eradication attempts. Wider findings of Ips typographus will also be discussed with a long-term view of Ips typographus establishment in the UK. Is it possible that this species will recolonise the UK, and if so are there any management practices that could help prevent or slow establishment?

Elevated carbon dioxide concentration impacts the semiochemically-mediated plant-insect interactions

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Abstract: The impact of global change on ecosystems has received growing scientific attention during the last decades. Numerous studies are now suggesting that abiotic environmental factors will modify plant physiology with cascade effect on higher trophic levels.
In this study, we tested the hypothesis that the predicted raise of carbon dioxide concentration will modify the semiochemically-mediated interactions in a multitrophic model including plants, aphids, aphid-tending ants, and aphid natural enemies. To do so, we raised all plants and insects under two contrasted carbon dioxide concentrations.
Due to the pest status of aphids and the dispersal ability of their winged morphs, we investigated the host plant choice of black bean aphids under changing environment and found positive impact of elevated CO2 concentrations for the winged morphs, but not for the apterous ones. These modifications of behaviors were not led by modifications of Vicia faba plant volatile emissions under elevated carbon dioxide concentrations. Because aphid honeydew volatiles are mediating the prey location behavior of aphid-natural enemies, we characterized the volatile profile of honeydew and found qualitative and quantitative modifications under elevated CO2 concentrations. These changes were not linked with a modification of hoverfly attraction and oviposition site selection. The raise of CO2 concentrations also increased the number of physical interactions between ants and aphids, leading to the reinforcement of the aphid-ant mutualism. Sugar composition of aphid honeydew is now investigated for a more comprehensive understanding of the impact of abiotic factors on aphid-ant mutualism.
We conclude that carbon dioxide concentration impacts these semiochemically-mediated interactions. New studies on the effect of warming on the same multitrophic interactions revealed quantitative impacts of elevated temperatures on the emission of plant volatiles and behavioral impacts on the aphid-ant mutualism.

Field assessments of the effects of elevated ozone and diesel exhaust emissions on insect pollination and natural enemy recruitment

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Abstract: Common atmospheric pollutants such as nitrogen oxides (NO and NO2, collectively NOx) released from diesel vehicle exhausts and tropospheric ozone (O3) are capable of disrupting the volatile organic compounds (VOCs) that many insects utilise for communication during critical stages of their life cycles, such as locating hosts. The disruption of these odour signals may have wide ranging, yet unquantified, impacts on insects and the important ecosystem services they provide (e.g. pollination and plant pest management), which are critical for the functioning of terrestrial ecosystems. While laboratory-based behavioural studies have demonstrated that air pollution may reduce the foraging efficiency of pollinators and herbivore natural enemies (e.g. predators and parasitoids), to-date there has been limited field-scale validation.

Using eight Free-Air Diesel and Ozone Exposure (FADOE) rings, we investigated the impact of diesel and ozone pollution, individually and in combination, on insect pollination services and natural enemy recruitment. Both pollutants had clear negative effects on insect counts and flower visitation by major pollinator groups, which coincided with decreases in yield metrics of our study plant (Brassica nigra). Numbers of true bugs, beetles and parasitoids, however, tended to increase under some pollution treatments. These results provide evidence of significant negative field-scale effects of air pollution on insect-derived pollination services. The complex nature of pest-natural enemy interactions, however, makes broad field-scale assumptions about natural enemy responses to air pollution difficult, requiring a more mechanistic understanding that targets individual ubiquitous species to maximise pest control.

Revival of the larch budmoth (Zeiraphera griseana) cycles in the European Alps

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Abstract: The regular cycles of the larch budmoth (LBM) in the European inner alpine valleys are a famous example for cycling population dynamics. Extensive investigations in the middle of the last century have shown that several mechanisms are involved in driving, stabilizing and synchronizing the population cycles across the alpine arch. Mechanisms include regulation by natural enemies, negative feedback of food quality, different performance of caterpillar ecotypes, and dispersal across landscapes.

While, by means of tree ring analyses, the regular LBM outbreaks could be dated back more than thousand years, no mass outbreaks were observed during almost four decades after 1981. Population cycling, however, continued with the same frequency as before, but with lower amplitudes and without visible discoloration of the larch stands. Starting in 2016, in accordance with the previous periodicity, large LBM outbreaks started in the Western Alps of France. They then travelled across the Alps affecting Switzerland in 2017 and 2018. The extent and intensity, however, did not quite reach the levels of the outbreaks in the middle of the last century. It is supposed that this resurrection of outbreaks was brought about by altered winter temperatures affecting egg survival and by improved synchrony of budburst and egg hatching.

Trends in bark beetle outbreaks and sanitation felling of spruce in Switzerland

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Abstract: The European spruce bark beetle (Ips typographus) represents an ongoing threat to Norway spruce across Europe. In Switzerland, Norway spruce represents the most common tree species covering approximately one quarter of the total forest area. Especially in mountainous regions, this tree species often fulfils important protection functions against natural hazards such as rockfalls or avalanches. Besides forestry losses, bark beetle disturbances can therefore directly influence the security of humans and infrastructure. In order to formulate appropriate management strategies, the understanding of infestation dynamics is crucial. Since 1984, the volume of Norway spruce killed by I. typographus as well as the results from pheromone trap monitoring have been yearly registered for the different forest districts of Switzerland. In our current work, we analyze this dataset for the first time in an in-depth manner, focusing on effects of climate factors (mean temperature, drought, storms, etc.) and comparing the infestation dynamics among the different geographic forest regions. Moreover, we assess the relationship between trap catches and the volume of infested Norway spruce. Our findings present the trends of the infestation dynamics in Switzerland over the last 37 years and provide important information for sustaining the various forest functions in the long run.

Biorational pest management in arable crops using semiochemicals and egg parasitoids

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Abstract: During the last 30 years, changes in agricultural systems, such as non-tillage and keeping soil occupied all year-round, have improved crop production significantly. However, they have also provided food in abundance for insects, thus provoking insect outbreaks and increased crop losses. A recent study on stink bugs and their adult parasitoid populations in nine soybean production regions in Brazil showed there was a very low level of parasitoid and predator communities due to overuse of pesticide application. To minimize insecticide application, studies are being conducted to develop more sustainable technologies for pest control. Semiochemicals applied synthetically or naturally, using companion plants that can repel pest or attract natural enemies, are among the critical tools that have been evaluated. Field experiments conducted in Brazil on soybean parcels treated with dispensers releasing the sesquiterpene (E,E)-a-farnesene attracted higher numbers of Platygastridae parasitoids, resulting in higher levels of parasitized stink bugs eggs compared to parasitism levels of non-treated soybean parcels. Another field experiment with maize cultivated with companion plants, such as Cajanus cajan and Napier grass (Pennisetum purpureum), showed that these areas attracted higher numbers of egg parasitoids and Braconidae wasps compared to areas with only maize or maize combined with Crotalária spectabilis. The results of these experiments and the underlying chemical ecology involved will be presented, and possible applications will be discussed.

Sesquipiperitol as stink bugs pheromones' constituent and biosynthesis intermediate

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Abstract: Sesquipiperitol (2,10-bisaboladien-1-ol, or 3-methyl-6-(6-methylhept-5-en-2-yl)cyclohex-2-en-1-ol) is a plant-produced sesquiterpene alcohol, a putative biological role of which in plants is still unknown. This compound can exist in eight stereoisomeric forms, yet absolute configurations of sesquipiperitols occurred in plants remained unidentified. It was reported that (+)-trans-sesquipiperitol occurred in roots of Argyranthemum adauctum spp. jacobaeifolium, and (-)-trans-sesquipiperitol was isolated from the foliage of Fitzroya cupressolides. Two Zingiberaceae plant species, Alpinia densibracteata and Zingiber officinale have also been reported to contain sesquipiperitol of undisclosed stereochemistry. Recently, (1S,6S,7R)-1,10-bisaboladien-1-ol (SSR-sesquipiperitol) had been found for the first time in animals as an intermediate in the harlequin bug, Murgantia histrionica, pheromone biosynthesis.1

We found that two more stink bug species, Tibraca limbativentris and Glyphepomis spinosa, known as rice pests in Brazil, produce sesquipiperitols. In case of the former, sesquipiperitol was shown as a pheromone component but it could possibly serve as a biosynthetic precursor to pheromones of both species. For precise stereochemical identifications of these and other naturally-occurring sesquipiperitols, we synthesized all eight stereoisomers starting from commercially available (S)- and (R)-citronellals. We exploited two synthetic strategies: a rhodium-catalyzed enantioselective addition to carbonyl group, and a Robinson annulation to prepare stereodefined sesquipiperitones. Reductions of each of these ketones (total four) produced two epimeric sesquipiperitols, the stereochemical assignment of which was conducted by preparations of Mosher ester and analyses thereof by NMR.

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Use of vibratory signals for stink bugs monitoring and control

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Abstract: Many species of stink bugs, mainly those of Pentatominae and Edessinae, are serious pests in crops such as legumes, grasses, grains, vegetables and fruit and nut trees. Their impact on agriculture has been increased by some invasive species affecting crops around the world. It is necessary develop management strategies for stink bugs based on integrated pest management (IPM) practices with efficient monitoring systems and alternatives for population control. In this way application of knowledge related to sexual communication and vibratory signals may contribute to some birational control alternatives. Applied biotremology offers a strong potential to contribute to reach this goal. The general pattern of reproductive behaviour of stink bugs starts at long range with the emission of aggregation or sexual pheromone by the males. Pheromones triggers emission of the female substrate-borne signals (calling signals) on the plant, at medium range. Female calling signals, transmitted through the plant, provide information on signaler identity and location. The calling phase of reproductive behaviour is followed by the courtship phase, at short range, which is characterized by duetting with courtship song vibratory signals, antennation and butting at close range. It is possible to interfere in stink bug communication at any of these phases. Some recent advances of applied biotremology for stink bugs management will be presented. Attention will be place on three principal areas of applications: 1- the use of vibratory signals in monitoring systems, 2- the disruption of stink bug mating by interference of vibratory communication and 3- applications in biological control.

Effect of green cover management on arthropods predation in Mediterranean vineyards

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Abstract: Green cover has been identified as an alternative management of vineyard soil to improve biodiversity and ecosystem services. We explore here the relationship between vegetation cover and arthropod predation, hypothesising that inter-row vegetation provides habitat and resources for generalist predators, improving pest regulation. We selected 26 vineyards located in south-eastern France with three different green cover managements: tillage, one inter-row of two tilled and complete inter-row vegetated vineyards, and evaluated both ground and canopy predation. In each vineyard, we set 96 for eight hours during the day living sentinel preys (Lucilia sp. larvae), 48 on the ground and 48 in the vine canopy. Larvae were then renewed for an 11 hours night session. Regular visual checking during the day allowed us to identify predators at preys. We found a clear and significant increase in larvae predation from tilled to complete vegetated vineyards. We observed spiders, harvestmen, and beetles but ants were by far the primary predator. They were responsible for more than 75% of larvae predation, with two key species, Camponotus vagus in the vine canopy and Cataglyphis cursor on the ground. These results highlight the underestimate role of ants as generalist predators and their likely role in pest regulation that is directly related to green cover management in vineyards. Therefore, the use of green cover in Mediterranean vineyards promotes predation by generalist arthropods and may be key to provide pest regulation services.

A multi-dimensional quantitative approach to study the evolution of social complexity

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Abstract: The current approach for research on the evolution of insect sociality is based on a qualitative and crude classification and suffers from several limitations: (i) It assumes that social traits always evolve together and in synchrony, which may falsely imply that social evolution always progresses along a single linear stepwise trajectory; (ii) It limits our ability to test the association between the level of sociality and quantitative "omics" molecular, physiological, and behavioral parameters. We are developing a novel approach that is based on quantitative indices for social complexity using bees as a model. As a first step, we compiled a comprehensive database of social traits for 70 species. Next, we performed data-driven statistical analyzes, which account for phylogenetic relations between species. Our approach enables quantification and mapping of sociality in species based on multiple types of data. Our results indicate a spectrum of sociality types in bees, which is wider than appreciated with the classical approach. We identified multiple axes that characterize regions of interest in the multidimensional trait space, suggesting non-trivial relations between different social complexity traits. Moreover, we discovered potential trajectories for social evolution by calculating the molecular evolutionary rate of focal genes.

Cues mediating social entrainment of circadian rhythms in honey bees

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Abstract: Honey bees (Apis mellifera) show task-related plasticity in circadian rhythms. Forager worker bees have strong circadian rhythms that are necessary for sun-compass orientation and for timing visits to flowers whereas "nurse" bees tend brood around the clock with attenuated or no activity rhythms. Nevertheless, nurses that are removed from the hive, show strong circadian rhythms that are in phase with ambient day-night cycles. These observations indicate that at least some pacemakers in their brain continue to measure time in the constantly dark and tightly thermoregulated nest environment. This premise is supported by immunocytomemistry analyses showing that clock gene protein expression similarly cycle in pacemaker neurons in the brains of foragers with, and nurse without, circadian rhythms in locomotor activity. The nurse clock is entrained by social cues, that can even override photic entrainment, but the nature of these social cues remain elusive. We hypothesize that surrogates of bee activity generate daily oscillations in the nest microenvironment, which in turn, entrain circadian rhythms of other bees to a common colony phase. Here we tested whether direct contact, substrate-borne vibrations, and nest volatiles can entrain circadian rhythms in honey bee workers and can mediate social synchronization. We manipulated the cues passing among bees and used circadian analyses and circular statistics to assess the degree of phase synchronization. We further used our new ICON pipeline to calculate the coupling function between the rhythms of pairs of bees. Our findings show that both direct contact between pairs of individually-isolated bees and activity-induced changes in the common environment can entrain circadian rhythms of young bees. Substrate-borne vibrations and changes in nest volatiles entrain circadian rhythms and can mediate social synchronization of honey bees to a common colony phase. These findings are consistent with a self-organization model for circadian rhythms synchronization in complex social insects colonies composed of dozens thousand individuals.

Side-effect testing of pesticides on beneficial organisms - the IOBC-WPRS approach

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Abstract: Integrated Pest Management combines diverse preventive and curative measures including pesticides to protect plants from pest organisms. These pesticides should not affect natural enemies or antagonists of plant pests and therefore reliable information about their potentially adverse effects on non-target organisms is necessary. In this context, the International Organisation for Biological and Integrated Control, West Palearctic Regional Section (IOBC-WPRS) had started in the 1970ties to develop a sequential pesticide side-effect testing concept to identify pesticides selective for beneficial organisms. Indicator species of beneficial organisms from different taxonomic groups against major pests in important crops were selected and species-specific standardized side-effect testing methods were developed. These methods follow a stepwise approach from a worst-case study in the laboratory with the most sensitive developmental stage of a beneficial exposed to pesticide residues on different substrates, to semi-field tests on plants with all beneficial developmental stages under controlled conditions up to field studies with naturally occurring or released populations of the target organisms. Pesticides are applied at the highest recommended field rate as commercial formulations. Main end- points of the laboratory tests include primary direct (lethal) and indirect (sublethal) effects such as mortality and decreased oviposition. All effects are combined to so-called efficacy values. The efficacy values are classified in four categories from harmless to harmful and were published in IOBC-WPRS Bulletins and in the online database (https://www.iobc-wprs.org/ip_ipm/IOBC_Pesticide_Side_Effect_Database.html). Between 1983 and 2000, nine Joint Testing Programmes with about 200 pesticides for up to 25 different beneficial indicator species were carried out. Over time, the methods partly had to be adapted for pesticides with new mode of actions. When the provision of data about side effects of pesticides on non-target organisms became obligatory for the authorization of pesticides in the EU, a „Joint Initiative for the validation of beneficial arthropod testing" with participants from the European Plant Protection Organisation (EPPO), pesticide industry, contract test laboratories and IOBC-WPRS was established to validate and standardize existing side-effect testing methods (mainly those of IOBC-WPRS) in ring-test groups for 12 relevant indicator species. The first tier tests for assessments of the effects of Plant Protection Products on Non-target Arthropods for regulatory purposes (EEC/91/414, EC 1107/2009) are based on these jointly established side-effect testing methods.

Microbial metabolites as key elements in the life cycle of entomopathogenic nematodes

Authors: Bode Helge, Molecular Biotechnology, Department of Biosciences, Goethe University Frankfurt, Germany

Abstract: Entomopathogenic nematodes of the genera Steinernema and Heterorhabditis live in symbiosis with bacteria of the genera Xenorhabdus and Photorhabdus, respectively. Genome analysis of these bacteria as well as their chemical analysis have revealed the presence of several specialized metabolites and their biosynthetic gene clusters that might be involved in the tripartite interaction of nematode host, bacterial symbionts and insect prey.
The talk will highlight recent methods to obtain and modify these metabolites in order to apply the metabolites themselves or the engineered bacteria in medicine or agriculture.

Spittlebugs in vineyards: influence of plant community characteristics on the abundance of Xylella fastidiosa vectors

Authors: Bodino Nicola, Fogliatto Silvia, Demichelis Stefano, Saladini Matteo, Vidotto Francesco, Ottati Sara and Bosco Domenico

Abstract: The bacterium Xylella fastidiosa (Xf) has been identified in Europe for the first time less than ten years ago. In Southern Italy, a strain of Xf subsp. pauca is the causal agent of the Olive Quick Decline Syndrome (OQDS) on olive, a destructive disease that killed millions of trees and is still spreading. Xylella fastidiosa is also a potential major threat to the European wine sector, as it is known as the causal agent of Pierce's disease of grapevine. Insect vectors of this bacterium, i.e. spittlebugs (Hemiptera: Aphrophoridae), can reach high populations in vineyards, hence the risk of X. fastidiosa outbreaks in wine-producing areas is significant. However, current knowledge on drivers of insect vector presence and abundance in the vineyard agroecosystem is scarce. The aim of this study was to investigate the influence of vegetation community characteristics and management strategy on presence and abundance of spittlebug nymphal and adult stages in the vineyard agroecosystem. A two-year field survey of spittlebug populations was carried out in six vineyards (three organic and three IPM) in North-western Italy. Nymphal samplings were carried out in April, at the time of nymph population peak. Randomly selected sampling units (n = 15, 0.25 m2) were performed in each vineyard. Vegetation characteristics were recorded within each insect sampling unit. Adult stage was sampled by sweeping net in June and September from three vegetation compartments of the vineyard: i) grapevine plants ii) ground cover herbaceous vegetation iii) spontaneous woody plants. All samplings were conservative. Our results show that spittlebug nymph abundance is negatively correlated with i) high values of mean Ellenberg indicator value of nitrogen, ii) high herbaceous cover percentage and iii) high herbaceous biomass. Also, the abundance of Philaenus spumarius (the main European vector of Xf) was negatively influenced by high cover percentage of monocots. Spontaneous woody plants host high numbers of adult spittlebugs (P. spumarius and Aphrophora alni) in summer, and density of P. spumarius adults on grapevine was similar to those observed on the other vegetation compartments – at least in vineyards with high spittlebug population. New insights on associations between plant community characteristics and density level of spittlebugs may pave the way to the design of environmentally-sound strategies to lower vector populations in X. fastidiosa susceptible agroecosystems, e.g. by promoting herbaceous cover not suitable to spittlebug nymphal development or by developing trap cropping systems at the plant community level.

Intergeneric imprinting and the impact of early experience on nest affiliation in hornets

Authors: Bodner Levona, Israel

Abstract: Social insects spend the first couple of days following eclosion inside their nests. During this time, they incorporate the odor signature (i.e., the cuticular hydrocarbon template) of their nest and nest members, and are practically being “imprinted” on their colony. We examined the potential plasticity of colony imprinting in the Oriental hornet (Vespa orientalis) by transferring newly-emerged hornets onto larvae-containing combs of German wasps (Vespula germanica). The hornets nursed the foster brood and exhibited the regular set of social behaviors in the heterospecific colony, including trophallactic interactions with their adult foster sisters. This result prompted us to investigate the impact of early exposure on nest imprinting in both behavioral and chemical levels. We tested the hornets' comb preferences in a T-maze and analyzed their cuticular hydrocarbon profiles, following one week in a foster German wasp colony, and compared both results with a control group (i.e., their biological sisters that were reared in their biological colony). We found that hornets from the foster colony showed stronger affiliation to the foster (German) nest, while exhibiting a chemical profile that resembled their biological sisters' and differed from that of their foster sisters. Our results exemplify the effect of early environmental and social exposure on nest affiliation, as well as the potential plasticity of recognition and colony imprinting in social insects.

Population dynamics of winter moth in the northeastern United States before and after the establishment of the parasitoid Cyzenis albicans.

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Abstract: Winter moth, Operophtera brumata L. has recently invaded the northeastern United States and caused widespread defoliation. We embarked on a 14 year project to collect life table data which involved estimating densities of different winter moth life stages at multiple research plots on two different tree species.. We also began introduction of the tachinid parasitoid, Cyzenis albicans, which has controlled winter moth at other locations in North America. An analysis of 14 years of life table data collected from outbreak populations of this species has revealed that populations are regulated by direct density-dependent mortality primarily in the larval stage. This mortality is mainly due to density dependent dispersal of larvae. Mortality of pupae in outbreak populations is not density-dependent. These dynamics contrast strongly with classic analyses of low-density populations of this insect. Introductions of the parasitoid Cyzenis albicans have resulted in successful establishment at several locations and sharp reductions in winter moth density at multiple locations. Once winter moth populations decline, mortality of pupae becomes density dependent, as it has in multiple previous studies.

Sawflies containing toxic peptides

Authors: Boevé Jean-Luc[1] and Rozenberg Raoul[2], [1]Royal Belgian Institute of Natural Sciences, Belgium, [2]Universite´ Catholique de Louvain, Belgium

Abstract: From the 1970’s, toxic peptides were detected and identified in the larvae of some Argidae (genus Arge) and Pergidae (Lophyrotoma, Perreyia) sawfly species (Hymenoptera: Symphyta). They caused the death of livestock in Australia, Denmark and South American countries. The chemicals were studied, here, to elucidate their involvement in ecology, evolution, physiology and behavior of the sawflies. Liquid chromatography–tandem mass spectrometry of extracts from single larvae revealed that the peptides occur commonly in the two sawfly families. A phylogenetic approach pointed to evidence that the peptides may have driven the evolution of these sawflies by allowing frequent “defense shifts”, that is, switches between cryptic and conspicuous appearances, and levels of gregariousness. The toxic peptides proved to vary in quality and quantity across species, and in quantity across populations. Such results led to canceling the use of a pergid (Heteroperreyia hubrichi) as a biocontrol agent of an invasive weed. In Arge berberidis the chemicals were detected not only at larval stage but also in the prepupal and adult stages. By isolating organs from larvae of Lophyrotoma zonalis and Arge pagana, the chemicals were detected mainly in the hemolymph and integument, and little or none in the digestive tube. Finally, bioassays revealed that Pergidae and especially Arge larvae are well defended against ants, with ant responses determined by the body size and behavior of the larva such as raising the abdomen. Thus, combined with other antipredator defense mechanisms, the toxic peptides seem to constitute an essential element in the biology and ecology of Argidae and Pergidae sawflies.

Are non-native mud dauber wasps (Hymenoptera: Sphecidae) dangerous for people and for their native European relatives?

Authors: Bogusch Petr, University of Hradec Kralove, Faculty of Science, Department of Biology, Czech Republic

Abstract: Three non-native species of the family Sphecidae have been recorded in various parts of Europe. In particular, Sceliphron curvatum has spreaded to many parts of the continent. Studies have investigated their potential threats to other hymenopterans and also to people. S. curvatum originates from India and surrounding countries and was first reported from Europe in 1979, with a record from south Austria. Recently it has been recorded in most of the continent except the northernmost parts and it has also been recorded in other parts of the world (Mexico, Argentina). The presence of this species is not welcomed by humans because it places its nests mainly inside buildings. The nests can make a mess in rooms and people may be fearful, especially of the insects’ provisions of paralyzed spiders. However, S. curvatum does not represent an important danger as the nests are usually placed on or in unused matter (paper boxes, old clothes, books, behind pictures or furniture) and the species is not aggressive. The specific nesting habits can help this species to spread very fast in various parts of the world, but it does not compete well with other species, which place their nests differently. Sceliphron caementarium and Chalybion californicum have their origins in North and Central America and they place their nests mainly on the surface of buildings, while the latter usually uses old nests of Sceliphron species and re-builds them for its own nesting purposes. They nest similarly to the native Sceliphron destillatorium. In several regions of South Europe (especially coastal regions of Slovenia, Croatia and Italy), S. caementarium is very numerous and has forced out the native S. destillatorium, which has become very rare or has locally disappeared. The second species, C. californicum is rare and its presence probably does not harm native species. Since these species negatively influence people (in the case of S. curvatum) or native species (S. caementarium) they must be considered to be invasive.

What are the main pollinators of almond trees and is the role of native solitary bees important?

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Abstract: Almonds are fruit trees, which are planted in south Europe in high numbers. The production is highly dependent on the effectivity of the pollination done especially by various species of bees. We have studied the insects present on flowers of almond trees in 12 orchards in the vicinity of the town Lleida in NE Spain in March 2019, when the trees were in flower. In each orchard, one person was capturing and observing all visible bees on the flowers. Additionally, we have captured other bees present in the orchard. The numbers of species recorded and dominances differed among the orchards, as well as the total number of specimens recorded. The honeybee (Apis mellifera) was most numerous in all orchards except those, where nesting blocks with horned mason bees (Osmia cornuta) were installed and this bee species was most numerous. We have recorded additional 15 species of bees and two species of hoverflies pollinating almond flowers, of which only Andrena nigroaenea was quite numerous. Capturing the bees in the surroundings of the trees, we have recorded that most of the wild bees occurring in almond orchards do not pollinate almond trees or only males sporadically gather nectar on the flowers. Most of the species were recorded on plants of the family Brassicaceae, which were numerous in herb layer. Almond trees are then dependent on mason bees and the honeybee and keeping these species in the orchard is very important for good pollination. The presence of species-rich communities of wild bees are not necessary for almond pollination but the bees are important for the biodiversity and natural character of the landscape in the vicinity of the orchard.

High doses of the attractant indole repel mosquitoes

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Abstract: N,N-Diethyl-meta-toluamide (DEET) is an effective mosquito repellent used for personal protection. However, this synthetic compound suffers from a several disadvantages, including plasticizing effects, oily feel and low user acceptability. More significantly, DEET exhibits a limited range of action due to its low volatility. New repellents with higher volatility and longer range of action are therefore desirable. Based on its chemical structure and known modulatory effects on odorant receptor (OR) function, we have hypothesized that indole may act as an OR modulator. We show that high indole concentrations not only inhibits OR function, but also elicit avoidance behavior in mosquitoes. These findings confirm that a structure-activity approach can lead to the discovery of potential mosquito repellents. In this study, using indole as a mosquito repellent may offer greater volatility and spatial repellence than DEET.

Seeing a Lot With a Little: Visual specialization in the miniaturized eyes of thrips (Thysanoptera)

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Abstract: Thrips (Thysanoptera) are an order of tiny, yet economically important insects. Several species are major agricultural pests, including Frankliniella occidentalis, the Western Flower Thrips (WFT), which causes severe economic impacts. There has been extensive research testing the response of WFT to visual cues to improve lures for pest management strategies. However, little is known about the fundamental aspects of WFT visual systems. Here we present data about the structure, optics, and visual genes present in WFT eyes. Despite possessing a mere 60 ommatidia in each eye, WFT display a tremendous degree of regionalised retinal specialization. They express five visual opsins, have putative spectral filters in a mosaic of enlarged ventral ommatidia, and display anatomical specialization in dorsal rhabdoms that may be analogous to a dorsal rim, which is used for orientation using celestial polarization patterns in many flying insects. Furthermore, we use 3D synchrotron µCT reconstructions of WFT eyes to model their visual system in simulated light environments. Using this approach, we can combine information about regionalized spatial, color, and polarization sensitivity in order to inform the design of improved trapping strategies utilizing visual lures that will be increasingly salient and attractive to WFT in agricultural settings.

Selection of natural enemies for augmentative biological control: sense and nonsense of ecological selection criteria

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Abstract: The selection of natural enemies species for augmentative biological control is based on answering three basic questions: 1. is the natural enemy able to significantly contribute to managing the population of the target pest in the target crop?; 2. are there any undesired side-effects on the crop, or on other natural enemies that are used in the same crop, or, in the case of non-native species, are significant effects on non-target species expected?; 3. can the natural enemy be economically mass-reared?

Insect ecology is the scientific study of how insects, individually or as a community, interact with the surrounding biotic and abiotic environment or ecosystem. Based on natural enemy species that are either successfully used in augmentative biological control programs and species that did not make it through the screening process, we will discuss the sense and nonsense of different ecological selection criteria.

Insight in ecology also informs how to optimally deploy specific species or combinations of species of natural enemies in crop specific biocontrol-based IPM programs.

The How and Why of insect air flows

Authors: Bomphrey Richard, Royal Veterinary College, United Kingdom

Abstract: Traditionally there have been substantial practical challenges in recording insect wing kinematics, describing aerodynamic force generation and understanding how insects monitor their own state within the physical environment. More recently, a suite of genetic, videography and computational methods have been used to explain the elusive links between form and function. I will describe how some of these innovations have opened new research avenues in fundamental aerodynamics, functional ecology and robotics.

Exploring the link between viral integrations and the piRNA pathway in Aedes mosquitoes

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Abstract: Arthropod-borne viruses such Dengue, Zika and Chikungunya are (re)-emerging public health threats. Despite having different genome structures and replication strategies, these viruses are all nonretroviral RNA viruses, thus they lack reverse transcriptase and integrase and complete their life cycle in the cytoplasm of their host cells. Arboviruses belong to large viral families which include additional viruses able to replicate exclusively in insect cells and are thus called Insect-Specific Viruses (ISVs).

Unexpectedly, we, and others, detected hundreds of ISV sequences integrated into the genome of the main arboviral vectors, Aedes spp. mosquitoes. These Nonretroviral Integrated RNA virus Sequences (NIRVS) are enriched in piRNA clusters and produce piRNAs. This observation and the physical contiguity between NIRVSs and transposable elements (TEs) in piRNA clusters, led to the hypothesis that NIRVSs contribute to mosquito immunity through piRNA-targeted processing of cognate viruses and are adaptive.

If NIRVSs behave like TE fragments of piRNA clusters, their distribution within mosquito genomes should diversify according to previous pathogen encounters. Alternatively, viral integrations may represent ancient viral relicts, among which only few may have been co-opted for antiviral functions.

We developed a computational approach to probe the genome of wild-collected mosquitoes and test for differences in the landscape of viral integrations in and outside piRNA clusters. We also applied computational and molecular approaches to probe the evolution of viral integrations in field mosquitoes and their activity after viral integration. We identified novel viral integrations in the genomes of both Aedes aegypti and Aedes albopictus wild-collected mosquitoes. We also showed that a limited number of viral integrations are adaptive and produce piRNAs following arboviral infection. Overall our results indicate that like TEs, not all viral integrations are the same, and they are organized through a redundant system that influence mosquito response to arboviruses, primarily through the piRNA pathway.

Safety Education is Critical for Grain Fumigation

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Abstract: Fumigation is an important part of an integrated pest management strategy for keeping stored grain in good condition. The stored grain environment may cause concern for the safety of fumigant applicators who need to enter the structure because of unsafe atmospheric conditions, possible grain entrapment, and the use of a potentially dangerous insecticide. Instructions and equipment for testing the atmosphere, knowledge about how entrapment occurs and how to avoid it, and safety precautions for using a severely toxic insecticide will be discussed. Atmosphere and phosphine monitors needed to test the air and keep applicators aware of the amount of fumigant in the area are needed for all fumigations. Being aware of the condition of the grain in storage and knowing whether any grain has been previously removed are important aspects to help prevent entrapment from occurring. Many steps must be taken and included in a fumigation management plan to keep applicators and workers safe from exposure to toxic insecticides. Education of applicators and employees is essential to keep everyone safe.

Historical plant flows predict current insect invasions

Authors: Bonnamour Aymeric, University of Lausanne, Switzerland

Abstract: Thousands of insect species have been introduced outside of their native range, causing important damage on ecosystems and human societies. Many insects are tightly associated with plants as they feed or live on plants. Consequently, the plant trade is one of the main pathways of alien insect introductions. Alien plants also facilitate the establishment and spread of alien insects, in particular of those that use these plants as hosts. Here, we tested the hypothesis that plant invasions precede insect invasions. If such time lag exists, recent plant invasions might be useful to predict future insect invasions.

We tested the predictive power of historical and current alien plant flows and of potentially confounding socioeconomic drivers on alien insect invasions. We found that alien insect flows were best explained by alien plant flows of 1900. We then used the observed time lag between plant and insect invasions to estimate the insect “invasion debt”. Based on recent plant flows, we found that alien insect invasions are expected to increase in Asia, Africa and South America.

Evolution of novel receptors and peripheral inputs in the olfactory system

Authors: Bontonou Gwénaëlle[1], Arguello Roman[3], Baticle Tess[1], Auer Thomas[1], Álvarez-Ocaña Raquel[1], Cruchet Steeve[1] and Benton Richard[2], [1]University of Lausanne, [2]University of Lausanne, Center for Integrative Genomics, Switzerland, [3]University of Lausanne, Switzerland

Abstract: Chemoreceptor gene families are characterized by extensive between-species copy number changes, but how these genomic changes relate to modifications in the neural circuitry in which they are expressed remains mysterious. Drosophila's Odorant receptor (Or) family is particularly useful for addressing this question because most Ors are expressed uniquely in single olfactory sensory neuron (OSN) types. Between-species changes in Or copy number, therefore, may indicate OSN diversification or reduction. We focus on a rapidly duplicated/deleted subfamily (named Or67a) in the D. melanogaster species group. Genomic analyses have uncovered a dynamic recent history involving many parallel receptor gains and losses, likely related to an increased mutation rate promoted by repeat-rich sequences surrounding Or67a genes. Physiology, expression, and molecular evolutionary analyses have revealed a previously unappreciated adaptive mechanism involving Or co-expression. These experiments have also identified an evolutionary "birth" of a young OSN population. Together, our Or67a results shed light on the early steps of olfactory system evolution and the intriguing relationship between chemoreceptor family turnover and sensory neuron diversification.

Strepsipteran Parasitism of White Leafhopper, Cofana spectra (Distant) in Lowland Rice Fields

Authors: Boonsa-nga Kunlayaa[1], Kunawong Chattraporn[1] and Jaikeang Unchalee[1], [1]Chiang Rai Rice Research Center, Division of Rice Research and Development, Rice Department, Thailand

Abstract: White leafhopper, Cofana spectra (Distant) (Hemiptera: Cicadellidae) is considered as a minor insect pest of rice in Thailand. Nymph and adult of White Leafhopper suck the sap in rice plants resulting in tiller reduction, stunting and yellowing from leaf tip downwards. Severe damage finally causes rice death. Recently, the survey of insect pest of rice in the North revealed important information that White leafhopper was found abundantly in the light traps, rice fields particularly those nearby the lights, and wheat fields. Concurrently, Halictophagus spectrus Yang (Strepsiptera: Halictophagidae) was also found as an endoparasitoid of the White leafhopper. Although Strepsiptera has been recorded as possible biocontrol agents, there was no information on the effective use of H. spectrus as the endoparasitoid for controlling White leaf hopper. The objective of this study was to investigate the population dynamic of White leafhopper and it's relative number infected by H. spectrus in the fields at Chiang Rai Rice Research Center from February 2017 to February 2018. Sampling and monitoring in the rice fields were conducted on a weekly basis by sweeping net. During the study, two peaks of White Leafhopper population were recorded i.e April-June and October-December. The highest percentage of stylopization of the White leafhopper by H. spectrus being 34.6 % was recorded in June 2017. The result indicated that the effect of parasitization by H. spectrus may be one of the factors suppressing the population levels of White leafhopper in the rice field. However, indepth study should be carried out further to gather information adequately for developing efficient biological control of White leafhopper by the endoparasitoid H. spectrus.

Solving the taxonomy of dacine fruit fly larvae (Diptera: Tephritidae) with the help of morphology and adult morphometrics

Authors: Boontop Yuvarin, Plant Protection Research and Development Office, Department of Agriculture, Bangkok, Thailand

Abstract: The tribe Dacini includes some of world's prime economic and quarantine pests. Larvae infest fruit and vegetables, causing serious production losses and widespread, phytosanitary barriers to global trade. Larval stages are most commonly encountered by regulatory officials certifying exports or performing quarantine inspections of imported goods, but these stages are notoriously difficult to identify using morphological characteristics. In this study, dacine fruit flies were surveyed in diverse, fruit orchards throughout Thailand. Adults were collected by lure trapping; larvae were collected for morphological study and rearing. Larvae of six species (all major pests) were re-described from reliably associated material: Bactrocera correcta, B. dorsalis, B latifrons, B. umbrosa, Zeugodacus cucurbitae and Z. tau. A dichotomous key was prepared to enable rapid identification of third instar larvae by using a combination of morphological features. Wing morphometrics were studied in these species and an additional four: B. carambolae, B. cilifera, B. tuberculata and B. zonata. Centroid sizes (calculated from xx wing metrics) differed significantly among sampled species ($P > 0.05$), with B. latifrons smallest (5.533 ± 0.401 mm) and B. tuberculata largest (6.377 ± 0.306 mm). Canonical variate analysis of the dataset revealed a clear pattern in which species of Zeugodacus clustered together and separated from the cluster comprising species of Bactrocera. This study provides a basis for ongoing molecular analysis to clarify the distinction among species and establish criteria for confirmatory, molecular diagnosis of larvae.

Pheromone-based products for the monitoring and management of tomato leafminer (Tuta absoluta) on tomatoes

Authors: Booysen Petrus Johannes Gerhardus[1], Schlemmer Marie-Louise[1], van Tonder Aletta Johanna[1], Liebenberg Jessica[1], Schlemmer Marie-Louise[1] and M Steyn Vernon[1], [1]Insect Science (Pty) Ltd, South Africa

Abstract: The tomato leafminer, Tuta absoluta (Meyrick) (Lepidoptera: Gelechiidae) is an economically important pest of tomato (Solanum esculentum L.), potato (Solanum tuberosum L.) and various other solanaceous crops. If not controlled in tomatoes, T. absoluta can cause severe crop damage leading to losses of up to 80 - 100%. With international markets enforcing lower chemical residues and increased resistance to various insecticides, the need for more sustainable management of T. absoluta is critical. Monitoring of T. absoluta is essential to enable growers to detect its presence and population growth to ensure timely management interventions. The Insect Science (Pty) Ltd pheromone lure (T.A. PheroLure®), loaded with T. absoluta female sex pheromone, was developed to monitor T. absoluta in South Africa. T.A. PheroLure® caught a mean of 53 moths/trap/week over six weeks in five trials located throughout South Africa and can therefore be used for effective monitoring of tomato leafminer. Two pheromone-based control products (attract-and-kill and mass trapping) were developed for the management of T. absoluta. The Insect Science (Pty) Ltd attract-and-kill product (Last Call™ T.A.) at 2000 droplets/ha effectively controlled (reduced by > 80%) T. absoluta moths for three weeks and suppressed (reduced by > 60%) T. absoluta moths for five weeks compared to a standard insecticide programme. Last Call™ T.A. at 4000 droplets/ha extended control of T. absoluta with one week. No fruit damage occurred for eight weeks in both the 2000 and 4000 droplets/ha treatment blocks. The Insect Science (Pty) Ltd mass trapping product (TrapAll™ T.A.) at 30 water traps/ha effectively suppressed tomato leafminer over a period of six weeks. Both Last Call™ T.A. and TrapAll™ T.A. can be used effectively in an integrated pest management programme to manage tomato leafminer in tomatoes.

Elucidating the mechanisms of aphid resistance in Triticum monococcum L. (Poaceae)

Authors: Borg Alexander, Rothamsted Research, United Kingdom

Abstract: The aim of this study is to characterise the antibiotic mechanisms underlying aphid resistance in T. monococcum MDR049, focusing on its secondary metabolites (SMs). Two hypotheses were tested: (i) induction of aphid resistance in MDR049 is aphid density-dependent and (ii) aphid resistance mechanisms are systematically induced upon aphid feeding.

MDR049 leaf extracts were antibiotic against S. avenae after 24hrs and 48hrs, reducing adult survival and number of nymphs. MDR049 has a threshold of 5 aphids to induce a significant antibiotic activity at the aphid feeding site. This activity is reversed at the same leaf as the feeding site and not affected at a different leaf of the feeding site. LCMS analysis shows MDR049 leaf SMs change in trends compared to Solstice with increasing aphid density with signs of a systemic reaction to aphid feeding in MDR049, confined to the same leaf as the feeding site. Bioassay guided fractionation has identified peaks potentially responsible for the antibiotic activity observed in MDR049.

In conclusion, SM changes in MDR049 are aphid-density dependent and may be related to its aphid resistance mechanisms. MDR049 shows signs of a systematic response to aphid feeding. The SMs potentially responsible for this aphid antibiotic activity have been isolated.

Migration pattern of diurnal Lepidoptera populations under a rural-to-urban gradient

Authors: Borges da Silva Elsa[1] and Ramos Ana Paula[2], [1]Forest Research Centre, Instituto Superior de Agronomia, Universidade de Lisboa, [2]Laboratório de Patologia Vegetal “Veríssimo de Almeida”, Instituto Superior de A

Abstract: The influence of the urban gradient on the abundance and richness of diurnal Lepidoptera was studied in three sites located in the perimeter of the School of Agriculture of Lisbon (rural area) and in a public garden (urban garden) in Lisbon, from spring to fall of 2018. The objectives were: 1) evaluate the impact of human activity (frequency of people and vehicles) on lepidopteran abundance and richness populations and the pattern of migration; 2) relate the abundance and richness of Lepidoptera with the floristic composition.

The results show the existence of an inversely proportional significant relationship between the abundance and richness of Lepidoptera and human presence, following a rural-to-urban gradient, depending also on the species. A seasonal pattern of abundance and richness of Lepidoptera population’s species was also observed with the increase in the urban garden suggesting the establishment of a migration pattern under a rural-to-urban gradient. The migration from the rural to the urban area, together with the existence of small private gardens with abundant flowering plant species in the interstices between these two zones, thus constitutes a green corridor, which acts like a food repository and/or shelter for Lepidoptera at the urban area of Lisbon.

Host-seeking behavior of ticks toward resistant and susceptible animals: identification of repellent compounds and their use for tick control

Authors: Borges Ligia, Federal University of Goias, Brazil

Abstract: We are working on tick-host interactions with a goal to identify behavior-modifying compounds that can be used for tick control. Two breeds of dogs, English cocker spaniel and beagle, were compared for susceptibility to the tick Rhipicephalus sanguineus sensu lato. Beagles were found to have lower tick infestation than cockers due the production of two repellents, benzaldehyde and 2-hexanone. Slow-release formulations containing those repellents reduced the number of R. sanguineus on dogs. We further examined the odor profiles of three dog breeds: beagles, cockers, and the miniature pinschers (putative resistant). The mean amounts of benzaldehyde and 2-hexanone were similar for beagles and miniature pinschers and higher than that observed for cockers. Furthermore, 6-methyl-5-hepten-2-one was significantly higher in miniature pinschers than for the other breeds and repelled R. sanguineus in a bioassay. Those results support the hypothesis that miniature pinschers are a tick-resistant dog breed. We also tested and compared semiochemicals produced by horses (susceptible) and donkeys (resistant). One compound, (E)-2-octenal, was detected exclusively in donkey extracts, displaying repellency against Amblyomma sculptum. (E)-2-octenal slow-release formulations were found to reduce A. sculptum numbers in humans in a naturally infested field. This volatile also repelled Rhipicephalus microplus Amblyomma dubitatum and Lutzomyia longipalpis.

Staying in the club: Exploring criteria governing metacommunity membership for obligate symbionts under host–symbiont feedback

Authors: Borges Renee[1], Venkateswaran Vignesh, [1]Centre for Ecological Sciences, Indian Institute of Science, India

Abstract: Metacommunity membership is influenced by habitat availability and trophic requirements. However, for symbiont metacommunities consisting of herbivores and their predators, symbiont-host interactions can curtail membership criteria in novel ways. Understanding such host–symbiont feedback effects on symbiont community membership is crucial for understanding symbiont community structure and function.

We investigate symbiont community colonizing host inflorescences during specific host developmental stages. By modelling Inflorescences as habitat microcosms and accounting for the various symbiont-host we demonstrate two factors uniquely constraining symbiont membership criteria. 1) Host–mutualistic symbiont feedback ensured that no other symbiont had higher persistence than the mutualists, thereby constraining membership for non-mutualists. 2) Larger symbiont colonization windows, in part driven by host inflorescence development, increased overall colonization success and symbiont persistence. We also determine that predators required a larger number of hosts than that of their prey for persistence in the community with valuable implications for top–down predator-aided symbiont community stability. Our study clearly demonstrates that factors influencing symbiont community membership can be fundamentally different from those of non-symbiont metacommunities owing to host–symbiont feedback effects and impacts on host microcosm development and these constraints governing symbiont community membership, function and structure require special attention. Finally, through my talk, I will justify the utility of natural insect microcosms to test theories in metacommunity ecology.

Releases of native and exotic natural enemies to control main apple pests

Authors: Borowiec Nicolas[1], Hance Thierry[2], [1]INRAE Sophia-Antipolis, France, [2]UCLouvain, Belgium

Abstract: Research in agricultural entomology must face the challenge of radically reducing the use of pesticides in the coming years. Different alternative techniques to pesticides are already in use, but a combination of methods is often required to achieve sufficient reductions in pest population levels. The releases of natural enemies in the frame of biological control is one of these techniques. In order to control the two main pests in apple orchards, the rosy apple aphid Dysaphis plantaginea (RAA) and the codling moth Cydia pomonella, we tested three different strategies: (i) the releases of the exotic parasitoid Mastrus ridens for its permanent establishment, (ii) the inundative releases of the native predator Forficula auricularia and (iii) the inundative releases of the native parasitoids Aphidius matricariae and Ephedrus cerasicola.

The first releases of Mastrus ridens in Europe were done during summer 2019. A total of 6 900 M. ridens were released in 23 sites from North-West to South-East France. Since post-release surveys will be done next summer, the success of establishment of the parasitoid is still unknown. However, progeny of released M. ridens have been already sampled in some sites in South-East France.

We performed earwig releases in spring and then follow RAA infestation as well as potential sides effects on other beneficials arthropods. This predator appeared to be very efficient at the colony level but failed to control aphid population at the tree scale.

When the release of aphid parasitoids was carried out at a low density of aphids, an effective control of the density of aphid populations is observed, that is similar to the level of control obtained when spraying chemical products authorized in organic farming. However, if the release was done at a high density level of aphids, the parasitoid failed to reduce the density of the pest. The implementation of this technique in the field needs nevertheless to be improved particularly with regard to the significant costs associated with it.

The intercompatibility of these three techniques in experimental orchards and the feasibility of their combined use in commercial orchards will be discussed.

Does acquisition of resistance to entomopathogenic virus influence the outcome of a host-parasitoid interaction? A case-study with the codling moth Cydia pomonella and its parasitoid Mastrus ridens.

Authors: Borowiec Nicolas[4], Moiroux Joffrey[1], Perrin Marie[2], Dib Hazem[3] and Delattre Thomas[3], [1]Avignon University, France, [2]Avignon University, France, [3]INRA, PSH Unit, Team Biological Control by Conservation, Avignon, France, [4]INRAE Sophia-Antipolis, France

Abstract: A wide range of tools is used for pest control, such as pesticides, pheromones, microorganisms or natural enemies. Repeated application of a method may result in the acquisition of resistance to this method, as commonly observed in the rapid appearance of resistance to insecticides in pest insects. Such acquisition of resistance to a given method may however be traded-off against, or, on the contrary, increase resistance to another control agent. The codling moth Cydia pomonella is a worldwide-distributed species which causes major losses in orchards. Among pest control methods, Cydia pomonella granulovirus (CpGV) has been successfully used for 15 years as a bioinsecticide until some insect populations with low susceptibility to the virus were detected for the first time in 2004 in southeast France. More recently, in 2019, the parasitoid Mastrus ridens was released in experimental fields to study its efficiency to control the codling moth in France. In this study, we compared in the lab a Cydia pomonella sensitive and resistant line with the CpGV to investigate how acquisition of resistance to this entomopathogenic virus shaped life history traits of this pest species, and how it influenced its resistance to chemical and biological insecticides and to the newly introduced parasitoid Mastrus ridens. Implications for pest management will be discussed.

Ants do drugs to fight disease

Authors: Bos Nick[1], Freitak Dalial[2] and Sundström Lotta[3], [1]University of Copenhagen, Denmark, [2]University of Graz, Austria, [3]University of Helsinki, Finland

Abstract: Defence against pathogens and parasites is extremely important for organisms in order to maintain their fitness. Immune responses can take on many forms, which can be divided between behavioural and physiological responses. One of these behavioural responses is self-medication, which occurs when an organism consumes or contacts biologically active compounds in order to clear or inhibit the infection. Here, we show that upon exposure to a fungal pathogen, ants (Formica fusca) change their diet preference to include Reactive Oxygen Species (ROS). This leads to higher resistance against fungal infection. Furthermore, we show that only infected ants benefit from feeding on ROS, as when healthy ants feed on the same diet, they show increased mortality. Thus, by showing a cost of medication in the absence of pathogens, we rule out the possibility of compensatory diet choice, and provide conclusive evidence for the first time, that ants engage in therapeutic self-medication.

Where do all the fungi go?

Authors: Bos Nick[1], Thomas-Poulsen Michael[1], Guimeraes Leandro[1], Kone N'golo[2], Palenzuela Romen[1] and Silue Simon[2], [1]University of Copenhagen, Denmark, [2]Nangui Abrogoua University, Ivory Coast

Abstract: Fungus-growing termite colonies are rarely infected by antagonistic fungi, and their fungus gardens are essentially free of other fungi with 99% of amplicon reads belonging to their Termitomyces symbiont. However, foraging for food is expected to open the way for antagonistic fungi to enter the nest and exploit the termites' fungal crop, raising the question as to how the termites achieve such a sterile environment while raising their monoculture.

Several potential barriers to diseases entering the nest have been suggested. First, as termites normally forage underneath self-built soil sheets, they could sterilize the foraging substrate they are foraging on. Furthermore, any returned food could potentially be sterilized by the workers through a gut passage. This is a feature unique to the fungus-growing termites, where all food first passes through their gut, before being deposited by defecation on the fungus comb.

To test these two potential barriers, we first analysed the diversity of fungi growing in termite foraging sites. To test whether fungal diversity in the foraged material decreases during the gut passage, we dissected worker guts and divided them into three compartments, and used a culture-based approach to identify fungal genera present in each of the compartments.

Foraging material did not appear sterilized, and fungal diversity did not decrease during gut passage. We therefore conclude that any sterilization of substrate is likely to happen after it has been deposited on the fungus comb, likely through an interplay between defences originating from the termites as well as those from the crop itself.

Gene tree symmetry in the age of genomics– a case study on Nomiinae

Authors: Bossert Silas[1], Danforth Bryan[2] and Brady Sean[3], [1]Cornell University Smithsonian National Museum of Natural History, United States, [2]Cornell University, United States, [3]National Museum of Natural History, United States

Abstract: Modern gene tree approaches that aim to solve notoriously difficult nodes of large-scale phylogenies suffer from uninformative genes and poorly resolved gene trees. The resulting gene tree estimation error, coined the 'Achilles' heel' of coalescent methods, can substantially distort the process of finding the true species tree. I present research on establishing a metric to identify suitable and less suitable loci, and provide first-hand suggestions to improve gene tree-based phylogenetic reconstruction of species trees.

The control of Tuta absoluta tomato leafminer in the region of Mostaganem (Algeria).

Authors: Boualem Malika[1], Ghelamallah Amine[1], Krache Farial[1], [1]University Abdelamid Ibn Badis of Mostaganem, Algeria

Abstract: Since 2008, the tomato leafminer Tuta absoluta (Meyrick, 1917) (Lepidoptera: Gelechiidae) has been considered in the Mediterranean basin and Algeria as a serious threat to greenhouse and field tomato production. This microlepidoptera attacks all the phenological stages of the crop and causes significant damage to leaves, stems and fruits, its damage can reach 100% losses. A number of research has been carried out to develop control strategies that can help mitigate the extent of this pest on glasshouse tomatoes in the Mostaganem region. Two plants (Urtica membranacea Poir.) and (Juniperus oxycedrus L.) have been used as bioinsecticides for their richness in bioactive substances (essential oil, aqueous and hydroalcoholic extracts). A biological control based on the use of predatory or parasitoid auxiliaries with the enhancement of the species of auxiliary insects identified as such under the bioclimatic conditions of the study area. The combination of all these regulatory factors has made it possible to control this pest to an interesting degree.

The Multi Target Method (MTM) for the control of stable, horse and tsetse flies in the FlyScreen project

Authors: Bouhsira Emilie[9], Lienard Emmanuel[9], Salou Ernest[2], Gimonneau Geoffrey[3], Rayaisse Jean-Baptiste[2], Ouma Johnson[1], Thaisungnoen Kornkanok[7], Desquesnes Marc[6], Franc Michel[9], Jacquiet Philippe[9], Chalermwong Piangjai[7], Guillet Pierre[1], Masmeatathip Roungthip[5], Jittapalapong Sathaporn[8], Onju Sathaporn[7], Shukri Sharif[9], Shah Viral[1] and Grimaud Yannick[4], [1]AtoZ Textile mills l.t.d., Arusha, Tanzania, [2]CIRDES, Bobo-Dioulasso, Burkina Faso, [3]CIRDES/CIRAD, UMR InterTryp, Bobo-Dioulasso, Burkina Faso, [4]GDS, La Reunion Island, Réunion, [5]Kasetsart University, Department of Entomology, Faculty of Agriculture, Kamphaeng Saen, Thailand, [6]Kasetsart University, Faculty of Veterinary Medicine, Bangkok CIRAD, UMR InterTryp, Bangkok, Thailand, [7]Kasetsart University, Faculty of Veterinary Medicine, Bangkok, Thailand, [8]Kasetsart University, Faculty of Veterinary Technology, Bangkok, Thailand, [9]Veterinary School of Toulouse, France

Abstract: Facing increasing needs to feed human populations requires, more than ever, to enhance quantity, quality, safety and security of agricultural products, and, at the same time, to reduce environmental contamination. Thus, in livestock production, it is required to control blood-feeding flies such as Tabanids and stable flies which are responsible of annual losses estimated at 130Kg of milk/cow and 25Kg of meat/ox. To the huge blood spoliation are added stress, loss of appetite and energy, immunosuppression and mechanical transmission of viruses (equine infectious anaemia, ovine catarrhal fever), bacteria (Q fever, anthrax) and parasites (Besnoitia, Trypanosoma), with dramatic medical and economic consequences. Control of hematophagous flies is most often neglected or occasional, since insecticide spraying on walls or animals (spray, pour on) is expensive, of short term efficacy and meets increasing chemo-resistance problems. Moreover, residues contamination of animal products and environment is unacceptable, for biological agriculture.

Tsetse fly control using insecticide impregnated fabric targets proved to be efficient in Africa, because Glossina spp. are low prolific and very sensitive to insecticides. Unfortunately, this does not apply to other hematophagous flies such as Tabanids (> 4,400 species present in all types of landscapes and climates), Stomoxys (one species is cosmopolite) and other hematophagous insects such as Haematobia and Musca crassirostris, which are highly prolific, and may develop early chemo-resistance to insecticides.

FlyScreen project aims at the development and optimization of efficient, low cost and low or non-polluting methods for the control of hematophagous insects. It consists in (i) design and optimize specific hematophagous colour baited attractant screen (excluding pollinators) (ii) Develop and evaluate in laboratory conditions various toxic systems including encapsulated (slow release) insecticides, UV-protection and attractants (iii) Evaluate and validate these screens in semi-natural and natural conditions to measure efficacy and safety (environmental contamination) and (iv) Promote low-cost and low-polluting control methods.

FlyScreen project was coordinated by CIRAD and supported by the French Research Agency (FlyScreen project ANR-15-CE35-0003). It has been carried out by a Consortium in partnership between France [CIRAD (UMR InterTryp), National Veterinary School of Toulouse (ENVT) (UMR IHAP), Montpellier 3 University (CEFE)], Thailand [Kasetsart University (Bangkok)], Burkina Faso [CIRDES, Bobo-Dioulasso] and Tanzania [AtoZ Textile Mills l.t.d.].

During this project, new insecticide impregnated plastic screens have been developed and give very good results for tsetse flies, and good results for stable and horse flies when populations are still sensitive to pyrethrinoides. Ecotoxicological tests have been performed by an independent start-up showing very low release of insecticide in the environment.

Improving the efficacy of two Metarhizium species combined with Spinosad to control two species of wireworm (Agriotes lineatus and Agriotes obscurus).

Authors: Bourdon Pierre-Antoine[3], Baxter Ian[1] and Butt Tariq[2], [1]Certis Europe, United Kingdom, [2]Swansea University, United Kingdom, [3]Swansea University, France

Abstract: Following the withdrawal of registration of neonicotinoid and mocap in 2018, wireworm management is challenged. Spinosad, a bioinsecticide, is one of the only products still registered for wireworm control; however, its efficacy is limited. Entomopathogenic fungi (EPF) are another option, but the time to kill the larvae do not prevent damage. A stress and kill strategy combining an insecticide with an EPF can reduce the time to death and increase the mortality. Two Metarhizium strains were tested against wireworm in combination with three sublethal doses of spinosad. Metarhizium brunneum Met52 and Metarhizium 16P alone were unable to kill any Agriotes lineatus and Agriotes sordidus larvae. The addition of sublethal doses of spinosad could increase significantly the mortality of the wireworm larvae; however, synergies were dose dependant and species dependant. Met52 combined with spinosad produced higher mortality and was faster to kill than Metarhizium 16P against both species of wireworms. Control of wireworm could be possible to achieve in the field, but the right combination between an EPF, the appropriate dose of stressing agent and the right wireworm species.

The utilization of the fungal volatile organic compounds 1-octen-3-ol and 3-octanone against wireworm, corn rootworm and garden chafer: toxicity and semiochemicals activity

Authors: Bourdon Pierre-Antoine[3], Myrta Arben [1], Midthassel Audun[1] and Butt Tariq[2], [1]Certis Europe, [2]Swansea University, [3]Swansea University, France

Abstract: New pest management solutions are needed to control soil insects. Fungal volatile organic compounds (VOCs) such as 1-octen-3-ol and 3-octanone could be part of the solution as these have fumigant properties and semiochemicals properties affecting various insects or mollusks. We tested the fumigants properties of these two volatiles against three soil pests: wireworm (Agriotes lineatus), corn rootworm (Diabrotica virgifera virgifera) and garden chafer (Phyllopertha horticola) in closed tubes with or without soil. The insects differed in their sensitivity to these VOCs. The lowest doses (1.25 and 2.5µl) were sufficient to kill corn rootworm and garden chafer but not wireworms which required a threshold of 5µl or more to die. The semiochemicals properties of the VOCs were assessed in 5L bucket with a choice trial (untreated vs treated maize). Low doses (100 or 200µl) of VOCs could influence the movement of the insects in the soil but not kill them. Corn rootworm and garden chafer were mostly attracted by low doses VOCs while wireworms were repelled by these. Fumigation in the field seemed unrealistic as it will require huge amount of VOCs; however, attract and kill or push pull strategies could be develop against soil insects to reduce crop damage.

Dietary preferences of Heteromurus nitidus (Collembola) among wheat phytopathogenic fungi of crop residues: implications for bioregulation

Authors: Bourgeois Thomas[2], Salmon Sandrine[1], Suffert Frédéric[3], Dupont Joëlle[1], Prado Soizic[1], Lacoste Sandrine[1], Biau Gwenola[1], Dury Gérard[1], [1]Muséum national d'Histoire naturelle, [2]UMR 7179 CNRS, France, [3]Université Paris-Saclay - INRAE

Abstract: Soil arthropods play a key role in agrosystems through several ecosystemic services. Among these services, they regulate fungal communities and could play a role in mitigating the impact of deleterious fungi overwintering in crops. In this study, we investigated the preferences of a springtail, Heteromurus nitidus, between two phytopathogenic fungi, Zymoseptoria tritici and Fusarium graminearum, and eleven fungi present on wheat plants by placing springtails in presence of fungi grown in vitro in pairs. We also tested the impact of long-term consumption of the phytopathogenic fungi on springtail populations and fungal development by feeding populations with the fungi for ten weeks. Our first results show that Z. tritici was more often preferred to other fungi offered than F. graminearum . During the long-term experiment, springtail populations fed on either Z. tritici or F. graminearum had a better growth than control populations. Moreover fungal cover at the end of the experiment was reduced by springtail presence. These results seem to highlight a potential capability of H. nitidus as a biological control agent against the pathogenic fungi tested and open the way to new tests in situ.

Peer Community In Entomology: a free recommendation process of unpublished scientific papers in Entomology based on peer reviews

Authors: Bourguet Denis[1], Guillemaud Thomas[2], Facon Benoit[3], [1]CBGP, Inra, France, [2]INRA, ISA (INRA/UNSA/CNRS), France, [3]PVBMT, Inra, France

Abstract: Peer Community in Entomology has been launched in 2019. It already counts 90 recommenders and has already received submissions of preprints for evaluation and recommendation. It is part of the global Peer Community in (PCI, https://peercommunityin.org) project.
In order to offer an alternative to the current system of publication - which is particularly expensive and not very transparent - we have initiated PCI: a non-profit scientific organization that aims to create specific communities of researchers reviewing and recommending, for free, unpublished preprints in their field (i.e. unpublished articles deposited on open online archives like arXiv.org and bioRxiv.org). Each PCI is a group of several hundred recommenders playing the role of editors who recommend such preprints based on peer-reviews to make them complete, reliable and citable articles, without the need for publication in 'traditional' journals (altough the authors can submit their recommended preprints afterwards). Evaluations and recommendations by a PCI are free of charge. When a recommender decides to recommend a preprint, he/she writes a recommendation text that is published along with all the editorial correspondence (reviews, recommender's decisions, authors' replies) by PCI Evol Biol. The preprint itself is not published by PCI: it remains in the preprint server where it has been posted by the authors.
The first Peer Community in has been launched in 2017: Peer Community in Evolutionary Biology (PCI Evol Biol). More than 700 recommenders have already joined PCI Evol Biol, PCI Paleontology, PCI Ecology, PCI Animal Science and PCI Entomology.

Sterile Insect Technique and population management of insect pests: success and challenges

Authors: Bourtzis Kostas, Insect Pest Control Laboratory, Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, Vienna, Austria

Abstract: Insects represent the most abundant and speciose group of animals on our planet. The great majority of them are beneficial or harmless. However, a small fraction of them are considered major pests for agriculture or transmit devastating diseases to animals and humans. The populations of these insect pests and disease vectors have so far mainly been controlled with broad spectrum insecticides. However, insecticides pose major threat to the health of ecosystems and humans while insecticide resistance evolves and has been frequently reported and therefore there is an urgent need of alternative methods for the management of these insect pests and disease vectors. The sterile insect technique (SIT) is an environment-friendly birth-control method, which has been successfully implemented for the last 70 years as a component of area-wide integrated pest management to suppress or locally eradicate populations of insect pests and disease vectors worldwide. In this presentation, we will outline the basic principles of SIT and will report on recent R&D activities at the FAO/IAEA Insect Pest Control Laboratory, Seibersdorf, Austria. We will also present a few SIT success stories and will discuss the major challenges for its large-scale implementation against insect species of agricultural, veterinary and human health importance.

Potential use of Coccinellids as predator of Bagrada hilaris (Hemiptera: Pentatomidae) in Chile

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Abstract: Bagrada hilaris (Burmeister) (Hemiptera: Pentatomidae), the painted bug, is a native species of Africa and one of the most invasive pentatomid pests in the world. In South America, B. hilaris was recently reported, for the first time, in the Santiago Metropolitan Region, Chile, in 2016. Despite the control measures adopted in Chile, which include reiterative applications of conventional insecticides, the populations of B. hilaris have been growing and have been recently found in all central regions of the country, mainly associated with horticultural crops of the Brassicaceae family. Although entomopathogenic fungi, several parasitoids (Scelionidae) and predators such as Bochartia sp. have been described, there have been no reports of efficient strategies using them in the field. This study reports for the first time the predation of coccinellids on immature Bagrada hilaris (Burmeister) (Hemiptera: Pentatomidae) in South America. In Chile, B. hilaris was found in association with three genera of coccinellid predators: Harmonia, Hippodamia and Eriopis. Therefore, we study i) the diversity of Coccinellidae species associated with B. hilaris on brassica and ii) predatory behavior assays of these Coccinellidae species on nymphs of B. hilaris. The evaluations were done using a General Linear Model (GLM) with a quasibinomial error distribution and logit link function. The results are discussed to explore new alternatives for controlling this pest.

Physiological consequences of climate change on the performance and metabolism of the eastern spruce budworm (Choristoneura fumiferana, Clemens)

Authors: Bowden Joe[1], Moise Eric[1], Spicer Heather[2] and Thomas Raymond[3],

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Abstract: Climate change is projected to have significant consequences for forest ecosystems, including for irruptive forest insects, such as the spruce budworm. Despite current knowledge that temperature affects insect performance (e.g., reproduction, body mass, feeding), the underpinning physiological mechanisms are not yet fully understood. Using environmental chambers, we established six temperatures (n=6) to simulate a range of historical and projected growing season temperatures for Newfoundland, Canada. We monitored growth, development, feeding and metabolic rate (using an infrared gas-exchange analyzer). Our results indicate that temperature significantly decreased development times for both pupae and adults (p <2.2 x10-16), but there was marginal consequence for pupal (p= 0.054) and none for adult mass (p= 0.952). At both fifth-instar and adult stages, an increase in temperature resulted in a significant increase in metabolic rate (L5: p= 0.043, and Adult: p= 0.014). Feeding assay results suggest that despite shorter maturation periods and greater metabolic losses, the lack of an effect on budworm mass can likely be attributed to the positive relationship observed between warming and compensatory feeding (p= 0.019 for net growth efficiency and p= 0.045 for growth rate). We will also present the results of compositional changes to the storage- and mitochondrial membrane specific- lipids. It is imperative to understand the physiological basis of the relationship between warming and performance on irruptive insects to comprehend how climate change continues to influence these economically, and ecologically, important species.

Molecular regulation of diapause initiation in the solitary bee Megachile rotundata

Authors: Bowsher Julia[1], Yocum George[3], Brar Gagandeep[1], Signor Sarah[1], Torson Alex[3] and Rinehart Joseph[2], [1]North Dakota State University, United States, [2]United States Department of Agriculture Agricultural Research Service, United States, [3]USDA-ARS

Abstract: Environmental cues regulate diapause initiation in facultatively diapausing insects. In the alfalfa leafcutting bee, Megachile rotundata, diapause seem to have a maternal component to its regulation. The goal of this work was to test whether methylation influences gene expression at the point of diapause initiation, and which genes were differentially expressed at that decision point. We compared prepupae that were diapause-destined and nondiapause-destined with whole genome bisulfite sequencing and RNAseq. Samples were collected early in the field season and late in the field season. We found that methylation rates were low across the genome regardless of diapause status. There was a significant overlap between genes that were differentially expressed and genes that were differentially methylated, but the direction of differential expression did not always correspond with methylation status. We identified differentially expressed genes involved in oxidative stress and other diapause-related pathways. Methylation may be important for the regulation of specific genes involved in diapause, but is not likely to be a general regulator of gene expression prior to diapause.

Telomere dynamics during development and overwintering in solitary bees

Authors: Bowsher Julia[2], Grula Courtney[2], Heidinger Britt[2] and Yocum George[1], [1]Edward T. Schafer Agricultural Research Center USDA-ARS, United States, [2]North Dakota State University, United States

Abstract: Adult insects have relatively short lifespans but show declines in performance with age. The mechanisms that underlie these age-associated declines in performance are not well understood. Decreasing telomere length is positively associated with aging in various organisms. Telomeres are repetitive sequences of non-coding DNA located at the end of chromosomes, which protect coding DNA during replication. Telomere attrition is associated with increasing age in many animals. Insects that go through metamorphosis can spend different lengths of time in each life stage. Cellular aging may depend on life stage and time spent in that stage, especially if that life stage is extended, as during diapause. This study aimed to determine the telomere dynamics throughout development, and overwintering in solitary bees, Osmia lignaria and Megachile rotundata. Bees from differing stages of development including prepupae, pupae, and multiple adult stages were collected and their DNA was extracted. Telomere length was measured using qPCR. Our results show a contradictory trend in telomere attrition, with telomeres elongating with age. Telomere length did not change during diapause, but increased only in emerged adults. These data can be used to demonstrate how bees age, and to determine if telomere loss is a driving mechanism of aging in solitary bees.

A new DNA metabarcoding approach to describe the diet of social wasps and evaluate their impact on biodiversity

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Abstract: For most invertebrates, it is difficult to access 'historical' samples such as older faeces due to the small size of the animals and the absence of permanent dejection sites. This project aimed at developing a method to study the diet of social wasps and provide an overall picture of their diet using the leftover prey DNA recovered from their nests.

By applying our method to the nests of two Polistine wasps (Polistine chinensis and P. humilis) in urban and sub-urban areas in New Zealand, our analysis provided an outline of the resource partitioning between these species and their potential impact on New Zealand native inverterbrates.

Our method allowed the amplification and sequencing of 96 samples collected from 48 wasps' nest, with on average 80,334 DNA reads (±6,435 sem) per sample. For both wasps species the main prey taxa detected comprised Thysanoptera, Lepidotera, Diptera, Coleoptera and Acariformes. Among these, a significant number of reads corresponded to pest species, which supports the hypothesis that wasps can have positive effect on the control of other insect pests. On the other hand, our study also revealed the presence of New Zealand native and endemic species, which highlights the ambivalent impact of these generalist predators.

The IMAgHO project: Increasing the Multifunctionality of Agroecosystems by Harnessing fOod webs

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Abstract: In a context of ever-increasing demand for food, the future of farming requires to develop sustainable agricultural practices. The IMAgHo project aims at harnessing naturally-occurring trophic interactions to maximise regulatory services in agroecosystems and thus maintain or increase yield while reducing chemical inputs. Key regulatory services (biological control and pollination), will be studied in oilseed rape crop through the deciphering of food web dynamics at very fine temporal scale (monthly sampling), and wide spatial scale (from plot to landscape) in a setting that allows the testing of critical environmental and management gradients. Three work packages have been developed to reach the projects' goal. First the dynamics of selected food webs will be described over two years with samples collected every month during the crop growing season (WP1). Massively parallel DNA sequencing and environmental DNA samples will be used to decrypt food webs and quantify regulatory services of carabids feeding on pests and weeds, parasitoids attacking aphids and domestic and wild bees collecting pollen. The structure, stability and other connectedness descriptors of these webs will then be analysed in relation to environmental gradients, as well as existing long term historical data on agricultural practices, agrochemical input and biodiversity (WP2). Finally, modelling and field experiments will be implemented to predict and test how modifications of food webs can cascade into increased ecosystem services and greater yield (WP3). Results from the project will lead to better management of monoculture and overall lower use of pesticides. This will have a substantial impact in economic term (less buying of pesticides) and in ecological term. The more ecological growing practices may also give a market edge or lead to higher resale value as customers are constantly demanding for production processes that are environmentally friendly.

Within and beyond stick insect evolution: trait evolution and historical biogeography based on an extremely comprehensive taxon sampling

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Abstract: Stick and leaf insects (Phasmatodea) are nocturnal herbivorous arthropods characterised by masquerading as plant parts. Despite their morphological diversity and worldwide tropical distribution, their traditional taxonomy is unstructured and lacks a solid basis for sensible classification. It was only until recently that Phasmatodea was considered one of the lesser-studied insect lineages. However, due to efforts of the past years, molecular phylogenies have begun to shed light on the phylogenetic relationships and raised doubt on the validity of the traditional classification. Using a set of seven nuclear and mitochondrial markers, we aim to revise the traditional concepts that were mainly based on morphological characters. We inferred the so far largest phasmatodean molecular phylogeny comprising over 1000 stick and leaf insect species. We are not only covering almost a third of the described species, but also presenting a vast amount of hidden and undescribed phasmatodean diversity. In combination with geographical data, we reconstructed the historical biogeography, which allows us to draw conclusions about distribution patterns of an insect group with rather low dispersal capability. Furthermore, our extensive taxon sample provides the optimal framework to discuss evolutionary relevant traits such as reproduction strategies and the capability of flight. We suppose that wings and ocelli were lost and possibly regained in several instances and that similar evolutionary processes may have shaped the evolution of organismic lineages beyond the stick and leaf insect clade.

From ancestral states to ancestral ecological networks

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Abstract: Intimate ecological interactions, such as those between parasites and their hosts, may persist over long time spans, coupling the evolutionary histories of the lineages involved. Most methods that reconstruct the coevolutionary history of such associations make the simplifying assumption that symbionts have a single host. We developed a Bayesian approach for inferring coevolutionary history based on a model that allows symbionts to use multiple simultaneous hosts and to preferentially colonise new hosts that are phylogenetically similar to other hosts in it's host repertoire. These features reveal the entire distribution of ancestral states at any given point in time, allowing us to build networks of all inferred interactions at different times in the past. By reconstructing ancestral networks, we show how specific host shifts, host-range expansions, and recolonisations of ancestral hosts have shaped the network of interactions between Pieridae butterflies and their angiosperm host plants over time, creating an evolutionarily stable modular and nested structure. Our approach can be used to test ideas about the evolution of ecological networks in many other systems besides herbivorous insects.

Behavior, freedom of choice, flexible niches and their link to the ecological resilience and stability debate

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Abstract: Despite that we need a clear hypothesis for how animals can stably coexist when conditions are adverse (e.g. to support diversity, the resilience of endangered ecosystems, or ecosystems services that we rely on for food), we have so far struggled to identify the core mechanisms that enable this ability. Consequently "how resilience is promoted" has become listed as one of the most important fundamental questions that remain to be answered in ecology. However, despite that we know that behavioral responses to natural (e.g. seasonal variation) or human-made habitat changes (e.g. agriculture) are common, we have barely addressed that the ability of individuals to behaviorally "choose" to step out of competitive dynamics when conditions are adverse could be the key to answering this question.

Such choices could, for example, be when individuals change their behavior in response to the resources available (e.g. per optimal foraging theory) or to avoid negative encounters, and we here present a novel network-based approach where we use the level of "freedom of choice" to approximate ecological response and recovery rate. Using this approach we conceptually show how behavior is likely to buffer competition and community dynamics before diversity effects have time to emerge. Furthermore, we also empirically use this approach to show how management manipulations, such as a switch to organic fertilization, immediately can change both functional redundancy and resilience within the available diversity. In our case, the reason for this was arguably that unstable prey communities (induced by inorganic fertilization) constrained predators' choices and made functioning depend on early competitive and community settings. Whereas, stable prey communities (induced by organic fertilization) on the other hand lead to an increased adaptability, reduced the influence of "the ghost of competition past", and made functioning reliable.

In summary we show that behavioral mechanisms are key measurements that needs to be incorporated into resilience and coexistence hypothesis. Not the least because our hypothesis for how diversity is regulated both implies that species niches are flexible and that their dynamics are preceded by a behavioral "sorting by competition", that we believe could lead to a paradigm shift in our understanding of how competing species co-exist. Furthermore, by allowing effects that are occurring within the available diversity to be assessed, we hope to enable a leap a towards a gaining more detailed understanding of how ecosystems could be managed. This is important, not the least because diversity effects often are slow to emerge and difficult to survey during the short time frame allowed by most funding schemes.

Converting molecular data to trophic networks: what needs to be considered and why

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Abstract: DNA-based approaches are widely used for assessing trophic interactions. In trophic networks of arthropod communities one of the major challenges is the high complexity they harbour: multiple consumer species are interacting with a wide range of prey taxa. But how do we translate the results from molecular screenings of different consumers into meaningful trophic networks?

We want to address this question in relation to a recently produced, large molecular dataset. In the framework of the BioAware project, molecular gut content samples of carabid beetles (Coleoptera: Carabidae) have been collected to assess their role as natural pest control agents in arable land. This unique dataset of over 10.000 individual samples of over 100 carabid species collected in 60 cereal fields across four European countries in two synchronized sampling sessions will be examined to assess carabid food choices in relation to environmental conditions.

Our findings suggest that consumer traits are important to be considered when translating molecular into trophic data. This adds highly needed methodological and conceptual considerations to how molecular data sets should be used for studying trophic networks.

Examining the reliability of biological control by assessing the season-wide trophic dynamics between pests, generalist predators and alternative prey

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Abstract: Modern food production often involves using pesticides and while this constant input is unsustainable, natural methods of pests control have yet to be refined. Among these, conservation biological control is the ecosystem service most likely to enable reductions in pesticide use. Despite this, current knowledge on what drives its efficacy has been insufficient to make it reliable. Because most research within crop-pest systems has been restricted to limited time points, we lack an understanding of season-wide dynamics between pests, predators and alternative prey. Knowing how predators adapt their behaviour to changing conditions is crucial to understanding how biological control could be managed. Such adaptations affect the redundancy of pest consumption, and increasing redundancy is likely to enhance the resilience of biological control. We investigated the temporal dynamics in trophic interactions between predators, pest and alternative prey, by molecularly analysing the gut content of several thousand predator individuals. Using cereal fields naturally infested by aphids, we experimentally manipulated pest and alternative prey availability, to assess how turnover in community structure affects predator diets and niche overlap. This allowed a high temporal resolution of interactions occurring throughout the entire season, to determine critical time points to maintaining a reliable biological control.

Reducing wireworm damage in potato: assessing trap crops and entomopathogenic fungi

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Abstract: Wireworms pose a serious problem in potato production in Central Europe and elsewhere as they damage tubers and make them vulnerable to attack of pathogens. Due to the ban of insecticides for wireworm control in many countries, there is a great need to develop alternatives for the control of elaterid pests. One such alternative control approach is the deployment of trap crops and ento-mopathogenic fungi. Whilst the former is intended to lure the larvae away from the crop, the latter should infect and kill wireworms to reduce their population densities. To test this approach under field conditions, two field experiments were conducted in Tyrol (Austria) where we tested the combination of trap crops (a mixture of six plant species) and Metarhizium brunneum to reduce the feeding pressure Agriotes larvae exert on potato tubers. The treatments involved the application of the fungus in the preceding crop and the main crop as well as trap crops and combinations thereof. Wireworm densities were monitored within and between potato ridges throughout crop development and collected larvae were tested for plant DNA to assess their food choices. Moreover, potato yield and damage to tubers was examined. We found that the combination of trap crops and the application of the fungus in potato reduced wireworm-induced damage by one third whilst wireworm densities seemed to be unaffected in the different treatments. Molecular gut content analysis showed that potatoes represent the most attractive host plant when comparing plant DNA detection frequencies between the crop and the trap crop species. These findings provide important implications for the refinement of a novel attract and kill approach to reduce wireworm damage in potato crops.

Redundancy and climate resilience of generalist predator food webs in Swedish barley crops

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Abstract: In general, increased biodiversity is expected to provide more resilient ecosystem processes. This is largely because in diverse communities there are more species that can contribute to the functions (functional redundancy), and because different species are likely to respond differently to environmental variation (response diversity). Unfortunately, attempts to empirically assess resilience of ecosystem processes in relation to relevant disturbances are few, not least in agricultural landscapes. We will here present results from a study investigating functional redundancy and climate resilience of generalist predators predating on pest aphids and a range of other prey types in Swedish barley crops. To assess functional redundancy we developed a new method linking interaction metrics with metabolic theory that allows for a quantification of redundancy at the level of ecosystem processes. Applying this method to our generalist predator food webs, we found that redundancy of aphid predation significantly increased with the complexity of landscapes surrounding the barley fields. To assess response diversity in relation to global warming we have investigated the activity niches of a large number of actively hunting generalist predators in relation to temperature. By combining these activity niches into a metric of climate resilience at the predator community level and applying it to existing datasets we are now assessing how climate resilience varies with landscape complexity and in field management. Results from this work will be presented at the congress.

First record in Europe of Psyllaephagous blastopsyllae associated to the eucalypt psyllid Blastopsylla occidentalis: a new case of fortuitous biological control

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Abstract: The psyllid Blastopsylla occidentalis Taylor (Hemiptera: Aphalaridae) is an Australian species that is invasive in Africa, South America and Europe. The species was first detected in Portugal in 2009. This psyllid use different Eucalyptus species as hosts, in particular E. camaldulensis, E. globulus, E. rudis and E. tereticornis. These Eucalyptus species occur in Portugal on urban and peri-urban areas for amenity and leisure purposes. Eucalyptus globulus is an economically important species widely used in plantations. Here we present the most recent geographical distribution of B. occidentalis in Portugal, and data on its abundance and potential impact. Field surveys conducted in four years, showed low population levels of B. occidentalis. On average, less than 20% of eucalypt buds were attacked. In 2019, the endoparasitoid Psyllaephagous blastopsyllae (Hymenoptera: Encyrtidae) was found associated to B. occidentalis. This is the first report in Europe of P. blastopsyllae. This parasitoid was first reported from Camaroon and was later introduced into South Africa and South American countries.

How critical are insect pests for Eucalyptus plantations in Iberia and how biological control may alleviate it?

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Abstract: The area planted with Eucalyptus in the Iberian Peninsula has increased about 4-fold during the last 40 years, reaching around 1.4 million ha at present. The first Australian invasive pest species affecting Eucalyptus plantations was reported in early 70's. Since then, the number of invasive pest species of Eucalyptus increased exponentially following global trends. During the last decade, almost every year one new species has been reported. Biological control has been a major aid to reduce the economic impact of these invasive species. More than 60% of the Eucalyptus invasive species are currently under complete or partial classical biological control. Significant positive benefit: cost ratio was demonstrated for the case of Gonipterus platensis under control by the egg parasitoid Anaphes nitens in Portugal. Although the success was incomplete, benefit estimates may have exceed 2000 million Euros. Further, an anticipation of the establishment of this parasitoid by just one year provided a benefit: cost ratio of 67. No negative impacts were registered whatsoever on non-target native insects for any of the introduced parasitoids. Interestingly, 85%, 6 out of 7 species of biological control agents currently present in Portugal arrived unintentionally, most of them following releases in other regions or other continents. Once a classical biological control is launched in one region it may originate significant positive externalities by natural spreading to other regions. In the case of A. nitens, further augmentative releases were conducted. Research programs are under way with the aim of introducing new control agents in Portugal and Spain, namely for the control of G. platensis and Thaumastocoris peregrinus. These include biological control organisms already released in other continents, such as Cleruchoides noackae, and new ones, never released outside Australia, such as the larval parasitoid Anagonia sp.. However, the process has been slow and the cost and time needed to complete all the studies required by legislation may hinder the initiatives. The current strict legislation for the introduction of new biological agents in many European countries is probably one of the most important constrains to biological control programs. We defend that present European regulations and countries legislation should be reviewed. In particular, the requirements for programs for which biological control was demonstrated to be safe and efficient in other regions of the world should be lessened.

The interplay of habitat composition and configuration on ant communities: effects at distinct landscape matrices

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Abstract: Ants (Hymenoptera, Formicidae) have been widely used as bioindicators of habitat loss and fragmentation due to their sensitive and rapid response to environmental changes and human impacts. Moreover, ants play a key role in ecosystem functioning and provide valuable ecosystem services (e.g., nutrient cycling, decomposition, seed dispersal, biological control).

In the scope of the CERES project – Connectivity of forest and riparian ecosystems of the SUDOE space, this work aims to show how forest and riparian habitat composition and configuration affects ant abundance and diversity, and how ant communities may be used to identify and prioritize the reestablishment of landscape connectivity. The study was conducted in two Mediterranean areas, in Portugal: the Sorraia and Tagus valleys. Ants were surveyed in June and July 2019, both inside Ecological Relevant Units (ERU), i.e., forest and riparian vegetation habitats, and within the three distinct dominant landscape matrices, i.e., Intensive Agriculture, Forest Production, and Extensive Agriculture systems. Samples were collected using pitfall traps in 280 sites. In each site, five pitfall traps were installed and left in the field for approximately 48 hours. Ant specimens were preserved and identified at the species level in the laboratory, under a stereomicroscope. ERU patches were mapped using World Imagery layer (RGB, 50cm, flyover 2018) and classified based on the location and vegetation attributes, leading to the following types of habitats: 1) Riparian Woody (rw); 2) Riparian Non-Woody (rNw); 3) Non-Riparian Woody (Nrw); and 4) Non-Riparian Non-Woody (NrNw). Landscape metrics related to connectivity and shape configuration were calculated for each ERU class, at the distinct dominant landscape matrices.

Results showed higher ant abundance in the ERU patches than in matrices for the Intensive Agriculture and Forest Production types. Ant abundance was particularly low in the agricultural areas. Large and complex riparian woody patches seem to be particularly relevant for ant communities, especially in Forest Production areas. In agricultural dominated matrix small forest patches and isolated trees play an important role in the maintenance of ant structural community. Ant functional traits and diversity metrics will be discussed in view of better understanding the functional importance of landscape features that appear to be of high connectivity value.

Evolution of alternative reproductive systems in Bacillus stick insects

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Abstract: Stick insects of the genus Bacillus feature a variety of reproductive strategies including canonical sex, parthenogenesis and hemiclonal reproduction (hybridogenesis). The different parthenogenetic and hybridogenetic lineages were suggested to be of interspecific hybrid origin between the same two sexual species, but it remains unknown whether they derive from independent hybridization events or whether a single event was followed by secondary diversification of reproductive modes. Here, we revisit the different species and hybrid lineages within the genus Bacillus using a de novo chromosome-level reference genome and RADseq data of > 500 wild-caught individuals. We corroborate that two hybridogenetic lineages and two parthenogenetic lineages show the genomic signatures of diploid or triploid F1 hybrid species with the maternal genome coming from the facultative sexual species B. rossius. We then phased the haplotypes in each hybrid lineage to infer the separate evolutionary history of each parental genome. Our preliminary phylogenomic analyses suggest that sex was lost after a single historical hybridisation event, followed by (multiple) transitions between parthenogenesis and hybridogenesis, subsequent hybridisations and ploidy changes. These findings indicate transitions between unorthodox modes of reproduction previously unknown to occur, suggesting that loss of sex per se can be a driver of reproductive mode diversification.

Deciphering the role of pollen-borne microbes in the development of Megachile rotundata

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Abstract: The alfalfa leaf cutting bee, Megachile rotundata F. is an important field crop pollinator. The females provision their offspring with pollen having diverse microbial community that can contribute to the health and survival. The Apilactobacillus clade is the most abundant microbe in the gut and provisions helping bees to digest pollen. Despite the apparent importance of the microbial community, evidence concerning the effects of provision microbes on M. rotundata physiology are lacking. To test this, M. rotundata larvae were reared on the pollen with antibiotics, sterile pollen, sterile pollen + Lactobacillus micheneri, natural pollen + Lactobacillus micheneri, and natural pollen (control). Results showed that there was no significant difference in larval and prepupal weight when fed on sterile pollen, sterile pollen + Lactobacillus micheneri and natural pollen + Lactobacillus micheneri as compared to control. Larvae spun significantly heavier cocoons and showed delayed development when fed with sterile pollen and as compared to control. As a follow up, we used 16S rRNA gene sequencing to assess whether the bee-microbiome interaction and quality of diet can shape the fitness of M. rotundata. This study will improve the understanding of the microbiome-bee symbiotic relationship in the field of bee health and nutrition.

The genetic mechanism of polyphagy in Noctuidae

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Abstract: Many species within the butterfly family Noctuidae are generalists and form notorious pests on various plant species. Yet, most insect herbivores show a degree of host specialisation, likely driven by co-evolutionary forces. Host-plant specialisation seems to be the rule rather than the exception. Still numerous insect species –as in the Noctuidae- have evolved the ability to feed on a large range of host plants from distant related families. The ability to do so seems to be dependent of a broad digestion and detoxification system due to the diversity and flexibility of genes involved in these processes.

How is a polyphagous insect able to cope with the variation of plant material and defences encountered during feeding? We studied how generalist cutworm moths are able to feed on a broad host plant range. By linking herbivore success with gene expression data we studied and compared the transcriptional response within Noctuidae species. We did so within an evolutionary framework, allowing us to study the evolution of (polyphagous) herbivory on a molecular, genetic scale.

Linking genomic loci with behavioral variation in Ixodes scapularis

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Abstract: Ixodes scapularis, the principal vector vector of the Lyme disease bacterium in eastern North America, can be divided into two primary lineages through single- and multi-locus genetic analysis. These lineages are broadly linked with variation in Lyme disease risk but specific associations between genomic loci and behavioral variation have yet to be identified. We describe variation among tick populations in Virginia across nearly 25,000 polymorphic loci in the context of variation in tick density, Lyme disease incidence, and observed differences in tick behavior. We found that ticks from different Virginia populations where Lyme disease risk varies substantially engage in different host-seeking behaviors and in their propensity to parasitize rodent hosts. Genomic analyses of ticks form these populations revealed functional differences in genes related to metabolism, development, and external stimulus response, suggesting that differences in tick behavior and heterogeneity in host use may be related to physiological processes and organism function. Although preliminary, our analyses shed light on the genetic underpinnings of host seeking and host use behavior in an important disease vector.

Military roles in vector control

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Abstract: The United States Department of Defense employs advanced-degreed entomologists as Preventative Medicine and Public Health Officers in the Army, Navy, and Air Force. While the primary function of these scientists is service member health, military entomologists can also provide support to vector control operations following natural disasters. Each of the services has various specialties and the Air Force maintains a capacity to conduct large-area aerial sprays to control disease vectors in combat zones and in response to declared emergencies. This talk will touch on the various capabilities of the individual services and highlight Air Force aerial spray operations, using recent responses to natural disasters as case studies.

Acoustic communication of bark and ambrosia beetles

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Abstract: Bark and ambrosia beetles including pinhole borers (Coleoptera: Curculionidae: Scolytinae and Platypodinae) are among the smallest wood- and bark-boring insects. They spend much or most of their lifetime inside plant tissue, a dark and chemically over-saturated environment, and hence acoustic communication appears to be widespread; however, sound production in these taxa is sorely understudied, perhaps because monitoring individuals communicating inside woody tissue is somewhat difficult. We collected the largest dataset to date of bark and ambrosia beetle sounds, consisting of distress calls of 55 species within 15 subtribes of both the Scolytinae and the Platypodinae. Based on this we analysed the presence and absence of acoustic communication and characterised the temporal, spectral, and amplitude features of the calls across these multiple tribes and genera. Depending on the species, either both sexes stridulated or only one. Some species had calls with different acoustic morphotypes (e.g., one, two, or three notes), and when both sexes stridulated, the sounds generally differed. We also performed a literature review and combined both acoustic and metadata to investigate the effects of the type of mating system - and its interactions with body size and phylogeny - on the use of acoustic communication. We found that the interaction between size and mating system plays a fundamental role in determining the presence and sex-dependence of acoustic communication in a species. Furthermore, we studied the context-dependence of the spectro-temporal parameters of the stridulatory sounds and the effect of the physical presence/absence of other individuals in the variability of such parameters. Physical interactions between individuals rather than acoustic stimulation from nearby males appeared to be a causative factor in the variability of stridulatory sounds.

Bridgehead effects in forest insect and pathogen invasions

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Abstract: Invasions of insects and pathogens are a major threat to forest ecosystems. Invasions typically originate in the native range of species; however, some successful invaders become very abundant in the invaded range which may lead to further invasions originating in the invaded range. This is known as the “bridgehead effect”. In this presentation, I will review the bridgehead effect concept and present some evidence for the existence of the effect based on interception and establishment data and population genetic studies of selected insects and pathogens (including some new results). Finally, as bridgehead invasions are likely to become more frequent, I will discuss potential measures to counter their occurrence.

Human transport networks drive global alien species flows

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Abstract: Since the Industrial Revolution increased international trade and human movement have resulted in the accidental movement of many species worldwide at an unprecedented scale. There has been much interest in identifying which regions have acted as major donors of invasive species and why. Darwin proposed that more species from the Northern hemisphere have invaded the Southern hemisphere than vice versa because “the northern forms have existed in their own homes in greater numbers, and have consequently been advanced through natural selection and competition to a higher stage of perfection or dominating power, than the southern forms”. More recently, it has been suggested that Old World plants have more frequently invaded the New World than vice versa because they share traits for quick colonization of disturbed habitats and are pre-adapted to invade. These are two examples of the many species trait hypotheses that have been proposed to explain historical patterns of global invasions. Alternatively, these patterns may simply reflect the direction and level of human transport. Here, we evaluate the extent to which global species flows are best explained by the biodiversity of donor regions or the worldwide network of human transport, using ants (Formicidae) as model system. To test if global flows of the 241 species of alien ants are simply driven by the available species pools of the donor regions, we compared the observed species flows to expected flows based on the native species richness of each region. Observed species flows differed significantly from expected flows based on native species richness. For example, Australia and North America have exported less species than expected and Europe has exported more species than expected. To test if these patterns can be explained by the level and direction of human transport, we analysed flows of transported species representing the level of species introductions through human transport before the establishment stage, using border interceptions from air and maritime ports in five countries on three different continents. We found that expected species flows based on human transport were consistent with observed species flows (establishments) to these countries. Our results imply that the direction of human-mediated transport is able to generate the observed species flows in contrast to species trait hypotheses based on the evolutionary superiority of regional faunas.

Impacts of prescribed burns on the nesting communities of ground-nesting bees in tallgrass prairies in Minnesota, USA

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Abstract: Nearly all wild bee conservation efforts focus on mitigating the effects of habitat loss by enhancing foraging resources like floral diversity, floral abundance and nectar quality. Tallgrass prairie restoration provides an ideal system in which to mitigate against wild bee declines and support their conservation efforts. Prescribed fire is a common management tool in tallgrass prairie systems because many plants require burning to persist in the landscape. While ground-nesting bees nest deep enough below the soil surface to avoid detrimental impacts of burning, it is unknown how the resulting changes to the vegetation structure and microhabitat of the soil surface influence their nesting choices. To determine if nesting by ground-nesting bees are influenced by burning, we used emergence traps to make direct measurements of areas used by bees for nesting. We placed twenty-one hand-designed and commercially available emergence traps in burned and unburned areas of four remnant prairie sites that were patch burned in the spring of 2019. Traps were rearranged weekly from June to August and collected 507 bees of 52 different species. The bee nesting abundance of actively nesting females was greater in the burned areas than the unburned areas, but species diversity of bee nesting was not significantly different. The results of this research demonstrate that patch burning in prairies supports ground-nesting bee nesting preferences and documents an often overlooked life history trait of ground-nesting bees.

Economic and socio-environmental impacts of insect resistance technology in Brazil: historical analysis, perspectives and future challenges

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Abstract: The advent of GMO crops has been one of the main technological advances in the agricultural sector in the last two decades. The insertion of genes that enable plants to produce proteins with insecticidal activity against major pests has provided farmers with an additional tool to deal with the complex process of integrated pest management. In Brazil, the introduction of this technology occurred in 2005, with the approval and launch of a cotton variety. Insect resistant (IR) maize was approved in the country in 2007 and soybeans in 2010. Due to its efficiency, there was intense adherence by farmers to technology. Today, the rate of IR crops adoption in the country are 65% for soybeans, 82% for maize and 85% for cotton (data from the 2018/19 harvest). Currently, the area cultivated with insect resistant varieties reaches 39 million hectares, making Brazil one of the largest global players in the adoption of such technology. The factors that best explain the success of the technology are those observed directly on farms. Taking the gains obtained in the field as a starting point, we have quantified the benefits that GMO plants resistant to insects have provided to the Brazilian agribusiness, from the authorization of its planting until the last harvest (2018/19 harvest), emphasizing its impacts in the economic, social and environmental areas. In addition, based on the agricultural growth scenario expected for the next ten years, the future impact of that technology on the control of target insects is also estimated. The discussion over the next few years is especially relevant because we are at a time when there are reports of population growth of insects resistant to Bt proteins, which would decrease the efficiency of the technology. In light of the risks pointed out, the importance of coordinated actions among farmers, the industry and the government is discussed so that the technology remains sustainable in medium and long terms. It is vital to preserve the efficiency of Bt plants so that they continue providing gains in the productive sector and maintain positive externalities in terms of wealth generation, job creation, more efficient use of resources and reduction of environmental impacts.

Urban hardwood forest diversity and structure drive carabid beetle assemblages

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Abstract: Urbanization impacts native ecosystems directly through replacement of native communities with urban infrastructure and indirectly through habitat fragmentation and degradation. Understanding how and to what extent urbanization has impacted forest composition and structure is vital because these forests continue to provide a diverse array of ecosystem services. We sampled 38 sites across an urbanization gradient. Cluster analysis revealed four groups of forest sites that differed in understory and overstory plant diversity structure and diversity (MRPP, $A = 0.14$, $p < 0.0001$) and abiotic factors (MRPP, $A= .19$, $p < .0001$). The first group consisted of closed canopy forests with depauperate understory dominated by native mesophytic species such Acer saplings & Virginia creeper and high levels of bare soil. Woodland-specialist carabids (Chlaenius emarginatus & Calathus gregarious) dominated these sites. The second group consisted of open-canopy forests with relatively intact native understory and overstory communities dominated by oak and hickory species. A mix of forest edge and open area carabids (Cyclotrachelus sodalis & Galerita janus) dominated these sites. The third and fourth groups consists of sites located in the smallest remnant forest patches that were also most disturbed. They were characterized by the highest levels of invasive plant species and differed primarily in Lonicera spp. (honeysuckle) dominance. Generalist and forest edge carabids dominated these sites. Our findings suggest that despite being degraded these remnant urban forest ecosystems serve as a refuge for native flora and fauna.

Airborne cues accelerate and enhance flowering without cost to growth and defence.

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Abstract: Volatile cues can induce and/or prime plant defences, but it is less well known if plants also respond by altering growth and reproduction-related parameters. Here we evaluated whether plant volatile cues can elicit changes in growth, flower production, net photosynthesis rate and defences in receiver plants and whether those responses are similar to those elicited in response to direct herbivore-feeding. Our results demonstrate that exposure to volatiles emitted from damaged neighbours accelerated the time to first flowering, and increased the number of flowers produced, net photosynthesis rate, without altering the fresh harvested plant biomass and volatile defences, compared to non-exposed plants. Earlier flowering was also observed for plants exposed to volatiles from undamaged plants. These responses differed from those of plants exposed to actual herbivore-feeding for which feeding enhanced net photosynthesis rate but reduced growth and had no effect on reproduction and defence in response to subsequent herbivory. These findings document that plant airborne cues can influence reproductive traits of receiver plants. In particular, the flower phenology is modulated, and photosynthesis is enhanced, suggesting that carbon allocation is directed toward reproduction.

Global phylogeography of the Bemisia tabaci cryptic species group by mitochondrial COI and nuclear ortholog sequence analyses, and niche-modeling to unravel phenotypic plasticity

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Abstract: The whitefly Bemisia tabaci cryptic/sibling species group consists of important pests and plant virus vectors corresponding to geographically structured phylogenetic clades. Here, the mitochondria cytochrome oxidase (mtCOI) sequences from whitefly individuals (n=1,923) was used to infer a global phylogeny, and the intragroup nucleotide (nt) divergence (corrected nt distances) was estimated, imposing 12.5% to establish species boundaries. Based on matrix correlation and niche modeling methods, respectively, whitefly 'occurrence' records were overlaid to determine if phylogenetic breaks were structured based on geographical affiliations or sharp transitions across environmental gradients i.e. indicative of geographic isolation. To determine if intra-clade genenic variation could be explained by spatial distribution, intra-clade divergence estimates and geographical distances for each clade were compared using a simple mantel test. To account for predicted environmental factor influences a partial mantel test was carried out in which fourteen agro-environmental variables were considered. Finally, climatic suitability, as a potential driver of diversification among endemic members to the major clades, was assessed by ecological niche modeling that considers environmental-, ecological-, and agricultural-related factors that could influenced ecological processes that may in turn delimit distribution and/or phenotypic plasticity of the cryptic species. Distance analysis resolved 14 lineages within and/or basal to the five recognized species clades (delimited by 2184 nuclear orthologs): American Tropics (AM-TROP) (1), Asia (ASIA) (3 lineages), Asia-Pacific-Australia (AS-PAC-AU) (6), North Africa-Mediterranean-Middle East (NAF-MED-ME) (1), or Sub-Saharan Africa (SSA) (1), plus the 'undefined' sweet potato-Uganda (UGswpot) (1) and Italian highlands-T mitotype (1). Well-supported patterns of geographic isolation ($rM=0.61$, $p<0.05$) influenced primarily by seasonal temperatures ($rM=0.4702$, $p=0.00001$) appeared to best explain extant diversification of species lineages. Similarly, niche predictions resolved an isolation-by-distance model of speciation, at >0.9 AUC support values in test and training datasets, with annual mean temperature and precipitation of the driest month explaining up to 80% of the variation in the model, suggesting these factors best explain the distribution of B. tabaci worldwide. Remaining challenges include increased overall sample size of certain represented species, better representation of non-agricultural species exemplers, validation of predicted habitat with genotype-phenotype character state associations, and analysis of effective gene flow within and between species and predicted sister groups within a species e.g. sibling or cryptic species status.

Disruption of targets at the psyllid-Ca.Liberibacter interface to abate early stages of the infection cycle leading to circular, propagative transmission

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Abstract: 'Ca. Liberibacter asiaticus' (CLas) is the obligate, fastidious bacterial pathogen that causes citrus greening disease, or Huanglongbing. The bacterium is transmitted in a circulative, propagative manner by Asian citrus psyllid (ACP) Diaphorina citri Kuwayama adults. Using the surrogate study system involving the potato psyllid Bactericera cockerelli Sulc. and the analogous bacterial pathogen of tomato/potato plants,' Ca. Liberibacter solanacearum' (CLso). The identification and functional characterization of effectors involved in invasion of the psyllid gut and blood, with presumed entry into the salivary glands was investigated using combined transcriptomic, proteomic, yeast-2 hybrid (Y2H) and co-immunoprecipitation (Co-IP) analyses. In silico annotation and differential expression analysis of contigs from ACP and/or PoP nymphs and adults, and adult midgut and salivary gland tissues identified transcripts and proteins with altered expression in response to CLas/CLso infection. Several differentially expressed transcripts were selected as bait for Y2H-detection in protein-protein interactions studies. Those positive by Y2H were subjected to verification by bait to prey co-transformation and Co-IP. Proteins positive in one or both assays were tested in 'knock down' experiments using dsRNA to induced RNA-interference (RNAi), with quantification by qPCR. Candidates of the greatest interest were those with a predicted role in entry, gut /salivary gland invasion, virulence, and systemic infection, that if disrupted by RNAi could abate Liberibacter accumulation in and exit from the gut, circulation in hemolymph, and acquisition in the salivary glands. Collectively, the results suggest a model for invasion in which Liberibacter- and prophage-encoded effectors that exploit psyllid cellular pathways, including membrane ruffling for entry into the gut, followed by cytoskeletal remodeling, and exocytosis leading to bacterial exit into the hemocoel. Following systemic invasion of the hemocoel and transport in the hemolymph (blood), CLas/CLso are predicted to use an endocytosis-like process to enter the salivary glands from where transmission to the plant host occurs post-acquisition.

Contributions of citizen science to understanding patterns and trends in the distribution of ladybirds in the UK

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Abstract: People have been contributing their wildlife observations from across the UK for centuries. Simple biological records (what, where and when a species was seen) can be made by anyone, anywhere. Technological developments such as smart phone apps are increasing the number of people participating in such citizen science initiatives. The information accruing from them is enabling us to track changes in wildlife over time and address many ecological questions. The UK Ladybird Survey is one of the volunteer recording schemes hosted by the Biological Records Centre (UK Centre for the Ecology & Hydrology) and encompasses the Harlequin Ladybird Survey which was initiated in 2005 in response to the arrival of the non-native species Harmonia axyridis within the UK. Formerly the Coccinellidae Recording Scheme, the UK Ladybird Survey has been active since the early 1970s. Much has changed over the last 50 years but the success of this citizen science initiative has contributed substantially to our understanding of the ecology of ladybirds and more broadly non-native species. Harmonia axyridis is a charismatic species that has been instrumental in engaging people in non-native species ecology and encouraging public participation in surveillance and monitoring. In 2019 we published the latest ladybird distribution trends using the UK Ladybird Survey dataset. Many species are showing declines in distribution but there have also been some expansions and indeed some new arrivals. Here we will provide an overview of the UK Ladybird Survey and celebrate the role of volunteers, through citizen science, in underpinning ecological studies with benefits for nature and people.

Resistance of wild potato species against Myzus persicae

Authors: Bruce Toby[1], Ali Jamin[1], [1]Keele University, United Kingdom

Abstract: Crop wild relatives have common ancestry with cultivated crops and provide increased genetic diversity. Wild relatives of potato have a vast history of use in breeding, even though a large number of species have not yet been tested for their future utilisation (Castañeda-Álvarez et al., 2015). Under natural selection they have evolved traits making them resistant to abiotic or biotic stresses (Maxted and Kell, 2009). They can be crossed with domesticated crops for crop genetic improvement (Maxted et al., 2016). The aim of the current study was to evaluate different genetic lines of wild potato Solanum stoloniferum for resistance to the aphid Myzus persicae. An aphid performance bioassay was done with the help of clip cages. We found that four accessions of wild potato had high levels of aphid resistance. Three out of the four were highly resistant with few aphids alive after 3 days and no surviving aphids after six days. The fourth line had low aphid survival. Nymph production was similarly affected with a marked in reduction in nymph production with the three most resistant lines and some residual nymph production in the fourth line. These lines could be used to breed aphid resistant potatoes.

Assessing a crop-rotation wide attract-and-kill approach for wireworms and adult click beetles in arable land

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Abstract: Due to their long belowground development, wireworms are durable by nature and hard to control, but cause tremendous damage worldwide. In Europe, larvae of the genus Agriotes spp. are most common and to date no sufficient control measure is available. Alternative control strategies are urgently needed and the use of entomopathogenic fungi (EPF) such as Metarhizium brunneum could be one component to develop a sustainable control strategy. Unfortunately it's efficacy in the field is low, but trap crops could help to boost the effectiveness of EPFs by providing improved conditions for M. brunneum to establish in the soil. We hypothesize that an optimized combination of (i) trap crops, (ii) entomopathogenic fungi and (iii) intensive soil cultivation can significantly reduce wireworm population and crop damage over a period of three years.

Influencing the oviposition of female click beetles could be another component to efficient wireworm control. To identify attractive plants and volatiles for female click beetles of the species Agriotes sputator, electroantennography (EAG) and olfactometer experiments will be performed. Identification of highly attractive plant species and volatiles is expected to provide the base for an advanced attract-and-kill strategy, concentrating eggs and emerging neonates in oviposition strips at field margins.

From red list to rogue: current research on the planthopper Pentastiridius leporinus, a vector of the fast spreading Syndrome “Basses Richesses” disease in sugar beet

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Abstract: The planthopper Pentastiridius leporinus (L.) (Hemiptera: Cixiidae) is the main vector of Candidatus Arsenophonus phytopathogenicus, a phloem-restricted γ-proteobacterium associated to the low-sugar content syndrome of sugar beet (Beta vulgaris L.) known as “basses richesses” (SBR). This disease was first identified after tremendous yield losses in eastern France in the nineties. In recent years, it has been rapidly expanding east and northward, thus becoming a major problem for sugar beet cultivation in Germany and Switzerland. The planthoppers spend most of their life as root-feeding nymphs, where they are protected from insecticide treatments. After sugar beet harvest, the nymphs are able to complete their life cycle in the subsequent winter wheat crops. Promising sustainable management strategies against SBR and its vector include crop rotation, breeding for highly-tolerant or resistant sugar beet varieties, and biological control of the insect vectors. To develop these, there is urgent need for a deeper understanding of the biology and chemical ecology of P. leporinus. Here we present an overview of our current research on the above-mentioned topics.

Status of entomological lidar

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Abstract: This will be a brief overview of our group’s latest accomplishments within the field of entomological lidar. Entolidars are capable of detection hundreds of thousands of insects per day, and several clues on target identity can be retrieved, for example, wing beat harmonics by kHz sampling, microstructural features by polarization or molecular and nanoscopic information by the implementation of lidar with multiple spectral bands. We currently explore the potentials and limitations regarding discriminating species and quantifying insect diversity by lidar. Our activities involve development of new spectroscopic lidar instruments which are 3D printed and sufficiently simple to test during in situ during field campaigns. We relate remotely sensed signals to detailed target analysis of ex vivo pinned specimen and develop new computational data pipelines for extracting meaningful information. Our new hyperspectral lidar techniques allow to distinguish insects both by their intrinsic nanostructures but also to monitor of fluorescence tagged insects during both night and daytime.

Unearthing the virome of Spodoptera species

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Abstract: The noctuid moth species, Spodoptera exigua and Spodoptera frugiperda, are two major polyphagous pests that are responsible for substantial yield losses worldwide. Besides the often ineffective conventional pesticides, there is a growing market for the application of specific biological control agents to combat these devastating pests. The production of such biological control agents requires a continuous moth mass rearing. Unfortunately, covert asymptomatic infections, both viral and non-viral, can have major impacts on the mass rearings. Covert viral infections can be triggered into symptomatic, overt infections by external triggers and cause major economic losses. Therefore, our research aimed to gain more insights in the virus diversity of two populations of the two pest species S. exigua and S. frugiperda. We unraveled the virome via Illumina sequencing DNA, RNA and small RNAs and showed that both known and new viruses are present in these Spodoptera populations. We confirmed their presence via PCR and reverse-transcription PCR. Although no symptoms were noted in the moth rearing, the interaction of the known and newly discovered viruses may influence the moth’s fitness posing a risk for mass rearing facilities or offering new opportunities for biological control by viruses.

Viruses of reared insects: the enemy within?

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Abstract: The outbreak of insect diseases severely threatens insect rearing. In particular, viral diseases can be devastating for the yield and quality of mass rearing systems. Here, I highlight disease-causing viruses in insects most commonly reared for food and feed, with a special focus on viruses threatening cricket rearing. In addition, I will discuss covert (latent/persistent) virus infections in insects, and how these can suddenly develop into overt (symptomatic) infections under stress conditions. In that context I will also elaborate on factors affecting the emergence of viral outbreaks in insect rearing, along with virus transmission routes. Lastly, I will give an overview of measures available to prevent and manage virus outbreaks.

Medical appointment for crickets – why do insect diseases matter in mass rearing systems?

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Abstract: Several species of crickets are reared as a source of protein with an ever-increasing number of start-up companies and projects engaging in cricket large scale rearing. In this presentation, I will talk about my work on cricket pathogens in wild and captive populations. I will also discuss my findings on the effect of abiotic factors on bacterial (Rickettsiella sp.)and viral diseases (Acheta domesticus densovirus) development in cricket rearing. Furthermore, I will concentrate on practical aspects of cricket rearing that render production systems resilient (or not) to diseases, including research done on egg sanitation. Finally, I will elaborate on the reasons why studying and understanding fundamental and applied aspects of cricket diseases is important to improve cricket rearing.

Evolution of symbiosis, colony organization and defense in termites

Authors: Buček Aleš[3], Šobotník Jan, Bourguignon Thomas[2] and Roisin Yves[1], [1]Evolutionary Biology and Ecology, CP 160/12, Université Libre de Bruxelles, Belgium, [2]Okinawa Institute of Science & Technology Graduate University, Japan, [3]Okinawa Institute of Science and Technology, Czech Republic

Abstract: Termites are the oldest social insect lineage, one of the few animal groups able to feed on lignocellulose and amongst the most abundant animal groups in tropical ecosystems. To understand the key evolutionary transitions during the ~ 140 Ma of extant termite evolution a robust molecular phylogenetic tree is required. To this end, we used datasets based on transcriptome sequences, ultraconserved element sequences, and mitochondrial genome sequences. I will summarize our current understanding of the termite phylogeny and how it informed the hypotheses on the evolution of the colony organization, the loss of symbiotic gut protozoa, and the evolution of the defensive soldier caste in termites. Our analyses challenge previous molecular phylogenies by recovering sister relationships between the comb-builders Sphaerotermitinae and Macrotermitinae, which changes our understanding of the chronology of the loss of protozoa and the origin of fungus-growing in termites. The termite phylogeny indicates that comb building is a derived trait within Termitidae and that externalization of some of the digestion to comb-like nest structures involving bacteria or fungi may not have driven the loss of protozoa from ancestral termitids, as previously hypothesized [1]. Our phylogeny of the second largest termite family - dry wood termites (Kalotermitidae) - uncovered their trans-oceanic dispersal capabilities and hinted at their ancestral potential to forage between separate wood pieces [2]. The major remaining challenge that I will discuss is the resolution of relationships within Termitidae family and particularly among one of its clades encompassing Cubitermitinae, Nasutitermitinae, Syntermitinae and polyphyletic Termitinae, that rapidly diversified ~ 35 Ma and which includes some of the most striking termite soldier defensive adaptations.

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Predator-prey naïveté as a mechanism contributing to explain the invasion success of non-native ladybeetles in Europe and in North America

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Abstract: Invasive species pose a major threat to global biodiversity. Despite the growing scientific literature on detrimental effects of invasive species, we often lack a mechanistic understanding why some species become invasive while others remain benign. Possibly, invasive predators might remain undetected by native predators and thus suffer less intraguild interference (naïve predator hypothesis). In addition, invasive predators might benefit from a lack of predator avoidance by native prey (naïve prey hypothesis). The ability to recognize non-native predators is expected to depend on cue similarity with native predators. Consequently, non-native ladybeetles bearing a unique set of cues might have the double advantage of naïve ants and aphids and thus outcompete native ladybeetles.

To test this, we compared ant aggression towards native and non-native ladybeetles in Europe and in North America. Thereby, we manipulated cuticular hydrocarbons on ladybeetle elytra to elucidate the role of these chemical cues in predator recognition. In addition, we compared aphid consumption and avoidance behavior upon direct contact with native and non-native ladybeetles as well as with their chemical cues only. We analyzed chemical ladybeetle cues to establish their species-specificity, which is a prerequisite for predator-prey naïveté. Finally, we related cue similarity between native and non-native ladybeetles with the strength of behavioral responses of ants and aphids.

In line with our expectations, we found higher ant aggression towards native European ladybeetle species compared to the invasive Harmonia axyridis. Ant aggression was strongly influenced by the presence of chemical cues on ladybeetle elytra. Similarity in chemical cues between H. axyridis and the native European ladybeetle H. variegata led to similar ant aggression. In Europe, the aphid Acyrthosiphon pisum avoided cues of native ladybeetle species but not of the invasive H. axyridis. Contrastingly, the American strain of A. pisum avoided cues of all ladybeetle species. A. pisum predation in our experiments, however, was largely determined by ladybeetle body size rather than by species origin and did not differ across continents.

We suggest that high cue dissimilarity to voracious native ladybeetles and large ladybeetle body size contribute to the intensity of competition with native ladybeetles and ultimately to the invasion success of non-native ladybeetles. However, differences in aphid avoidance behavior between Europe and North America also suggest that rapid adaptation within few decades can normalize novel biotic interactions among insects. Nonetheless, small native ladybeetles (e.g. Adalia bipunctata in Europe) that co-occur in space and time with invasive ladybeetles are at particular risk.

Phylogeny and evolution of the New Zealand stick insects (Phasmatodea)

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Abstract: The New Zealand stick insect fauna includes approximately 20 species. These species are related to sub-tropical taxa from New Caledonia. We have been investigating their phylogenetic relationships, patterns of introgression and adaptation to the cool, temperate environments of New Zealand. Using transcriptomes and whole genome sequencing we describe the reticulate patterns of evolution among taxa caused by extensive hybridization. This has also resulted in the frequent development of parthenogenesis. We also show how colonization of cool environments has left an imprint on the genome sequences of these species.

Phylogenomics of Cynipoidea

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Abstract: A complete phylogeny of Hymenoptera has been sought after for over 100 years. While many trees and phylogenetic hypotheses have been published, their topologies have been limited by the number of characters available, the number of taxa coded or sequenced, or most typically, both of these issues. With the advent of next generation sequencing of ultraconserved elements (UCE's), the major hurdle of tackling both taxon sampling and data abundance/quality has been overcome. Herewith we present a comprehensive phylogeny of Hymenoptera based on around 1000 terminal species. Our taxon sampling aimed at representing lineages relative to their diversity in the analyses. Experts for each major clade selected representative taxa, many of which were derived from pinned specimens deposited in the USNM and no new fieldwork was needed to fill in taxonomic gaps. The resulting trees are based on variety of analyses ranging from 301 to 1687 UCE loci. We summarize the recovered topologies and compare/contrast these results with previous analyses.

The Expanding Range of the Asian Chestnut Gall Wasp Dryocosmus kuriphilus Yasumatsu (Hymenoptera: Cynipidae) in North America

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Abstract: The Asian chestnut gall wasp, Dryocosmus kuriphilus Yasumatsu (Hymenoptera: Cynipidae) is an invasive species of global concern, and in North America it induces gall formation on chestnut species including Castanea mollissima Blume, C. crenata Siebold & Zucc., and C. sativa Mill., as well as the American chestnut, C. dentata (Marsh.) Borkh. The Asian chestnut gall wasp was first introduced into the United States in the 1970's, and since its initial introduction in Georgia, it has been reported to have spread to 13 other states. It has been documented as far to the northeast as Connecticut and Massachusetts, as far to the northwest as Michigan, and has recently been reported in Ontario, Canada. The introduction and spread of D. kuriphilus is of particular concern given the goal to restore American chestnuts into the North American landscape. This study explores the continuing spread of D. kuriphilus, providing new state records and evidence of the expansion of the range of this gall-forming invasive species in the United States to encompass all of the Mid-Atlantic States. The effectiveness of Torymus sinensis Kamijo (Hymenoptera: Torymidae) as a biological control agent will also be discussed.

Thermal diversity of ant communities at large and small scales

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Abstract: Ectotherm distributions and fitness will depend on their ability to adapt and acclimate to the ongoing increases in temperature. The thermal adaptation hypothesis predicts that more thermally variable environments favor organisms with wider thermal ranges and thermal limits which track climate. To test this, we used ants because they are globally distributed and, like other ectotherms, sensitive to temperature. We measured critical thermal minima and maxima (CTmin and CTmax) of 132 North American ant species across 15.7° of latitude from warm deserts to alpine tundra. Across 31 ant communities we found that ants were cold tolerant in cooler environments particularly at the community level where CTmin positively correlates with mean annual temperature (CTmin=0.20MAT+2.7; R2 = 0.30, p=0.001). In contrast, CTmax did not covary with environmental temperatures at the community or species level, but instead showed a strong phylogenetic signal suggesting that CTmax might be phylogenetically conserved.

The absence of CTmax tracking environmental temperatures and the high variation of this trait in each of our communities could be caused by the fact that CTmax is not a fixed trait but can be acclimatized to the changes in microclimates. Thus, air temperature averages might not be good predictors of the fine tuning of CTmax which could be achieved at the local scale.

To evaluate this, we focused on a single community experiencing significant differences in mean monthly temperatures across seasons and quantified CTmax of 27 ant species. On average species sampled during the winter had lower CTmax compared to the summer and spring. While some species showed no changes across the seasons, heat tolerance of others varied in a predictive fashion. Four out of five seasonal generalists—species actively foraging in all three focal months—had, on average, 6°C higher CTmax at the end of the summer. We show that heat tolerance can be plastic, and this should be considered when examining species level adaptations at large scales. Thermally plastic species might have a competitive advantage in communities under global warming with consequences for community composition and structure. For example, among the thermally plastic species was the invasive fire ant, Solenopsis invicta, suggesting that plasticity in thermal tolerance could be another trait enabling success of this invasive species. Thus, exploring the notion of thermal plasticity should be increasingly important for models that hope to predict the future of native and invasive species distributions.

Essentials of ecological knowledge that applied biological control urgently needs

Authors: Bukovinszky Tibor[1], Groot Tom[1], Calvo Francisco Javier[2], [1]Koppert Biological Systems, Netherlands, [2]R&D Koppert Biological Systems, Spain

Abstract: The call to increase the contribution of biological control in IPM is louder than ever before, but current research efforts are often not geared towards meeting this demand. We argue that more focus on currently largely ignored applied problems is needed in order to increase the efficiency of developing new biological control products. While finding natural enemies in nature is relatively easy, selecting the right ones to develop into products for augmentative biological control is much harder, and time consuming. There are several known selection criteria that are typically assessed in controlled laboratory and semi-field assays. Such assays typically quantify biological parameters essential in early phase of candidate screening, for example population growth rate, prey/ host acceptance, consumption rates. Besides these parameters, there is another group of criteria that a successful candidate biological control agent needs to pass. Such criteria examine versatile aspects of the candidate's suitability to be produced at an industrial scale as well as to be shipped to the growers arriving in good shape. Other criteria are related to the complexities of the often highly artificial agro-environmental conditions where the agents are released and need to perform. The evaluation at this relatively late point of product development, when already a significant time and financial commitments have been made, will ultimately "make or break" a product. Also, with the ongoing intensification of growing conditions, the importance of screening in this phase, will likely increase. We argue that such problems pertaining to the selection of candidates are not high enough on the agenda of biocontrol research. In this presentation we review the complexities based on published examples and our own extensive experience. We discuss how reducing the gap between the current scientific efforts and the realistic field situation at growers' site may increase the efficiency at which new biocontrol agents are developed.

Colour heritability in a variable aposematic insect

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Abstract: Despite the fact their colouration has been shown to work as an aposematic signal, and is thus expected to be under purifying selection, Hibiscus harlequin bugs (Tectocoris diophthalmus) show an impressive level of variation in their iridescent colouration both across and within populations. Previous work has shown that part of this variation may be due to plasticity in response to temperature. However, populations vary both in the extent of plasticity, and in the distribution of different colour patterns, suggesting a heritable component. No studies have yet examined heritability of colour in this species. Here we focus on a single population in the southern part of range, as these populations contain the greatest colour variation. We reared full-sib families of know pedigree in the laboratory and analysed the extent of iridescent colouration once they eclosed to adulthood. We then looked for evidence of heritability and antagonistic sexual selection acting on colour in this species. We found surprisingly low levels of heritability, particularly in males. There was however a sex by genotype interaction for iridescent cover, in the form of a negative intersexual genetic correlation: in families where sons had high iridescent cover the daughters had low, and vice-versa. Thus antagonistic sexual selection is unlikely to be maintaining diversity in colouration in this species.

A new association between insect and nudivirus producing virus-like particles

Authors: Burke Gaelen, University of Georgia, United States

Abstract: Some lineages of parasitoid wasps have evolved a remarkable strategy in their parasitism arsenal: they utilize domesticated endogenous viruses (DEVs) to breach host defenses. The most well-known examples are Polydnaviruses (PDVs), which are found in three diverse clades of parasitoid wasps, likely representing three unique origins. Despite their independent evolution, PDV genomes share some key characteristics. PDV genomes are integrated into the genomes of wasps, and their genome architecture has been rearranged compared to viral ancestors into two separate components: proviral segments containing virulence genes and replication genes. In addition to PDVs, DEVs have been documented in other parasitoid wasp species, and their recent genomic characterization has shown that these DEVs differ from the PDV paradigm. We have discovered another independently-derived DEV in Fopius arisanus that produces virus-like particles (VLPs) that do not contain nucleic acids. These data highlight existing diversity in viral symbiont genome architecture, which has important implications for symbiont function in hosts. In host insects, PDVs rely upon gene expression from existing DNAs for virulence. In contrast, the lack of DNAs in F. arisanus VLPs prevents delivery of virulence genes into host cells, likely necessitating other mechanisms for promoting parasitism in host insects.

Influence of increasing summer temperatures on an invasive forest pest

Authors: Burke Gaelen[1], Mech Angela[2], Rusty Rhea J.[4], J. K. Gandhi Kamal[1], Tobin Patrick[3] and Teskey Robert[1], [1]University of Georgia, United States, [2]University of Maine, United States, [3]University of Washington, Seattle, Washington, United States, [4]USDA Forest Service, United States

Abstract: Higher temperatures predicted under current climate change models are expected to have an overall positive effect on the success of invasive forest pests by increasing biological attributes such as survivability, geographic range, and fecundity. These changes in life history factors may result in negative cascading effects on forested ecosystems. However, heat may be a limiting factor for invasive insects that undergo summer diapause, such as the non-native hemlock woolly adelgid (Adelges tsugae) (Hemiptera: Adelgidae), which is causing widespread mortality of eastern hemlock (Tsuga canadensis) in eastern North America. The thermal ecology of A. tsugae was examined in the southernmost limit of hemlock's contiguous range by determining A. tsugae survivorship under increasing temperature regimens and heat waves. A positive correlation was found between increasing temperatures, duration of exposure, and A. tsugae mortality. These results showed evidence for a cumulative effect of temperature. Adelges tsugae mortality was minimal (< 20%) when exposed to 20° and 25°C, but markedly increased at temperatures above 30°C (up to 100%). High temperatures resulted in a significant increase in A. tsugae mortality over time and similar trends were exhibited in field populations. Field mortality of A. tsugae ranged from 8.5% to 62.8% in hemlock stands and was strongly correlated with temperature regimes. In addition, a controlled experiment was designed to determine whether any of the beneficial bacterial endosymbionts of A. tsugae are sensitive to heat stress and may be causing the decrease in host fitness. In response to lower A. tsugae densities, hemlock appears to be avoiding the anticipated rapid dieback and mortality caused by this pest.

Joint species distribution models of saproxylic beetle species: implications for forest management and climate change

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Abstract: Saproxylic insects play a key role in a variety of forest ecosystem functions. Modern forestry practices result in low levels of dead wood compared to natural forest systems leading to loss of habitat for saproxylic communities. Saproxylic beetles are important for the decomposition of dead wood and are therefore crucial for nutrient cycling and maintaining healthy forest ecosystems. However, little is known about how their large-scale distributions will change under future forest scenarios with a changing climate and in a landscape with varying forestry practices and dead wood amounts.

Distributions of species and assembly of communities result from complex processes involving local and regional environmental conditions, species traits, and species interactions such as competition and facilitation. Additionally, these processes change through space and time, adding further complexity. Traditionally it has been difficult to model all these important factors simultaneously, and most research focuses on only a few of the many possible sources of variation in species distributions. Here we use a hierarchical species distribution model (HMSC) to understand the relationship between climate, habitat, forest management practices, species traits, phylogenetic relationships, and species interactions of saproxylic beetles across Norway. The model is a form of Joint Species Distribution Models (JSDMs) which, contrary to stacked species distribution models that combine models for each species, has the advantage of also drawing information from the co-occurrence patterns of species.

Using window trap records of 457 saproxylic beetle species from 468 sites sampled over three decades, we find that many saproxylic species are rare, and their abundance is best predicted by a combination of forest management and climatic covariates. Our current approach aims at including beetle species traits, like wing to mass ratio as proxy for dispersal capacity, and phylogenetic relatedness among the beetles in an HMSC to better predict species occurrences and disentangle the importance of each predictor. Because the model formulation is very tightly linked to the ecological theory of community assembly, we discuss how facilitation, competitive exclusion, and random processes may shape beetle communities. Importantly, mature and unmanaged forests provide key habitat for many rare and red listed species but are underrepresented in managed forest landscapes and should be preserved. HMSCs of saproxylic beetle communities provide a new and promising avenue of community research across a range of spatial scales to better understand these communities and make predictions how future forestry practices and climate change will impact these communities.

The fate of flies in fruit: implications of Drosophila suzukii infestations in fruit

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Abstract: Drosophila suzukii (SWD, spotted-wing drosophila) is a globally invasive pest of soft skinned fruit which has undergone a dramatic range expansion during the last decade. Since 2008, SWD has been detected throughout North America, Europe, and South America in addition to its presumed native range in mainland Asia and Japan. Much of this recent movement has been potentially facilitated through trade. Larval SWD feed internally within host fruit, and at low infestation rates, eggs and small larvae may escape detection. There is presumed zero tolerance for SWD larval presence in fresh market or whole frozen fruit, and purchasers may reject whole shipments of fruit if any SWD are observed. Significant research efforts have focused on pre harvest management tactics to prevent infestation, including insecticide use, exclusion netting, and biological controls. However, in highly preferred hosts or fruit which ripen during peak fly activity may still experience infestation even with pre harvest management. This presentation will review post harvest monitoring and management strategies for SWD with a focus on the effect of cold storage.

Molecular evidence suggesting the re-examination of the taxonomy of the groundnut/soya bean leaf miner (Aproaerema sp.) (Lepidoptera: Gelechiidae)

Authors: Buthelezi Makhosi, Mangosuthu University of Technology, South Africa

Abstract: Mitochondrial DNA COI gene analyses of the groundnut/soya bean leaf miner (GSLM) conducted in South Africa linked the South African GSLM to the Australian Aproaerema simplexella (Walker) and the Indian Aproaerema modicella (Deventer). Thus, the genetic relatedness of the South African GSLM, the Australian A. simplexela and the Indian A. modicella was examined by performing MtDNA and nuclear DNA analyses (COI, COII, cytb, 28S and EF-1 ALPHA) on 44 specimens collected from South Africa, four from Mozambique, and three each from single locations in India and Australia. In the phylogenetic trees for COI, COII, cytb and EF-1 ALPHA, a similar pattern was observed in the way that the sequences assembled into different groups; i.e. some sequences of A. simplexella from Australia were grouped separately from the others, but some Australian sequences grouped with those of the GSLM from South Africa, India and Mozambique. In the phylogenetic tree for 28S, all sequences grouped together. Genetic pairwise distances ranged from 0.97 to 3.60% (COI), 0.19% to 2.32% (COII), 0.25 to 9.77% (cytb) and 0.48 to 6.99% (EF-1 ALPHA). Results of this study indicate that these populations are genetically related and presumably constitute a single species. Thus, further molecular and morphological studies need to be undertaken in order to resolve this apparent conundrum on the taxonomy of these populations.

The smelly sex lives of blow flies

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Abstract: Blowflies (Diptera: Calliphoridae) are a biodiverse family that occupy a wide range of ecological niches. In carrion-breeding species, adults aggregate and breed around decaying animal matter, which is an ephemeral and speciose environment. Under these conditions, there is intense competition for mates, and a high risk of misguided mating investment. As such, it is likely that blowflies have evolved highly specific sexual signals to mediate mate recognition and sexual attraction. Most observations of blowfly sexual behaviour have focused on visual cues, and it appears that vision is an important aspect of blowfly communication. By contrast, very little attention has been given to chemical communication in blowflies, which is also likely to be important considering the prevalence of pheromones throughout other calyptrate fly groups. Cuticular hydrocarbons (CHCs), are long-chain hydrocarbons that are expressed on the cuticle of virtually all insects, and are common pheromones across many dipteran taxa. Within Calliphoridae, CHCs have been found to be highly species-specific. However, there is no evidence that they facilitate sexual communication. To assess whether CHCs may have a communicative function, we combined behavioural assays, gas-chromatography mass-spectrometry, and genetic data to analyse and compare CHCs between 10 Australian blowfly species. This presentation reports species- and sex-specific differences, and discusses the potential role for CHCs to mediate the sexual behaviour of flies.

Orthoptera Conservation in Italy: the Zeuneriana marmorata case. (Orthoptera, Ensifera)

Authors: Buzzetti Filippo Maria[2], Fanin Yannick, Leandri Fausto and Fontana Paolo[1], [1]Fondazione Edmund Mach, Italy, [2]Fondazione Museo Civico di Rovereto

Abstract: Listed as EN (Endangered) by IUCN in the Red List of European Orthoptera, Zeuneriana marmorata (Fieber, 1853) is under conservation project in Italy. Known current populations are in NE Adriatic coast of Italy, inland of Slovenia and one recently discovered in Italian inland.

These sub-populations are assumed to be remnant of a larger metapopulation that was most likely living in the wet habitats of the plains around the North Adriatic Sea and the Po river. Habitat loss and fragmentation due to human activity contributed dramatically to the disappearance of the species in most of its range. Regarding the Italian populations, study (bioacoustic) and conservation (translocation, area management) actions are applied to date and planned for the future.

Orthopteroid insects collections at the Museo Civico di Rovereto (Italy): the Galvagni collection and the Fontana collection

Authors: Buzzetti Filippo Maria[2], Fontana Paolo[1] and Stancher Gionata[2], [1]Fondazione Edmund Mach, Italy, [2]Fondazione Museo Civico di Rovereto

Abstract: The Museo Civico of Rovereto was founded in 1851 and hosts several art and science collections. Concerning Zoology, the entomology is noteworthy, consisting of the collection Halbherr (Coleoptera), the collection Tamanini (Hemiptera with several types especially among Gerromorpha), plus the recently acquired collections Galvagni (30,000 specimens: Orthoptera, Dermaptera, Blattodea, Mantodea, Phasmatodea) and Fontana (25,000 specimens: Orthoptera, Dermaptera, Blattodea, Mantodea, Phasmatodea).

Within a couple of years the entomological collections of the Civic Museum of Rovereto have been enriched with more than 50,000 identified specimens (2147 species of Orthoptera).

Thanks to the recently acquired entomological collections, the Rovereto Civic Museum becomes a reference point for Orthoptera studies, resulting attractive also for further donations such as the Fontana Orthopteroid collection recently acquired.

A biogeographic and systematic analysis of endemic damselflies in Vanuatu (Vanuatubasis: Ceonagrionidae: Odonata)

Authors: Bybee Seth[3], Ferguson Daniel[2] and Saxton Natalie[1], [1]Brigham Young University, United States, [2]Brigham Young University, United States, [3]Department of Biology, Brigham Young University, United States

Abstract: In this study we examined the phylogenetics relationships of the damselfly genus Vanuatubasis (Odonata: Zygoptera: Coenagrionidae), an endemic to the island archipelago of Vanuatu. We reconstructed a phylogeny of Vanuatubasis using all three previously described Vanuatubasis species, along with an additional 16 morphospecies representing putative undescribed taxa that were recently collected during extensive field work from 2017-2019. We sequenced the mitochondrial loci CO1 and 12S and the nuclear locus ITS for all taxa. Our molecular data are fairly limited in an effort to minimize missing data when including a larger taxon sampling of closely related taxa from previous studies. By so doing we were able to include 26 species of Nesobasis, the hypothesized closest relative to Vanuatubasis, and an endemic to Fiji. Phylogenetic reconstruction was conducted under both maximum likelihood and Bayesian inference methods and both were highly congruent and exhibited high support across most of our topologies. However, some low support and differences are seen within the Vanuatubasis grouping. Our analyses support Vanuatubasis as monophyletic and being placed within Nesobasis rendering it non-monophyletic. The phylogenetic analyses give more understanding of the relationships between the Vanuatubasis species across Vanuatu. Morphospecies from islands that were closer in distance were more closely related than those from farther islands. Though weather conditions and time of year may have been a factor, we did not observe any Vanuatubasis on islands with large active volcanoes. In the future, we plan to add additional molecular data and taxa to better understand the evolution of the group, particularly taxa from throughout the South Pacific.

Aphid-induced changes in the phloem exudate metabolome of wheat and positive effects on aphid offspring suggest niche construction by Sitobion avenae

Authors: Bühler Andreas[1], Schweiger Rabea[1], Wall Saskia[1], Wimmelbücker Maximilian[1], [1]University of Bielefeld, Germany

Abstract: Plant phloem sap imposes nutritional challenges on aphids. Previous studies revealed that aphids may change the phloem sap metabolome. However, it is unclear how these changes affect aphid performance. In this study, wheat (Triticum aestivum) leaves or ears were infested with grain aphids (Sitobion avenae) for 10 days or left uninfested. The performance of S. avenae offspring colonies on these differently treated plant parts as well as the preference behaviour of the aphids were assessed. Moreover, phloem exudates were collected and analysed for their amino acid composition and metabolic fingerprints of putative specialised metabolites. In the first days, nymphs showed higher survival on previously aphid-infested leaves than on control leaves, though colonies increased to similar sizes over 12 days. Positive effects of previous aphid infestation were more pronounced on ears, with colonies on previously aphid-infested plants growing substantially larger. In the choice bioassays, S. avenae showed a preference for previously aphid-infested ears, while on leaves no preference was observed. Taken together, our study indicates niche construction by S. avenae, which was transient on wheat leaves and more pronounced and longer lasting on ears. The findings may be partly explained by aphid-induced metabolic differences between the corresponding phloem exudates.

Effects of frequency and timing of methyl jasmonate treatment on pine weevil damage received by Norway spruce seedlings

Authors: Bylund Helena[1], Chen Yayuan[1], Puentes Adriana[1] and Björkman Christer[1], [1]Swedish University of Agricultural Sciences, Sweden

Abstract: It has been shown that induced defence in conifer seedlings can be triggered by treatment with methyl jasmonate (MeJA) on the above-ground parts of seedlings to reduce pine weevil (Hylobius abietis) damage. Thus, enhancing the plant's own defences can provide a novel and sustainable potential plant protection strategy. However, few studies have addressed the practical issues surrounding MeJA treatment such as treatment frequency and timing, optimal seedling age and if it is compatible with plant nursery practices. In this paper, we examined if levels of pine weevil damage differ depend on the frequency (once or twice) and timing (before or after nursery winter storage) of MeJA treatment, and if these effects differ depending on plant age. Norway spruce (Picea abies) seedlings from two different age cohorts (1 year and 1,5 year old plants) were each grouped into four MeJA (10mM) treatments as follows: One MeJA application before nursery winter storage, one MeJA application after winter storage but before spring planting, two MeJA applications: before storage and before planting, and no MeJA applications at either time point). A lab and field experiment was set-up to examine differences in pine weevil damage among treatments. Seedlings were exposed to pine weevils in a non-choice lab experiment, and in the field we followed survival and levels of damage both the year of planting and the following year. We found that the timing and frequency of MeJA treatment significantly affects the amount of damage inflicted by pine weevils, and these effects were mostly consistent among age cohorts. Previous application, before winter storage, provided the most effective protection compared to the other treatments. This reduction in damage was comparable to that provided by a currently used method of in nurseries, Conniflex. Thus, our results indicate that MeJA treatment can be conducted in line with nursery practices (before winter storage) for plant age cohorts usually used for re-planting, and provide adequate protection the following year.

Spinning in Embioptera (Part 1): a behavioural perspective

Authors: Büsse Sebastian[2], Edgerly Janice[1], [1]Department of Biology, Santa Clara University, United States, [2]Department of Functional Morphology and Biomechanics, Institute of Zoology, Kiel University, Germany

Abstract: Webspinners (Embioptera) are unique in their ability to spin silk by stepping with their front feet against the substrate to release dozens of fibers as they fashion a domicile. Their silk fibers are among the finest known but via complex spinning behaviours, the webspinner produces thick sheets and tubes. Despite the apparent fragility of such structures, the occupants are protected from predators and rainfall. We have quantified spinning behaviours of two dozen species from across the range of the order and found stereotypy in their spin-steps. An individual displays 26 possible spin-steps as she constructs a silk framework around her body and then thickens the emerging structure with reinforcement steps. Even though individuals express the same actions, the emphases and stepping combinations display a phylogenetic signal to some degree. However, individuals in some species show high intraspecific similarity while individuals of other species are spontaneous and unpredictable. Embiopteran body shapes are highly constrained throughout the entire range because of uniformity of lifestyle—living in tightly spun silken tubes. Despite this morphological homogeneity, analysis of variation in spin styles revealed that species with higher intraspecific similarity tend to live in regions with greater seasonality, higher temperatures and less rainfall. One interpretation is that individuals living in more predictable climes, such as tropical rainforests, are more spontaneous, while those from Mediterranean climes display more predictable species-specific spin-step routines. We will discuss methods for discovering phylogenetic signal and environmental correlates as they relate to the diversification of spinning behaviour.

Spinning in Embioptera (Part 2): a biomechanical perspective

Authors: Büsse Sebastian[2], Edgerly Janice[1], [1]Department of Biology, Santa Clara University, United States, [2]Department of Functional Morphology and Biomechanics, Institute of Zoology, Kiel University, Germany

Abstract: Using the legs for multiple functions in addition to walking, potentially imposes constraints and compromises. Within this context, webspinners (Embioptera) show a unique morphological adaptation: they use their front feet to produce silk for building a shelter. The morphology of the so-called spinning-tarsus is well studied; however, the actual process of silk ejection, is addressed only vaguely. The spinning apparatus, located within the prothoracic basitarsus, is composed of: i) multinucleated silk glands enclosing a reservoir used for silk storage; ii) the ejection duct with canal cage; iii) hollow, cuticular hair-like tubes (silk-ejectors) located on the ventral surface of the spinning tarsus.

We here present morphological and experimental evidence for a "passive" pressure-induced spinning mechanism induced by external mechanical stimuli. Material distribution of the tarsal cuticle and anatomy of the spinning apparatus provide both deformability of the basitarsus and mechanical resistance for proper pressure generation; resulting in ejection of the silk, when the silk-ejectors contact the surface. When the first contact between single threads and substrate is established, it is sufficient pulling off the tarsus to continue silk spinning. Furthermore, we experimentally induced silk production in anaesthetised individuals by applying a mechanical stimulus to the spinning-tarsus. As silk spinning is induced by likely any mechanical contact of the ventral surface of the spinning-tarsus, the proposed mechanism results in a complex behaviour for both application of the silk as well as for contact avoidance of the spinning apparatus with the substrate during locomotion.

Korean species of the genus Caloptilia Hübner, 1825 (Lepidoptera: Gracillariidae)

Authors: Byun Bong-Kyu[1], Kim Da-Som[2], [1]Hannam University, South Korea, [2]National Science Museum of Korea

Abstract: In this study, a total of 27 species of the genus Caloptilia Hübner, 1825 belonging to the family Gracillariidae are recognized from Korea. Among them, seven species, Caloptilia acericola Kumata, 1966, C. celtidis Kumata, 1982, C. dentata Liu & Yuan, 1990, C. kadsurae Kumata, 1966, C. monticola Kumata, 1966, C. recitata (Meyrick, 1918) and C. soyella (van Deventer, 1904), are reported for the first time from Korea. All the known species are enumerated with their available information. Adults and genitalia of all species are redescribed and illustrated.

Review of the subfamily Phyllocnistinae (Lepidoptera: Gracillariidae) in Korea

Authors: Byun Bong-Kyu[1], Kim Da-Som[2], Lee Ji-Young[1], [1]Hannam University, South Korea, [2]National Science Museum of Korea

Abstract: This study was conducted to review of the subfamily Phyllocnistinae, belonging to the family Gracillariidae, in Korea. Only one species, Phyllocnistis citrella, has been known from Korea to date. In this study, a total of 7 species of the subfamily are recognized from Korea. Among them, three new species Phyllocnistis sp. nov. 1, Phyllocnistis sp. nov. 2 and Phyllocnistis sp. nov. 3 are described as new to science. Also, three species, Phyllocnistis chlorantica, P indistincta and P. saligna are reported for the first time from Korea. All the known species are enumerated with their available information including images of adults and genitalia of all species are redescribed and illustrated.

Reverse chemical ecology applied to odorant receptors in the crop pest insect Spodoptera littoralis

Authors: Caballero Vidal Gabriela[3], Jacquin-Joly Emmanuelle[2], Montagné Nicolas[1], Bouysset Cédric[4], Golebiowski Jérôme[4] and Fiorucci Sébastien[4], [1]iEES-Paris, INRAE, Sorbonne Université, Versailles, France, [2]INRA, Institute of Ecology and Environmental Sciences (iEES) - Paris, France, [3]INRAE, Sorbonne Université, Institute of Ecology & Environmental Sciences of Paris, Versailles and Paris, France, [4]Institute of Chemistry of Nice, UMR CNRS, Université Côte d'Azur, Nice, France

Abstract: Insects detect, via their odorant receptors (OR), a variety of volatile compounds found in the environment and use them to carry out vital activities such as identifying food sources and sexual partners. The identification of attractive or repellent semiochemicals that interfere with crop pest behaviors is a major issue for their biocontrol. Yet, their application for the control of pest Lepidoptera mainly targets adults, whereas the caterpillars represent the feeding stage.

In this context, this work consisted in searching semiochemicals active on the behavior of caterpillars in a model crop pest, the moth Spodoptera littoralis, using a reverse chemical ecology targeting the larval ORs. First, a transcriptomic study allowed us to identify the repertoire of chemosensory genes expressed in the larva. Then, the function of some ORs was determined via their heterologous expression in Drosophila, in order to identify which olfactory cues are detected by larvae. Last, we combined in silico ligand-targeted modeling, functional analyzes of ORs expressed in Drosophila and behavioral assays to identify new ligands for the targeted ORs that are active on the larval behavior. This work validates the use of ORs as targets to accelerate the discovery of new semiochemicals active on behaviors, which, in the long term could be used for the bioncontrol of herbivorous caterpillars. The data obtained also provide fundamental knowledge in the field of neurobiology and the ethology of larvae.

Bacteriocyte differentiation and cell death in the aphid/Buchnera symbiotic system

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Abstract: Symbiosis is a key source of ecological and evolutionary diversification of eukaryotic organisms throughout the animal and plant kingdoms. In insects that are obligatorily dependent on intracellular bacterial symbionts, novel host cells, the bacteriocytes, have evolved for harboring beneficial microbial partners. These cells constitute a fascinating riddle in developmental and evolutionary cell biology, as the molecular mechanisms governing their homeostasis in response to host physiology remain largely unsolved. Using the pea aphid/Buchnera aphidicola symbiotic system, we demonstrated that bacteriocytes not only house symbiotic bacteria, but they are a core tissue in aphid physiology: (i) they are sensors of nutritional stress and respond to amino acid depletion by entirely reprogramming their transcription and modifying their sizes and numbers, (ii) they are highly dynamic cells, adjusting their growth and death, and their symbiont load to the variation of the aphid demand throughout its developmental cycle. These studies led to the discovery of a non-apoptotic and non-autophagic form of cell death, novel for insects, involved in the elimination of senescent bacteriocytes. Combining molecular and cellular approaches we characterized aphid bacteriocyte cell death as a multi-step process that starts with the hypervacuolation of the endoplasmic reticulum, and is followed by a cascade of cellular stress responses including the formation of autophagosomes in intervacuolar spaces, activation of oxygen reactive species, and Buchnera endosymbiont degradation by the lysosomal system. To address the molecular mechanisms governing bacteriocyte cell death, we annotated and studied the expression patterns of apoptosis pathway genes in the pea aphid. We found that, while the executive pathway of apoptosis is incomplete, with homologs for only four out of the eight proteins present in Drosophila melanogaster, apoptosis inhibitors underwent a large gene expansion, with over 30 Inhibitor-of-Apoptosis Proteins (IAPs) (contrary to 4 to 7 in other insects). Tissue-specific qRT-PCR and RNAseq analyses have shown that only two apoptotic effectors are induced in senescent bacteriocytes, while several apoptosis inhibitors are concomitantly over-expressed. We have confirmed the anti-apoptotic role of these bacteriocyte cell death-associated IAPs in heterologous expression experiments using a tractable in vivo model, the D. melanogaster developing eye. The induction of a restricted set of strong anti-apoptotic IAPs provides a possible mechanism whereby apoptosis is prevented in senescent bacteriocytes, enabling the emergence of a novel cell death process. Considering that aphid IAPs are differentially expressed in different life stages and tissues, this suggests an as yet not understood functional diversification.

Agriculturally Relevant Venom Peptides Derived from Arthropods. A Systematic Review Of Known Venom Peptides With A View To Their Development As Novel Bioinsecticides

Authors: Calvert Robert, Newcastle University, United Kingdom

Abstract: The European Green Deal aims to, by 2030, improve insect pest management (IPM) strategies whilst halving the current usage of chemical and non-environmentally friendly pesticides used in agriculture. A recent study has highlighted that the European Green Deal could result in a crop yield reduction of 10-20 percent if only current IPM strategies are utilised. Looking towards insect antagonists, such as spiders and parasitoid wasps, we discover a treasure trove of insecticidal venom peptides, many with novel modes of action. Though promising, only κ/ω-ACTX-Hv1a derived from the spider Hadronyche versuta has been developed by Vestaron Corp as a bioinsecticide in the USA. The development of new biological insecticides derived from arthropod venom peptides could help mitigate this loss, whilst minimising off-target effects on ecosystems. This systematic review used the PRISMA guidelines to collate published insecticidal venom peptides derived from arthropods into a potential database and makes recommendations for their future development.

Early establishment of the omnivorous predator Nesidiocoris tenuis increased uptake of biological control in tomato. Is it an alternative for others?

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Abstract: The tobacco whitefly, Bemisia tabaci and the tomato borer Tuta absoluta are major pests in tomato crops. Laboratory trials showed that Nesidiocoris tenuis could be an effective biological control agent of T. absoluta. Nevertheless, to be effective against T. absoluta under greenhouse conditions, it was necessary to develop an alternative release method. The adult predators were released on seedlings before transplanting to inoculate the plants with predator eggs. Nymphs started to emerge immediately after transplanting, once the plants were inside the greenhouse. With this method, the predator was already present in the greenhouse before the occurrence and in sufficient numbers to provide effective whitely and T. absoluta control. Here we present the results from the experiments conducted to develop this early release method and to evaluate the possibilities of other natural enemies for augmentative biological control when combined with this release estrategy. Additionally, we show the implications of the implementation of this new tactic in the uptake of augmentative biological control in southern European tomato crops and how this could serve as an example for other areas.

SCAN-Clim: a tool to support climate suitability analysis of plant pests based on climate classification.

Authors: Campese Caterina[1] and Maiorano Andrea[1], [1]European Food Safety Authority

Abstract: Climate suitability analysis is a crucial step in evaluating the likelihood of establishment of an invasive pest in an area. SCAN-Clim is a tool designed to perform climate suitability analysis based on climate classifications, thus evidencing the occurrence of climates that favour pest development and persistence in a specific area. The current version is the first prototype of the tool, developed in R and publicly available (https://zenodo.org/record/5780031#.YhZh6OjMKUI). The tool is currently used to support EFSA climate suitability analysis for pest categorisation and for quantitative pest risk assessment, under EU mandate. Tested on over 34 EFSA opinions, SCAN-Clim significantly improved the production of climate suitability maps, guaranteeing a standardised map format and providing clear documentation on the tool inputs and outputs. Further improvements will include the development of an interactive web app that will be freely accessible for registered users through the EFSA R4EU Portal (expected to be delivered in 2022).

Climate suitability analysis in the context of EFSA Pest Risk Assessment. Amyelois transitella, the navel-orange worm, as a case study.

Authors: Campese Caterina[1], Maiorano Andrea[1] and Van der Werf Wopke[2], [1]European Food Safety Authority, [2]Wageningen University & Research

Abstract: EFSA conducts plant pest risk assessments (PRA) under EU mandate. The assessment of the potential area of establishment is based on the presence of suitable hosts in combination with suitable climate. We conduct systematic literature search to collect data on pest distribution and eco-physiology, to develop pest-specific climate suitability models. We detail the full process, applied to the polyphagous pest Amyelois transitella, currently present in North and South America, but absent from the EU territory. Following two EC mandates, EFSA completed a pest categorisation and it is currently conducting a PRA. For this PRA, we collected 771 scientific documents, screened at title-abstract level. Out of these 191 studies were further screened as full-text. Ninety-seven studies were selected for data extraction. Out of these, 69 contained information on pest distribution and 51 on eco-physiology. We extracted 160 geographical-presence-records, out of which 91 related to specific locations with geographical coordinates. Climate suitability analysis was conducted based on the Köppen–Geiger climate classification and modelling with Climex. Preliminary results showed that, if the insect enters in the EU territory, it is more likely to establish in Southern and Mediterranean areas of the EU, where it could cause an impact on susceptible EU crops.

Effects of thermal extremes on male bumble bee reproduction

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Abstract: Bumble bee populations are increasingly under threat from habitat fragmentation, pesticides, pathogens, and climate change. Climate is likely a prime driver of declines in abundance and distribution, as bumble bees are limited by their thermal tolerance. However, the tolerance of whole organisms often exceeds that of their gametes; for example, insects can be sterilized by temperatures below their upper thermal tolerances. In Bombus, males are independent from the colony and can withstand extreme temperatures, but whether these temperatures compromise spermatozoa is unclear. Using commercially-reared Bombus impatiens males, we measured how exposure to sublethal temperatures near male critical thermal minimum and maximum impact spermatozoa viability. We measured temperature effects on spermatozoa in intact males and outside the body to determine if males are potentially protecting spermatozoa. A live dead assay and cell counter were used to estimate sperm count and viability. Males exposed to 45^{0}C for 85 minutes had significantly lower spermatozoa viability (control= 80%, heat= 58%). However, males exposed to 4^{0}C for 85 min had no significant decrease in spermatozoa viability (control=82%, cold= 76%). We discuss how exposure time may influence temperature effects on viability and the role of males in protecting sperm from damage due to temperature exposure.

Influence of conservation agriculture on carabid community's diet revealed by high throughput sequencing

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Abstract: Conservation agriculture is developing rapidly as part of the promotion of environmentally friendly agriculture. However, the consequences of conservation agriculture on trophic interactions and biological control remain poorly known. We used DNA-based gut content analyses to reveal the diet of the entire carabid community of winter wheat fields cultivated under different soil management systems (conservation and conventional) in Brittany, France.

In five pairs of fields, 985 carabid individuals belonging to 35 species were trapped alive in April, May, and June, the period of highest carabid abundance in the region and habitat under study. To avoid overrepresentation of the consumer DNA, we used regurgitates for large carabids. For small carabids, the whole body was processed.

DNA was amplified using fwhF2 and fwhR2n primer pairs (Vamos et al., 2017), targeting a 254bp fragment of the mitochondrial COI region. Amplicons were sequenced employing MiSeq Illumina run v2 and sequences were treated using a modified Dada2 pipeline using a custom-made reference database for taxonomic assignation.

739 single ASVs were detected mostly corresponding to invertebrate pests, such as slugs and aphids, but also to other predators, such as spiders and to organisms involved in the decomposition of organic matter, such as earthworms and springtails.

Profiling smallholder vegetable crops production landscape ecologies for sustainable management of viral diseases and associated vectors

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Abstract: Studies to assess viral diseases and insect vector abundance were carried out in three major vegetable crops production landscape ecologies: at low (Coast), medium (Morogoro) and high (Iringa) altitudes from 2016 to 2018 in Tanzania. Vegetable crops are grown with and in the immediate surroundings of multiple crop and non-crop plant species that serve as good sources of inoculum for plant viruses and the associated insect vectors that affect vegetable crops in smallholder farming systems. There was a high incidence (60-94%) of plants infected with viral diseases in the smallholder vegetable fields. Similarly, there was a high abundance of insect vectors such as aphids, whiteflies, leaf hoppers and thrips. The study showed that 87.5% of the farmers were aware of viral diseases as one of the major production constraints to vegetable crops production. There was a fair knowledge of the insect pests, including aphids, caterpillars, leaf minors and whiteflies. However, the respondents were less aware of the biology (cause, mode of transmission and spread), ecology (cropping practices and host range) and integrated management of the viral diseases and associated insect vectors. Thus, majority of the farmers resorted to use of pesticides as their first and 'only' line of defense. Unfortunately, this has not only failed to decrease viral disease incidences, but it has also led to ineffective pest control, partly due to lack of knowledge of disease and pest species identity and diversity, biology and production ecology and sustainable management strategies. The study findings were used to create awareness among vegetable producers, agricultural extension officers, agro-dealers, scientists and government plant health regulatory agencies on the importance of understanding the ecology and biology of crop-infecting diseases and associated insect vectors. The study results will be discussed in the context of understanding virus-vector interactions in smallholder cropping ecologies, to advise IPM strategies that encourage the use of cultural practices to manage the viral diseases and insect vectors, with reduced pesticides usage.

Potential for insecticide resistance on Kenyan populations of Tuta absoluta

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Abstract: Tomato (Solanum lycopersicum) is one of the most important vegetable crops cultivated for the domestic market in East Africa. In East Africa particularly in Kenya, most tomato growers are small scale farmers, practice open field cultivation and are faced with invasive pest species. Tuta absoluta (Meyrick, 1917) (Lepidoptera: Gelechiidae), commonly referred to as the South American tomato moth, is a major invasive pest species in Kenya threatening tomato production. Traditionally this pest has been controlled using conventional insecticides in many parts of the world where it has been introduced. Several classes of insecticides have been used in the management of this pest including organophosphates, pyrethroids, diamides and spinosyns. This over-reliance and overuse of pesticides has led to insecticide resistance development of T. absoluta in many parts of the world.

Diamides include the most recent class of insecticides that has been widely used to manage T. absoluta in Kenya. Its popularity stem from its narrow spectrum, its low mammalian toxicity and less non-target effects. Recently, control failures have been reported by Kenyan farmers. This calls for investigations of a possible resistance of T. absoluta to diamides. Its detection will inform stakeholders of the need to incorporate insecticides with different modes of action as well as incorporate other management techniques and will aid in strengthening current pest management techniques. Integrated pest management packages for tomatoes have been developed through collaborative efforts of various institutions notably KARLO (Kenya) and Ohio State University. These packages include proper use of chemicals through the development of appropriate rotations for pest management.

Counting bees like birds: Roadside bumble bee monitoring in Canada

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Abstract: A number of bumble bee species are known to have declined dramatically, but sparse monitoring data has made it difficult to assess the magnitude of these declines across the broad ranges of some of these species in North America. Extensive, simple and effective monitoring programs are needed across the continent to establish range-wide trends. In this study we sampled bumble bees with hand-netting along roadsides in northwestern Canada, using established breeding bird survey routes as a basis of our effort. Within each 36-km transect, bees were sampled for ten minutes at each of ten sites. Early results show that species that have declined in southern Canada and the United States (e.g. Bombus bohemicus, B. occidentalis, and B. suckleyi) are still present in the northwest, and probably at historical densities.

Predators under spotlights! Behavioral responses of Orius insidiosus to supplemental light spectra and intensity: first step towards selection of light favoring predator in a tri-trophic system

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Abstract: Supplemental lighting (SL) is now considered as an efficient tool to disrupt pest activity, including in greenhouses. Despite its current use in controlled environments, SL potential to favor biocontrol agents have been overlooked, especially regarding predators. Our approach is to use Light Emitting Diodes (LEDs) to control SL environments (spectra × intensity × photoperiod combinations) and screen different SL combinations to identify optimal conditions for arthropod predators. As light both have direct and indirect (plant or prey mediated) effects on predators in “plant-herbivore-predator” tri-trophic systems, SL-related responses of the whole system must be considered. We selected an economically relevant study system, linked to an actual horticultural concern. The greenhouse cucumber (Cucumis sativus) is a model plant since the beginning of SL sources’ development. Its photobiology is now well known, and SL conditions have been accordingly optimized in commercial greenhouses. Like various crops, cucumbers are susceptible to thrips activity, impacting both plant performance and fruit quality. The thrips Frankliniella occidentalis (Pergande) is considered as a major international pest, causing substantial losses in greenhouses worldwide. As F. occidentalis pesticide resistance globally strengthens, biocontrol should increasingly appear as an appealing alternative. The predatory bug Orius insidiosus (Say) is an efficient generalist biocontrol agent, widely use against thrips. However, its photobiology remains mostly unknown and diapause issues are frequent under greenhouse conditions, disrupting biocontrol. To select optimal SL conditions for O. insidiosus and ensure biocontrol enhancement in commercial greenhouses, predator’s responses to light environment will be investigated at various spatiotemporal scales. The presented experiment corresponds to the first step and focus on O. insidiosus predation performance at small scale. Both prey and predator were exposed to monochromatic spectra treatments under a range of light intensities, based on previous works with other bug species and wavelengths used to promote crop productivity. Locomotion (walking time, distance, speed, etc.) and alimentation (time before first capture, time spent eating, attack/defense, etc.) were analyzed from video tracking data. Results were used to identify the most favorable light spectra × intensity combinations for O. insidiosus, to consider them in subsequent experiments. To our knowledge, those observations are the first concerning O. insidiosus behavior under SL at small scale, as well as being the initial act towards optimizing SL conditions for this widespread biocontrol agent.

Promoters and effectors for the development of a Killer-Rescue system in Aedes aegypti (Diptera, Culicidae)

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Abstract: Mosquito-borne diseases are a severe public health burden, causing morbidity and mortality worldwide. The mosquito Aedes aegypti is found in tropical and sub-tropical regions throughout the world and is a vector for multiple arboviruses including chikungunya, Zika, and dengue; no safe and effective vaccines currently exist for these diseases. The primary preventative method for reducing new infections from these diseases is mosquito population control, primarily eliminating larval habits by physical or chemical measures. Chemical insecticides are themselves challenged by emerging resistance, and are also relatively non-selective.

Recent advances in genetics-based vector control methods such as gene drives could modify populations of disease vectors such as Ae. aegypti to make them less able to transmit pathogens. This has caused both excitement about the prospect of disease eradication and concerns around safeguards. Drive mechanisms that balance these competing interests for invasiveness and control are therefore highly desirable.

Here we characterise our work towards building the components of one such system as a Killer-Rescue drive. This simple toxin-antidote system requires effective lethal genes and efficient rescues, and is attractive due to its inability to spread to neighbouring populations and self-limitation over time. We have developed and tested a variety of lethal genes; through the bipartite Tet-OFF system. This has allowed us to systematically characterise different combinations of lethal proteins, gene expression and insertional effects, while simultaneously developing novel tools for the mosquito research community.

We characterised the expression pattern of two different transgene insertions of a midgut specific promoter (Carboxypeptidase A - AeCPA) driving the transactivator tTA, by crossing the mosquito lines with a TRE line expressing a fluorophore, and then tested them against a range of inducible lethal effectors.

The two AeCPA lines demonstrated high expression of tTA from the late larval stage onwards in the midgut of both males and females, but with different levels of ectopic expression, highlighting the importance of the transgene insertion site for expression.

Regarding the analysis of the different lethal genes crossed with the promoter lines, we observed death, reduction in female fecundity or no effect depending on the combination of promoter and lethal lines tested. The Tet-OFF system has proven useful in the evaluation of the different components required for the potential development of a Killer-Rescue system in Ae. aegypti, allowing the identification of a number of promising promoter-effector combinations.

Focus on Antarctic Springtails: the true “pachyderms” of the Continent

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Abstract: From an evolutionary standpoint, springtails (Collembola) are considered an archaic terrestrial group, part of the earliest diversification of hexapods, and differing from derived insects in the peculiar structure of (internal) mouth parts and by the primitive lack of wings. With ca. 9000 described species, springtails can be found in almost every terrestrial environment of the planet, including the Antarctic, where a basic ecosystem supports the development of communities of a limited number of taxa that are active only during the summer season.

Together with mites, springtails are the most diverse group of Antarctic land invertebrates and amongst the largest strictly terrestrial animals of the Continent. In Antarctica, springtails have a long evolutionary history and must have survived multiple glacial cycles in refugia. Consistent with the scale of isolation of Antarctic terrestrial habitats and the limited active dispersal capabilities of springtails, most population genetic studies so far performed on Antarctic species have showed moderate to high levels of intraspecific genetic divergence. However, the extreme environmental conditions of Antarctica may have preserved successful morphological traits even if clear genetic divergence has taken place, fostering morphological stasis. It is consequently likely that a large number of cryptic taxa may be present. Therefore, we have recently investigated the morphology and genetic differentiation of springtail species through a multidisciplinary comparative analysis, testing the efficacy of an integrative taxonomic approach to assess whether or not cryptic speciation is at play in Maritime and Continental Antarctica.

In addition, metabarcoding analyses of the gut microbial communities of some springtail species, and sequencing of the transcriptome of specimens stressed at temperatures higher than measured in their natural environment, as well as mitogenome comparison among taxa subject to different evolutionary pressures, were also performed. The aim of these studies was to evaluate the resilience of specimens exposed to climate change, and to characterize the microbiomes associated with species from the two Antarctic bioregions.

The results of combined morphological and genetic studies clearly suggest that Cryptopygus terranovus and Friesea antarctica both comprise complexes of at least three cryptic species. Some mitochondrial genes involved in the oxidative phosphorylation process are under positive selection. RNA-seq results from C. terranovus detect differences in the gene expression related to protein unfolding, protein degradation and synthesis of fatty acids between springtails arbitrarily stressed at +6°C, with respect to control conditions. Data obtained from the microbiome analyses highlight (as previously detected in non-polar species) the occurrence of interesting OTUs, including from genera such as Streptomyces and Bacillus.

Invasion biology of the American Boatman Trichocorixa verticalis verticalis in Western Europe: The role of ecophysiology and biological interactions

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Abstract: The corixid (lesser water boatman) Trichocorixa verticalis verticalis (Fieber, 1851) originates from North America is the only aquatic Hemipteran alien to Europe, where it is concentrated on the Atlantic coastal plain in the south west of the Iberian Peninsula. Recent studies of its ecophysiology, ecology and interactions with native corixids are reviewed. The main questions addressed are: (1) What is its potential non-native range within Europe and beyond? (2) How does its physiological performance compare to that of native species? (3) What physiological/biological factors determine why it is so dominant in saline wetlands yet so much rarer in low salinity wetlands? (4) How does its trophic ecology relate to that of native species? (5) What effects is it having on other aquatic communities? We show that this species has the potential to disperse across a high proportion of the coastal European lowlands across a wide range of latitudes, and the projections are not significantly modified by climate change. The invasion success of Trichocorixa verticalis in permanent, saline wetlands seems to be mediated by high plasticity in response to changes in temperature and salinity, together with high plasticity in diet. However, the most important factors seem to be its higher fecundity compared to native corixids, and ability to reproduce throughout the year. Moreover, although its eggs are not resistant to drought, epizoochory of eggs by waterbirds such as flamingos may contribute to the expansion of this alien species around the Mediterranean region. As in the native range, Tricocorixa verticalis is an important predator in its introduced range, and is likely to reduce the abundance of native Anostraca such as brine shrimps, thus increasing phytoplankton abundance through trophic cascades. According to microcosm experiments, Trichocorixa verticalis is able to live and reproduce in freshwater in the presence of native corixids, so its rarity in fresher wetlands may be explained by its greater susceptibility to parasitic mites, together with a higher predation rate by Odonata larvae compared to native corixids. The presence of Trichocorixa verticalis has been shown to modify the distribution and co-occurrence patterns of native corixids, niche differentiation being the main mechanism to avoid competition among the invasive and native species, enabling coexistence and resource partitioning.

Finding odor-linked resources in a turbulent and complex odor landscape

Authors: Cardé Ring, Department of Entomology University of California Riverside, CA, United States

Abstract: Many insects locate resources such as a mate, host or food by tracking the odor plumes these resources generate to their source. As the plume is carried downwind, it becomes more spatially dispersed and dilute, but filaments above behavioral threshold can persist for long distances. Plume tracking can extend to 100s of meters. Flying insects track along a plume by flying upwind, sensing the wind's direction by the optomotor reaction, not by detecting a concentration gradient or by mechanoreception of wind flow.

In the case of moths, there should be strong selective pressure for males quickly locating calling (pheromone-emitting) females. Females as well may compete for mates. In many moth lineages, a female can be triggered into imitating calling after detecting pheromone from nearby females. Such contagious calling should concentrate males in their vicinity and also attractant more males. Females can also be induced to call by host-plant volatiles (HPVs).

We now know that most moth pheromones are blends of 2-4 compounds, often released in precise ratios, thereby creating a species-specific communication channel. A second factor seemingly concentrating males and females near their host plants is the detection of HPVs. This seems to be reflected in many cases wherein addition of HPV to the pheromone blend increases capture of males. What remains to be discovered is how influential HPVs are in concentrating males in host plant patches to position themselves in the likely vicinity of calling females.

Similarly, female anthropophilic mosquitoes also may use odors from human hosts as cues for house entering, which can occur well before biting.

These and other recent studies suggest that volatile "habitat" chemical cues, released over larger areas in larger quantities, may concentrate responders in areas where more specific, resource-linked odors are more apt to be found.

Lessons learned from fruit fly eradication efforts in California

Authors: Carey James, University of California, Davis, United States

Abstract: Drawing from analyses of and multiple publications on the 70-year/10,000 fly database containing detection details for individual flies involving 17 different fruit fly species in California, I will offer answers to the following questions: What are the probabilities of first and subsequent fruit fly outbreaks in a randomly-chosen 10 x 10 km grid cells in the state? What is the spatial distribution of outbreak risk? What is the meaning of zero capture? O a single fly? Which species of fruit fly is the most invasive? Does the interval between new outbreaks change after each outbreak? Once eradication is declared what is the interval before fruit fly recurrence? How concerned should grower be in located just outside of a regulated area? Why is eradication so difficult? I will end with a synopsis of lessons learned including policy implications for future intervention programs on tephritids.

Development of Leishmania parasites in Culicoides

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Abstract: Leishmaniases are vector-borne diseases whose etiological agents are protozoan parasites of the genus Leishmania (Kinetoplastida: Trypanosomatidae). The genus consists of four subgenera, three of them, Leishmania, Viannia and Sauroleishmania, are transmitted by phlebotomine sand flies (Diptera: Phlebotominae) which represent their only proven vectors. Some authors reported wild-caught biting midges PCR-positive for Leishmania but we experimentally demonstrated that Culicoides nubeculosus and Culicoides sonorensis are refractory to development of the principal Old-World parasites, namely L. major, L. infantum and L. donovani.

On the other hand, the vectors of the most ancient phylogenetic group of leishmania, parasites of the subgenus Mundinia, are not known. The recently established subgenus Mundinia consists of 5 species known before as L. enriettii complex – L. enriettii, L. macropodum, L. orientalis, L. martiniquensis and the unnamed species from Ghana. First two species are parasites of guinea pigs and red kangaroos, respectively, but rest three are causing human diseases characterized by symptoms varying from self-healing skin lesions to visceral form. In Australia, biting midges of the subgenus Forcipomyia (Lasiohelea) were found with heavy late stage infection of L. macropodum and recent studies demonstrated development of Leishmania orientalis in Culicoides sonorensis.

Here we studied experimental infections of eight leishmanial strains belonging to five Mundinia species. Infection rates and parasite localization in C. sonorensis was compared to several sand fly species, namely Phlebotomus argentipes, Phlebotomus duboscqi and Lutzomyia migonei. Our experiments demonstrated high susceptibility of C. sonorensis to L. orientalis and suggest that Mundinia parasites could be transmitted by midges rather than sand flies. Therefore, we propose that biting midges should be assessed in the field when searching for the vectors of L. enriettii, L. martiniquensis and other related parasites of subgenus Mundinia.

Ticks Find Hosts Using Infrared Homing

Authors: Carr Ann[2] and Salgado Vincent[1], [1]BASF, United States, [2]Vanderbilt University, United States

Abstract: Ticks are second only to mosquitoes as vectors of disease to humans and animals. Commercial insect repellents provide an effective means of personal protection against potentially infectious tick bites by disrupting host-seeking, but their mechanism of action and indeed the sensory cues used in host-seeking are not well understood. While there is anecdotal evidence that ticks and other ectoparasites are attracted to heat, it has never been demonstrated that they sense radiant heat. Using a novel thermotaxis assay to investigate the detection range, temperature dependence and repellent sensitivity of heat perception in ticks and to identify the sensory organ responsible for this sense, we showed that Amblyomma americanum and Dermacentor variabilis ticks home in on objects at human body temperature by sensing radiant heat with the Haller's organ posterior capsule, a covered spherical pit organ that was previously thought to be olfactory. An aperture in the capsule cover confers directionality and highly reflective interior surfaces of the capsule concentrate radiation, to provide enough sensitivity to locate a human from several meters away. Low concentrations of the insect repellents DEET, picaridin, 2-undecanone, citronellal and nootkatone eliminated thermotaxis without affecting olfaction-stimulated tick host-seeking behavior. We anticipate that this discovery will significantly aid insect repellent research and provide novel targets for the development of innovative integrated pest management programs and personal protection strategies for ectoparasites and vector-borne disease.

The Evolution and Diversity of Parental Care in Insects

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Abstract: Insects exhibit a stunning variety of ecologies and life histories, which has contributed to and been influenced by the evolution of a tremendous diversity of parental care strategies. Yet, outside of eusociality, the evolution of insect parental care has been the subject of limited systematic study. Elaborated non-eusocial insect parental care is well represented in certain groups of beetles, flies, cockroaches, and heteropterans. At the same time, it is unclear how often parental care has evolved, what forms it takes, and the extent to which it is phylogenetically enabled or constrained. We review the diversity of insects in which parental care has arisen, plumbing lesser known instances to build a stronger data set. Incorporating recent phylogenetic advances, we compare among taxa to test hypotheses about the eco-evolutionary conditions under which selection favors added investment in individual offspring. By combining these approaches, we aim to form a deeper understanding of how, when, and where parental care evolves within the Insecta, and how their capacities and constraints have shaped both insect niche evolution and resulted in types of parental care unobserved in other animals. We expect our findings from insects to help inform and broaden the prevailing vertebrate-biased theory about the eco-evolutionary dynamics of parental care.

'Neoclassical' Biological Control: prescriptive eco-evolution of native biological control agents

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Abstract: In Classical Biological Control, 'invasive' species are reunited with their natural enemies, re-establishing lost ecological connections as if turning back the eco-evolutionary clock to match the native range. Most environmental weeds, however, receive little or no management, leaving trophic relationships to perhaps ultimately arise from within the resident community. 'Neo-classical' Biological Control is a prospective approach that leverages the latent adaptive potential of native herbivores to exploit established non-native species. By spinning the eco-evolutionary clock forward, it aims to control populations by accelerating their ecological integration into resident communities.

We believe that two fundamental drivers of Neoclassical opportunities are predicted to be phylogenetic niche conservatism and ecological opportunity. Prescribed evolution in wild insect herbivores is feasible because naturalized plants frequently have native family members and even congeners in their new ranges, much more so than expected by chance. Related plants in turn commonly share related herbivores within and among continents. When introduced, those plants can be evolutionary traps for partially pre-adapted resident herbivores, hindering their survival and reproduction or exposing them to novel risks. Neo-classical interventions seek to resolve critical deficits in pre-adaptation that limit the spread of resident herbivores onto targeted non-natives. And secondly, when those plants are abundant and underexploited, differences in ecological opportunity suggest that even struggling 'maladapted' herbivore lineages, if able to persist upon them, will sometimes show disproportionately increased fitness compared to 'adapted' lineages feeding on highly contested native hosts.

Those eco-evolutionary dynamics and related genetic and ecological factors can reinforce the field efficacy of prescribed interventions such as mass rearing under selection to improve phenotypic match to local opportunities. Such work may be conducted in the same semi-field facilities that are used to screen Classical control agents for nontarget risks. Translating resulting fitness gains into natural wild is the challenge. We will touch on multiple scenarios where Neoclassical Biological Control practices could be trialed to extend the reach of current control efforts in an Epoch of increasingly novel ecosystems

Identification and characterisation of a Masculinizer homolog in the diamondback moth Plutella xylostella

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Abstract: Recently, a novel sex-determination system was identified in the silkworm (Bombyx mori) in which a piRNA encoded on the female-specific W chromosome silences a Z-linked gene (Masculinizer) which would otherwise initiate male sex-determination and dosage compensation. Masculinizer provides various opportunities for developing improved genetic pest management tools. A pest lepidopteran in which a genetic pest management system has been developed, but which would benefit greatly from such improved designs, is the diamondback moth, Plutella xylostella. However, Masculinizer has not yet been identified in this species. Here, focusing on the previously described 'masculinizing' domain of B. mori Masculinizer, we identify P. xylostella Masculinizer (PxyMasc). We show that PxyMasc is Z-linked, regulates sex-specific alternative splicing of doublesex and is necessary for male survival. Similar results in B. mori suggest this survival effect is possibly through failure to initiate male dosage compensation. The highly conserved function and location of this gene between these two distantly related lepidopterans suggests a deep role for Masculinizer in the sex-determination systems of the Lepidoptera.

Study of an insecticide, the sulfoxaflor, on learning and memory honeybee's

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Abstract: Honey bees are major pollinators of crops and wild plants, and are therefore essential to the agricultural economy and wild plant diversity. Unfortunately, despite their important role in human activities, there is clear evidence of the decline of honey bee colonies worldwide. Several studies have shown that pesticide exposure is involved in this decline. Among insecticides, neonicotinoids are the most widely used to control a wide range of insect pests. These insecticides target neuronal nicotinic acetylcholine receptors (nAChRs) which play an important role in cognitive function. Recently, sulfoxaflor (SFX) has been used to replace neonicotinoid insecticides. In the present study, we have evaluated the effect of sublethal concentration of SFX on honey bees Apis mellifera learning and memory processes. Using the proboscis extension response paradigm, we found that, depending on the conditions, SFX can impair learning and memory recovery. Relative quantitative PCR experiments demonstrated different nAChRs expression levels in the bee brain after SFX exposure. These results demonstrated that a sublethal dose of SFX could affect bee learning performance and modulate the expression of specific nAChR subunits in the brain.

Pheromones transport: role of aerosols and multiscale antennae on odor capture

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Abstract: Understanding the role of aerosols in pheromone transport is of fundamental interest as aerosol phase can alter the transport properties, accessibility and chemical reactivity of the pheromones in the air. To lay the foundations of our approach in which pheromones partition between a gas phase and an aerosol phase, we will first present the key concepts from thermodynamic theory that are needed to discuss the complex physico-chemical processes at stakes and their consequences. The multiscale modeling of the phase exchanges of pheromone when transported in the air will subsequently be presented. Then, a running experiment with Bombyx moths reacting to air flows differently loaded with aerosols will be described, highlighting their double-edge sword impact. Finally, we will consider the flow around pectinate antennae, for which a mechanistic understanding of odor capture is still lacking. We focus on the functional, two-scales sub-structure of an antenna of Samia cynthia (Lepidoptera, Saturniidae): a brush of sensory filliform sensilla attached to one rami, the supporting tubular structure. We had to plit the structure of the antenna because 3D printing cannot currently fabricate multiscale structures spanning the antennal four orders of magnitude. A semi-analytical model to compute mass transfer, originally developed for heat transfer in pipes, is then adapted. Particle Image velocimetry (PIV) is used with scaled-up physical models for estimating the leakiness of the structure, i.e. the proportion of flow passing through the structure rather than around. The combination of these experimental and modeling approaches delivers the capture efficiency over a biologically relevant range of air speed. We found that two distinct processes are setting pheromone capture efficiency. At low Re numbers, leakiness at the higher organizational scale, i.e. the entire substructure, determines the efficiency of odor capture. At higher Re numbers, advection at the lower organizational scale of a single sensillum is determining efficiency. We then study how to embed the sub-structure within an entire antenna and observe that the multiscale architecture of the pectinate antenna is highly adapted for odor capture over a large range of flow speeds. We end up comparing the efficiency of pectinate antenna with more classical, cylindrical forms and consider why the multiscale antennae have evolved so many times, as well as the possible relationship between antennal forms and pheromone diffusive coefficients.

“Sensory neuron membrane proteins (SNMPs)” indicate distinct roles in olfactory signal detection in insects

Authors: Cassau Sina, Martin-Luther-University Halle Wittenberg

Abstract: The sense of smell enables insects the recognition of vital olfactory signals that are essential for their survival. The detection of various odorants is dependent on a complex interplay of proteins expressed by the insects' olfactory sensory neurons (OSNs) and the adjacent support cells which are housed together in the main chemosensory units on the antenna, named sensilla. Among the well-studied odorant binding proteins (OBPs) and various families of olfactory receptors, another class of proteins appear to play an important role in the detection of distinct odorants, termed the sensory neuron membrane proteins (SNMPs). SNMPs are classified as CD36 proteins due to their sequence identity to this family of two-transmembrane receptors of various lipophilic compounds. Here we assess the distribution pattern of two SNMP homologs in the antenna of the hemimetabolic desert locust Schistocerca gregaria via immunohistochemical investigation. To further elucidate the role of SNMPs in insect olfaction, we performed functional investigations with HEK293 cells expressing each SNMP homolog utilizing fluorescent lipid analogs. The data suggests that SNMPs play an important role in detecting and possibly even eliminating specific lipophilic compounds, which may aggregate in the sensillum lymph after the initial detection of odorants.

Connecting the pieces: Evolution of genitalia in Cimicoidea and the phylogenetic revision of the group (Heteroptera: Cimicomorpha)

Authors: Cassis Gerasimos[1], Tatarnic Nikolai[3] and Bonduriansky Russell[2], [1]University of New South Wales, [3]Western Australian Museum, Australia, [2]University of New South Wales (UNSW), Sydney, Australia

Abstract: Cimicoidea is a superfamily of predaceous and ectoparasitic insects that include the infamous human bedbugs. Most species of Cimicoidea practice traumatic insemination, where the male pierces the abdomen of the female and ejaculate directly into the haemoceol. Traumatic insemination is regarded as textbook case of sexually antagonistic coevolution, with elaboration of both male and female genital morphology across the Cimicoidea. Knowledge of genital morphology across the Cimicoidea is still in its infancy, with many of the key works dating to the 1960s and 1970s. To address this shortfall, we have employed microCT methods to virtually dissect male and female genitalia separately and, where possible, in copula. These data have been compiled to (1) assess genital complexity and variation for exemplars of the bedbug, batbug and minute pirate bug families, and (2) optimise character evolution in a phylogenetic context and determine if they exhibit a phylogenetic signal. The consensus tree produced revealed highly unresolved relationships with most families. This limited support between the distribution of traumatic inseminating characters on the phylogeny and currently available phylogenies showing relationships in the Cimicoidea, is likely due to the lack of a well-resolved phylogeny of the Cimicoidea. Higher taxonomic relationships within the Cimicoidea is still in a state of controversy, and several alternative hypotheses for relationships exists. We furthermore, aimed to reconstruct the evolutionary relationship in the Cimcoidea by next-generation sequencing (NGS) to target ultraconserved elements (UCEs) across all Cimicoidea.

Insights into DEET's mode of action in ticks

Authors: Cassone Bryan[1] and Koloski Cody[1], [1]Brandon University, Canada

Abstract: DEET is far and away the most common active ingredient in commercial repellents, providing effective protection against blood-sucking insects and ticks. However, its mode of action appears complex and is not yet fully understood. Since ticks possess a unique sensory structure, the Haller's organ, the specific genes and pathways associated with DEET repellence may differ from insects. Using the American dog tick, Dermacentor variabilis, as our model system, we carried out a series of transcriptional studies to explore the genetic basis of DEET repellence and the relative roles of the Haller's organ and other tissues (synganglion, palps, salivary glands) in DEET recognition. Further, we used a variety of behavioural assays to explore natural insensitivity and the effects of concentration on the repellency. Overall, our studies furthers our understanding of DEET repellence in hard ticks.

Insights into the repellency effect of DEET on human-biting ticks (Dermacentor variabilis)

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Abstract: Developed for use by the United States military nearly eight decades ago, N,N-Diethyl-m-toluamide (DEET) is considered the gold standard in repellents. Despite its widespread commercial availability, the precise mechanisms underlying the mode of action of its active ingredient remain unclear. Most of the research has focused on mosquitoes and fruit flies, and indicate the repellent affects insect taste, smell, and also acts on contact. However, little is known about the underlying basis of DEET repellency in human-biting ticks, including the American dog tick (Dermacentor variabilis). In these studies, we present evidence that DEET acts as both an olfactory confusant and mild acaricide. We further disentangle the relative roles of the Haller's organ in the repellency effect. Finally, we explore natural insensitivity to DEET and the effects of concentration on the repellency of D. variabilis in Manitoba, Canada.

How do trees protect trees from herbivores in urban environments?

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Abstract: Trees are key components of human well-being in urban areas, in particular through urban cooling and improved citizen physical and mental health. Yet, several pest insects are prone to cause major damage and to threaten the health of urban trees. Over the past decades, ecologists had a mounting interest for tree-pest interactions in urban ecosystems and several studies showed that tree-pest interactions are strongly affected by the urban environments. Yet, discrepancies among existing studies are such that it is still unclear what are the main factors driving pest insect damage on urban trees. For instance, the urban environment may enhance herbivory through the heat island effect, favouring the activity of ectothermous herbivorous insects. Alternatively, because of the fragmentation of habitats, the urban environment may alter the diversity and distribution of insectivorous birds, thereby affecting the strength of the top-down control they exert on herbivore populations. Yet, trees, and in particular tree density, are key determinants of both urban temperatures and bird habitats. In this study, we ask how urban temperatures and tree density jointly affect (i) insect herbivory on urban trees and (ii) the top-down control of herbivory by herbivores' enemies. We selected a total of 49 trees from three species along two orthogonal ecological gradients in Bordeaux city (South-Western France): one temperature gradient defined as summer temperatures in a circular buffer of 200m radius centered on sampled trees and one gradient of tree density defined as the percentage of canopy cover in a circular buffer of 20m radius around sampled trees. In each tree, we measured insect herbivory as the percentage of leaf area impacted by insect herbivores. We additionally installed artificial clay caterpillars in the same trees to study predator activity. By linking insect herbivory with predation pressure along well defined ecological gradients, our study will help understand the ecological drivers responsible for tree health in urban environments.

Cephalonomia tarsalis, a promising parasitoid for the control of the sawtoothed grain beetle

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Abstract: The sawtoothed grain beetle, Oryzaephilus surinamensis (L.) (Coleoptera: Silvanidae) is an important pest in stored rice, particularly because it has developed resistance to some pyrethroids, more precisely to deltamethrin. Cephalonomia tarsalis (Ashmead) (Hymenoptera: Bethylidae) is a specialized parasitoid that attacks larval stages of this beetle and can be an alternative control agent.

We have studied the dispersion of this parasitoid, and we have shown that females were able to disperse, to locate sawtoothed grain beetles and parasitize them when placed at the bottom of a 1.5m paddy rice column (20cm diameter). This result suggests that this parasitoid would be able to find and parasitize these hosts in piles of stored rice, where most of the pest populations are concealed in the 1m upper layer. We have also shown that under optimum environmental conditions (28ºC, 70% relative humidity) this parasitoid can prevent sawtoothed grain beetle population growth, because the final size was more than 90% lower than the population of the control treatment without parasitoids. This suggests that, with periodical releases of the parasitoid, beetle populations could be maintained under control.

Control of the maize weevil, Sitophilus zeamais, with the larval parasitoid Anisopteromalus calandrae in rice big bags

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Abstract: The maize weevil, Sitophilus zeamais, is a key pest of stored rice that is currently controlled mainly with pesticides. This procedure has well-known associated drawbacks, as the presence of toxic residues in the grain and a decline of efficacy due to repeated applications of the few available active ingredients. Under optimum conditions in laboratory tests, the larval parasitoid Anisopteromalus calandrae (Hymenoptera: Pteromalidae) is effective in preventing the weevil population to reach pest density. However, few data are available on its performance when released in commercial situations.

We have demonstrated that females were able to locate hosts and parasitize them when placed in a 1.5m paddy rice column (20cm diameter). Females were not only able to reach the bottom of the column, but also to reduce up to 90% the weevil population. Moreover, when females were released in commercial bags (500kg paddy rice, 1x1x1m in size), they also reached the bottom of the bag and reduced the weevil population up to 50-60%, depending on the season. The presence in the bags of a secondary pest, the lesser grain borer Rhyzopertha dominica which is also a host for this parasitoid, did not interfere with the control of the maize weevil.

Genetic diet specialization in phytozoophagous and zoophytophagous mirids

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Abstract: The Miridae have a true omnivorous diet that includes varying proportions of animal and plant resources. Species belonging to this family can, therefore, be classified on a spectrum varying from phytozoophagy to zoophytophagy according to the relative proportion of plant and animal resources in their diet. The differences in diet composition can be as important within the species, than between species. Genetic variability in omnivorous populations generates diet specialization (individuals of the same population may consume a different proportion of available resources). Here, we compare genetic diet specialization among three North American species of Miridae, namely the tarnished plang bug Lygus lineolaris, the mullein bug Campylomma verbasci and Dicyphus hesperus. These species form a spectrum from phytozoophagous to zoophytophagous. The consequences of genetic diet specialization in these economically important species in agricultural environments is discussed.

Biocontrol of Aculops lycopersici (Massee) (Acari, Eriophyidae) on tomato with releases of Transeius montdorensis

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Abstract: Aculops lycopersici is an increasing pest in protected tomato crops without a biocontrol solution. Despite that several promising predatory mites have been described in laboratory, results in field conditions have not been successful enough to implement augmentative programs. The introduction of astigmatid mites has been recently implemented as a method to improve the establishment of the predatory mites in different crops. In this study, preventive strategies have been tested with releases of Transeius montdorensis complemented with this feeding system. A trial on potted tomato plants placed in a climatic chamber showed that the pest did not develop after release on the plants where the predator had been established. Success was obtained in all three evaluated treatments, with different timing and ratios of releases. Two of these strategies were tested in a greenhouse in walk-in cages. After artificial infestation, successful control was also obtained as long as the climate conditions allowed to keep high predator populations. A program of releases was then evaluated in an experimental greenhouse. Natural infestation of the tomato plants with the pest occurred in all the control plots without predators, where severe damage occurred. The plots with predators were only colonized by the pest when high populations had already developed in the control plots, and no damages were recorded. Additional trials have been performed in Spain and Holland both in experimental and commercial greenhouses, where lower dosages have been tested. Different machineries have been examined to release the mite populations that allow to reduce the labor costs. A commercial biocontrol program is discussed for different crop conditions.

Phylogenomics of the braconid subfamily Doryctinae: towards a complete genus sampling of an extraordinarily diverse, cosmopolitan taxon

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Abstract: The Doryctinae is a highly diverse, morphologically heterogeneous braconid wasp subfamily with currently over 200 recognised genera and more than 1,700 described species. This cosmopolitan group is mainly represented by ectoparasitoids of xylophagous beetle larvae, though it also contains some phytophagous species. Previous phylogenetic studies on the subfamily, based on rather few gene markers and a limited taxon sampling, showed that its generic relationships are largely congruent with the geographical distribution, and not with its current tribal classification. They also failed to recover doryctine monophyly but with weak support. Here we present preliminary results of an ongoing study that seeks to reconstruct the phylogenomic relationships among all the currently within the subfamily based on both mitochondrial and ultraconserved elements, and that also is characterizing the mitochondrial genome of representative members of the main doryctine clades (Neotropical, Afrotropical-Holarctic-Oriental, Australian and Holcobraconini clades). Our phylogeny estimates will serve to propose a stable higher taxonomic classification for the subfamily, and will serve to conduct further studies about its origin, diversification and evolution of hosts preferences.

Evolution of raptorial legs in assassin bugs (Hemiptera: Heteroptera: Reduvioidea)

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Abstract: Assassin bugs (Reduvioidea) are amongst the most morphologically and ecologically diverse lineages of predators, with approximately 7000 described species. Predacious reduvioids are either generalists or specialists of various arthropods and possess an astounding variety of leg modifications to handle prey. However, the evolutionary history of these modifications remains limited by the lack of a comprehensively robust phylogenetic hypothesis and detailed assessments of leg modifications across Reduvioidea. Here we reevaluate raptorial modifications with a phylogenetic dataset comprised of various data types and significantly improved taxon sampling. Reconstructing the evolutionary history of raptorial characters will serve as a framework for understanding the complex morphological diversity in this group of predators.

Temporal comparison of pheromone gland chemical content and volatile emissions between Bactrocera tryoni and Bactrocera neohumeralis

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Abstract: Bactrocera tryoni and Bactrocera neohumeralis are closely related sibling pest species that occur sympatrically in eastern Australia. They are often distinguished morphologically by the colour of the humeral calli, which is yellow in B. tryoni and brown in B. neohumeralis. Also, they differ in their time of mating: B. tryoni mates during a small window at dusk whereas B. neohumeralis mates during the middle of the day. This difference in mating time is an important factor that contributes to the maintenance of reproductive isolation between them. During courtship, sexually mature males from both species release a volatile blend from a specialized gland located in the rectum. The content of the rectal gland secretions is complex and interspecific comparisons so far have been limited the six aliphatic amides, which constitute the major components of the blend. Recent data, however, has revealed the presence of additional compounds in rectal gland extracts in B. tryoni and it is unclear if B. neohumeralis also contains additional compounds.

The current study compares the chemical profiles of pheromone rectal gland content and volatile emissions in B. tryoni and B. neohumeralis during courtship using solid-phase microextraction followed by gas chromatography-mass spectrometry. While the six amides remain the major components in the gland in both species, we identified two compounds, ethyl isobutyrate and 2-ethyl-1-hexanol, that differ significantly in their relative proportions, and diethyl succinate, which is only present in B. tryoni. Upon identity confirmation with authentic standards and functional validation, the variations in the non-amide components of the rectal gland may represent an additional reproductive isolation mechanism in addition to the mating time difference. In addition, it could aid to the development of strategies for the regulation and control of these two pests.

Management of the Redbanded Stink Bug (Piezodorus guildinii) the Mid-Southern United States Soybean

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Abstract: The redbanded stink bug, Piezodorus guildinii (Westwood), has recently become a significant pest of soybeans in Mississippi and other southeastern United States. The first description of the redbanded stink bug originated from the Caribbean island of St. Vincent. The redbanded stink bug was first reported in the United States in the early 1970s but the time of its arrival in North America is still unclear (Panizzi.2005). As of 2016, the redbanded stink bug has been recorded in several southern states including Alabama, Florida, Louisiana, Mississippi, New Mexico, South Carolina, and Texas (Temple et al. 2013). Redbanded stink bugs are of particular concern because they appear to be much more damaging to seed than traditional species commonly found in the Mid-South. This study indicated that during severe outbreaks even the most aggressive foliar insecticide treatments at various thresholds were not enough to avoid seed quality and yield loss.

Novaluron Impacts Lygus Ovarian Development and Maturation

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Abstract: The tarnished plant bug (TPB), Lygus lineolaris (Palisot de Beauvois) (Miridae: Hemiptera) is the most economically important pest in cotton in the mid-south region. It is highly polyphagous, and the most widely distributed species of Lygus in North America. Novaluron is an insect growth regulator and chitin synthesis inhibitor, which has primarily been used for its ovicidal and larvacidal activities. Here, we examined the impacts of novaluron on TPB ovarian (telotrophic ovariole) development and maturation, including fecundity and egg hatching. Results indicate that novaluron has a detrimental effect on ovarian development and maturation as revealed from histological studies resulting in degenerated follicular epithelial cells coupled with distorted oocytes exhibiting large vacuoles in vitellogenic sites. Field exposure results showed a significant reduction in percent hatch rate and nymphs/female/day compared to TPB from non-treated fields. Laboratory studies on joint exposure of males and females or single sex exposure indicated no significant differences in fecundity compared to controls. However, significant differences in egg hatch rate were observed with least eggs hatching following joint exposure or exposure of only females. On the contrary, in the male exposure treatment, significantly more eggs hatched than in the female only or the joint exposure treatments. Thus, the effects of novaluron may be female specific. This in turn can reduce overall nymph populations in the field through sublethal effects on adult female TPB. Also, impacts vary depending on adult age at the time of exposure, but effects persist throughout the life of the adult. Taken together, our results support the application of novaluron on young TPB adult populations to disrupt ovarian development and maturation and hence its fecundity and hatchability.

Metabarcoding high elevation leaf litter arthropods in southern Appalachia - diversity and endemism

Authors: Caterino Michael, Clemson University, United States

Abstract: The highest peaks of the southern Appalachian Mountains (USA) harbor a unique and relictual spruce-fir forests that hosts many endemic species. While a handful of arthropod lineages have been examined and found to have diversified in the region, the vast majority have received only cursory study. These communities are threatened by invasive species and habitat loss through climate change. However, the dearth of information on their diversity and uniqueness provides a weak foundation for conservation management. We have undertaken thorough arthropod community inventories using a voucher-based COI plus 16S multiplexed metabarcoding approach. Results to date indicate good success rates and generally high levels of divergence among putatively conspecific populations across peaks. This suggests that levels of endemism and cryptic species richness are much higher than currently supposed.

Functional characterization of codling moth chemoreceptors

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Abstract: The codling moth Cydia pomonella is a worldwide pest of apple, pear and walnut orchards, whose sensing of chemicals plays a dominant role in its ecology, from mate-location to host selection, oviposition and larval feeding. To decipher chemical sensing of this pest insect, we have performed transcriptome analyses to identify moth chemosensory genes, including those encoding Odorant receptors and Ionotropic receptors. Using heterologous expression, in both olfactory sensory neurons of transgenic Drosophila melanogaster and in human embryonic kidney cells, together with gas chromatography, electrophysiological recordings and fluorescent imaging, we have characterized the physiological and pharmacological properties of several of these receptors, confirming that they form functional cation channels. Our findings represent an important advance in the study of chemical sensing of the codling moth towards the development of sustainable control strategies manipulating its chemosensory communication.

Functional characterization of Drosophila suzukii OR69a transcript variants unveiled response to kairomones and to a candidate pheromone

Authors: Cattaneo Alberto Maria[1] and Walker William[2], [1]Swedish University of Agricultural Sciences, Switzerland, [2]USDA-ARS, United States

Abstract: Drosophila suzukii is among the main pests of berries, to which control, application of insecticides, is challenging and it urges alternative strategies. Methods based on targeting chemical sensing and interfering with the behavior of this pest insect are promising, and is facilitated by the functional characterization of chemosensory receptors with the aim to identify novel behaviorally active ligands. Previously, we functionally characterized subunits of the OR69a locus of Drosophila melanogaster as being capable to bind both pheromones and kairomones, representing possible candidates within the genus Drosophila for broad behavioral interference control strategies based on targeting chemosensory communication. By means of heterologous expression in empty ab3A olfactory neurons of D. melanogaster together with Single Sensillum Recording (SSR), we screened three OR69a-subunits we have identified in D. suzukii with a panel of 48 ligands. In these subunits, we characterized olfactory responses to several compounds, including two possible kairomones and a possible fly-emitted volatile compound. Similarities and differences were observed in the olfactory tuning of these receptors, relative to their D. melanogaster homologues, reflecting potential evolutionary adaptations relevant to the ecology of the species.

Public perceptions of the benefits of biological control

Authors: Catton Haley, Agriculture and Agri-Food Canada, Canada

Abstract: Public perceptions of biological control are critical to the continuation of the discipline, but are dynamic, complex, and sometimes surprising. Public perceptions result from an integration of many factors beyond the general training of entomologists such as psychology, perceptions and acceptance of risk, media influences, and history. Depending on the biological control agent, region, target species, and culture of stakeholders involved, multiple publics with different values, motivations, and perceptions of risk may exist. In recent decades, scientific advances in modern biological control have been remarkable, but social aspects have lagged far behind. This talk will discuss what different publics may exist, what is known about public perceptions, and why the benefits of biological control are undervalued. Case studies and recommendations for improving public perceptions of biological control will be discussed. The biological control community must increasingly and proactively respect social aspects such as a public's values, motivations, perceptions and acceptance of risk to avoid and solve conflicts. This objective can be achieved by collaborating with social scientists, publicizing successes, improving communication, and identifying risk- and value-based disagreements for possible resolution. Only then can public perceptions of modern biological control rise to match the value of this discipline to ecology and society.

Contributions of a non-native cover crop to native parasitoids in controlling the pest wheat stem sawfly

Authors: Cavallini Laissa[1], Peterson Robert K. D. and Weaver David K, [1]Montana State University

Abstract: Wheat stem sawfly, Cephus cinctus, is a major pest of wheat, causing losses that exceed $350 million annually in North America. Two native parasitoids, Bracon cephi and B. lissogaster, suppress C. cinctus populations in wheat fields. The success of natural enemies is linked to access to supplemental food in the field, which increases their life span and benefits their reproductive parameters. To assess the benefits of supplemental nutrition to these parasitoids, we conducted greenhouse experiments with cowpea, Vigna unguiculata, as an extrafloral nectar source for parasitoids. Cages containing individual females were placed on living plants enclosing either cowpea inflorescence stalk extrafloral nectar (IS-EFN) or the leaf stipel extrafloral nectar (LS-EFN), with water as the negative control and buckwheat nectar as the positive control. Females were observed daily to assess longevity, while egg load and volume were assessed 2, 5, and 10 days after placement. Results show that IS-EFN increases longevity in both parasitoids. B. lissogaster kept constant egg load and volume, while B. cephi increased reproductive parameters with IS-EFN. Our results show cowpea IS-EFN improves our parasitoids longevity and reproductive parameters. Therefore, cowpea should be considered as a food supplement crop in conservation biocontrol programs to reduce C. cinctus populations.

Nutritional dimensions of locust research and management

Authors: Cease Arianne, Global Institute of Sustainability, Arizona State University, United States

Abstract: As transboundary migratory pests, locusts, present complex agricultural challenges that are best addressed with an interdisciplinary systems approach. During outbreak years, species like the desert locust (Schistocerca gregaria) can cause 80–100% crop losses in effected areas and cost hundreds of millions of US dollars to control. At high densities locusts switch from a solitarious to a gregarious/swarming form. Many abiotic and biotic factors affect locust population dynamics; however, macronutrient balance (e.g. protein and carbohydrates) has emerged as a potential modulator of locust phase polyphenism and outbreaks. Despite a general paradigm that terrestrial herbivores should be protein limited, we present evidence from both the field and lab, across multiple continents, that locusts prefer carbohydrate-biased diets and perform better on diets rich in carbohydrates. These results have potentially broad implications for land-management practices and their interactions with locust plagues. The Global Locust Initiative is working across boundaries and sectors to explore this space.

LIFE FOR SPECIES: Contribution by the LIFE FOR SPECIES project to the protection of threatened entomofauna in Latvia (LIFE19 GIE/LV/000857)

Authors: Cekstere Gunta[2], Telnov Dmitry[3] and Dzenis Jekabs[1], [1]Nature Conservation Agency, [2]University of Latvia, [3]University of Latvia, Institute of Biology, Latvia

Abstract: The current regulations, which determine the list of the specially protected species and micro-reserve species in Latvia, were issued several years ago. During this time, scientific information on the species occurrence and threatening factors has been gathered, as well as changes have taken place in Latvian economy. Thus the project LIFE FOR SPECIES main activities and results to protect Europe's threatened insect species in Latvia relate to: assessment of threatened insect species (for instance, beetles, dragon-flies, butterflies, etc.) based on IUCN criteria (i); development of species data sheets and Red Data Book (ii); compiling of a new list of protected species and micro-reserve species (iii); development of criteria for including threatened species in the national regulations on legally protected/micro-reserve species and a flexible system for updating the list (iv); drawing a draft legislative amendment for improving the national legislation (v); improvements of the quality and quantity of data in the National Biodiversity Data System OZOLS (vi); increase of capacity of governmental institutions, experts, stakeholder involvement and awareness of the general public (vii).

The project LIFE FOR SPECIES (LIFE19 GIE/LV/000857) is implementing by UL, NCA, LOB and DU (2020-2024) with financial support of EU LIFE program and the State Regional Development Agency.

Game of viruses: JEV is coming

Authors: Cernicchiaro Natalia, Valent Biosciences LLC, United States

Abstract: As demonstrated by the introduction of other flaviviruses (WNV, Zika) in the American continent, United States represents a region favorable for potential entry and spread of other vector-borne viruses that can potentially pose a similar risk of introduction. The objective of our study was to quantify the probability of Japanese Encephalitis Virus (JEV) introduction in the United States using qualitative and quantitative risk assessment frameworks. Of all pathways of entry considered, the probability of introduction of JEV through infected adult mosquitoes via aircraft was deemed very high. We predicted a median 95% probability that at least one infected mosquito is introduced via aircraft from JEV-affected countries, most likely from Eastern China to the US Mediterranean California and East coast, every year. Although the probability of transmission of JEV ranged from low to high, the probability of establishment was deemed negligible under current conditions. Though JEV has not established in the US, the conditions are rapidly changing, and as such newer pathways may dictate the future emergence and spread of JEV in the US. Based on our models, prevention and control plans should be placed towards vector control as well as surveillance efforts on the west and east coasts.

Inventing the Future: Understanding and developing the tools that agencies need for combating vector borne diseases

Authors: Cernicchiaro Natalia, Valent Biosciences LLC, United States

Abstract: Vector borne diseases like Dengue and Malaria have a major impact on human lives. Vaccinations are few and for more than a century the best-known defense is vector control. There used to be a time when blanketing huge areas with arsenic was effective in managing vector borne diseases but in modern times the need for environmentally rational approaches have increased. Research has shown that vector specific control is a better approach for rational use of pesticides. For example, although spot treatments using residual biological larvicide is the common approach, broadcasting liquid Bti larvicide droplets as part of an integrated vector management approach has a greater impact on the container breeding Aedes aegypti and on the diseases such as Chikungunya and Dengue that are transmitted by Ae. aegypti. This underscores the importance of working closely with public agencies in order to understand what is needed as a tool. A blanket approach that works on other insect pests is not a guarantee that it will work on all mosquitoes of disease importance. The talk will focus on new approaches that have been developed due to successful collaboration in research and development between public and private agencies in the United States.

Role of endogenized lef-4 and lef-8 nudiviral genes in Virus-Like-Particle production in the parasitoid wasp Venturia canescens

Authors: Cerqueira de Araujo Alexandra[2], Huguet Elisabeth[1], Leobold Matthieu[2], Bézier Annie[2], Musset Karine[2], Uzbekov Rustem[3], Drezen Jean-Michel[2] and Josse Thibaut[2], [1]IRBI-CNRS-University of Tours, France, [2]UMR 7261, CNRS - Université de Tours, France, [3]Université de Tours, Département des Microscopies

Abstract: Nudiviruses are large double-stranded DNA viruses related to baculoviruses that are endogenized in genomes of certain parasitic wasps. These wasp-virus associations allow the production of viral or virus-like particles that ensure wasp parasitism success within lepidopteran hosts. Venturia canescens is an ichneumonid wasp belonging to the Campopleginae subfamily that has endogenized alphanudivirus genes to produce “Virus-Like Particules” which package proteic virulence factors. The aim of this study was to determine whether alphanudivirus gene functions have been conserved following endogenization. The expression dynamics of alphanudivirus genes was monitored by a RNA-seq approach and the functional role of lef-4 and lef-8 genes predicted to encode viral RNA polymerase components was investigated by RNA interference. As described for baculovirus infections and for endogenized nudivirus genes in Braconid wasp species producing bracoviruses, a transcriptional cascade involving early and late expressed alphanudivirus genes could be observed. Lef-4 and lef-8 expression was also required for the expression of alphanudivirus late genes allowing correct particle formation. Together with previous literature, the results show that endogenization of nudiviruses in parasitoid wasps has repeatedly led to the conservation of the viral RNA polymerase function, allowing the production of viruses or viral-like particles that enable wasp parasitic success.

Chrysomelidae (leaf beetles) is the most diverse beetle family (Coleoptera) documented in Peru, a Neotropical biodiversity hotspot

Authors: Chaboo Caroline, University of Nebraska-Lincoln, United States

Abstract: Peru is known for its exceptionally high species richness, endemism, and habitat complexity, yet little is known about its beetle fauna. This presentation reviews results from a 10-year study of annual surveys using structured, semi-structured and unstructured trapping of beetles in Peru. The beetles were sorted, curated, digitized and sorted to families, then sent to beetle experts for further study and identifications. We documented 100 families, with ten new family records for Peru—Biphyllidae, Bothrideridae, Eucinetidae, Omethidae, Monotomidae, Rhipiceridae, Scirtidae, Scraptiidae, Silvanidae, and Throscidae, along with many new generic and species records. Many new genera and species have been described so far. Remarkably, Chrysomelidae (leaf beetles) is found to be the most diverse family, with 1 786 species and 278 genera, of the 100 families we document in Peru. Within Chrysomelidae, Cassidinae s. l. (leaf-mining and tortoise beetles) is documented as the most diverse subfamilies. These two findings about Chrysomelidae in Peru are counter to global diversity patterns. In the ancient and remarkably complex terrain of Peru, many factors have influenced speciation to make Peru one of the most biodiverse countries on Earth. Peru's extraordinary high plant-species richness undoubtedly also plays a role in the hyperdiversity of herbivorous insects like Chrysomelidae.

Ten International Symposia on the Chrysomelidae - a retrospective and an outlook

Authors: Chaboo Caroline[2], Schmitt Michael[1], [1]Universitaet Greifswald Allgemeine & Systematische Zoologie, Greifswald, Germany, [2]University of Nebraska-Lincoln, United States,

Abstract: The series of ten symposia dedicated to all aspects of the biology of leaf and seed beetles began in 1984 within the frame of the 17th International Congress of Entomology in Germany. David G. Furth organised the first five, nearly always jointly with local co-organisers. From 2004, Michael Schmitt organised the next five, also in co-operation with colleagues from the respective host country. From the beginning, these symposia were highly welcomed by the community of leaf beetle workers worldwide. The proceedings volumes were published originally with different publishers. Since 2008, we have compiled special volumes of ZooKeys as the series "Research on Chrysomelidae" (RoC). The symposia are not only valuable platforms of discussion and co-operation but also made the group of leaf beetle enthusiasts an intensively communicating society. From symposium no. 11 on, Caroline S. Chaboo will take responsibility for the organisation of these symposia, calling on colleagues everywhere to support, promote, and expand leaf beetle research.

Discovery of novel engineered Cry proteins to control fall armyworm

Authors: Chae Hyunsook[1], Wen Zhimou, Bramlett Matthew and Chen Jeng S, [1]Syngenta Seeds, United States

Abstract: Fall armyworm (FAW) is one of the most devastating insect pests in crop fields of the Americas and is rapidly expanding its range worldwide. Although GM traits can be an effective way to control FAW, it is very rare to find native genes that provide the necessary level of FAW control in crop fields. Protein engineering enabled us to discover novel chimeric Cry proteins devised from inactive parent sequences. Some of these chimeras show excellent efficacy against FAW from Brazil and North America. One of these shared here is IC3002. IC3002 also effectively controls Vip3A-resistant FAW and Cry1F-resistant FAW indicating the protein acts through a novel mode of action compared to these existing traits. In addition, IC3002 is efficacious against key soybean pests, Soybean looper and Velvetbean caterpillar. When IC3002 was introduced into corn and soybean, transgenic events showed strong efficacy against target pests, but no adverse plant phenotypes. This suggests that in planta expression of the gene does not compromise plant growth or reproduction but can protect plants from FAW related damage. IC3002 will be a differentiating FAW control trait that will give growers another tool to help them reduce yield loss due to the pests.

Horizontal and vertical transmission of an entomopathogenic fungus, Metarhizium anisopliae, among Bactrocera dorsalis fruit flies

Authors: Chailleux Anaïs[2], Brévault Thierry and Dosso Fatime[1], [1]- CIRAD, UPR HortSys, Centre commun ISRA-IRD, Dakar, Senegal - Biopass, Cirad-IRD-ISRA-UCAD, Dakar, [2]Senegal

Abstract: Entomovectoring is a novel pest management technique that relies on the use of insects to deliver highly targeted and continuous pest or disease control. The control of the Oriental fruit fly, Bactrocera dorsalis (Hendel) (Diptera, Tephritidae), using males of the same species as vectors of spores of the entomopathogenic fungus, Metarhizium anisopliae (Sorokin) (Hypocreales, Clavicipitaceae), is a promising avenue. However, triggering epizootics in a fly population requires high rate of transmission of the pathogen among individuals. In the present study, horizontal transmission of spores from contaminated vs. non-contaminated wild or mass-reared sterile B. dorsalis males to wild females was assessed under laboratory conditions with a focus on mating success of each male category and mortality of wild females. Additionally, a field cage experiment was conducted to assess the effect of contamination or sterility on population dynamics. Vertical transmission of fungal spores was evaluated under laboratory conditions to assess the effect of contamination on egg laying and hatching rate. Contamination and sterility by themselves did not significantly affect the mating success of males, whereas cumulated sterility and contamination of males reduced their mating success. During mating, males were able to transmit infectious doses to females leading to 34 % female mortality. Female fecundity and egg hatching were also affected by fungal contamination. These results are key to model the dynamics of a fungal epizootics within a population of B. dorsalis fruit flies so as to optimize the field implementation of the technique.

Improving pest management of field-grown tomato in Senegal: the combination of net and biological control

Authors: Chailleux Anaïs[2], CORREA Philippe[1], Deletre Emilie, Haran Julien, Diarra Bousso Ba Mame, Diakhate Massamba, Kane Modou, Ndjiliw Saliou, Simon Serge, Sylla Serigne and Brévault Thierry, [1]-CIRAD, UPR HortSys, Centre Commun ISRA-IRD, Senegal -Biopass, Cirad-IRD-ISRA-UCAD, Dakar, Senegal -UCAD-FST, ED SEV, Dakar, Senegal, [2]Senegal

Abstract: The need to produce healthier food with low impact of cropping systems on the environment implies a combination of ecologically intensive methods to effectively control pests. We investigated how net-houses can be used in combination with a generalist predator to protect tomato crops from the tomato leafminer, Tuta absoluta (Lepidoptera, Gelechiidae), and other minor pests in smallholder farmers in Senegal. Net-houses have been developed to protect tomato crops from large size arthropod pests, such as the tomato fruitworm, Helicoverpa armigera (Lepidoptera, Noctuidae). However, this technique delays crop colonization by large size pests but also natural enemies, and often favors the outbreak of some others. Field surveys were carried out to search for natural enemies and insectarium plants for the setup of augmentative biological control in tomato crops in Senegal. The indigenous predatory mirid bug, Nesidiocoris tenuis (Heteroptera: Miridae), and its insectarium plants were identified and evaluated under laboratory conditions. Then, we tested the combination of the net, the false sesame as an insectarium plant, and the predatory bug using pre-plant release in an experimental station. Pests, including the tomato leafminer, were successfully controlled and tomato yield significantly increased. These results support the upscaling of this method for the benefit of African smallholder farmers.

Impact of insecticides application in paddy fields: tendency and consequences of the parasitoid in the rice hispa (Dicladispa armigera)

Authors: Chaiwong Jintana[1], Paoteerasarn Pakorn[1] and Thanikkul Ploypirin[1], [1]Division of Rice Research and Development, Rice Department, Thailand

Abstract: Rice hispa, Dicladispa armigera (Olivier) is one of the major pests in rice that which occasionally found in rice fields. Previous studies reported the outbreak of rice hispa has cropped up in 1932, 1984, and 1998 in central Thailand including in Chachoengsao, Nakhon Pathom, Suphan Buri, and Chainat provinces but no report of further outbreaks. In 2018, outbreaks were found again in Chachoengsao, Suphan Buri, and Chainat province surprisingly. The information according to the farmers in Si Prachan District, Suphan Buri provinces referred to the continuous outbreaks by rice hispa on every crop from 2015 to till date. In this study, we conducted with the purpose to study the effect of insecticides on parasitoids of rice hispa and the data will be helpful to deal with any outbreak situations in the future. Our study was carried out in two crop seasons between September 2018 to March 2019. We randomly collected some samples of rice hispa eggs, nymphs, and pupa along with the higher number of parasites. Our findings revealed that they are mostly ingested by Trichogramma spp., parasitoid on eggs, larva parasitoid Bracon spp., and Trichomalopsis spp., parasitoid on the pupa. Interestingly, the mortality rate of rice hispa in insecticide method that is proposed to apply more than 2 times in a season had only 9.4 %. Conversely, the mortality rate of rice hispa has increased to 90.2% in the non-insecticide method and majorly ingested by Bracon spp. and Trichomalopsis spp., which are parasitoids of larva and pupa rice hispa.

Spatio-temporal evolution of egg parasitoids of the processionary moth, Thaumetopoea pityocampa (Denis & Schiffermüller 1775) (Lep, Thaumetopoeidae) in cedar and pine forests at Algeria

Authors: Chakali Gahdab, Agronomic National High School, Algeria

Abstract: The processionary moth, Thaumetopoea pityocampa is the main defoliator pest in both cedar and pine forests at northern Algeria. Worldwide this pest populations are naturally controlled by parasitoids therefore it's very important to identify and quantify the main species. Study of 604 egg batches collected from the biosphere reserve at cedars of Chrea, Djurdjura and Theniet El-Had as well as from the pine forests of the sub-humid and semi-arid areas highlighted three species of egg parasitoids: Ooencyrtus pityocampae (Mercet) (Hymenoptera, Encyrtidae), considered as polyphagous, Baryscapus servadeii (Domenichini) (Hymenoptera, Eulophidae), a specialist of the genus Thaumetopoea emerging in synchronization with their hosts oviposition patterns. These two parasitoids were found in all the prospected sites of the two bioclimatic stages. However, the third species Trichogramma embryophagum (Hartig) (Hymenoptera, Trichogrammatidae) was presented only in pure cedar forests of altitudinal areas. The extension of theses oophagous antagonists is related to the evolution of the gradation of the two processionary clades (pityocampa clade and Eastern North African clade). The analysis of the egg batches showed an average of 246 + 47 eggs per batch from cedar forests, and 142 + 40 eggs per batch from pine forests, with an average parasitism rate ranging from 6 to 16%. The parasitoids Baryscapus servadeii and Ooencyrtus pityocampea were found at varying rates of parasitism, up to 48% per egg mass in the cedar plantation, and up to 28% in pine settlements. The parasitoid Trichogramma embryophagum was collected only in cedar plantations, at a rate not exceeding 3% despite its frequency of presence in the eggs located at the both ends of the ovipositions in elongated form 4 to 6 centimeters. A strategic evolution of the parasitoids species listed and their distribution through the cedar groves and the pine forests is noted. The ecological conditions of the prospected ecotypes participate in the spatial distribution of parasitoids in their distribution areas. This result showed that these parasitoids preferred the cedar forests, which may offer the best condition for their development. The performance of these parasitoids is highly related to the altitudinal variable that has impacted the intra-interspecific competition between the egg parasitoid species. Results are discussed focusing on the evolution of the egg parasitoids populations aiming its practical use in future biological control strategies.

Challenges and Sustainability of Commercial Beekeeping and Pollination in the United States

Authors: Chakrabarti Priyadarshini[1], Sagili Ramesh[2], Breece Carolyn[2], Topitzhofer Ellen[2] and M. Lucas Hannah[2], [1]Honey Bee Lab Oregon State University, Agriculture and Life Sciences Building, Corvallis, OR, United States, [2]Oregon State University, United States

Abstract: Pests, poor nutrition and pesticides are considered primary stressors among multiple factors implicated in honey bee colony losses. Migratory beekeeper colonies encounter a variety of challenges including high density of colonies, timely monitoring and management of pests/diseases, and nutritional stress resulting from crop pollination. In the wake of significant honey bee colony losses, best management practices are becoming increasingly important. This presentation will discuss the challenges facing commercial beekeepers in the USA, and relevant research efforts to understand and address these challenges with a goal of developing appropriate best management practices for sustainable apiculture and pollination.

Understanding the nutritional landscape available to bees

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Abstract: Significant annual honey bee colony losses have been reported in the USA and across the world over the past years. Malnutrition is one among several causative factors for such declines. Optimal nutrition serves as the first line of defense against multiple stressors such as parasites/pathogens and pesticides. Given the importance of nutrition, it is imperative to understand bee nutrition holistically, identifying dietary sources that may fulfill bee nutritional needs. Pollen is the primary source of protein for bees and is critical for brood rearing and colony growth. Currently, there is significant gap in knowledge regarding the chemical and nutritional composition of pollen. Targeted sterol analysis and untargeted metabolomics were conducted on five commercially available crop pollens, three bee-collected crop pollens, three vegetable oils (often added to artificial protein supplements by beekeepers), and one commonly used artificial protein supplement. This study reports key phytosterols and metabolites present across a spectrum of bee diets, including some of the major bee-pollinated crop pollens in the western United States. Significant differences were observed in sterol concentrations among the dietary sources tested. Among all quantified sterols, the highest concentrations were observed for 24-methylenecholesterol and further, pollen samples exhibited the highest 24-methylenecholesterol among all diet sources that were tested. Also, 236 metabolites were identified across all dietary sources examined. Information gleaned from this study is crucial in understanding the nutritional landscape available to all bee pollinators and may further assist in future efforts to develop comprehensive database of nutrients and metabolites present in all bee diets.

Recent advances in understanding the impact of agriculture on pollinators

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Abstract: Research has shown that agricultural practices act as a major stress on pollinator populations, driving their declines. However, the main focus of empirical work has been on how the impact of both local and landscape level agricultural intensification impacts pollinators within farms. Here we summarize recent advances in our understanding of how agricultural intensification impacts insect pollinators and pollination in adjacent ecosystems. We will consider pollinator abundance, species diversity, health and function and identify key priorities for research.

Location, location, location: Why eyespot location matters to butterflies!

Authors: Chan Ian[1], Monteiro Antonia[1], Naing Lin[1], Lee Yueying[1] and Ching Ngan Zhe[1], [1]Department of Biological Sciences, National University of Singapore, Singapore

Abstract: Eyespots are circular “eye-like” markings on animals and can be found on the wings of numerous butterfly species. A previous comparative study of 450 nymphalid species revealed that there are markedly fewer eyespots on forewings than on hindwings, e.g. Bicyclus anynana butterflies have two forewing eyespots and seven hindwing eyespots, but the reasons for this asymmetry remain poorly understood. Through experiments involving mantis predators preying upon wildtype and Spotty variants (with two additional eyespots on the ventral forewing) of Bicyclus anynana butterflies, we demonstrate that butterflies with more forewing eyespots are attacked more often on the eyespots of both wings. We further show that these butterflies exhibit a greater amount of damage to the forewing sectors which contain eyespots, and that they are significantly disadvantaged in terms of survival and fecundity. These results suggest that having too many forewing eyespots is detrimental for butterflies. We propose that flight performance is more severely hindered when forewings, as opposed to hindwings, are damaged and butterflies would therefore benefit from placing their attack-deflecting eyespots primarily on the more expendable hindwings. These results help explain the asymmetric eyespot distribution patterns previously observed across nymphalids.

The contribution of phenolics to the antioxidant potentials of propolis from Tetragonula laeviceps and T. pegdeni with its correlation to dominant plant sources in different regions in Thailand

Authors: Chanchao Chanpen[1], Meemongkolkiat Thitipan[1], Khongkarat Phanthiwa[1], Rod-im Preecha[2] and Duangphakdee Orawan[2], [1]Chulalongkorn University, [2]Ratchaburi Campus, King Mongkut's University of Technology Thonburi

Abstract: Propolis from two dominant stingless bee species in Thailand, Tetragonula laeviceps and T. pegdeni were collected from four locations in Ratchaburi and one location in Chiangmai provinces. In each location, the dominant plants are different. Samples were extracted in methanol (MeOH) and sequentially partitioned with hexane, dichloromethane (DCM) and MeOH. All partitioned extracts were examined by three antioxidant methods [1,1-diphenyl-2-picrylhydrazyl (DPPH), 2,2'-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) and ferric reducing ability (FRAP) assays]. For DPPH assay, MeOH partitioned extract of T. laeviceps from Bankha district (MPE7) was the most active. While DCM partitioned extract of T. pegdeni from Suan phueng district (DPE2) was the most active by ABTS and FRAP assay. The DPE2 also showed the highest phenolic and flavonoid contents. The identification and quantification of twelve phenolic compounds with the highest concentration of vitexin in MPE7 and MPE5 are reported by high performance liquid chromatography (HPLC). Interestingly, kaempferol was only detected in DPE2. The different antioxidant potentials among sites are expected due to specific flora of each location. Furthermore, significant difference in this bioactivity was found between both species in the same location suggesting the different preference of flora. These results verified the potential of extracts to effectively scavenge radicals.

Carbon Nanomaterials in Drosophila suzukii (Diptera:Drosophilidae) control

Authors: Chaniotakis Nikos[2], Belenioti Maria[2] and Chaniotakis Manos[1], [1]Sole proprietorship: BioMarkerImaging, [2]University of Crete, Department of Chemistry, Laboratory of Analytical Chemistry

Abstract: Crop losses due to insect infection are one of the greatest issues to address in agriculture and food production. In order to control these kinds of pests, such as D. suzukii, farmers usually resort to the use of insecticides. Unfortunately, their efficacy is limited, while the environmental impact is devastating. Nanotechnology can provide new means for a variety of industrial activities, providing novel tools in many human activities. Nanomaterials can provide solutions for pest management in agriculture without harming the environment. There are only a few studies in which D. melanogaster is used as model species to study the toxicity of nanomaterials. Based on these preliminary results, it is proposed here that NPs could be used successfully in pest management formulation. We used different carbon nanomaterials to study their effects on larval and adult Drosophila suzukii. It is shown that dietary uptake of certain carbon nanomaterials has no detectable effect on egg to adult survivorship. However, when the adult species were exposed to the same nanomaterials through the skin via spraying, led to a total locomotor function impairment and mortality.

Development of a Scrub Typhus Diagnostic Platform Incorporating Cell-Surface Display Technology

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Abstract: Scrub typhus (ST), also known as tsutsugamushi disease and caused by rickettsia Orientia tsutsugamushi, is an underestimated fatal epidemic in the Asia-Pacific region, resulting in a million human infections each year. ST is easily misdiagnosed as a clinical diagnosis is based on non-specific skin eschar and flu-like symptoms. Thus, the lack of accurate, convenient, and low-cost detection methods for ST poses a global health threat. To address this problem, we adopted baculovirus surface-display technology to express three variants of TSA56, the major membrane antigen of O. tsutsugamushi, as well as the passenger domain of ScaC (ScaC-PD), on insect Sf21 cell surfaces rather than biosafety level 3 bacteria in an enzyme-linked immunosorbent assay (ELISA). Recombinant TSA56 and ScaC-PD were all properly expressed and displayed on Sf21 cells. This cell-based ELISA presented high accuracy (96.3%), sensitivity (98.6%), and specificity (84.6%) when tested against the ST-positive rat sera. Results using human sera were also highly consistent with the results of immunofluorescence analyses. By adopting this approach, we circumvented complex purification and refolding processes and reduced the need for expensive equipment and extensively trained operators. Thus, our system has the potential to become a widely used serological platform for diagnosing ST.

Display of acetylcholinesterase on cell surface for enzymatic analyses and pesticide detection

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Abstract: Insecticides detection in agricultural products is usually tedious and expensive. Thus, a convenient method is needed to screen for their toxicity in the fruits and vegetables. In this study, two highly toxic major pesticide groups, organophosphates (OP) and carbamates (CB), frequently used in agriculture, including the field application for killing fall armyworm, are studied. Since acetylcholinesterase (AChE) is the target of OP and CB compounds to kill insects, the detection of pesticide residues could rely on the inhibition of AChE activity by these pesticides. AChE hydrolyzes an alternative substrate, acetylthiocholine (ATCh), into thiocholine and acetic acid. Thus, AChE activity is frequently measured by the colorimetric Ellman's method, whereby thiocholine reacts with 5,5'-dithio-bis-2-nitrobenzoic acid (DTNB, Ellman's reagent) to yield yellow 5-thio-2-nitrobenzoate (TNB), which can be observed by the naked eye or be measured at 412 nm. This colorimetric method is especially important for the rapid detection of OP and CB pesticides in agricultural products, as the presence of such pesticides will inhibit the enzyme activity and eliminate the yellow coloring. In this study, we have developed a novel cell surface display technology by insect baculovirus expression system to efficiently express acetylcholinesterase on insect cell membrane in 96-well plates for the detection of OP and CB pesticide residue with high efficiency. This measure should help for the safe application of pesticides to control insect pests including fall armyworm.

Bioflows through migration hotspots are dominated by hoverflies (Diptera: Syrphidae): uncovering key genetic/physiological adaptations and orientation strategies

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Abstract: Insect migrants number in the trillions and carry out vital ecological roles. Understanding their migration routes, seasonal patterns of abundance and associated orientation behaviours remains a formidable task, but is necessary if we are to understand the contribution these organisms make when moving between distant ecosystems. Our studies utilise migration hotspots: geographic sites that occupy major flyways and provide topological funnelling to concentrate huge numbers of active migrants. Our research takes a comparative approach, identifying differences in migratory assemblages and numbers across multiple sites spanning Western to Eastern Europe. Using traditional techniques of trapping, counts and transects, together with high-resolution imaging, we provide evidence for huge seasonal bioflows that are dominated by Diptera, numbers of which may reach >10 million / day through a single funnel point. To uncover the orientation strategies of the most abundant of these Diptera, the hoverflies, we have developed a flight simulator based on magnetic tethering and computer vision algorithms to automatically record responses to various cues. We find evidence for strong orientation behaviour due south, but only when the sun is visible, additionally, this behaviour is maintained under time-shift conditions. Finally, using a range of genomic techniques, we have identified differentially expressed transcripts between migrant and non-migrant forms of the marmalade hoverfly, together with a fully sequenced genome these have allowed us to begin to uncover the pathways involved in long-distance migration.

Individual tracking reveals consistent headings in migrating hawkmoths

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Abstract: In comparison to vertebrates, the migratory pathways of insects and behaviour en route are relatively poorly understood. While individual tracking can allow for insects to be monitored during migration, this technique is rarely applied, primarily due to most insect species being too small to carry radio-transmitters. Here we present the first study to individually track nocturnal migrating insects, to identify migratory routes and understand factors affecting flight behaviour. Using a Cessna 172 aeroplane, we tracked individual hawkmoths (Acherontia atropos, Sphingidae), fitted with 0.25 g radio-transmitters. During tracking, all moths maintained consistent headings, which persisted across days in some individuals. However, there was variation in headings among individuals and between animals from different origins. Analysis of high-resolution wind data determined that moths maintained seasonally-adaptive headings regardless of wind direction, indicating that they compensated for wind drift en route.

Migratory routes of the invasive fall armyworm in eastern Asia

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Abstract: The fall armyworm (FAW), an invasive pest from the Americas, is rapidly spreading through the Old World, and has recently invaded the Indochinese Peninsula, China and Korea. In the Americas, FAW migrates from winter-breeding areas in the south into summer-breeding areas throughout North America where it is a major pest of corn. Asian populations are also likely to evolve migrations into the corn-producing regions of eastern China, where they will pose a serious threat to food security. To evaluate the invasion risk in East Asia, the potential routes and mechanisms by which FAW moved from Africa into India, Indochina and then into China was modelled by a trajectory simulation approach, combined with flight behaviour and meteorological data. Our results reveal that (i) FAW could potentially have reached India and Indochina by natural migration from Africa with the help of Somali Jet, which is characterized by persistent, high-speed winds over the Arabian Sea, southern Asia, and the Bay of Bengal; (ii) that FAW will annually expand from its new year-round breeding regions in the Indochinese Peninsula and southern China into the two main corn-producing regions of eastern China (North China and Northeast China) by July, via separate eastern and western migration pathways involving the northward movement of four generations; and (iii) there is a high risk that FAW will invade Japan and Korea in the summer monsoon season in June and July. Information on migration pathways and timings can be used to inform integrated pest management strategies for this emerging pest.

Radar observations of the seasonal migration of the oriental armyworm moth, Mythimna separata, and other insects

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Abstract: The migrations of the oriental armyworm moth, Mythimna separata (Walker), and other insects over the Bohai Sea were observed by entomological scanning radar at a site on Changdao Island in the center of the sea. Aerial samples of the insect migrants were collected using a searchlight trap, thus long-distance and across sea movement of M.separata populations in the surrounding regions could be detected and well studied using data from the entomological scanning radar, a standardized light trap network, field surveys, atmospheric trajectory simulations and a next-generation meso-scale numerical weather prediction system. Our main results were summarized as follows. Seasonal migrations of M.separata moths over Beihuang from May to October in 2003 to 2017 governed by wind streams exhibited three main migratory stages: 9 May to 28 June, 28 June to 17 August, and 17 August to 6 October, which were consistent with the results of ovarian dissection. Northward migration of M.separata moths usually started in early May and persisted until mid-August, then the migration pattern shifted and southward migration (i.e., return migration) occurred during late August to October. It is also suggested that the migration of M.separata performed a closed loop between the central and eastern China and the northeastern China, and the Changdao Island was distinctive on its vital pathway. Furthermore, displacement speed and direction of insect targets were measured to obtain individuals' flight heading and speed. Abiotic meteorological cues adjusting the long-distance migratory movement were also identified incorporating with the combination approaches of the numerical weather simulation and the entomological scanning radar. Furthermore, the seasonally aerial migration fluxes of M.separata population and other insects flying over the island were estimated to explore their adaptive strategies to atmospheric features in migration arena.

Epitope specific conditional discrimination of FREPs expression in An. stephensi

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Abstract: Hemocytes are the blood cells of mosquitoes' circulatory system, which imparts a selective immune response against various micro-organsims/pathogens. Among diverse members of PRR family, FREPs have been recognized as key modulator of cellular immune responses, however, their physiological relavance has not been investigated in detail. A comprehensive In-silico analysis of 24 putative FREPs from Anopheles stephensi, predicts a common evolutionary relationship across blood feeding mosquitoes and Drosophila. Finding of at least seven putative transcripts in our hemocyte RNAseq data in response to Plasmodium vivax prompted us to access their potential immune-physiological responses. AsFREPs showed a highly selective response of individual FREPs against blood meal, exogenous bacterial challenge and Plasmodum vivax infection. Our study revealed relatively high affinity of FREP13 and another FREP towards gram negative bacteria and P.vivax infection respectively. Functional knock down assay reveals that FREP13 is not only involved in regulation of TEP1 mediated immune response but also modulate microbiota during blood feeding which may indirectly work against plasmodium infection.

Molecular mechanism for metabolic adaptation to muscle hypoxia during flight in migratory locusts

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Abstract: Animals indigenous to very high altitudes have evolved a distinctive suite of physiological traits to cope with the environmental hypoxia. We have used Tibetan migratory locusts as an ideal model to study the physiological and molecular mechanisms of insects for hypoxia adaptation. We previously demonstrated that modulation of mitochondrial respiration in flight muscle contributes to adaptation of Tibetan locusts to hypoxia (Zhang et al. 2012 Proc. R. Soc. B.). Transcriptome analysis revealed the different molecular pathways enriched in aerobic metabolisms between Tibetan and lowland locusts under hypoxia (Zhao et al. 2013 BMC Genome). We further performed whole-Genome genetic analysis and functional studies and found that the Tibetan locusts regulate the hypoxia-induced metabolic adaptation through mediating the activity of insulin signaling pathway (Ding et al. 2018 Nat. Commun.). Here, in this report, we show that one hypoxia-inducible factor (HIF) is mutated in the Tibetan locusts. The mutation endows them with long flight capacity under hypoxia. Our findings provide novel insight into the evolution of metabolic adaptation to muscle hypoxia during flight in insects.

Systematic and taxonomic study of the egg parasitoid family Scelionidae in China

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Abstract: Species of the family Scelionidae are important egg parasitoids of 9 orders of insects and spiders. Many species have been successfully used as biological agents against insect pests in agriculture and forestry. Due to its large number of species, host diversity and specificity, Scelionidae may serve as an ideal group for testing the adaptive evolution of host use and the mechanism of host finding. However, the Chinese fauna of Scelionidae taxonomically remains a large void in our knowledge. In addition, the interrelationships within the family are largely unclear, which in turn have impeded research on how these wasps have adapted to different hosts. My project aims to thoroughly revise the Chinese fauna of Scelionidae, including their taxonomy, distribution, host range, biology, and phylogenetic hypotheses and adaptive evolution patterns of host use across multiple hierarchical levels in the family. We are hoping to provide scientific basics for further biological study of these wasps and their implications in pest biological control as well as baseline data for biodiversity conservation in China.

Biocontrol characteristics of the fruit fly pupal parasitoid Trichopria drosophilae (Hymenoptera: Diapriidae) emerging from different hosts.

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Abstract: Trichopria drosophilae (Hymenoptera: Diapriidae) is an important pupal endoparasitoid of Drosophila melanogaster Meigen (Diptera: Drosophilidae) and some other fruit fly species, such as D. suzukii, a very important invasive and economic pest. Studies of T. drosophilae suggest that this could be a good biological control agent for fruit fly pests. In this research, we compared the parasitic characteristics of T. drosophilae reared in D. melanogaster (TD m) with those reared in D. hydei (TD h). TD h had a larger size than TD m . The number of maximum mature eggs of a female TD h was 133.6 ± 6.9, compared with the significantly lower value of 104.8 ± 11.4 for TD m . Mated TD h female wasp continuously produced female offspring up to 6 days after mating, compared with only 3 days for TD m . In addition, the offspring female ratio of TD h, i.e., 82.32%, was significantly higher than that of TD m, i.e., 61.37%. Under starvation treatment, TD h survived longer than TD m. TD h also survived longer than TD m at high temperatures, such as 37 °C, although they both survived well at low temperatures, such as 18 °C and 4 °C. Old-age TD h females maintained a high parasitism rate and offspring female ratio, while they were declined in old-age TD m . Overall, TD h had an advantage in terms of body size, fecundity, stress resistance ability and the parasitism rate compared with TD m . Therefore, T. drosophilae from D. hydei could improve biocontrol efficacy with enormous economic benefits in the field, especially in the control of many frugivorous Drosophilidae species worldwide.

Larval secretions of two Drosophila endoparasitoids with distinct infection strategies.

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Abstract: Parasitic wasps are exceedingly diverse and the most successful group of biological control agents. Successful parasitization and development of wasps depend not only on diverse parasitic strategies but also on their diverse parasitic factors, including venom, polydnavirus (PDVs), and teratocytes. However, for the wasps with venom only, there may exist some novel parasitic factors, like larval secretions, to regulate host development and immunity, as well as manipulate host nutrition. Leptopilina boulardi and Leptopilina heterotoma, two species of Drosophila larval-pupal endoparasitoids, which have two distinct infection strategies: L. boulardi evades host immune response, and L. heterotoma breaks host immune response. Therefore, these two wasp larvae might secret different immune related proteins. Here, we dissected the larvae of two parasitic wasps from the hosts, cultured them in vitro and collected their larval secretions. We used mass spectrometry to sequence peptides of the secretory proteins and then mapped the peptide spectral data against the larval transcriptomes to identify putative genes for each group. In total, we obtained 948 and 168 larval secretory proteins from L. boulardi and L. heterotoma, respectively. The protein numbers of L. boulardi were much higher than L. heterotoma, which indicated that the L. boulardi needed more proteins to evade host immune response. The present study greatly contributes to the understanding of the biological diversity of larval secreted proteins which have been seldom reported, and is helpful to study the regulation of secretions into host to facilitate the development of wasp larvae.

The developmental transcriptome of Trichopria drosophilae (Hymenoptera: Diapriidae) and insights into cuticular protein genes

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Abstract: The pupal endoparasitoid wasp Trichopria drosophilae (Hymenoptera: Diapriidae) plays an important role in biological control of many frugivorous fruit fly species including Drosophila suzukii, a well-known invasive pest. Here, we report the transcriptomes of T. drosophilae among different developmental stages. A total of 601,148,438 high-quality reads were obtained and de novo assembled into 187,704 unigenes with an average length of 1096 bp. Among them, 21,735 unigenes were annotated into 52 Gene Ontology terms and 36,898 were assigned to 25 Cluster of Orthologous Groups categories, whereas 30,585 unigenes were mapped to 270 Kyoto Encyclopedia of Genes and Genomes different pathways. Numbers of differentially expressed genes were found through comparisons between different developmental stages. We further identified 137 cuticular protein genes (CPs) from T. drosophilae transcriptome, including 59 from CPR family, 2 from Tweedle family, 1 from CPF family, 46 from CPAP family, and 29 from other CP families. We analyzed expression patterns of the CPs at different developmental stages of T. drosophilae, and found some stage-specific CPs. Quantitative real-time PCR results confirmed RNA sequencing findings based on the relative expression levels of eight randomly selected CPs. This study provides a valuable transcriptomic resource for a comprehensive understanding of the development and physiology of T. drosophilae, and will help to improve their parasitism efficiency for biological control purposes.

The impact of cover crops on the predatory mite Anystis baccarum (Acari, Anystidae) and the leafhopper pest Empoasca onukii (Hemiptera, Cicadellidae) in a tea plantation

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Abstract: BACKGROUND: Empoasca onukii, the tea green leafhopper, is a key pest of tea, whose control often requires the extensive use of insecticides. As a predator of the tea green leafhopper, the mite, Anystis baccarum, is a potential biological control agent worldwide, though little is known about how intercropping cover crops can impact its suppressing effect on E. onukii. Therefore, we conducted a field experiment to investigate how the relationship of the abundance of the predatory mite and its leafhopper prey is influenced by different two cover crops and a manually weeded inter-row treatment as a contrast to naturally growing vegetation in a tea plantation in China.

RESULTS: The abundance of A. baccarum was signi?cantly higher in tea canopies of intercropped treatments than in canopies over natural ground cover. Litter samples showed higher abundances of A. baccarum when tea was intercropped with Paspalum notatum than with natural ground cover, in the first year of treatment. The abundance of E. onukii in tea canopies was higher over the bare ground treatment in the first year but the opposite was observed in the second year.

CONCLUSIONS: Results suggest that the abundance of A. baccarum in a tea plantation is influenced by intercropping and it can affect its leafhopper prey, albeit, with varying levels of suppression. For informing biological control and suppression of pests, long term experiments are needed to investigate the interactions of both pest and predator with cover crop treatments.

WAKE mediates Drosophila male-male courtship activity through insulin-like signaling pathway

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Abstract: WAKE is highly important to neurological functions in Drosophila, implicated in circadian and sleep maintenance and it is an essential regulator in asymmetric cell division (ACD) of neuroprecursor cells in developmental stage. In this study, we evidenced WAKE deficits in insulin producing cells (IPCs) that prompts inter-male courtship underlie insulin/insulin-like growth factor signaling (IIS) pathway. This is an interesting discover but how IIS induced male to male courtship needs further study.

Large-scale annotation and evolution analysis of microRNAs in insects

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Abstract: MicroRNAs are small no-coding RNAs with crucial biological functions. Accumulation of miRNAs is believed to contribute significantly to the increase in morphology complexity of animal evolution. Insects have been through at least two round of morphological innovations during the evolution. However, the question how miRNAs evolved in insects and how miRNA evolution related to these important evolution events such as the appearance of wing and metamorphosis in insect remains elusive. To address these issues, we annotated miRNAs from 152 arthropod genomes (including 132 insects represent major evolutionary clades of Insecta) using homologous searching and de novo method. We obtained 15680 miRNA genes and 489 miRNA families. By adding the presence and absence of miRNA families to a phylogenetic tree constructed by protein-coding genes, we use Dollo parsimony model to reconstruct the gain and loss of miRNA in insect evolution. Our result showed that the common ancestor of insects shared 64 conserved miRNA families. After derived from Apterygota ancestor, winged-insect gained 5 miRNAs at the stem of Pterygota and 3 at the stem of Neoptera. After that, miRNA evolution became quiescent with no miRNA gained at the clades of Polyneoptera and Paraneoptera, and only one gain and loss at Endopterygota. In Endopterygota, we show two independent rounds of miRNA innovations occurred at the stem of Hymenoptera and Lepidoptera. Meanwhile, we show an extensive loss of conserved miRNAs in paraneoptera (especially Coccidae) and twisted-wing insect (Strepsiptera), which concur with the morphological simplification in these clades. Our result suggests the gain and loss of miRNAs is consistent with the morphological evolution of insects, and provide new insight into the miRNA evolution in insects.

Species and phylogenetic diversity within the tribe Alysiini (Hymenoptera, Braconidae, Alysiinae) from China

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Abstract: Hymenoptera are one of the four hyperdiverse orders of holometabolan insects, in which more than 90% species are Apocrita. However, the research on species richness and phylogenetic diversity in the Parasitoid hymenoptera are largely unknown. The tribe Alysiini belonging to the order Hymenopetra, are known as koinobiont endoparasitoids of larval cyclorrhaphous Diptera, which play an important role in the biological control. Here, we systematically assessed the taxon biodiversity in the parasitoids, Alysiini using both morphological and molecular data across the China for the first time. We found distinct 26 genera, additional seven subgenera and 98 new species in the tribe Alysiini (with one new genera and one new subgenera) from total 2400 specimens. Moreover, we present the first phylogenetic hypothesis for these tribe and species richness by the whole mitochondrial genome and barcoding sequencing respectively, combined with morphological matrix. We found that the species in Alysiini are phylogenetically diverse and closely related parasitoids use main host taxon. Various Bayesian inferences using different data partitions and phylogenetic methods recovered similar phylogenetic trees with strong statistical support for almost all nodes. Our results demonstrated the general pattern that most genera of Alysiini are much diverse in the humid, shady habitat like Yunnan, Hainan province (especially new species are often found in these area) or mountainous regions like Zhejiang and Sichuan province. Such patterns are strongly coincided with the distribution of host use and habitat. We supported that the species richness is related with host habitat, together with morphological traits and genetic heterogeneity, highlighting the important influence of host-association, evolutionary constraints and environmental phenology on the diversification in the tribe Alysiini.

The flightin gene is necessary for the emission of vibrational signals in the rice brown planthopper (Nilaparvata lugens St?l)

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Abstract: In duet-based courtship, species- and sex-specific vibrational signals enable animals to identify the species and sex of the singer and also provide the necessary information to locate a partner. Substrate-borne communication has been described in a wide variety of insects. Here, we focused on the gene necessary for the emission of male vibrational signals and whether male songs fulfil such functional roles in mating systems in the brown planthopper (BPH, Nilaparvata lugens). We generated mute BPH adult males by RNA interference of the flightin gene, which encodes a myosin-binding protein expressed exclusively in the dorsal longitudinal muscle (DLM) in the basal two abdominal segments for driving vibration of the male-specific tymbal structure in short-winged (brachypterous) BPH adults. Transmission electron microscopy observation showed that flightin knockdown disrupted the normal sarcomere structure of abdominal DLM. No courtship song could be detected in the brachypterous males after RNAi of flightin. Behavior and competition trials showed that the lack of male courtship songs prolonged copulation latency and even caused female rejection. Unexpectedly, the mute males exhibited greater competitiveness when competing against normal males.

Male homosexual mating behaviors in Bactrocera dorsalis

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Abstract: The variety and ubiquity of same-sex courtship, pair bonding and copulation have been observed in a wide range of species, and it is always a puzzle to interpret the reason to such behavior. Many hypotheses have been proposed to explain the persistence of same-sex sexual behavior, some hypotheses have hold, but others haven't explained this particular phenomenon. In our study, the sex pheromone identification hypothesis was verified by us in Bactrocera dorsalis. As the case in Drosophila, cis-vaccenyl acetate (cVA) and 7-tricosene (7-T) have roles in mediating male-male mating behavior in B.dorsalis, as cVA increase the frequency of male-male mating behaviors at low concentrations, and 7-T could significantly reduce male-male mating frequency. Then we used genetic approaches to investigate the consequence of odorant receptor manipulation on male-male mating behaviors. And the results showed six odorant receptors (BdorOr2d, BdorOr2e, BdorOr7, BdorOr13b, BdorOr2a, BdorOr10) play roles in mediating male-male mating behavior in B.dorsalis. Further, studies confirmed that BdorOr2d, BdorOr2e, BdorOr7, BdorOr13b could participate in regulating male-male mating behavior as cVA recognition receptors, and BdorOr2a, BdorOr10 are important recognition receptors for 7-T. As the results indicated that one of the reasons for male-male mating behaviors could be that the sex pheromone cannot be correctly identified. This study described the existence of same-sex sexual mating behavior in B.dorsalis for the first time, and the results in this study could providelines of evidence and information to utilize sex pheromone and their odorant receptors to manipulate male-male mating behavior of B.dorsalis to accomplish green, sustainable and specific pest control.

Insecticide exposure alters epigenetic modifications in the Colorado potato beetle, Leptinotarsa decemlineata

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Abstract: Although it is widely assumed that insects eventually evolve resistance to commonly used insecticides, the evolutionary processes underlying insecticide resistance remain poorly understood. Insecticide resistance seems to arise in response to the frequency and intensity of insecticide exposure, suggesting insecticide exposure itself may increase the rate of mutation or cause heritable physiological changes in pest organisms. Environmental stress has been shown to influence epigenetic modifications such as DNA methylation, which can be heritable across generations. We studied if changes in DNA methylation may be associated with the evolution of insecticide resistance. Using a whole genome bisulfite resequencing study, we tested how insecticide exposure influenced patterns of DNA methylation in the Colorado potato beetle, a widely adaptable beetle. We exposed third instar larvae to treatments that varied in toxicity (water, LC50 dose of imidacloprid, LC10 dose of imidacloprid, and a LC¬10 dose of a modified imidacloprid compound). After dosing them, we reared beetles to adult we tested how the treatments influenced % DNA methylation and patterns of differential methylation in the parent and F2 generation. All beetles exposed to imidacloprid showed significantly lower levels of % of CpG methylation, which was significant in the F¬2 generation but not the parent generation. We found differential levels of methylation across over 100k sites, but 221 differentially methylated sites exceeded the more conservative cut-off. Although the majority of the 221 differentially methylated sites fell in genomic regions that were not annotated, a few annotated genes were differentially methylated.

Biological and chemical control of coconut rhinoceros beetle (Oryctes rhinoceros), a recent invasive pest on Oahu, Hawaii.

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Abstract: Coconut rhinoceros beetle (CRB, Oryctes rhinoceros) is a large scarab beetle native to Southeast Asia and a serious pest of palm species, most notably coconut and oil palms. CRB adults damage palms, particularly younger ones, by boring into the center of the crown, where they injure the young, growing tissues and feed on the sap. Adult CRBs were found at the Honolulu International Airport and the adjacent Joint Base Pearl Harbor-Hickam (JBPHH) on Oahu in December 2013. Further examination revealed CRB larvae in mulch at JBPHH, representing the first time a breeding population of CRB had been confirmed in Hawaii. CRB has been identified by USDA Animal and Plant Health Inspection Service (APHIS) as one of the most damaging invasive insect pests of coconut and other palm species whose introduction could result in significant economic losses to commercial coconut and palm nurseries, and Hawaii's residents and tourists who appreciate palm trees for their aesthetic and cultural values. Since then, USDA APHIS, in collaboration with Hawaii Department of Agriculture (HDOA), University of Hawaii at Manoa, Hawaii Invasive Species Council, and other entities, launched the CRB eradication program, the largest invasive species eradication program in Hawaii's history. This presentation reports our latest research updates on biological and chemical control of CRB. Due to the strict regulations on importing biological control agents into Hawaii set by HDOA, our approach for biological control research is to collect locally occurring entomopathogenic fungi and nematodes, and then screen them for effective strains in both lab assays and field trials. We collected over 60 entomopathogenic fungal strains and over 20 entomopathogenic nematode strains from various landscape sites on Oahu. Based on our multiple lab assays, we identified 6 Metarhizium strains that caused > 70% mortality of CRB larvae. A small-scale field trial with 3 most effective Metarhizium strains resulted in > 40% mortality of CRB larvae in field condition. Larger scale field trials will be conducted as soon as permission from HDOA is obtained. For chemical control, we focus on low-risk systemic insecticides. Based on our multiple lab assays, we identified that acephate and imidacloprid were very effective, causing 40% paralysis of CRB adults within 4 hours, 50% mortality of CRB adults within one day, and 100% mortality of CRB adults within three days. Based on these lab assay results, we conducted a field trial with 125 coconut palms for 2 years. Field trial results did not yield significant difference among treatments, but resulted in an area-wide reduction of CRB population indicated by the decreased number of CRB adults caught by traps. Most up-to-date research results will be presented at 2022 ICE.

Functional morphology of Trichadenotecnum male and female genitalia analyzed using µCT (Insecta: Psocodea: Psocomorpha)

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Abstract: Although the great genital diversity of the barklouse genus Trichadenotecnum has been described in previous studies, the specific function of the genital structures during the copulation process has received less investigative attention. We reconstructed the 3D models of each structure and muscle of the male and female genitalia of T. incognitum in copula and those of uncopulated male and female of T. pseudomedium. By comparing the changes in male and female genital structures and related muscles in copulated and uncopulated states, the function of each genital structure can be described. During the Trichadenotecnum copulation process, we found that the female subgenital plate was hooked into the male body by the distal process on the male paraproct and was fixed by the male epiproct, hypandrium and phallosome. In addition, the presence of sexually antagonistic coevolution was suggested by tightly contacting structures, i.e., thorny male hypandrium and female gonopore plate. These results not only give us a new understanding of the copulating process of Trichadenotecnum but also explain the reasons why each genital structure is extremely diversified in the genus.

Survival and Behavior of Melanotus communis (Coleoptera: Elateridae) in Florida Sugarcane Soils

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Abstract: Wireworms (Coleoptera: Elateridae) are major economic pests of Florida sugarcane (Saccharum spp. hybrid). The corn wireworm, Melanotus communis (Gyllenhal), is the most important wireworm pest of Florida sugarcane occurring in both sandy and muck soils. The objective of this study was to determine survivability, preference, and dispersal of wireworms in sandy and muck soils. There was no significant difference in starved wireworm survival between the soils after 2 mo. However, the starved wireworms gained more weight in muck soil than sand. Wireworms dispersed at similar rates towards oat baits in both soil types. Interestingly, in free choice tests, wireworms showed a high preference to reside in muck versus sandy soil which corresponds to the greater wireworm weight change found in muck versus sandy soil. The high preference for muck and greater weight gain in muck found in this study partially explains why M. communis is more abundant in muck soils than sandy soils in Florida sugarcane.

Assessing the contribution of the bacterial symbiont Rickettsia to the salivary functions of the sweet potato whitefly Bemisia tabaci

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Abstract: Now ranked among the top 100 most damaging invasive pests worldwide, the sweet potato whitefly, Bemisia tabaci MEAM1 is a generalist insect capable of feeding on and transmitting viruses to numerous high-value crops. Development of effective and sustainable whitefly control methods requires a fundamental understanding of the molecular mechanisms underlying host plant exploitation and feeding behaviors necessary for virus transmission, which we currently lack for B. tabaci MEAM1 and other globally important whitefly species. Sufficient nutrient ingestion, and transmission of many plant viruses depend on aphids, whiteflies, and related hemipterans engaging in prolonged uptake of plant sap from the phloem. Studies on aphids demonstrate that this process is made possible by delivery of effector proteins into the plant during bouts of salivation that precede sap ingestion. Salivary effector proteins suppress plant defenses and phloem occlusion to enable prolonged sap uptake by the vector, during which virus acquisition can occur. However, effector discovery and functional validation has only been carried out for a handful of hemipteran organisms. As new insect effectors are being discovered, we are also learning that bacterial symbionts can have profound effects on saliva content and activity. For example, proteins from an obligate symbiont of aphids can enter saliva and subsequently modify plant defenses and aphid performance. Considering that most hemipterans, including whiteflies, are host to a suite of obligate and facultative vertically-transmitted bacterial symbionts, it is essential to consider symbiont contributions to the salivary proteome. We present a work that uses a combined transcriptomic and proteomic approach to characterize the contributions of the whitefly host and a key facultative symbiont that enhances whitefly fitness, to saliva composition and function of two B. tabaci MEAM1 populations that share >98% similarity in nuclear genomes, but differ in the presence of Rickettsia.

Age-stage, two-sex life table: important basis for achieving successful biological control programs

Authors: Chi Hsin, National Chung Hsing University, Taiwan

Abstract: The age-stage, two-sex life table incorporates the age-stage structure of a population and the male individuals - two critical parameters that are missing in female-based life tables. It is an important tool for population ecology studies and pest management programs. Because both the predation rate and the vulnerability of prey vary with the stage, and male predators and the male pests are components of the predator-prey system, it is obvious that using the age-stage, two-sex life table is vital to understanding the intricacies involved in planning successful biological control programs.

Comparative demography and mass rearing of Aedes aegypti fed on live mice versus pig blood using a novel perforated feeder

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Abstract: A novel thermal-constant blood-feeder covered with a perforated film and using pig blood was developed for rearing Aedes aegypti (L.) (Diptera: Culicidae). The perforated film was used as a substitute for the membrane or parafilm that is normally used in conventional blood-feeders to prevent the mosquitoes from directly contacting the blood. The efficiency of this perforated blood feeder was assessed by using live mice and comparing the engorgement rate of female mosquitoes and their demographic parameters. In a no-choice test, no significant differences were observed in the engorgement rates and fecundity between females fed on perforated feeders containing pig blood and those fed on live mice. In a three-minute-long free-choice test, the accumulated engorgement rate was significantly higher in mosquitoes feeding on the perforated feeders than in those feeding on live mice. The demographic characteristics indicated that mosquitoes fed on the perforated feeder containing pig blood had a higher immature survival rate and prolonged adult male and female longevity. Although a lower intrinsic rate of increase and lower finite rate of increase were observed when female adults fed on the perforated feeder, computer projection of the population growth was comparable using both blood sources. Mass-rearing analysis showed that the perforated blood feeder was much more cost-effective than using live mice. These results demonstrate that the perforated blood feeder containing pig blood is more effective and cost efficient than using live mice for maintaining and mass rearing of mosquitoes in the laboratory.

Differential life-history responses in Neolema abbreviata, a biological control agent for Tradescantia fluminensis under water and nitrogen gradients

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Abstract: Due to their sessile nature, plants inexorably endure both transient and chronic environmental stressors with subsequent impact on their interactions with other trophic groups. Water and nitrogen variability are key abiotic factors mediating the interaction between plants and insect herbivores. For insects used in classical biological control of plants, such factors may determine extent of herbivory, population dynamics and ultimately field establishment and persistence. We conducted a full factorial experiment to determine the impact of water and fertiliser variability on the performance of Neolema abbreviata (Lacordaire) (Coleoptera: Chrysomelidae) and its host plant Tradescantia fluminensis Vell (Commelinaceae). Water and fertiliser variability strongly influenced T. fluminensis biomass accumulation and foliar nitrogen content. These changes in host plant quality resulted in preferential oviposition selection by the beetles with optimally irrigated plants that received moderate fertilizer being most favoured. Larval performance, in terms of weight gain and time to pupation, was highest in this treatment providing support for the preference–performance hypothesis. There were similarities in feeding performance and subsequent performance among plant treatments between larvae and adults suggesting uniform nutritional quality requirements between the life-stages. Overall, our study reveals differential effects of paired abiotic stressors and performance among herbivorous insects with both juvenile and adult feeding life-stages. The study, therefore, calls for multi-trait and factor evaluation to understand the impact of plant quality on insect life history traits. Our findings

Olfactometer bioassays help defining ecological host range of a candidate biocontrol agent of Halyomorpha halys

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Abstract: In agriculture, management of invasive arthropod species involves multiple strategies, including the introduction and release of exotic natural enemies, e.g., parasitoids. However, a risk assessment must be preliminarily conducted to evaluate possible non-target effects on local biodiversity of the introduced natural enemy after its establishment. For egg parasitoids, location of target and non-target hosts is firstly determined by effective responses towards odours emitted by plants as a consequence of herbivore attack (synomones), and/or by the different host instars (kairomones). Hence, evaluation of host-associated odour attractiveness during pre-release risk assessment can be crucial for determining the likelihood of parasitoid interaction with non-target species in open field conditions. In a quarantine laboratory, using Y-tube olfactometer bioassays, we investigated the ability of the Asian egg parasitoid Trissolcus mitsukurii (Ashmead) (Hymenoptera: Scelionidae) to exploit odours associated with the coevolved invasive pest Halyomorpha halys Stål (Hemiptera Pentatomidae) and with non-target stink bugs native to Southern Europe. Our results demonstrated attraction of T. mitsukurii towards plants exposed to feeding and egg deposition by H. halys and by the native pest Nezara viridula L., but not towards physogastric females or eggs alone. Noteworthy, T. mitsukurii was not attracted to the other non-target species tested and was repelled by plants bearing eggs of the beneficial predator Arma custos F. These laboratory studies contribute to a deeper understanding of the potential non-target risks of T. mitsukurii as a potential biocontrol agent, alternative to Trissolcus japonicus (Ashmead), against H. halys.

Side effects of some insecticides on two Halyomorpha halys egg parasitoids, Trissolcus japonicus and Trissolcus mitsukurii

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Abstract: Halyomorpha halys is an invasive species native to eastern Asia accidentally introduced to America and Europe, causing severe damage in agriculture.

The egg parasitoid Trissolcus japonicus is the main natural enemy of H. halys in Asia, and adventive populations were discovered recently in USA and Europe. In Italy a second Asian egg parasitoid, Trissolcus mitsukurii, was detected parasitizing egg masses of H. halys. Both parasitoid species appear to be widely distributed in northern Italy. In Italy, the possibility for the application of a classical biological control program is currently being debated. A management approach involving the use of biological control in specialized crop cultures entails the need to determine the sensitivity of the parasitoids to commonly used agrochemicals and measure their persistence of these pesticides at levels harmful to the natural enemies over time.

Females and males of T. japonicus and T. mitsukurii used in our studies were obtained from lab-reared colonies using H. halys eggs as host. T. japonicus originated from the USDA Beijing colony, while T. mitsukurii was field collected in northern Italy. The insecticides whose selectivity was assessed in semi-field trials included Coragen (rynaxypyr; 0,2 ml/L), Steward (indoxacarb; 0,17 g/L), Delegate (spinetoram; 0,26 g/L) and Karate zeon 1.5 (lambda-cyhalothrin; 0,2 ml/L). An untreated control was added to the insecticide tests. The products were applied in the field on apple trees (Fuji variety) with a portable sprayer and the treated shoots were collected at three successive dates: T+0, T+5 and T+8 days after the treatment. The shoots were brought to the laboratory and placed in plastic cages. Ten females (3 replicates) were added to each cage, provided with honey, and incubated in a thermostatic cell (26±1 °C; 65% RH; 16:8 h light/dark).

Parasitoid mortality was assessed at 24 and 48 h (apparently insecticide-affected specimens were categorized as dead). The mortality values were transformed with the Schneider-Orelli formula to obtain the correct mortality rate. Results showed a low mortality of T. japonicus in the control that was always = 10%. On the same day of field application of the insecticides (T+0), Coragen and Steward showed good selectivity towards female T. japonicus, with a mortality rate of three and zero percent respectively. After 48 h of exposure, Coragen was confirmed to be quite selective, while Steward mortality increased significantly (87%). Similar results were observed when field-treated shoots were exposed to parasitoids after 5 or 8 days from treatment (T+5 and T+8). Karate Zeon and Delegate were shown to not be selective for T. japonicus from the start at T+0, with a mortality of 53 and 100% respectively. At T+5 and T+8 Delegate activity remained almost constant at high levels, while the toxicity of Karate Zeon tended to decrease over time. The same trends were observed for treated T. mitsukurii females and for males of both species.

Forensically Important Acari Associated with Rabbit Carcasses Placed at Four Different Ecoregions in Malaysia

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Abstract: Recent development in forensic acarology has raised the interest of researchers on the importance of Acari in death investigations. The understanding of how ecoregion differences could affect mites' diversity and abundance is important as they are useful as forensic indicators to detect location of death as well as minimum post-mortem interval (mPMI). Therefore, the aim of this study was to determine the diversity and abundance of forensically important mites at four different ecoregions in Malaysia. Three rabbit carcasses (n = 3) were placed at each different locality namely forest, highland, village, and oil palm plantation. One hundred gram of soil samples were collected from beneath and around the decomposing carcasses every three days until the carcasses reached the skeletonization stage (i.e., 40 days). The soils were then placed in the Berlese-Tullgren funnel for the extraction of mites and proceeded with slide mounting for family identification. The ambient temperature and the amount of precipitation for each location were recorded. The abundance of mites in the forest was significantly higher than the other study sites ($P < 0.05$) with the mean abundance of 7.47 ±7.52. Mites recovered from the highland (5.30 ±8.58) and oil palm plantation (4.23 ±5.49) were significantly higher than those from the village (1.92, ±3.52). The most abundant family of mites of forensic importance in the forest was Macrochelidae; Histiostomatidae on the highland, and Acaridae for both village and oil palm plantation. The soils samples collected from beneath and around the carcasses contain significantly more mites than those in the control soil ($P<0.05$). The introduction of carrion to the soil ecosystem has caused significant changes in the diversity and abundance of mites and further study is therefore needed to validate these changes as geographical and mPMI indicators in forensic investigations.

Temperature affects the wings area melanization of Idea leuconoe clara.

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Abstract: Idea leuconoe clara, the large tree nymph, is known for its presence in Southeast Asia butterfly gardens because of its large wingspan and black and white colour contrast. The distribution of black spots and the degree of coarseness and melanization of the wings are usually adopted for species identification. Patterns of latitudinal and teperature variation in the phenotype or genotype of a butterfly may lead the wings of the same butterfly to have different coloration. There are several records of the melanized I. leuconoe in literature and specimens collections from Taiwan and Southeast Asia. To test the effects of the development temperature on melanization of the wings of I. leuconoe, we reared 600 larvae under six constant temperatures (15- 40 °C) and found only two melanized adults (67-80% of wings area) under 35 °C and 40 °C; The mortality is 99% under these two high temperature treatments. We further characterized heat/cold-shock-treatments on 100 individuals during their wandering stage for 12 days. In response to the 10 °C cold treatment, the degree of melanization of the wings was 59-69% (2 melanized adults); on the other hand, in response to the 35 °C treatment melanization of the wings was 66-75% (4 melanized adults), and in response to the lethal 40 °C could reach up to 79-82% (5 melanized adults). In wandering stage heat-shock treatment, 9 individuals were melanized, the melanization rate was raised to 12% because of extreme temperatures and the mortality rate of I. leuconoe was reduced to 33%. We conclude that wing colour patterns to extreme temperature treatments results from a combined effect worked precisely on wandering, early pupal stage. These mechanisms might have been exploited in the colour-pattern of I. leuconoe to prevent individuals from some specific rearing conditions like wet and hot season.

Monitoring of Auchenorrhyncha species known or potential vectors for phytoplasma, in grapevine from Romania

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Abstract: The viticulture is one of the most important agroecosystems in Romania covering about 190 thousand hectares. The phytoplasmoses diseases and their associated insect vectors are a group of phytosanitary risk factors that increasingly threaten the grapevine agroecosystem. The aim of this work was to evaluate the presence and abundance of the Auchenorrhyncha species known in the literature as confirmed or potential vectors for the grapevine phytoplasmas. The survey was conducted from 2016 to 2018 in eighty vine plots located in vineyards from four viticulture regions, Banat, Crișana and Maramureș (Western Romania) and Moldova (Eastern Romania). The insects were monitored using yellow sticky traps of 30x20cm, which were replaced at two weeks interval, from June to October. A total of 38903 specimens belonging to twenty-one species confirmed or potential vectors for grapevine phytoplasmas were collected. The most abundant species was the leafhopper Scaphoideus titanus, the principal natural vector of the Flavescence doree phytoplasma in European grapevine, representing 46.9% of all captured insects. Other species with considerable abundance were Neoaliturus fenestratus (14.5%), Fieberiela florii (11.6%) and Reptalus quinqecostatus (6.5%) associated with Stolbur phytoplasma. For each species, the main ecological indices, abundance, dominance, constancy and indices of ecological signification were calculated.

Are insects sentient?

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Abstract: Nobel laureate Karl von Frisch famously claimed that bees not only do not feel pain, but in fact lack basic nociception. There would have been enough evidence even 50 years ago to debunk this myth, but we now know that most if not all animals have nociceptors, mechanoreceptors specialised for damaging or at least potentially damaging stimuli. The question of whether bees (and other animals) subjectively experience suffering is formally impossible to answer, hence we need to reason by common sense, probability and analogy to other animals. Using the same criteria as for other animals such as lobsters and fish, my team explores whether bees have the subjective experience of pain. We have also in the past discovered a positive emotion-like state in bees. These experiments as well as those by other teams working on emotions in insects indicate that, by the same criteria as those used for vertebrate animals, bees must be counted as sentient animals.

How bees use scanning behaviour for visual pattern recognition

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Abstract: Bumblebees have remarkable visual learning capacities and are a simple model for understanding visual processing in a miniature network. The mechanisms underlying bee visual discrimination are still poorly understood. Biederman's theory on human visual object recognition suggests that objects can be described by a combination of their simple components. Global visual perception in humans may be derived by eye saccades moving between local features. Accordingly, critical questions in bee vision are whether and how bees process localised elemental information within stimuli to generate a global perception. Here, we explore insights from Biederman's theory studying which visual features (vertices or edges) may be important for bees in the visual recognition and which strategy they may use to infer a holistic perception. After training bumblebees to discriminate a square and a triangle, bees were tested to identify triangles and squares with deletion of vertices or edges. We show that bees can still recognise these visual stimuli without either vertices or edges. Given the conditioned stimuli, different bees have distinctive preferences in using edges or vertices for pattern recognition. Using 3D video tracking, we discover that bees only scan the bottom of the presented shapes and focus on the left side of stimuli, which was also found in other sensory modalities in vertebrates. Our results suggest that bumblebees perceive the natural environment via local features as humans do. They then integrate these features to produce a global perception by flying between these elemental features. Additionnally, our results have been modelled into a virtual arena, which allow us to have a better understanding of the bee flight behaviour during a visual experiment.

The Mind of the Bee

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Abstract: Bees have a diverse instinctual repertoire that exceeds in complexity that of most vertebrates. This repertoire allows the social organisation of such feats as the construction of precisely hexagonal honeycombs, an exact climate control system inside their home, the provision of the hive with commodities that must be harvested over a large territory (nectar, pollen, resin, and water), as well as a symbolic communication system that allows them to inform hive members about the location of these commodities. However, the richness of bees' instincts has traditionally been contrasted with the notion that bees' small brains allow little behavioural flexibility and learning behaviour. This view has been entirely overturned in recent years, when it was discovered that bees display abilities such as counting, attention, simple tool use, learning by observation and metacognition (knowing their own knowledge). Thus, some scholars now discuss the possibility of consciousness-like phenomena in the bees. These observations raise the obvious question of how such capacities may be implemented at a neuronal level in the miniature brains of insects. We need to understand the neural circuits, not just the size of brain regions, which underlie these feats. Neural network analyses show that cognitive features found in insects, such as numerosity, attention and categorisation-like processes, may require only very limited neuron numbers. Using computational models of the bees' visual system, we explore whether seemingly advanced cognitive capacities might 'pop out' of the properties of relatively basic neural processes in the insect brain's visual processing area, and their connection with the mushroom bodies, higher order learning centres in the brains of insects.

Using drones to track bees

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Abstract: Insect telemetry involves the use of tracking technology to understand invertebrate movement and behaviour. Current techniques either rely on a battery powered tag which may impact the flight behaviour of the insect, or a lighter, passive tag used in tandem with a harmonic radar dish which has a tracking range of approximately 500m. Here we show how a piezoelectric tag used in conjunction with an antennae array carried by a drone can be used to track bees at a landscape scale. Through the use of the drone, it becomes possible to track bees over much greater distances compared to existing tracking techniques at a fraction of the cost. We present preliminary results using a prototype of the antennae array to track bees and discuss future applications of this novel tracking technology.

What can harmonic radar tracking reveal about the mating flights of honeybee drones and queens?

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Abstract: Honeybees (Apis mellifera) are arguably a domesticated species, with considerable economic and cultural importance, and have been kept for thousands of years. Nonetheless, there is much about their mating behavior that remains mysterious, since they mate in flight, away from the hive, making observation extremely difficult. Male honeybees (drones) gather in large numbers in areas known as Drone Congregation Areas (DCAs), presumably for the purposes of mating, and DCA locations are thought to persist for many years. Most of what is known about drone movements and DCAs comes from sampling drones approaching pheromone lures or tethered queens, which could potentially alter their behavior and does not allow tracking of individual flight paths. Virgin queen honeybees mate during short nuptial flights, but little is known about the structure or destination of these flights, or even whether mating takes place at DCAs, as commonly presumed. We used harmonic radar technology to track the flight paths of individual drones and virgin queens in an agricultural landscape, allowing us to examine for the first time the movements of individual bees in search of a mate. After attaching a lightweight transponder to the thorax of a bee, we scan across 360 degrees, locating the bee's position every 3 seconds. Using a dataset of hundreds of drone flights, collected over three years, we demonstrate that multiple drones converged on the same locations, even in the absence of pheromone lures and that these DCAs persisted over at least two years. Since no individual drones live overwinter, this demonstrates that the locations at which DCAs form must be defined by the landscape and that individual drones, from different hive locations, are capable of converging on the same spot. We will present findings on the structure of the orientation flights of drones and virgin queens and show how the flight paths of drones change with experience as they frequent DCAs. Finally, we ask whether the spatial structure of drone flights can provide any insight into where DCAs form and what features of the landscape bees use to locate them.

Genome-wide analysis of T. absoluta populations across South America

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Abstract: Tuta absoluta's recent expansion across South America currently represents a serious threat to the tomato agriculture industry. Massive pesticide use is the predominant method of control, and as a result, strong selective pressures have led to resistance development in populations of Tuta absoluta to various insecticides. In order to determine whether resistance developed in one population is likely to be genetically dispersed to other populations, it is necessary to first understand the population structure of Tuta absoluta. Previous analyses relied on microsatellite or mitochondrial sequences, which may lack power to discern distinct populations. Toward this end, we have sequenced whole genomes of 55 Tuta absoluta moths collected from sites across South America, as well as a collection site in Spain, to identify the populations in which gene flow is likely occurring. Analysis suggests the presence of three South American clusters which are clearly separated based on geography and genetic distance, although there is evidence of migration events between clusters. In addition, we conclude that the Spanish populations likely arose from a single population in Chile, confirming previous reports. In the future, this data can be used to inform growers on the best insecticides to use on their crops.

Molecular diagnostic assay to distinguish Tuta absoluta, Phthorimaea operculella, and Keiferia lycopersicella

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Abstract: In the past 15 years, the tomato pest Tuta absoluta has transformed from a regional pest of South America to a worldwide threat to tomato production. With current reports of Tuta absoluta presence across Europe, Africa, and sectors of Asia, there is a growing need to improve monitoring efforts in the United States to prevent introduction of this pest. A major challenge is the presence of morphologically similar moths Phthorimaea operculella and Keiferia lycopersicella, which prey on the same host plants as Tuta absoluta. Currently, identification requires dissection of adult moths, which can be labor intensive and requires a well-preserved intact specimen. This makes identification of Tuta absoluta presence in field traps difficult, especially when traps are left out for extended amounts of time. To tackle this, we used published draft genomes of the three species to identify two distinguishing loci, and developed a multiplexed quantitative PCR assay that can identify each species in a single reaction based on fluorescence from tagged oligonucleotide probes. This assay can reliably identify the three species with as little as 16 picograms of genomic DNA input. We tested sensitivity in an environmental collection setting by spiking local insect bycatch from traps with Tuta absoluta DNA; in all cases Tuta absoluta was positively identified. We expect this diagnostic to aid in monitoring and eradication efforts by allowing detection even when intact specimens are unavailable.

Risk-dependent brood parasitism by the predatory mite Neoseiulus californicus

Authors: Choh Yasuyuki[1], Janssen Arne[2], [1]Chiba University, Japan, [2]University of Amsterdam, Netherlands

Abstract: Two predatory mite species Neoseiulus califronicus and Gynaeseius liturivorus cooccur on the same plant individuals in crop fields, where they feed on the same prey species such as larvae of western flower thrips. In turn, the thrips prey on the predator eggs. In addition, the two mite species are reciprocal intraguild predators, attacking each other's juveniles. Although N. californicus is a stronger intraguild predator, eggs of both species are observed at the same oviposition sites such as leaf veins and hairs. Adult female G. liturivorus are known to reduce the predation risk of their eggs by thrips larvae by guarding their eggs. As a consequence, eggs of N. californicus close by guarded eggs of G. liturivorus might also be protected against attacks by thrips larvae. We therefore tested whether adult female N. californicus preferred ovipositing at sites where G. liturivorus had oviposited. N. californicus preferred laying eggs at oviposition sites with G. liturivorus eggs over sites without eggs but not at sites with eggs of conspecifics or another predatory mite species (Phytoseiulus persimilis) in the presence of thrips larvae. Moreover, such a preference was not found in the presence of two-spotted spider mites instead of thrips larvae as a food source. Although adult female N. californicus did not protect their eggs against thrips larvae, their eggs survived better from thrips larvae in the presence of G. liturivorus and its eggs. These results show that N. californicus reduces the predation risk of their eggs by ovipositing close to G. liturivorus eggs.

Classification of Culex pipiens complex using geometric morphometric

Authors: Choi Kwang Shik, Jeon Jiseung

Abstract: Traditionally, the D/V ratio of male genitalia and ommatidial number have been used to identify the Culex pipiens complex. However, it is difficult to identify the complex species due to morphological similarity. In this study, geometric morphometric (GM) was applied to the wings of Culex pipiens molestus and Culex pipiens pallens in the complex to supplement the traditional classification method before the molecular diagnostics step. Female mosquitoes were collected from nine regions in ROK between July and September 2021, and Cx. p. molestus and Cx. p. pallens were identified using the molecular markers. In addition, as an outgroup for comparison, Aedes albopictus was additionally collected and compared with Culex pipiens complex. As a result of morphometric analysis of Culex pipiens complex and Ae. albopictus, the morphological difference of the wings was revealed clearly. It was also shown that Cx. p. molestus and Cx. p. pallens, which are closely related to each other, were clearly separated. Therefore, it is expected that GM would be able to apply to various mosquito species that have difficulties in morphological classification.

Diagnostics development and species distribution of Culex pipiens complex in the Republic of Korea

Authors: Choi Kwang Shik, Ryu Jihun

Abstract: Culex pipiens complex, which is the most common in the urban area, has not yet caused a disease in the Republic of Korea (ROK) although Culex pipiens molestus and Culex pipiens pallens in the complex in ROK are known to have the vector competence. However, it is difficult to distinguish morphological differences between Culex pipiens complex species in ROK. Therefore, in this study, we collected from a total of 48 sites near residential areas in ROK, designed species-specific primers for the species, and analyzed the distribution of the Culex pipiens complex species. As a result, Cx. p. molestus and Cx. p. pallens were collected together in all of the study regions except Ullengdo where the number of collected samples were small (5 samples). Among the total of 1,063 individuals, 70.1% of the samples were Cx. p. molestus and 29.9% were Cx. p. pallens. Since there has been no research of these species distributions in ROK so far, the results of this study would be used as important data for the Culex pipiens complex research.

Receptor interference (Receptor-i) using small peptides to control the fire ant and slug

Authors: Choi Man-yeon[2], Vander Meer Robert[2] and Ahn Seung-Joon[1], [1]Mississippi State University, [2]USDA-ARS, United States,

Abstract: Insect pest management (IPM) is critical to prevent crop and livestock losses by Arthropod pests directly and indirectly by diseases vectored through arthropods, and to improve sustainable food production and security. Discovery of new insecticides has always been a goal in IPM, but it is a long iterative process with high risks and low chance of success. To discover potential insecticidal candidates screening is a critically important procedure. Insect G-protein coupled receptors (GPCRs) as a target for new specific class of pesticides holds great potential because GPCRs are involved in almost all physiological processes. We developed a novel GPCR-based screening method using a GPCR of neuropeptides, and successfully screened small bioactive peptides to be evaluated as control agents to manage populations of the fire ant and slug pest. Our research results provide an insight in the evolutional process with the neuropeptides and their receptors in the animal system. We also explore the feasibility and implementation of the novel screen technology for application to major economic pests.

First report of Pheromermis vesparum parasitic on Korean Vespa mandarinia

Authors: Choi Moon Bo[1], Kwon Ohseok[2] and Kim Seo Hyun[1], [1]Department of Plant Protection and Quarantine, College of Agriculture and Life S, [2]Kyungpook National University, South Korea

Abstract: We present this first report of an individual of the Mermithidae which was identified on V. mandarinia workers caught in a wasp trap in the Jirisan National Park in July 2021. This nematode was found to be parasitic on the abdomen of V. mandarinia, and because identification by appearance was impossible it was identified using molecular biology methods. A phylogenetic study based on sequencing of the 18S ribosomal RNA gene identified this nematode as Pheromermis vesparum. This is the first report of this species from Korea. In future research, we aim to analyze the frequency of their occurrence and host specificity to facilitate their use as a natural enemy for the biological control of V. mandarinia.

Foraging behavior of an invasive alien hornet (Vespa velutina) at Apis mellifera hives in Korea: foraging duration, attack attempts, and success rate

Authors: Choi Moonbo[1], Kwon Ohseok[1], [1]Kyungpook National University, South Korea

Abstract: The introduction of an invasive alien hornet (Vespa velutina) to Korea in 2003 has caused severe economic impacts on the beekeeping industry. We observed this hornet attacking honeybees at hives to develop control and management approaches for the species. We recorded duration of foraging attacks, number of attack attempts, and success rate from July to October, compared V. velutina attacks with those of a native wasp (V. simillima), and compared foraging behavior on a rainy day and a sunny day. The foraging success rate was 84.2% overall but exceeded 97% in September. V. velutina was a more efficient predator than V. simillima, with shorter attacks but a higher success rate. The data showed that local honeybees have not yet developed adequate defense mechanisms against predation by this new invasive species.

Temporal trend of species richness of macromoths across three southern mountains of South Korea

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Abstract: The purpose of the study was to track the changes in species richness of macromoths in mixed deciduous and coniferous forests during the last decade. Macromoths were collected from 2003 to 2019 at 27 sites on three mountains in southern South Korea: 11 sites of Mt. Hallasan (HL, maximum height 1,950m), 11 sites of Mt. Jirisan (JR, maximum height 1,915 m), and five sites of Mt. Seungdalsan (SD, maximum height 333m). Ultraviolet light traps (22 Watt and 12 volts) were employed to collect moths from May to October and the collected samples were identified to the species level, if possible. We questioned that (1) Have moth communities in the Korean mountains been declined in the last decade?, (2) If moth communities have been declined, which taxonomic group and elevation zone were severely affected?, and (3) What factors were showing the higher correlation with the declining moth communities? We will show the trend of change in species richness and the causal factors of the change of moths in three mountain areas of southern South Korea.

Occurrence of Tomato Russet Mites, Aculops lycopersici Massee (Acari: Eriophyidae) in a Greenhouse and Selection of an Eco-friendly Organic Insecticide

Authors: Choi YongSeok, Bioenvironmental Division, Chungnam Agricultural Research and Extension Services, South Korea

Abstract: The first occurrence of the tomato russet mite, Aculops lycopersici Massee was in mid-late April, and the maximum occurrence was in mid-late June in 2013 and 2014. However, in 2015, the density of tomato russet mites increased in July. This pattern is thought to be attributed to temperature fluctuations, in which, low temperatures at night promoted their reproduction and long periods of high temperatures during the day promoted their dispersion. Comparison of the use of 11 Eco-friendly organic insecticides (EOIs) showed that, the mortality rates after application of 0.6% matrin(EOIMa) and 10% clove oil (EOICo) were 92.1% and 95.1%, respectively, when administered at 500-fold diluted concentrations. At 1,000-fold and 2,000-fold diluted concentrations, the mortality rates of EOIMa were 90.4% and 88.2%, respectively. In a field test, the mortality rates of EOIMa at the 1,000-fold diluted concentration and of EOICo at the 500-fold diluted concentration were 91.5% and 93.9%, respectively. In conclusion, theses two EOIs are sufficient to replace pesticides, and EOIMa seems to be particularly useful as a prophylactic given that it induced a mortality rate of 88.2% at a 2,000-fold diluted concentration.

Acute and residual toxicities of chordotonal organ modulator insecticides against two aphid species

Authors: Chong Juang, Clemson University Pee Dee Research & Education Center, South Carolina, United States

Abstract: Sucking insects, such as aphids and whiteflies, are major pests of ornamental plants grown in glasshouses and outdoor nurseries. Sucking pest management on ornamental plants have traditionally relied on neonicotinoids. As neonicotinoids face increased scrutiny due to their detrimental effects on pollinators, growers are replacing neonicotinoids with other chemistries, such as the chordotonal organ modulators, which include afidopyropen, pymetrozine and pyrifluquinazon (IRAC Group 9), and flonicamid (IRAC Group 29). No concerted efforts have been undertaken to compare the acute and residual efficacy of the four compounds. This study include 2 glasshouse and laboratory experiments to compare the acute and residual efficacy of afidopyropen (Ventigra), pymetrozine (Endeavor), pyrifluquinazon (Rycar) and flonicamid (Aria) against the potato aphid (Macrosiphum euphorbiae) and the chrysanthemum aphid (Macrosiphoniella sanborni). The products were applied to roses (for the potato aphid) and chrysanthemums (for the chrysanthemum aphid) at the lowest and highest label rates registered in the United States. In the first (acute toxicity) experiment, leaves infested with aphids were detached from plants grown in a greenhouse and dipped in insecticidal solutions. The leaves were then air-dried, and maintained in Petri dishes with the leaf petioles inserted into a cup of water through a hole drilled at the bottom of the Petri dishes (henceforth to be referred to as the observational arenas). The dipped aphid cohorts were monitored in the laboratory over 7 days to record mortality and population growth. Results suggested that afidopyropen resulted in the fastest reduction in the population of both aphid species, but all products achieved complete elimination of the aphid cohorts within 7 days. Application rates did not appear to influence of speed by which the aphid cohorts were eliminated. In the second (residual toxicity) experiment, the insecticides were sprayed to potted plants maintained in glasshouses. The aphid population on randomly selected leaves were recorded at 1, 3, 5, 7, 14, 21 and 28 days after treatment (Experiment 2A). One leaf was collected from each plant at 1, 3, 5, 7, 14, 21 and 28 days after treatment, and 10 adult aphids were introduced onto each leaf. The leaves were kept in the observational arenas, and monitored for 9 days after introduction (Experiment 2B). In Experiment 2A, both aphid species were eliminated from the treated plants (of all products and rates) within 7 days of introduction. The populations of both aphid species begin to rebound within 21 days of treatment, regardless of products and application rates. In Experiment 2B, introduced adult aphids were not killed by the residue on the leaves and continued to produce offspring. The offspring, however, die as soon as they began to feed on the leaves. This study generated recommendations on product selection and reapplication interval that can be utilized by growers.

RNA-Based biocontrols: the bio-delivery challenges

Authors: Christiaens Olivier[1], Lacombe Ruben[1], Coorevits Arnout[1], Dehertogh Astrid[1], Dewulf Nathalie[1], Begheyn Myriam[1] and Cappelle Kaat[2], [1]Syngenta Crop Protection LLC, [2]Syngenta Ghent Innovation Center, Belgium

Abstract: For most insect pest species tested so far, it has proven difficult to achieve a commercially relevant activity level using an insecticidal RNA-based biocontrol. Multiple loss mechanisms have been described, including external factors, such as the environment and feeding behavior, and internal factors related to the physiology of the insect. Generally, differences in RNAi efficiency are described only qualitatively, as it is not straightforward to obtain exact numbers and compare between different delivery methods, feeding behaviors etc.

In this work, the differences were quantified more precisely to increase our understanding of physiology-related loss mechanisms. Four species from diverse orders were selected for 1) being candidate targets for an RNA-based biocontrol product, and 2) showing a varying degree of RNAi efficiency. Using both injection and feeding delivery methods, lethal dose and lethal time were accurately specified and linked to the precise amount taken up using a feeding tracker. In addition, the QuantiGene Plex method, routinely used to quantify dsRNA expression levels in GM plants, was adapted to detect dsRNA in the insect body. A similar robust quantification method was developed to compare degradation rates in the insects' hemolymph and gut. Putting all this data together increased our understanding of the limitations of exploiting RNAi in these commercially relevant pests, and revealed some interesting discrepancies between RNAi efficiency and known loss mechanisms.

Defensive responses of rice cultivars resistant to Cnaphalocrocis medinalis (Lepidoptera: Crambidae)

Authors: Chuang Wen-Po[1], Liao Chung-Ta[2] and Guo Tzu-Wei[1], [1]National Taiwan University, Taiwan, [2]Taichung District Agricultural Research and Extension Station, COA, Taiwan

Abstract: Cnaphalocrocis medinalis (Guenée) (Lepidoptera: Crambidae) is an economically important pest of rice, Oryza sativa L. (Poaceae), throughout Asia, where damage caused by larvae, particularly during grain-filling stages, significantly increases yield losses. There is, therefore, a pressing need to develop cultivars that are resistant to C. medinalis. In this study, we assessed growth and mortality of first and third instar C. medinalis larvae fed on six rice cultivars that had previously been identified as resistant to the pest, and we quantified production of defense enzymes in plants exposed to herbivory. We found that mortality rates were highest in larvae fed on the resistant cultivars Baiqiaowan, Sasanishiki, Qingliu, and Kasalasu, while relative growth rates were lower for larvae fed on Baiqiaowan and Qingliu. Higher levels of phenylalanine ammonia lyase were expressed in the resistant cultivars. Qingliu plants exposed to herbivory by C. medinalis produced higher levels of jasmonyl isoleucine and salicylic acid (SA) than plants of the susceptible cultivar TN1, and levels of SA in Qingliu plants were intrinsically higher prior to feeding by C. medinalis.

Benefit of drought on a herbivore of herbaceous plants: Does drought create enemy free space and reduce competition?

Authors: Chuang Wen-Po[2], Lin Po-An[3], Felton Gary W.[1], Sun Cheng-Han[2], Liu Chia-Ming[4], Ho Chuan-Kai[2], Ou Jia-Ang[2] and Kinoshita Natsuko[5], [1]Department of Entomology Pennsylvania State University University Park, PA, United States, [2]National Taiwan University, Taiwan, [3]Pennsylvania State University, United States, [4]University of Tsukuba, Japan

Abstract: Drought stress is known to benefit insect herbivores in some instances; however, the mechanisms that lead to these benefits remain debated. To understand the impact of drought on quality of host plant and the interactions of insect herbivore with the arthropod community associated with host plant, we conducted a manipulative field study using a specialist herbivore Pieris rapae, and its host plant, Rorippa indica, in two populations. The results revealed that moderate water deficit increased the survival of P. rapae on R. indica, which was associated with reduced abundance of other herbivores and natural enemies. Water deficit increased the resistance of R. indica to most herbivores indicating by the reduced abundance in field and decreased relative growth rate of herbivore when fed with drought stressed R. indica. However, the performance of P. rapae larvae were not affected by changes in quality of R. indica, suggesting ability to utilize host plant with different quality. Our findings suggested beneficial impacts of drought to certain specialist herbivores, and in contrast, detrimental to most other herbivores. The present study provides insight to how drought may benefit insect herbivores and the importance of interactions among arthropods associated with plant in determining the impact of drought on insect herbivores.

The role of transmission dynamics mathematical models in guiding malaria vector control policy

Authors: Churcher Thomas, Imperial College London, United Kingdom

Abstract: The use of vector control to control malaria is complicated. There is no silver bullet to kill mosquitoes and different interventions will need to be layered together to adequately control the disease. Malaria is currently primarily controlled using long-lasting insecticidal nets and indoor residual spraying of insecticide though the rise of insecticide resistant mosquitoes and a proliferation of new bednets and alternative technologies means that it is very unclear how best to control the disease. The optimum and most cost-effective mix of interventions will vary from setting to setting according to its unique epidemiology and mosquito population. This complexity means that transmission dynamics mathematical models parameterised on entomological data are increasingly being used to guide decision making. The statisticians George Box and Norman Draper wrote that “All models are wrong; the practical question is how wrong do they have to be to not be useful”. This session will take a sober look at current evidence for the use of these models in guiding vector control policy and implementation. It will investigate in what situations they should be used and discus what needs to be done to make sure results are not overly interpreted.

TaxonWorks-powered Orthoptera Species File (OSF): An integrated web-based workbench for orthopterists

Authors: Cigliano Maria, Museo de La Plata, CEPAVE-CONICET, Argentina

Abstract: The Orthoptera Species File (OSF, http://orthoptera.speciesfile.org/) is the most up to date and complete taxonomic database of the world’s Orthoptera (grasshoppers, locusts, katydids, crickets), both living and fossil. Nowadays, the classification of Orthoptera shown in OSF is used worldwide as the general reference for the group. The field of cybertaxonomy represents the confluence of traditional taxonomic goals with new ones, powered by the full potential of digital technology, information science, and computer engineering. An introduction to TaxonWorks (http://taxonworks.org), the new platform that integrates the best features of Species File software with new ones will be presented. TaxonWorks is an integrated web-based workbench for taxonomists and biodiversity scientists. It is designed to capture, organize, and enrich data, share and refine it with collaborators, and package it for analysis and publication. This new platform, constituted by a collection of open source tools and services that cover all aspects of the taxonomic workflow will help to maximize the efficiency of taxonomic work allowing the exchange of data among the orthopterists’ community and helping to expand and enhance our knowledge of Orthoptera. The potential of using OSF for integrating many of the most recent cybertaxonomic tools will be discussed. The presentation will explore the status of OSF within TaxonWorks as it stands now, discussing the new features developed that will be used to add, explore, retrieve, and download data from OSF.

Symbiotic bacteria affect the clearance rate of a plant pathogen from its insect host

Authors: Civitello Dave[1] and Gerardo Nicole[1], [1]Emory University, United States

Abstract: Many insects form intimate, long-term associations, known as symbioses, with select microbes. Symbionts influence the ecological functions and evolution of insects, allowing them to exploit unique resources and occupy otherwise inaccessible niches. Work in several insect systems has shown that, in addition to direct benefits on host fitness, bacterial symbioses can affect the establishment and transmission of insect-vectored pathogens. The squash bug Anasa tristis is an agriculturally important pest of plants in the family Cucurbitaceae and a known vector of Serratia marcescens, the causative agent of Cucurbit Yellow Vine Disease (CYVD). Burkholderia species bacteria have a symbiotic relationship with A. tristis, significantly accelerating their development and increasing their survival. Furthermore, certain Burkholderia strains have been shown to suppress the growth of S. marcescens in vivo. We hypothesized that association with Burkholderia affects the establishment of S. marcescens in squash bugs. To test this, we reared insects aposymbiotically and with different Burkholderia isolates, infected them with a phytopathogenic strain of S. marcescens, then sampled them periodically to assess pathogen clearance. We observed variation in clearance rates among Burkholderia isolates, but by and large, squash bugs harboring Burkholderia cleared S. marcescens significantly faster than their aposymbiotic counterparts. Work in this system furthers our current understanding of how symbionts affect the vectoring of pathogens. We hope to leverage these results to design novel and effective vector control for this system.

Adaptation of diapause induction cue enables range expansion of a biological control agent across latitude

Authors: Clark Eliza[2], Stahlke Amanda[3], Bean Dan[1], Bitume Ellyn[4] and Hohenlohe Paul[3], [1]Colorado Department of Agriculture, United States, [2]Colorado State University, United States, [3]University of Idaho, United States, [4]USDA Forest Service, Hawaii, United States

Abstract:

Background

Eco-evolutionary theory predicts that species undergoing range expansions will evolve due to spatial sorting, genetic drift or selection in small edge populations, and adaptation to novel environments. For diapausing species, adapting to environmental cues that indicate seasonal change and vary across the range is crucial. Phenological mismatches in diapause timing can reduce the number of generations per year and reduce establishment. The northern tamarisk leaf beetle (Diorhabda carinulata), biological control agent for the invasive plant Tamarix spp. in the United States, originally failed to establish in southern latitudes due to mistimed diapause in response to shorter summer daylengths. In the past decade, however, the beetle has rapidly expanded its range to these areas without the aid of humans. This range expansion is uniquely situated to study the impacts of local adaptation during range expansions across heterogeneous environments.

Methods

Adaptation to daylength across latitude has been shown in D. carinulata at a population level. Here, we define a new trait, days until diapause at one daylength, to study adaptation to daylength at an individual level. We measured the heritability of days until diapause in one northern population in both home and away environments using a paternal half-sibling breeding design. To study adaptation to daylength across the entire range of D. carinulata, we measured days until diapause in both northern and southern environments for females from eight populations collected at varying latitudes.

Results

We found that days until diapause was highly heritable for the population in its home environment and not significantly heritable in a novel environment. When we compared populations across the range, we found significant differences between the diapause behaviors of northern core beetles and southern edge beetles in each environment. Northern populations in the northern environment took multiple days to enter diapause with lots of phenotypic variance, while northern populations in the southern environment entered diapause quickly with little phenotypic variance. Similarly, southern beetles in the southern environment took multiple days to enter diapause with lots of phenotypic variance, but most southern beetles in the northern environments did not ever enter diapause.

Conclusions

Heritability of days until diapause indicates that adaptive evolution of this trait is possible, but only when populations are near their home environment, indicating that the range expansion must proceed slowly enough that genetic variation on which selection can act is maintained. The number of days to diapause has evolved in populations across the range to better match the summer daylengths at their latitudes. These results can be used in conjunction with genomic studies on individuals to better predict the rate of range expansion and inform research on ecological factors important to range expansions.

DNA metabarcoding vs. Morphotaxomy methodologies to identify Arthropods and Non-Arthropods for biomonitoring of European rivers

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Abstract: The present study has been developed under the Biowat kit_E!11892 project, which aims to validate a novel genomic tool for the identification of European freshwater macroinvertebrates and develop a protocol for its standard application in biodiversity assessments. The study has been carried out in rivers of Mediterranean Region (Spain), Continental Region (Germany) and Boreal Region (Finland). Two methods were used in parallel: the traditional morpho-taxonomy and metabarcoding tools. The genetic marker was selected according to a preliminary study comparing two commonly used mitochondrial marker regions: 16S and COI. A set of primers specific for 16S gene for arthropod and non-arthropod invertebrates were prepared. Results based on morphological and metabarcoding methods were compared. 93 macroinvertebrate families were identified by morphological (74 Arthropod and 19 Non-Arthropod). Of the families observed by both methods, metabarcoding observed 89% of the observations made by morphology. Of the total of Arthropod families only 8 were not identified with metabarcoding. In brief, the comparison of morpho-taxonomical and metabarcoding data for the studied rivers showed a good correlation. But some discordances were found between both methods due to the different level taxonomic resolution (family, genus, species). These discrepancies highlight the potential of DNA metabarcoding to provide more resolutive taxonomic inventories, as compared with morphological approach. The ecological status class (ESC) of the studied rivers were stablished based on both methodologies. Thus, in 75% of cases, remained the same with both approaches. In 13.9% of cases the ESC decreased by one class and increased by one class in 11.1% of cases.

10 Years of Operational Barrier Spraying in Panama City Beach, Fl. USA

Authors: Clauson James, None, United States

Abstract: With the advent of barrier sprayers that spray misting insecticides 30 feet and further, Beach Mosquito Control District incorporates this methodology in our integrated approach to controlling mosquitoes within our district. We utilize our high power misting sprayer (Buffalo Turbine) to access areas where mosquitoes harbor or rest. We use this technique in and around parks and schools. We have data that show positive results and feel this is a valuable tool in controlling adult mosquitoes.

Understanding the Australian termite diversity anomaly: how precipitation affects termite diversity in Northern Queensland

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Abstract: Termites are critical components of tropical systems where they are thought to decompose up to 50% of plant organic material in litter, wood and soil. Termites have adaptations (e.g., the ability to scavenge and store water in their mounds) allowing them to thrive in habitats with variable rainfall and remain active during droughts. One frequently drought-affected area, the Australian tropics, is thought to show a unique pattern of termite distribution, with termite diversity and abundance lower in rainforests, peaking in drier savannah ecosystems. This pattern, if true, is opposite to what is found in tropical regions around the globe where termite diversity and abundance is highest in rainforests. Our study aims to survey termite turnover across a precipitation gradient and examine the causes and consequences of this anomaly. In five sites in Northern Queensland ranging from 600--5000 mm annual rainfall, we collected samples from 50 m transects and 50 m x 50 m plots and measured termite abundance and diversity, deadwood occupancy, and termite mound abundance. We analyzed turnover of feeding types and landscape types among sites with differing rainfall. We observed dramatic decreases in termite abundance in both mounds and deadwood corresponding to an increase in rainfall (107 mounds per ¼ hectare plot in the driest site, compared to 1 mound per plot in the wettest). Of the 18 termite species encountered in this study, none were soil feeders; litter-feeding termites were found only in the savannah sites, while wood feeders were found in both rainforest and savannah sites. These results support the termite diversity anomaly and point to turnover in feeding guild with greater diversity in savannah, suggesting that part of the anomaly lies in the adaptations to food resources across habitats. We found that presence of several common species of termites including Amitermes laurensis, Nasutitermes magnus, and Microcerotermes cerratus, corresponded more closely with habitat type than with distance from other sites. These results suggest that termite communities assemble in large part based on habitat type. Rainfall is an important factor in termite community assembly shaping the termite diversity distribution although why so few termites are found in the rainforest remains elusive.

Mechanisms of ecological and sexual divergence in the European corn borer

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Abstract: The adaptation of pest arthropod species to local environments and producer control practices pose challenges to crop production across agroecosystems. The European corn borer, Ostrinia nubilalis, is a pest of cultivated maize in North America and Eurasia, and a model for elucidating the genomic interactions underlying differentially-adapted subpopulations. Sympatric strains that differ in sexual communication system can also vary in response to temperature and photoperiod via adjustments to diapause traits causing latitudinal differences in number of annual mating generations (voltinism). Distinct phenotypes persist despite relatively high reciprocal gene flow and hybridization. Specifically, pheromone strain variants differ in the ratio of E and Z isomers of the sex pheromone produced by females and preferentially responded to by males of the same strain. The autosomal pheromone gland fatty acyl-reductase (pgfar) gene controls strain-specific E and Z isomer ratios in female pheromones, and male pheromone response phenotype (Resp) maps to a suite of neurogenesis-related genes on the Z-chromosome. Linkage disequilibrium between strain specific alleles at pgfar and Resp suggest sexual co-selection for compatible sexual communication traits at the population level. Additionally, the genetic architecture of diapause duration involves functional interaction (epistasis) between co-adapted alleles on the Z-chromosome of major genes influencing circadian rhythm: period (per) and pigment dispersing factor receptor (pdfr). A segregating non-recombining Z-chromosome inversion also contributes to the maintenance of “optimal” co-adapted allelic combinations at per and pdfr, as evidenced by maintenance of the inversion at higher frequencies between populations differing in pheromone and diapause traits. Cyclical changes in allele frequency at per and the autosomal cryptochrome 1 gene are correlated with population transitions across regions of one, two, and three generations, demonstrating a possible genetic basis of latitudinal plasticity in voltinism traits. These genomic and ecological interactions contribute to the distribution of European corn borer variants, phenotypic plasticity, and capacity to adapt to changing environmental conditions.

Certain botanical nematicides also show repellency against ticks.

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Abstract: Our lab has explored the multiple bioactivities of monoterpenes from plants, and we have shown some of them to be insecticidal, acaricidal, repellent, or synergistic with conventional insecticides. This presentation will report on the nematicidal activity of a range of monoterpenoids that are plant-volatiles. Data from bioassays on the plant-parasitic soybean cyst nematode (Heterodera glycines) and the free-living nematode (C. elegans) will reveal that several volatile monoterpenes have nematicidal activity. Our investigations of a nicotinic acetylcholine receptor from the animal-parasitic swine roundworm (Ascaris suum) have demonstrated that some of the volatile monoterpenoids have inhibitory activity at that receptor. A natural terpene oral parasiticide could have potential as a therapeutic for swine. As we evaluate results from these three anti-nematode studies, we are alert for any patterns or consistent trends regarding which specific monoterpenes or classes of terpenes (e.g. aromatics, cyclics, bicyclics, or acyclics) (e.g. functional groups) are most active.

Citronella Oil Derivatives and Their Repellent Properties

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Abstract: The field of mosquito control has long been searching for molecules that can be used as mosquito repellents to fight against the spread of vector-borne diseases. A breakthrough was made while researchers were examining the essential oil associated with lemongrass (Cymbopogon nardus). Citronella oil was extracted from the plant and was proven to be an effective oil for repelling mosquitoes, especially in short-term evaluations. The multiple components of this oil have also been extracted and screened for their ability to repel mosquitoes. Citronellol, a major component of citronella oil, has proven to be quite effective when used as a spatial repellent. Our lab has now used citronellol as a parent molecule to which we have been able to make a series of derivatives. These biorational derivatives have shown high levels of efficacy when screened against multiple genera of mosquitoes in our laboratory spatial repellency assays in both short and long-term situations.

Terpene Repellents: Beyond Amides and Pyrethroids

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Abstract: Amide repellents, such as DEET, picaridin, and IR-3535 dominated the repellent market for years/decades. Recently the pyrethroid permethrin has shown utility as a contact repellent on clothing and other fabrics, and most volatile pyrethroids have activity as spatial repellents. Amides and pyrethroids are both useful, but both also have limitations. Terpenes are emerging as a promising third class of repellents; certain monoterpenoids in citronella oil and other plant essential oils show repellency, but they don't show much residual efficacy. The one newer botanical product on the market is the monoterpenoid p-menthane-3,8-diol, which shows modest activity as a contact repellent and minimal activity as a spatial repellent. Certain sesquiterpenoids show good activity, and provide better residual time. Many questions still remain: how broad-spectrum is their activity? Do they work against ticks? Do they have the same mechanism of action as amides or pyrethroids? Can biorational analogues and derivatives offer enhanced activity or residual times? The traditional amide-type repellents lack strong efficacy against ticks, but several terpene repellents and biorational derivatives of them show excellent potency against the black-legged tick (deer tick) Ixodes scapularis and the American dog tick Dermacentor variabilis. Comparisons in repellency in the lab will be reported between classes of commercial repellents, specific terpenoids, and between species of ticks.

Does the rearing of Telenomus remus Nixon in the laboratory, for successive generations, changes its characteristics for Spodoptera frugiperda (J.E. Smith) biological control?

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Abstract: We evaluated whether rearing the egg parasitoid wasp Telenomus remus Nixon for successive generations in the laboratory alters its characteristics as a biological control agent of Spodoptera frugiperda (J.E. Smith). The experiment began with collection of a population with characteristics close to the wild insects. A pool of three different strains were released in a cornfield, and S. frugiperda egg masses were placed on corn plant leaves. The presumably parasitized egg masses were brought to the laboratory, and the parasitized eggs were selected and reared at 25°C and 75% RH; after emergence, adult wasps were offered only S. frugiperda eggs and pure honey. The wasps' biological characteristics were assessed at generations F1, F6, F11 and F17, including the short-range flight capacity, parasitism and life span. The flight test unit consisted of a PVC pipe 15 cm in diameter and 20 cm long, covered inside with black paper. The pipe was closed with a clear plastic cap, with entomological glue inside to catch flying T. remus, and a 0.5 cm-wide glue ring around the inside of the pipe at a height of 3.5 cm from the bottom, to capture walking parasitoids. Parasitism was evaluated by counting the number of dark (parasitized) eggs of S. frugiperda egg masses offered daily; female wasps were monitored until they died. T. remus flight capacity decreased from generations F1 to F17, with the proportion of flyers changing from 60% in F1 to 40% in F17. Parasitism capacity was similar across generations, 250 eggs on average, except in F17, which was lower, 97 eggs. The F1 and F6 life spans were similar, around 12 days; F11 was four days shorter and wasps in F17 lived only two days on average. In conclusion, laboratory rearing of T. remus over successive generations changes its flight ability, longevity and parasitism in relation to wild populations. The mechanisms of this change are unknown; perhaps laboratory rearing selects for individuals adapted to artificial conditions, considering that for haplodiploids parasitoids as T. remus inbreeding (endogamy depression) do not occurs.

Effects of a lipid-enriched diet on adults of Trichogramma pretiosum Riley

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Abstract: The use of lipids in rearing has long been neglected. Parasitoids such as Trichogramma pretiosum Riley, as with most hymenopteran parasitoids, are unable to synthesize lipids de novo, differing from phytophagous insects, which can synthesize lipids in the adult stage. Lipid reserves are essential for fueling oogenesis and somatic functions. For parasitoids such as T. pretiosum the lipids contained in the host eggs will provide the needed energy for the wasp embryo to develop, and therefore are essential for viability. Adult female wasps can obtain lipids by consuming part of the host egg yolk (host feeding), and in this way stimulate oogenesis. However, the energy invested in producing eggs depletes lipid reserves faster than they can be renewed. It is believed that providing lipids from an alternative source, through the adult diet, would stimulate egg production and thus the capacity for parasitism, which is desirable since this is a biological control agent. Here, females of T. pretiosum were continuously fed with acacia honey enriched with 10% vegetable oils with a fatty-acid profile similar to that of Anagasta kuehniella (Zeller) eggs, by thermal process (water bath at 70°C). Females fed with honey enriched with oleic acid-rich vegetable oil parasitized 10% more eggs than females fed only pure honey, in 72 hours. However, the parasitoids' life span was reduced by about 40%. Neither the flight performance nor the quality of the offspring of parasitoids fed a lipid-rich diet was adversely affected. These results reveal the potential of a lipid-rich diet to increase lipid allocation to reproduction. Presumably, providing lipids from a plant source could rapidly renew the female's fat reserves and allow her to invest more energy in egg production. However, the increase in parasitism capacity occurred only under certain experimental conditions. Simply mixing vegetable oil in honey at room temperature (25°C) had no significant impact on the number of parasitized eggs. The use of an organic solvent, DMSO (5%), was also inconclusive. Therefore, the method of incorporating the lipid source into the diet (honey) is critical and needs to be explored. Further research into lipid supplementation is needed to determine which fatty acids can cause an increase in parasitism. Today, honey-only is used as a food source to rear this oophagous parasitoid. As Trichogramma species are now widely used in biological control programs, adding lipids to the diet of adults of this parasitoid could be of great interest to biological control companies.

South American Spodoptera Complex: Biology, Thermal Requirements and Ecological Zoning

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Abstract: Species of the Spodoptera Guenée complex, Spodoptera frugiperda (J.E. Smith), S. eridania (Stoll), S. albula (Walker) and S. cosmioides (Walker) are serious crop pests worldwide. All these species have a wide range of host plants as well as a high biotic potential. Satisfactory control of this pest complex might be achieved through Integrated Pest Management (IPM). Optimal use of IPM requires knowledge of bioecological aspects and the population dynamics of each species in the different producing regions.

Considering the importance of the Spodoptera pest complex for agriculture, the present study determined the biology, thermal requirements and ecological zoning of these species, considering the agricultural calendar of three highly important crop plants worldwide and in Brazil, soybean, corn (first and second crops) and cotton.
Pupal development of S. albula did not occur at 18°C and of S. eridania at 34°C. Egg-adult viability of S. frugiperda and S. eridania was higher at 25°C, and of S. cosmioides and S. albula was higher at 28°C. Pupae originated from larvae reared at lower temperatures were heavier than pupae originated from larva exposed to higher temperatures, except for S. albula, which had lighter pupae at 18°C. A higher proportion of deformed pupae was recorded at lower temperatures. The duration of the egg-adult period was inversely proportional to the temperature up to 32°C, above which the larval periods of S. cosmioides, S. frugiperda and S. albula were prolonged. The fertility of S. frugiperda, S. eridania and S. albula was lower in extreme temperatures, while S. cosmioides showed a decrease in fertility only at high temperatures. The thermal requirements were: S. frugiperda, Temperature threshold– Tt= 13.04°C and Thermal constant– K=390.06 Degree Days (DD); S. eridania, Tt=11.90 and K=495.96 DD; S. cosmioides, Tt=13.23, K= 462.02 DD and S. albula, Tt=13.19°C, K=478.49 DD. Using the lower threshold temperature and the thermal constant, we estimated the number of generations of each species in three crops (corn – 1st and 2nd harvests, soybean and cotton) grown in different Brazilian municipalities, considering their crop calendar. We used the ArcMap application in ArcGis Pro to organize and represent the estimated number of generations for each Spodoptera species in each crop and municipality. The number of generations was higher in municipalities in the North and Northeast regions where temperatures are highest. S. frugiperda had the highest number of generations in all crops, indicating that it is best adapted to temperature conditions in Brazil. Corn supported the highest number of generations of all species, because it is grown over a longer period.

Rearing Systems as Ecological Niches: The Interplay of Genetics and N-Dimensional Hypervolumes

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Abstract: Insect rearing systems are treated here as artificial niches. As with all ecological niches, there is a dynamic interplay between genetic potential and environmental conditions. Understanding this interplay in the rearing environment is important to designing rearing systems to meet the expectations of the rearing systems' purpose. Drawing from examples from mulberry silkworms (Bombyx mori) rearing (the oldest rearing systems) through modern highly automated processes such as those designed for pink bollworms (Pectinophora gossypiella) and boll weevils (Anthonomus grandis), the interplay of genes and the rearing environment is explored. In accord with treating the rearing process as an n-dimensional (Hutchisonian) hypervolume, the interplay of rearing system components can be explored, helping to shed light on where phenotypic outcomes match or depart from genetic potential. In this presentation, several examples of how rearing system components may succeed or fail in matching the genetic template. These examples are taken from nutritional and environmental factors as they interplay with genetic bases of immunology and life history. One of the most illuminating examples will be the responses to oxidative stress in silkworms and waxworms (Galleria mellonella L.). Other examples of "niche/gene matching" are taken from mass-rearing systems developed for tarnished plant bugs (Lygus Hesperus), green lacewings (Chrysoperla rufilabris), and cactus moths (Cactoblastis factotum).

Vibratory communication in a complex world: the role of media and the use of communication with signals of different modalities in insects.

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Abstract: Communication holds insect societies together and among many tasks enables mating females and males of solitary species to find each other in the field. The process from recognition and location to copulation runs through complex calling, courting and rivalry phases by information exchange with chemical, mechanical and visual signals, transmitted through different media. Plants represent for majority of insects the most natural and common surroundings where they find shelter, feed and mate. Local air currents, different architecture and specific mechanical properties of plants restrict communication by visual, chemical, airborne and contact mechanical signals to short distances. The majority of insects use the substrate-borne vibratory component of signals produced by different mechanisms to exchange information at longer distances along the plant. Plants as non-inert transmission medium change transmitted vibratory signal's amplitude, temporal and frequency characteristics. The amplitude decreases non-linearly with the distance, signal duration increases by echoes at the air/substrate phase border and frequency spectra change according to resonance properties of the substrate. Insects tune their vibratory emissions with mechanical properties of plants by incorporating information into signal's parameter less influenced by impacts of the transmission medium and environmental noise. During evolution they developed specific high sensitive receptors and underlying neuronal network, adapted to extract the relevant information from modified vibratory signals. Phytophagous and plant-dwelling stink bugs of the subfamily Pentatominae (Heteroptera: Pentatomidae) represent an instructive group of insects with well investigated multimodal communication running at different distances through air and substrate. Plant-borne communication represents just the intermediate phase of information exchange between long range chemical communication in the field and short range communication on a plant by visual and contact chemical and mechanical signals. Adaptation of vibratory signal characteristics, produced by different mechanisms and tuned with mechanical properties of plants are correlated with characteristics of group mechanosensory system and discussed in view of their function during species recognition and isolation, courting and social conflicts, reflected in female and male rivalry.

Trichoderma harzianum strain T22 enhances indirect plant defenses against stink bug egg deposition

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Abstract: In the recent years, there is increasing evidence showing plant growth-promoting fungi such as Trichoderma spp. do not only promote plant growth, but also direct and indirect plant defenses against a wide range of pests, such as herbivore insects. However, no information up to now is available on the role played by plant growth-promoting fungi in mediating egg parasitoid attraction to plant induced by stink bug oviposition. To fill this gap, a multitrophic model system consisting of tomato plant, Solanum lycopersicum, southern green stink bug, Nezara viridula, egg parasitoid, Trissolcus basalis and plant growth-promoting fungi, Trichoderma harzianum strain T22 was used. In olfactometer experiments, it has been found that root colonization by T. harzianum strain T22 enhanced T. basalis attraction towards oviposition-induced plant volatiles (OIPVs) released by tomato plants in response to egg laying by N. viridula. In fact, the egg parasitoid preferred OIPVs emitted by tomato plants inoculated with the beneficial soil microbe compared with OIPVs emitted by non-inoculated plants. Then, the chemical nature of OIPVs to attempt to explain which compounds could mediate parasitoid olfactory responses we analyzed.

Social immunity in fungus-farming termites

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Abstract: As epitomized by epidemics and pandemics throughout human history, including the ongoing SARS CoV-2 pandemic, social life carries risks of substantial and rapid spread of infectious diseases. Social insects, including termites that live in pathogen-rich environments have evolved remarkably robust social immunity mitigation strategies that effectively prevent diseases from spreading within colonies. However, experiments have been conducted on only a small portion of the vast diversity of termite species, with most work being on soil- and wood-dwelling species. Consequently, it is currently unknown to what extent mound-building termites face the same pathogenic pressures and exhibit the same social immune behaviours, strategies and immune responses as their wood-dwelling counterparts. Using the mound-building fungus-farming termite Macrotermes bellicosus, we identified and characterized ecologically relevant entomopathogens. We also performed a behavioural experiment and two survivorship experiments to test the hypotheses that M. bellicosus exhibits a sophisticated, and caste-specialized pathogen defense system. Here we present preliminary analyses, and more broadly discuss the evolution of termite immunity and the implications of social life for robust defence.

Tick-tock: New repellency strategies needed for the changing times

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Abstract: Ticks are one of the most devastating vectors of human pathogens, but they are often eclipsed by their flashier “cousins”, mosquitoes. Ticks vector Borellia, Anaplasmosis, Babesiosis, Erlichiosis, Powassan, Francisella, Rikettsia pathogens, and were responsible for 59,349 reported human illnesses in the US in 2017. This number greatly underestimates the number of illnesses due to ticks because of the challenge in diagnosing tick-borne illness. Additionally, the geographic range of native and invasive ticks is expanding. In one example, in 2017 a new species of tick was reported in the United States for the first time, Asian longhorned tick. It has since been detected in 13 US States. In the natural range, these ticks have transmitted pathogens to humans, it is still unclear what the domestic threat will be. All of these outcomes have a serious impact on human health, medical burden, and quality of life, and will require a multi-pronged approach to control the impact of these diseases, including better diagnostics, surveillance, treatment and intervention. Here we present a new set of active ingredients as topical repellents to protect humans from ticks.

Characterization of the circadian clock in the Pea Aphid

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Abstract: Aphids are strongly photoperiodic insects. They reproduce parthenogenetically in spring and sexually in autumn, and this change is controlled by the shortening of day length. The involvement of the circadian clock in photoperiodism has already been established in mammals, plants, and fungi, but it is still controversial in insects. To answer this question, we began by characterizing the neuroanatomy of the aphid circadian clock and localizing the clock-related neuropeptides. Using immunohistochemistry with antibodies against the clock proteins Period and Cryptochrome, we found that the clock consists of four neuronal clusters that oscillate daily. By doing a 3D reconstruction of the CRY-positive neurons, we found that they project toward the Pars Intercerebralis, where also insulin-producing cells are located. Furthermore, we used antibodies against neuropeptides that are clock related in Drosophila melanogaster and found that IPNamide, Diuretic Hormone 31, and Allatostatin A are expressed in some aphid clock neurons, suggesting that they may also be associated with the clock in aphids. Briefly, we have found that the expression pattern of neuropeptides can be very different in different insect species, even if the peptide sequence itself is highly conserved. This laid the groundwork for future functional analysis of the aphid clock neurons and neuropeptides.

Predatory Mirids as Crop Pests: Importance of Host Plants, Prey Type, and Endosymbiotic bacteria

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Abstract: Omnivory, the feeding on both plant and prey materials, is common in agroecosystems. Understanding the feeding habits of omnivorous consumers is particularly important for mirid bugs, because several biological control agents in this family may also inflict economic damage to crop plants. In recent studies, we explored the influence of plant genotype, availability of various prey types, and the presence of bacterial endosymbionts on plant-feeding and fitness components of several mirid bugs. Results show that compared to wild genotypes, commonly cultivated tomato is more suitable for the development, survival and reproduction of Nesidiocoris tenuis. However, the oviposition preference for the cultivated genotype is lost in the presence of prey. In another system, plant-feeding and crop damage were found to be influenced differentially by the presence of various prey species on pepper plants; red spider mite, sweet potato whitefly, western flower thrips, and moth eggs differed in their nutritional suitability for Creontiades pallidus which in turn affected level of fruit damaged by the bug. Finally, an on-going study suggests that two Rickettsia species, R. bellii and R. Limoniae, influence the ability of Macrolophus pygmaeus to exploit both plant and prey materials. These bacteria are highly abundant and probably fixed in bug populations, and are found in distinctly different cells in parts of the gut and in Malpighian tubes. Taken together, these results demonstrate the great challenge faced by biological control practitioners that employ omnivorous natural enemies. It seems that elaborate, specific research is needed of each mirid-cropping system combination if we are to maximize pest suppression and at the same time prevent bug-inflicted crop damage.

Ecology of native Drosophila parasitoids in Central Europe

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Abstract: The alien vinegar fly Drosophila suzukii calls for landscape-level control because it can re-infest orchards from semi-natural habitats that provide year-round food resources, oviposition sites and refuges. In Central Europe, several species of native pupal parasitoids have been identified that are able to utilize pupae of D. suzukii for reproduction. These parasitoids could help to reduce populations of the invasive pest on a landscape level.

To unravel the ecology of these parasitoids we first performed field collections in agricultural and semi-natural habitats with sentinel traps that contained pupae of four native Drosophila species. Subsequent laboratory experiments with the three most common parasitoid species, Pachycrepoideus vindemmiae, Trichopria drosophilae and Spalangia erythromera, were conducted to investigate host choice in the presence of D. suzukii. To validate our findings, we finally released the three parasitoid species in a semi-field experiment and evaluated their parasitization of D. suzukii and two native Drosophila species. Our results show that the parasitoid species differ in their host finding and host choices but that D. suzukii is among the preferred hosts. We discuss our findings in the light of efficacy and potential non-target effects and point to the challenges that still lay ahead in the use of native parasitoids for D. suzukii control.

Climate change adaptation strategies in Latin America as part of a Resilient Agricultural production system

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Abstract: Climate change is affecting the agricultural production in Latin America, and represents a challenge for agricultural production and plant protection, since it favours the movement of pests to new areas due to the increase in temperature and change in climatic conditions. Climate conditions have an important influence in the development of pests, diseases and biological control agents. Biological control plays an important role as part of Integrated Pest Management and sustainable production. Therefore, is important to investigate the effect of the abiotic condition changes, such as the increment of temperature, humidity, flooding and drought conditions on the distribution range of both agricultural pests and their biocontrol agents. This study presents the different strategies putting in place, and join efforts looking forward to have a more Resilient Agricultural production system, evaluating the effects of climate change on the pests and biological control agents and using sustainable practices and tools as part of the adaptation process to climate change. The Climate Smart Agriculture approach will be discussed as a possible way of facing some of the current challenges in the region and increasing sustainable production in Latin America.

Bottom-up and top-down effects on insect herbivore fitness under global change

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Abstract: Insect herbivores can be affected by selective forces from natural enemies (top-down) and host plants (bottom-up). The quality of plants as food for insect herbivores as well as the potential pressure by natural enemies can vary directly and indirectly with environmental factors such as temperature, water and nutrient availability, atmospheric gases, etc. Many of these environmental factors are already and will continue to rapidly change due to global environmental change. The different environmental factors that are changing can have variable effects on insect herbivore fitness via top-down and bottom-up forces, which makes the response of insect herbivores to global change hard to predict. For instance, some plants can respond positively to some environmental changes (e.g., nutrient pollution), which can result in positive effects for herbivores. However, other environmental factors can have a negative effect on plant quality (e.g., drought), resulting in an indirect negative effect on herbivores. Natural enemies are likely going to be negatively affected by many environmental changes (e.g., change in precipitation, temperature), which may result in enemy release and a positive effect for herbivores. We conducted a meta-analysis to synthesize the current knowledge on the indirect effects of global change on insect herbivores via bottom-up and top-down forces. We tested the overall effect that global change has on top-down and bottom-up forces on insect herbivore fitness. We further tested the effects of different types of global change on the responses of insect herbivores to top-down and bottom-up forces, and how these responses can vary with insect guild, type of habitat where the experiments were performed, type of fitness measure taken, and type of natural enemies (e.g., parasitoids vs. predators). Knowing the many possible effects that global change can have on top-down and bottom-up controls of insect herbivore can help with conservation efforts and pest controls.

Genome-wide macroevolutionary signatures of key innovations in butterflies colonizing new host plants

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Abstract: The exuberant proliferation of herbivorous insects is generally attributed to their associations with plants. Yet, despite numerous studies on insect-plant interactions, a rigorous integration of the macroevolutionary and genomic consequences of the evolutionary dynamics of host-plant shifts has not been achieved. The arms race between swallowtail butterflies and their host plants provides a preeminent model for addressing this gap. Here we show that host-plant shifts are associated with genome-wide adaptive molecular evolution, followed by repeated bursts of higher speciation rates. We find that this antagonistic insect-plant interaction began 55 million years ago for the ancestor of swallowtails and a highly toxic plant group, the birthwort genus Aristolochia, both of which occurred in a northern region centered on the Bering Land Bridge. Despite strong host-plant conservatism, several ancient shifts to new plant families now allow repeated tests of genome-wide signatures of macroevolutionary changes and estimation of diversification rates across their phylogeny. Phylogenetic branches with host-plant shifts had more genes under positive selection and faster diversification, contributing to an increase in global diversification through time. Our study links ecological changes, genome-wide adaptations and macroevolutionary consequences, lending support to the importance of ecological interactions as evolutionary drivers over long time periods.

Mechanisms of herbivore-induced plant responses and perspectives for improvement of stink bug biocontrol

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Abstract: Several stink bugs, such as Halyomorpha halys and Nezara viridula, are serious crop pests globally. Classical and conservation biological control, combined with other sustainable control methods, are considered effective solutions for management of these stink bugs. Future strategies might target plant resistance, focusing on indirect defences (attraction of egg parasitoids) and direct defences (antibiosis and antixenosis). The aim of this presentation is to review the current knowledge related to physiological and molecular aspects of bi-trophic and tri-trophic plants – stink bugs – parasitoids communication. Egg deposition combined with feeding punctures and walking activity by different stink bug species induces in plants the emission of volatiles that recruit stink bug egg parasitoids, thus preventing eggs from hatching. Furthermore, combinations of biological and molecular investigations indicate that naturally laid eggs and/or adult feeding by H. halys are perceived as a warning signal by faba bean and tomato plants, which activate a mechanism of enhanced direct defence that affects the developing progeny and repels nymphs. Indeed, higher expression of jasmonic acid-dependent genes was detected in oviposition-experienced plants compared to control plants when challenged by nymphs. The magnitude of plant response and/or the type of pathway activated by the herbivore attack may change with the stink bug species, plant species and type of plant-herbivore interaction. Understanding how plants modulate stink bug-induced responses is important for the development of management strategies based on improving plants' indirect and direct defences in combination with biocontrol.

The learning curve: specialist and generalist insect response to ozone-altered floral scents.

Authors: Cook Brynn[2] and Roulston T'ai[1], [1]University of Virginia, Blandy Experimental Farm, United States, [2]University of Virginia, United States

Abstract: Plant volatiles can act as important long-distance signals for host-searching insects. However, some air pollutants, which have increased dramatically following the industrial revolution, may react with volatiles and alter these cues. In following with emerging studies, we find that the air pollutant ozone causes floral scents to become less attractive to a pollinating moth, Manduca sexta, as well as two cucumber beetles Acalymma vittatum and Diabrotica undecimpucntata. However, some insects may be equipped to use behavioral plasticity to overcome ozone-induced changes in evolved signal-cue matching by learning the altered floral scents. Here we find that M. sexta can readily learn the ozone-altered plume, even when the ozone-altered plume and reward are temporally decoupled, as they would be in a field setting. Somewhat more surprisingly, given the dearth of literature on specialist-insect olfactory cue learning, the specialist beetle A. vittatum was also able to learn the ozone-altered plume via association. This work thus demonstrates both the potential threat of air pollution to insects as well as the importance of considering insect learning and learning abilities in future studies investigating how insects respond to anthropogenically-altered signals.

Not just a ‘dirty needle’: the influence of Stomoxys calcitrans on lumpy skin disease

Authors: Cook Charlotte[3], Moffat Katy[1], Greaves David R. [4], Darpel Karin [1] and Beard Pip[2], [1]The Pirbright Institute, [2]The Pirbright Institute; The Roslin Institute, [3]The Pirbright Institute; University of Oxford, [4]University of Oxford

Abstract: The poxvirus lumpy skin disease virus (LSDV) is mechanically transmitted by haematophagous arthropods including stable flies (Stomoxys calcitrans), causing severe systemic disease in cattle. Arthropod vectors that transmit viruses mechanically are regarded as playing little role in disease beyond transmission. We examined this theory by studying S. calcitrans and LSDV. Addition of S. calcitrans secreted saliva to LSDV had no impact on viral survival or replication in vitro. The impact of S. calcitrans on LSD was examined using an experimental LSD bovine model. Three groups of ten cattle were inoculated intradermally with 1x106 pfu of LSDV. Group 1 received virus alone, group 2 received virus mixed with 10ug S. calcitrans saliva, and group 3 received virus inoculated into a site that S. calcitrans had spot-fed on. Fewer cattle in group 2 developed LSD (3/10) than group 1 (6/10) and group 3 (7/10), indicating that S. calcitrans saliva inhibits LSDV infectivity in vivo. Cutaneous lesions and viraemia appeared more rapidly in group 3 than group 1, revealing that pre-feeding S. calcitrans on inoculation sites accelerates disease kinetics. S. calcitrans are therefore more than a simple conduit for virus transmission: through bite trauma and saliva deposition they influence LSDV infection and disease.

The Final Solution: Preventing Stable Flies from Developing in Vegetable Crop Residues

Authors: Cook David, Department of Primary Industries and Regional Development Western Australia, Australia

Abstract: Post-harvest residues of most leafy vegetables rot within days after harvest and provide an ideal environment for stable flies to complete their development. The resultant adult flies that emerge seek blood meals several times a day and significantly affect livestock and rural residents nearby. Numerous methodologies have been tried to reduce stable fly development from vegetable crop residues left in situ after harvest but have either had limited success or are neither practical nor economically viable for vegetable producers to adopt. Our research clearly confirmed the best method for managing and having a major impact on stable fly development from vegetable crop residues involved 2 simple steps: (1) Burial of crop residues using either a mouldboard plough, stone burier or a deep, slow rotary hoe; followed by (2) Compaction of the sandy soil using a fixed landroller at rates equivalent to 5t/m2. Compacting sandy soil almost totally prevented adult stable fly emergence from the soil. The hard barrier of soil near the surface prevent the newly-emerged adults from digging their way to the soil surface. Burying and compacting sandy soil over the crop residues provides key production benefits to growers including: (i) retention of all the organic matter from the residues (ii) less soil wind erosion from moist, compacted sand (iii) no need to use insecticides to control stable flies. The option of burying crop residues and compacting the sandy soil above the residues offers a unique physical solution to preventing the emergence of adult stable flies from the residues without the need to use pesticides.

Biology and chemical ecology of spotted lanternfly

Authors: Cooperband Miriam, Otis Laboratory USDA-APHIS-PPQ-S&T, United States

Abstract: In the five years since the discovery of Spotted Lanternfly in Pennsylvania, in the United States, it has spread to neighboring states and populations have multiplied unchecked. At the onset, we had few tools for monitoring and detection of this pest. We set out to improve our understanding of the biology and behavior of this species, with the ultimate goal of identifying strong attractants or semiochemicals that could be used in survey, detection, and control. We now know much more about its host preferences, host suitability, basic biology, adult phenology, have identified approximately 15 kairomones, and have found evidence that they may use pheromones. This talk will summarize our research and results in the context of Spotted Lanternfly biology and chemical ecology.

Population ecology of a forest insect with prolonged quiescence and its consequences on classical biological control

Authors: Corley Juan, Bariloche Institute of Research in Forestry, Agriculture and Livestock (IFAB, INTA-CONICET) and Ecology Department, Comahue National University, Bariloche, Arg, Argentina

Abstract: Prolonged or extended diapause is a life history feature of many forest insects living in unpredictable environments. It is considered an adaptive risk-spreading strategy, as it creates heterogeneity within populations by extending the life cycle of a fraction of individuals. Developmental quiescence can vary largely among species in kind, duration, stage and triggering factors. However, it can have dynamic consequences on single populations and on species interactions. I analyze the population dynamics of a forest insect pest that undergoes prolonged quiescence and through simple modeling, explore its significance on the interaction with parasitoids. I illustrate my case with a system involving a major forest pest, the woodwasp Sirex noctilio and two of its parasitoid species that have been introduced into different geographical regions through classical biological control programs. Recent work has provided evidence for prolonged developmental quiescence at the egg stage or early larval stage correlated to the ambient temperature in the Sirex wasp. A consequence of this is a variable, multi-year life cycle in some invaded regions. Through simple models, I show how multi-year cycles may affect population outbreaks. Because delayed emergence can also affect adult size, and consequently longevity, fecundity and dispersal potential the consequences are likely to be more complex. I also suggest that the physiological relationship between the parasitoids and the development patterns of its host, can have an impact on the success of classical biological control programs deployed. I conclude that for given environments and in the light of climate change, multi-year emergence and the way in which it affects population growth, should be carefully pondered to understand observed population patterns of forest insects and spread rates of invasive species. In turn, how parasitoids deal with host development under given climatic conditions, should be considered with other selection criteria of natural enemies of alien pests.

The standing challenges for the successful management of insect pests in plantation forestry in Argentina

Authors: Corley Juan, Bariloche Institute of Research in Forestry, Agriculture and Livestock (IFAB, INTA-CONICET) and Ecology Department, Comahue National University, Bariloche, Arg, Argentina

Abstract: Plantation forestry in South America is dominated by non-native tree species. A likely consequence of this, is that most pest issues are also non-native, largely arriving accidentally from native or previously invaded ranges. In contrast with most food or fodder producing crops, tree plantations cover larger spatial and temporal scales and so pest issues require management practices that consider their spatial and temporal dynamics. This, and the fact that many pests are non-native, are probably the reasons why classical biological control is often the practice used in plantation forestry.

In pine and eucalypt plantations in Argentina, thirty-five alien forest insects have established populations and only 23% (eight species) are exclusively found there; the rest being shared with a least one neighboring country. Despite the fact that information on the distribution changes, population dynamics, and spread of established forest insects in commercial forests of Argentina is limited, many probably cause still little damage. For all those alien species present that cause some impact (6), classical biological control plans are in course or else planned. For none however, population size prior to management and the economic impact have been estimated nor the efficacy of control actions has been quantified. To improve our knowledge on the factors underlying success or failure of pest management practices against established pests of plantation forests in Argentina, population information is urgently needed. A key matter is understanding those issues that favour the arrival and population growth of alien insects, including the relative roles of top-down vs bottom-up regulating factors and identifying the main mortality factors present. The development of sensitive, cost-efficient and repeatable monitoring protocols is thus a necessary step in this direction, as are, cross border pest databases of pests and natural enemies, that include geographical information. Considering the observed changes in global climate, detailed climate matching studies based on physiological studies of potential natural enemies, may improve the chances for success.

Plant-insect-entomopathogen interactions: Do host plants have a role in the outcome of mixed pathogen infection and successful pathogen transmission?

Authors: Cory Jenny[1], Deschodt Pauline[1], Dang Brandon[1] and Hercus Jess[1], [1]Simon Fraser University, Canada

Abstract: Plants can play a major role in the interaction between insects and their pathogens. Differences in plant quality can have significant impacts on insect growth and condition, which can affect their susceptibility to pathogen infection either directly or indirectly. Moreover, insects are commonly challenged by multiple pathogen species, yet little is known about how nutrition affects the outcome. Different host plants could influence pathogen co-infection in terms of host survival, pathogen replication and subsequent pathogen transmission to uninfected hosts. Additionally, traits that enable a pathogen to be a good competitor within the host on a specific host plant might not be the same as those that are needed for successful transmission within the host population. Our earlier work has shown that host nutrition significantly affects host survival to infection, as well as pathogen replication within the host and the outcome varies with pathogen type.

In a spray assay, using the cabbage looper, Trichoplusia ni, its nucleopolyhedrovirus (TnSNPV) and the entomopathogenic fungus, Beauveria bassiana, and two of its host plants, broccoli and tomato, we asked whether host plant species and mixed infection could alter pathogen efficacy in controlling the cabbage looper. Then using the same host plants, we measured pathogen transmission within T.ni populations. We challenged T.ni larvae with either a single pathogen species, two pathogens simultaneously or two pathogens asynchronously. Before death, randomly selected challenged larvae were transferred onto caged host plants (broccoli and tomato). After death, 20 healthy larvae were added to each plant. Using destructive samplings 1, 3 and 5 days after introduction, collected larvae were then reared on artificial diet until death or pupation to estimate pathogen transmission.

We hypothesized that the likelihood of healthy larvae being infected by a pathogen in the field will vary depending on; host plant architecture, plant nutrient composition and secondary chemicals; spatial structure of pathogen transmission stages as well as temperature and humidity. The results showed that host likelihood of being infected is highly dependent on the host plant and pathogen infection pathway. The results presented give insight into the complex interactions which can modulate pathogen transmission in the field.

Vector Control Products and Approaches: Contributions from the U.S. National Institute of Allergy and Infectious Diseases

Authors: Costero-Saint Denis Adriana[1] and Ghenbot Ghiorghis[1], [1]National Institute of Allergy and Infectious Diseases, National Institutes of Health, United States

Abstract: The National Institute of Allergy and Infectious Diseases (NIAID) part of the National Institutes of Health (NIH) in the U.S. Department of Health and Human Services (DHHS) provides funding (competitive grants) and resources (preclinical services) to investigators interested in basic and translational research leading to vector control approaches and products. The Vector Biology Program at NIAID supports over 100 grants on all aspects of basic research on arthropod vectors of human pathogens and snail reservoirs of Schistosoma parasites. Vectors currently supported include: mosquitoes, sand flies, black flies, tsetse flies, triatomine bugs, ticks and snails. Research projects range from physiology, pathogen/vector interactions, vector immunity, vector microbiome, to ecological and epidemiological studies, including clinical trials of vector interventions to assess their impact on disease transmission. The translational component of the Program supports the generation of evidence that allows investigators to reach out to funders to advance their product development efforts and for support to scale up; and to regulatory agencies to register the products. Examples of successful products that have followed this path will be presented and include ZAP Males (MosquitoMate) for dengue control and Ivermectin for malaria control.

Nutritional ecology, infection and immune defence — exploring the mechanisms

Authors: Cotter Sheena[2] and Al Shareefi Ekhlas[1], [1]University of Babylon, Iraq, [2]University of Lincoln, United Kingdom

Abstract: Many insects have been shown to switch diets after infection, to ones that improve the outcome of infection, known as self medication. However, how diet improves infection outcomes is often unclear. Diet can impact the outcome of parasitic infection in three, non-mutually exclusive ways: 1) by changing the physiological environment of the host, 2) by enhancing the immune response and 3) by altering the presence of host microbiota. We show that there are no clear patterns in the effects of diet across taxa and that good evidence for the mechanisms by which diet exerts its effects are often lacking. More studies are required to understand the mechanisms of action if we are to discern patterns that can be generalised across host and parasite taxa.

Sci-comics for #scicomm

Authors: Couret Jannelle[1] and Rothwell Aya[2], [1]University of Rhode Island Department of Biological Sciences, United States, [2]University of Rhode Island, United States

Abstract: Sci-comics are a product of graphic/comic art and compelling story-telling that primarily aim to educate, but also entertain. We present the tragicomic life-story of a mosquito larva in order to demystify the step-by-step process of creating a sci-comic inspired by published research articles, as well as highlight the important ground-rules for successful collaborations between graphic artists and scientists. This and other sci-comic success stories suggest that this genre has broad potential to enhance the impact of other forms of science communication. A preliminary study of the impact of sci-comics in an undergraduate entomology course demonstrates that students improved their understanding of research results when primary literature was accompanied by related sci-comics than when articles were read alone. The collaborative vision for sci-comics presented here is fun and rewarding, and creates products that can memorably capture and convey scientific concepts and research results.

The more you know: Targeted social media #scicomm for different demographics

Authors: Coyle David, Department of Forestry and Environmental Conservation, Clemson University, Clemson, South Carolina, United States

Abstract: Social media is exponentially increasing in its use as a scientific communication (#scicomm) tool. Many people, including professionals and non-professionals, are using social media to talk about the natural world. As an educator, especially one in an academic setting (e.g. Cooperative Extension in the U.S.), time and resources are seemingly on a continual decline. AS such, it is imperative that we maximize our time, energy, and resources. Social media is a great way to reach a lot of people, but it is important to know your audience in order to maximize the efficacy of your message. Different demographics gravitate towards different social media platforms. Knowing who uses what, and then using targeted messages, can greatly increase the chances that your #scicomm is effective. This talk will discuss different social media platforms and common demographics associated with them in an effort to help attendees more efficiently use social media.

Studies on the host diversity of the spiraling whitefly (Aleurodicus rugioperculatus Martin) and the physiological and biochemical changes accompanying the fly infestation in Cocos nucifera L.

Authors: CR Arunkumar[1] and Job Joseph[2], [1]Department of Botany St.Berchmans College Changanassery Kerala India, India, [2]Division of Plant Physiology and Biochemistry Department of Botany University of Calicut Kerala India, India

Abstract: Aleurodicus rugioperculatus Martin. was an important agricultural pest, known as spiraling whitefly which was found to be present mainly in agricultural crops. The whitefly infestation on crop plants was always associated with black sooty mold. The objectives of the present study were the preparation of an inventory of the host diversity of the fly and the determination of the physiological and biochemical changes in the coconut plants(Cocos nucifera L.) due to whitefly infestation . The fly was found to be inhabiting all most all of the crop plants and natural vegetation of the study area. The infestation made several biochemical changes in the infected plants. Mainly the stress related compounds were produced in higher amounts in the infected coconut leaves. Significant increase was noted in the contents of flavonoids, proline, total sugar, amino acid and total protein. It was also observed that the reactive oxygen species were formed at an elevated rate in the infected tissue. The enzymatic antioxidants such as catalase, ascorbate peroxidase and sod and non-enzymatic antioxidants such as glutathione, ascorbate and phenol were also detected in higher amounts in the infected leaves. As a result of the infection there was a significant decline in the contents of chlorophyll a, chlorophyll b, total chlorophyll and carotenoid. Consequently the activity of photosystem I and II were also reduced in the infected leaves.

Identification of the Bactrocera white pupae (wp) gene provides new opportunities for developing genetic sexing strains for SIT

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Abstract: Suppression or elimination of insect pest populations can be achieved using the Sterile Insect Technique (SIT). The release of sterilized males, rather than bi-sex releases, requires genetic sexing strains with the ability to selectively eliminate females and this can be achieved using dimorphic pupal color phenotypes. Here we report a recessive gene mutation in Bactrocera dorsalis that causes the white pupae (wp) phenotype by preventing the puparium from developing into wild type brown colors. The B. dorsalis wp- locus was introgressed into the genetic background of a related species, B. tryoni (brown pupae), over twelve generations to produce a wp- Bactrocera introgression line. Whole genome sequencing identified a 2.5 Mb region in the introgression line containing 81 genes from B. dorsalis that controlled the wp phenotype. One of these genes was highly expressed during pupal development, however, wp- flies contained a 37 bp truncating mutation predicted to cause a total loss of protein function. CRISPR/Cas9 mutagenesis in B. tryoni provided functional support for a role in pigmentation, as injected individuals developed mosaic white and tan puparium colors, and progeny with recessive white pupae phenotypes were subsequently produced. Gene technology has the potential to engineer white pupae phenotypes in a range of Tephritids, although the construction of a genetic sexing strain will require insertion or translocation of a functional copy of the wp+ gene to the male Y-chromosome for dimorphic pigmentation.

Manipulating pollen macronutrient ratios to improve honey bee (Apis mellifera) resilience to pesticide stress

Authors: Crone Makaylee[2], Grozinger Christina[1], Biddinger David[3], [1]Distinguished Professor of Entomology at Pennsylvania State University Director of the Center for Pollinator Research, United States, [2]Ecology Ph.D. Candidate in the Department of Entomology at Pennsylvania State University Center for Pollinator Research, United States, [3]Entomology, Penn State Fruit Research & Extension Center, Biglerville, PA, United States

Abstract: Many stressors are known to contribute to a decline in honey bee (Apis mellifera) health. One of the best ways bees can combat these stressors is by consuming pollen from multiple sources. A diet lacking in pollen quality or quantity has been shown to decrease the survival of bees parasitized by the ectoparasite Varroa destructor, increase the level of viral loads present, and increase pesticide susceptibility.

Our study sought to determine whether the protein or lipid portion of pollen contributes most to pesticide resilience by feeding groups pollen of varying protein to lipid ratios and challenging bees with the pesticide stressor chlorpyrifos. We also examined the differential expression of genes associated with diet and overall health by using qRT-PCR to determine the mechanisms responsible for differences in survival between dietary treatment groups. The goal of this study is to determine the most beneficial diet for honey bee health to inform beekeepers and land managers of best practices for supplementing floral resources for bees.

Impact of elevated CO2 on insect-plant interactions in a forest ecosystem.

Authors: Crowley Liam[1], Pritchard Jerry[1], Sadler Jon[1] and Hayward Scott[1], [1]University of Birmingham, United Kingdom

Abstract: Elevated atmospheric concentrations of carbon dioxide (eCO2) is a key driver of global climate change. Increasing CO2 can also profoundly alter insect-plant interactions via its effects on plant biochemistry, physiology and ecology. The full extent of these potential impacts, however, remains unclear specially in complex ecosystems such as forests. The new Birmingham Institute of Forest Research (BIFoR) Free Atmosphere Carbon Enrichment (FACE) facility provides a unique opportunity to investigate these responses in a mature, temperate woodland.

Insect herbivory and insect-mediated pollination are two key ecological process affecting nutrient flow and plant reproductive success within forested ecosystems. Thus, understanding the responses of insect herbivores and pollinators to eCO2 is critical to predicting the consequences of future climate scenarios for the wider ecosystem.

Leaf-mining insect larvae are a useful feeding guild to study these responses in a forest ecosystem as they are sessile, abundant and leave a clear trace of their life history. Here we present data showing the impact of eCO2 on leaf-miner species abundance, distribution and feeding rate. The details of how plant-pollinator interactions may be altered under future climate conditions are also discussed, using common Bluebell, Hyacinthoides non-scripta, and its pollinators as a model. Associated variables are measured in both interactions in an attempt to provide a mechanistic understanding of the driving force behind observed trends.

Ploidy levels regulate cell fate during metamorphosis in Drosophila melanogaster

Authors: Cruz Josefa [1], Martín David[3], Franch-Marro Xavier[3], Franch Marro Xavier[2], Subirana-Bonet Jordi[1], [1]IBE (CSIC-UPF), [2]IBE (UPF-CSIC), [3]Institute of Evolutionary Biology (CSIC-UPF), Spain

Abstract: Tissue remodeling is an important process during morphogenesis. In insects, organ remodeling takes place during the metamorphosis. At the metamorphic transition larval cells die, whereas imaginal cells survive and differentiate into the cells of the adult organism. Remarkably, we found that both processes (death and differentiation) depend on the presence of the ecdysone-dependent transcription factor E93. E93 expression in the prothoracic gland (PG), the main endocrine larval organ, induces its degeneration by apoptosis and autophagy. In contrast, in wing imaginal cells, E93 promotes cell differentiation. The molecular context that determines the fate of the larval cells and the adult precursors upon activation of E93 remains unknown. One of the main features that distinguish these two populations of cells is their DNA content. Whereas imaginal cells are mainly diploid, larval cells, as those of the PG, shows a high grade of polyploidy. Interestingly, conversion of PG polyploids cells into diploid by depleting Fzr impaired the degeneration of the organ. In contrast, polyploidization of wing imaginal cells resulted in an increase in cell death during metamorphosis in the adult wing. Altogether, our results indicate that E93 induces either cell death or differentiation depending on the DNA content of larval and imaginal cells.

Suppression of prophenoloxidase activation is required for vector competence for a persistent plant virus

Authors: Cui Feng[1], Wang We[1], Lu Hong[1], Yu Jinting[1], Kang Le[1] and Chen Xiaofang[1], [1]Institute of Zoology, Chinese Academy of Sciences, China

Abstract: Rice stripe virus (RSV) is the cause of one of the most destructive rice disease epidemics in eastern Asian countries. This virus is transmitted by the small brown planthopper in a persistent-propagative mode. However, factors associated with vector competence for RSV remain elusive. Here, we reported that the proteolytic activation of prophenoloxidase (PPO) played a role in vector competence for RSV transmission.

Neopolyploidy in plants and its impact on insect herbivore communities

Authors: Cure Anne[2], Porturas Laura[1] and Segraves Kari[2], [1]Pennsylvania State University, [2]Syracuse University, United States

Abstract: Insect herbivores are a key component of many ecosystems, having a major impact on plant community composition and structure. A common yet overlooked factor that could affect patterns of insect herbivory is the evolution of whole-genome duplication (WGD) or polyploidy in plants. Newly formed polyploids, or neopolyploids, often have physiological and morphological changes that might cause cascading effects in the associated herbivore community. Despite these potential linkages between WGD and herbivory, we know little about how WGD alters herbivore-plant interactions. Here we determined how insect herbivores respond to neopolyploid hosts by examining if the community of insect herbivores change in response to neopolyploidy, and in turn, if neopolyploidy alters patterns of attack by insect herbivores. We tested the effects of WGD on insect communities by placing diploid and neopolyploid red clover (Trifolium pratense) in a common garden and assessed insect community composition, abundance, and attack rates.

Estimation of developmental thermal parameters of the Chilean leafroller, Proeulia auraria (Clarke) (Lepidoptera: Tortricidae), using non-linear models.

Authors: Curkovic Tomislav[2], Arraztio Diego[2], Leiva Flaminio[2], Solis Gabriela[2], Neira Jose[2], Morales Luis[2], Gutierrez Pablo[3] and Tapia Roberto[1], [1]Agriculture and Livestock Service Dept. Agriculture, Chile, [2]University of Chile, Chile, [3]University of O´Higgins, Chile

Abstract: Proeulia auraria (Lepidoptera: Tortricidae) is a native to Chile leafroller, affecting fruit orchards and vineyards yields. Besides, historically it is the sixth species in terms of quarantine rejections during post-harvest inspections to our fruit for exports. Thus, our group has worked to develop a phenological model as a predictive tool for precise pest management under field conditions. P. auraria larvae, pupae, and eggs were collected in severely infested vineyards, brought to the lab, and reared on artificial diet. Once adults were obtained, couples were placed in courtship arenas where females laid eggs. 0-12-hours eggs were taken to climatic chambers set at constant temperatures (8 temperatures between 8 and 34º C). Development (days) was checked every 2-3 days, for over 100-130 individuals/stage or instar, in each temperature regime, determining the time when eggs hatched, and larvae and pupae molt. Most phenological models developed to date for insect species, have estimated thermal parameters (lower threshold and degree-days) using linear models fitted to data (developmental rate vs. rearing temperatures, at several thermic regimes). However, the linear approach is not able to estimate the upper threshold nor the optimal range of temperature. On the other hand, the use of non-linear models (we used those published by Briere, Kontodimas, Ratkowsky among others) has been reviewed most recently, having the advantage of estimating both, the threshold and optimum, but not the respective degree-days. Our work estimated all four thermal parameters with a new approach for calculation of degree-days, using several of these non-linear models, by computing the derivative of development rate with respect to temperature, and obtaining the mean positive value between the lower and upper thresholds. These parameters were used later for validation in field tests, where the development was checked daily, and the canopy temperature was periodically registered, to estimate the actual degree-days experimented by the individuals. Those were contrasted with predictions based on the thermal parameters, obtaining significantly better predictions when parameters obtained with the non-linear models were used.

Molecular identification of Irish mosquitoes via direct and indirect sources

Authors: Curran Thomas[3], McDevitt Allan[5], Browett Samuel[6], O'Neill David[6], Ruiz Arrondo Ignacio[1], John McMahon Barry[4], O'Hanlon Aidan[2], O'Reilly Catherine[6], Harrington Andrew[6] and O'Meara Denise[6], [1]Centre of Rickettsiosis and Arthropod-Borne Diseases, Hospital San Pedro–CIBIR,, [2]National Museum of Ireland, [3]South East Technological University, Ireland, [4]University College Dublin, [5]University of Salford, [6]Waterford Institute of Technology

Abstract: Ecosystem services provided by insects include soil aeration, plant pollination and pest control. Insects also pose concern, particularly vectors for disease, such as some of the 3500 mosquitoes that occur worldwide. Across Europe, cases of mosquito borne diseases have been recorded and are associated with anthropogenic changes. Mosquito monitoring is vital to create informed mitigation measures in advance of potential disease outbreaks. Morphological identification of mosquito larvae and adults requires a high level of expertise and is susceptible to error. Here, we demonstrate the application of DNA technology to identify mosquitoes from larvae, adults and indirectly from the diet of bats using a combination of DNA-based techniques including Sanger sequencing, DNA metabarcoding and real-time PCR (qPCR). Sanger sequencing facilitated the identification of previously unrecorded mosquito species in Ireland (Culex torrentium). Using DNA metabarcoding on bat faecal pellets a highly diverse diet was revealed and included the identification of four mosquito species, one of which was also previously unrecorded in Ireland, (Culex quinquefasciatus). Finally, species-specific qPCR assays were designed and optimised and allowed for the rapid detection of mosquitoes. The combination of these molecular techniques have facilitated the identification of mosquito species occurring in Ireland via direct and indirect approaches.

From lab bench to tailgate – the state of molecular diagnostics in invasive species surveillance and early detection

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Abstract: Vigilant biosurveillance is necessary to protect our forests from invasive alien species. Early detection is critical to effective control and management, but is challenging due to the diversity of pests and their pathways of spread, as well as the difficulty in assessing their risk of establishment. Genomics can provide powerful solutions to these biosurveillance challenges and can tell us the story of invasion. One exciting prospect is the development of genomic tools that can be used outside the laboratory environment. These 'point of need' approaches unshackles molecular diagnostics from the laboratory bench and releases them into the wild. We provide emerging examples of these field-based molecular diagnostics for several high risk forest invasive species.

Genomics-based tools for biosurveillance of Asian gypsy moths

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Abstract: Genomics-based approaches are becoming increasingly relevant for the design of assays aimed at detecting, identifying and monitoring forest invasive alien species. A good example of this type of application is provided by the Asian gypsy moth (AGM). Indeed, AGM ranks high on the list of unwanted alien pests in North America, and measures to prevent its accidental introduction and establishment are given high priority by plant protection authorities. Several features of AGM make it a particularly rewarding research subject from both fundamental and applied science perspectives. “AGM” designates a complex of difficult-to-distinguish Lymantria dispar subspecies and closely-related Lymantria species, some of which appear confined to Japan (L. dispar japonica, L. umbrosa, L. albescens, L. postalba), while the most widely distributed one, L. dispar asiatica, is found over most of mainland Asia. Its range overlaps with that of the European gypsy moth (EGM; L. dispar dispar) at its western-most limit, where the two subspecies appear to interbreed. EGM is already present in North America, following an accidental introduction in 1869. However, it has a narrower host range than AGM and, unlike the latter, its females are flightless, reducing its ability to spread rapidly in newly invaded habitats.

Research conducted by our group has involved the development of molecular tools that help distinguish EGM from AGM-complex species and subspecies in egg samples intercepted on foreign vessels entering North American ports, as well as in moths caught in pheromone traps. To this end, we carried out comparative mitochondrial genomics, which enabled the identification of markers suitable for the development of diagnostic TaqMan assays. In parallel, we initiated a study focused on the identification of genome-wide SNPs that can be used to identify the geographic origins of intercepted samples; this type of information is useful in characterizing introduction pathways. Do date, a proof-of-concept study based on eight populations sampled from across the range of L. dispar showed strong population structure and a high success of assignment of unknowns to source populations. A full scale study involving ~80 sampling sites and 25+ countries is now almost completed.

AGM-EGM hybrid populations in eastern Europe often feature females that display strong flight capability while bearing an EGM mitochondrial genomic signature. Because such specimens could be wrongly identified as flightless EGM on the basis of mitochondrial markers, and fail to be screened out during ship inspection, we recently set out to identify the genomic determinants of female flight capability in gypsy moths, using three analytical approaches in parallel; it is hoped that flight capability genes can be used to identify all specimens originating from populations with flight-capable females.

Insights into the role of insulin-like peptides in aphid photoperiodism

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Abstract: Aphids were the first animals to be described as photoperiodic due to their seasonal response characterized by a reproductive switch. During the favourable seasons (spring and summer), aphid’s populations consist of viviparous parthenogenetic females, whereas during the harsh seasons (autumn and winter) they switch to produce a single sexual generation of oviparous females and males that mate and lay diapausing cold-resistant eggs that can overcome the unfavourable environmental conditions. Aphids exhibiting the complete cycle are called holocyclic, but there are also anholocyclic lineages that represent natural mutants, which have lost the ability to respond to photoperiodic changes and thus can help us study how the process is regulated. Previous studies have demonstrated that the main elements of a putative photoperiodic clock are located in the aphid brain, especially in the medial region comprising the pars intercerebralis and pars lateralis areas. Moreover, the insulin-signalling pathway could be involved in the seasonal response, as it has been described in other insect species. In order to shed some light on the role of this mechanism, we analysed Acyrthosiphon pisum brains at the embryonic and adult stages by immunohistochemistry (IHC) to locate ILP4 (Insulin-Like Peptide 4), a neuropeptide previously shown to be differentially produced under diverse photoperiods. A possible link between the circadian clock and photoperiodism was also investigated by quantifying the expression of ilp1 and ilp4 genes by RT-qPCR during a time-course experiment along one day and a half. A similar experimental design was used to quantify ILP4 protein levels by IHC by measuring the intensity of cell’s fluorescence signal under a confocal microscope. Our results clearly show that ILP4 is synthesized in two groups of four cells in the pars intercerebralis and then it is axonally transported to the ventral region of the brain, possibly to the corpora cardiaca or corpora allata, where it could potentially modulate the secretion of some downstream hormones implicated in the photoperiodic response. Although no evident rhythmicity behaviour was observed, ILP1 and ILP4 change their expression patterns along the day and between long and short photoperiods in the holocyclic strain. On the other hand, no statistical differences were observed in ILP1 and ILP4 transcripts and proteins in anholocyclic aphids. In conclusion, our results highly support an active role of insulin-like peptides in the aphid seasonal response.

Strategic information provision in social insects

Authors: Czaczkes Tomer, Animal Comparative Economics lab, Department of Zoology University of Regensburg, Germany

Abstract: Social information use is extremely widespread throughout the animal kingdom, and how animals choose to use information has been extensively studied. However, for information to be used, it must be provided. The study of strategic information provision has been comparatively neglected. Foraging eusocial insects, such as ants and bees, famously communicate the availability of resources to their fellow foragers. Foragers have to make critical decisions about whether to communicate, and if so, how much. To do this, they need to integrate a wide variety of inputs in order to ensure successful foraging by their fellow foragers. At a basic level foragers need to decide whether a resource is worth recruiting to, and this depends on the resource quality other foragers are finding. Moreover, foragers need to tune their recruitment to the need for navigational help. At lower light levels, when individual navigation is hindered, ants deposit more pheromone. Foragers can even use their subjective experience of information need to tune recruitment: ants which make mistakes when trying to relocate a food source deposit more pheromone once they eventually find it. Even more intriguingly, foragers may tune their recruitment to their degree of certainty – ants which are about to make an error deposit less pheromone than ants which will go on to make correct decisions. Foraging social insects are in the rare situation of all being in the same boat – unlike predator-prey or mate communications, the foragers all have basically the same role, and so are in an ideal position to know what information is needed, and help each other based on their own experiences

VectorNet – A European network for medical and veterinary entomology

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Abstract: Public and animal health authorities face many challenges in surveillance and control of vector-borne diseases (VBDs). Those challenges are principally due to the multitude of interactions between vertebrate hosts, pathogens and vectors in continuously changing environments. VectorNet, a joint project of the European Food Safety Authority (EFSA) and the European Centre for Disease Prevention and Control (ECDC) facilitates risk assessments of VBD threats through the collection, mapping and sharing of distribution data for ticks, mosquitoes, sand flies and biting midges that are vectors of pathogens of importance to animal and/or human health in Europe. We describe the development of the network that celebrated its 10th anniversary in 2020 and the value of its most tangible outputs, the vector distribution maps, that are freely available online.

Effects of organic farming and landscape structure on biological pest control in Flemish apple orchards

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Abstract: Relying on natural predator-prey dynamics, biological pest control is often seen as a key element to achieve sustainable farming. Determining the potential of biological control for the suppression of pests, however, requires a profound understanding of how communities of pests and their natural enemies are influenced by local farming practices and landscape characteristics. Here, we used piecewise structural equation modelling to test direct and indirect effects of landscape composition, landscape configuration and local management practices on natural enemy communities, the pest control service they provide and ultimately pest infestation and crop damage. We sampled arthropods in 24 organic or Integrated Pest Management (IPM) orchards as well as in hedgerows bordering semi-natural grasslands to provide benchmark predator communities that developed free of pesticides and fertilizers. Pest control levels were quantified using sentinel eggs of codling moth and pest infestation as well as pest damage were estimated during harvest. Our results show higher predator abundance and richness in organic orchards relative to IPM orchards, but no higher predation levels. Biological control by natural enemies did not affect pest infestation in either of the management types, indicating that biological pest control alone seems to be an ineffective means to guarantee crop protection.

A role for Aedes aegypti Gr34 in sugar homeostasis

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Abstract: Mosquitoes are vectors of deadly human diseases in the world, and vector control remains a crucial part of the arsenal for disease prevention. Female mosquitoes feed not only on blood from vertebrate hosts but also on nectar from flowers and plants. It is known that nectar components such as sucrose and glucose are essential for survival, and as an energy source for flying, and for reproduction in female mosquitoes. Female mosquitoes must control the consumption and metabolism of dietary carbohydrates to achieve sugar homeostasis. Previous studies have shown that Drosophila Gr43a functions as a nutrient sensor in the brain that is important for sensing levels of fructose in circulating hemolymph. Loss of DmGr43a results in dysregulation of feeding behavior control by internal fed and starved states. Interestingly, Gr43a is among few gustatory receptors that are highly conserved, and found in most insect species. We therefore investigated the role of the yellow fever mosquito Aedes aegypti ortholog of DmGr43a, AaegGr34, by generating a mutant using CRISPR/Cas9 gene editing. We will present results of physiological and behavioral analysis of AaegGr34 mutants, which indicate a role for this receptor in carbohydrate homeostasis.

The ionotropic receptor IR56d is selectively required for perception of medium-chain fatty acids

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Abstract: Fat represents a calorically potent food source that yields approximately twice the amount of energy as carbohydrates or proteins per unit of mass. The highly palatable taste of free fatty acids (FAs), one of the building blocks of fat, promotes food consumption, activates reward circuitry, and is thought to contribute to hedonic feeding underlying many metabolism-related disorders. Despite a role in the etiology of metabolic diseases, little is known about how dietary fats are detected by the gustatory system to promote feeding. Neurons expressing the Ionotropic Receptor 56d (IR56d) are required for reflexive feeding responses to the medium-chain fatty acid, hexanoic acid. Short-, medium-, and long-chain fatty acids are appetitive to flies, but the role of IR56d in detecting these classes of fatty acids remain unknown. To determine the selectivity of the IR56d receptor, we generated IR56dnull flies and measured their response to a panel of fatty acids representing each of these classes. We find that that IR56d is required for medium-chain fatty acid taste perception, but not for perception of short- or long-chain fatty acids. Conversely, functional imaging reveals that neurons expressing IR56d are responsive to short-, medium- and long-chain fatty acids, suggesting the presence of additional receptors that are selective to short- and long-chain fatty acids. To determine whether flies can differentiate between different classes of fatty acids, we measured taste discrimination using an aversive taste memory assay. Flies are unable to discriminate between different medium-chain fatty acids, but are able discriminate between medium- and short-chain as well as medium- and long-chain fatty acids. Taken together, these findings suggest that the IR56d receptor is selective for medium-chain fatty acid taste perception. Further, these findings reveal that flies are capable of distinguishing between tastants of the same modality through neurons that are broadly tuned to short, medium, and long chain fatty acids.

Getting chased up the mountain: high elevation stress may limit ability of montane insects to respond to climate change

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Abstract: Climate change is expected to shift species distributions as populations grow in favorable habitats and decline in harsh ones. Montane animals escape warming conditions at low elevation by moving upslope, but may be physiologically constrained by conditions there. Losses of individual insect species along altitudinal gradients are likely to have profound effects on terrestrial communities, especially in montane environments where species diversity is low. Effects of high elevation were studied for montane populations of the leaf beetle Chrysomela aeneicollis, where allele frequencies at nuclear genes and the mitochondrion vary along latitudinal and altitudinal gradients. A population presence survey conducted along a steep altitudinal transect (1600-3800 m) from 1981 to 2018 revealed that populations expand to low elevation following wet winters and retreat during drought. Quantitative surveys of a 45-site population network conducted from 2012-2018 along multiple altitudinal transects shows that when beetles are abundant, population size peaks at 3135 m, highest altitude populations are at the southern edge of the range, and populations decline and extirpate during drought, especially at low elevation. To examine effects of elevation on measures of performance and fitness, beetles from a genetically-introgressed population (Bishop Creek- BC) were examined. In nature, fecundity of females transplanted along natural altitudinal transects was measured, as was activity of the electron transport enzyme cytochrome c oxidase (CytOx). To examine effects of environmental hypoxia independent of other factors limiting persistence at high elevation, larval development and metabolic rates were measured for larvae reared under otherwise common garden conditions at low (1250 m) and high (3800 m) elevation. In nature, fecundity declined with increasing elevation, independent of air temperature. CytOx activity was higher at high than low elevation, especially for individuals possessing genotypes of southern origin. Laboratory-reared larvae with southern mitochondrial haplotypes developed equally well at both elevations, but larvae with northern haplotypes developed more slowly at high elevation. Metabolic rates showed a similar pattern, suggesting that slower development rates at high elevation may be due to reduction in metabolic rate. These findings suggest that physiological effects of environmental hypoxia may contribute to other factors known to restrict insects' ability to persist at high elevation, ultimately disrupting associated ecological communities (e.g. loss of specialist beetle predators and other enemies). However, some populations may possess genetic variation that allows for local adaption to high elevation.

Genetic control of molting and metamorphosis in the silkworm

Authors: Daimon Takaaki, Kyoto University, Japan

Abstract: The number of larval instars in insects varies greatly across insect taxa, and can even vary at the intraspecific level. However, little is known about how the number of larval instar is fixed in each species or can be changed depending on the environment. The silkworm, Bombyx mori, would provide unique bioresources to elucidate this question, as there are several “moltinism” strains that exhibit variations in the number of larval molts. We have been working on moltinism mutants of Bombyx, and identified the genes responsible for the dimolting (mod) mutant and Molitinism (M) locus. We are hopeful that our studies will pave the way for a greater understanding of physiological control, developmental plasticity, and evolutionary history of the number of larval molts in insects, which may reflect adaptive strategies of insects to diverse environmental conditions.

Hox-mediated repression of ecdysone biosynthesis confers intraspecific variation in the number of larval instars in Bombyx

Authors: Daimon Takaaki, Kyoto University, Japan

Abstract: In insects, the number of larval molts varies inter- and intra-specifically, and it is widely accepted that the variation in the number of larval molts is an adaptive response to diverse environmental conditions. However, the molecular mechanism that underlies the variety and plasticity in the number of larval molts is largely unknown. In the silkworm, Bombyx mori, there are strains that molt three, four, or five times, and these numbers are determined by allelic variation at a single autosomal locus, Moltinism (M). Here, we demonstrate that the Hox gene Sex combs reduced (Scr) is responsible for the phenotypes of the M locus. Our results suggest that Scr represses the biosynthesis of molting hormones in the PG, thereby regulating the incremental increase in body size during each larval instar. While the role of Hox genes in conferring segmental identify along the body axis and in molding segment-specific structure later in development has been well-established, our study identifies an unexpected role of Hox gene in hormone biosynthesis. This new role means that in addition to shaping segment-specific morphology, Hox genes also drive the evolution of life history traits by regulating animal physiology.

DIPA-CRISPR is a simple and accessible method for insect gene editing

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Abstract: Current approaches for insect gene editing require microinjection of materials into early embryos. This severely limits the application of gene editing to a great number of insect species, especially to those whose reproduction systems preclude access to early embryos for injection. To overcome these limitations, we here develop a simple and accessible method for insect gene editing, termed Direct Parental CRISPR (DIPA-CRISPR). We show that injection of Cas9 ribonucleoproteins (RNPs) into the haemocoel of adult females efficiently introduces heritable mutations in developing oocytes. Importantly, commercially available standard Cas9 protein can be directly used for DIPA-CRISPR, which makes this approach highly practical and feasible. DIPA-CRISPR enables highly efficient gene editing in the cockroaches, on which conventional approaches cannot be applied, and in the model beetle Tribolium castaneum. Furthermore, we show that DIPA-CRISPR-mediated targeted gene knock-in can be achieved in beetles by co-injection of single-stranded oligodeoxynucleotides (ssODNs) with Cas9 RNPs. Due to its simplicity and accessibility, DIPA-CRISPR will greatly extend the application of gene editing technology to a wide variety of insects.

Integrated Pest Management in UK Forestry

Authors: Dainton Katrina, Forest Research, Northern Research Station, Scotland, United Kingdom

Abstract: Forests are essential to the health of the planet. They support biodiversity, provide ecosystem services, sequester carbon, mitigate climate change, and promote human health and wellbeing (Sing et al., 2018). Insect pests that damage and kill trees can drastically alter landscapes and ecosystems. Bark beetles, for example, have killed millions of hectares of forest across Europe and North America (Hlásny et al., 2019). In the UK, where forests are smaller and less contiguous, tree damage and mortality tend to be more localised, although several diseases (i.e. Dutch elm disease, Ash dieback and Phytophthora ramorum) have had widescale impacts on specific tree species.

To mitigate the negative effects on trees and landscapes it is necessary to manage these tree health threats. Different management options are available, some of which can themselves directly impact landscape scale change, e.g. felling and removing trees. Integrated pest management (IPM) approaches promote the use of preventative measures to protect trees from pests whilst reducing the need for more drastic reactive methods.

In this presentation I will introduce and share preliminary results from my PhD project (supervised by University of Edinburgh, Scotland's Rural College and Forest Research) which aims to evaluate and enhance IPM awareness and use in UK forestry. This research will assess the methods being used to manage insect pests in UK forestry. It will also investigate forest manager perspectives on the opportunities and challenges of taking an IPM approach. Identifying current challenges, including if there is a gap for new practices, will inform the focus of a case study, including laboratory and field trials.

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Insect conservation on golf courses: Integrating recreational land management and urban biodiversity conservation

Authors: Dale Adam[2], Cope Grace[2], Daniels Jaret[1] and Perry Rebecca[2], [1]Florida Museum of Natural History University of Florida, United States, [2]University of Florida Entomology and Nematology Department, United States

Abstract: Urbanization is the leading form of land use change and driver of biodiversity loss. As urbanization progresses, habitats are fragmented and vegetation is replaced with impervious surfaces. Golf courses are among the largest, most ubiquitous maintained green spaces within many urban areas. Although their primary function is recreation, a large portion of golf course land is primarily aesthetic, which presents opportunities to create more ecologically functional space and provide valuable urban conservation services. Many courses around the world are converting out-of-play areas to naturalized or wildflower habitats, but few do so using evidence that maximizes their conservation benefit. Based on previous research, we know that factors commonly associated with golf courses, like elevated nutrient content and reduced plant diversity may affect conservation efforts. Here, we aim to develop evidence-based guidelines that maximize the conservation benefits of golf course out-of-play areas. First, we ask if flowering plant species richness influences the effect of wildflower habitats on solitary bee and natural enemy conservation. Then we determine if this effect translates to biological control of key golf course pests in adjacent in-play areas. Finally, we test the hypothesis that soil nitrogen availability, associated with golf course turfgrass fertilization, affects host plant quality and butterfly fitness, and if that effect depends on plant species richness. Our results indicate that golf courses can provide valuable resources for urban pollinators and other beneficial insects, both flying and ground-dwelling. Interestingly, plant species richness does matter for beneficial insect conservation, but is not as important in translating to insect pest control. Nitrogen is an important factor that must be considered when evaluating the effects of urbanization on insect conservation efforts. Thus our results have important implications for tailoring insect conservation practices to golf courses and other urban green spaces to maximize their ecological value.

The association of symbiotic Rickettsia with omnivorous mirid bugs (Hemiptera)

Authors: Dally Maria, Hebrew University, Israel

Abstract: Bacterial symbionts are common in arthropods, where some of them are known to influence host nutrition and diet breadth. It was therefore interesting to explore the involvement of symbionts in the nutritional ecology of omnivorous insects, consumers that feed on both prey and plant food sources. Like most other insects, omnivorous consumers harbor symbiotic bacteria in their body. Omnivorous bugs of the genus Macrolophus (Heteroptera: Miridae) are mainly predatory but may also feed on plants. M. pygmaeus and M. melanotoma (=M. caliginosus) are key natural enemies of various economically important agricultural pests. To test for possible involvement of symbiotic bacteria in plant feeding habits of M. pygmaeus and M. melanotoma, we first determined that the microbiome of all tested individuals is dominated by Wolbachia (reported to induce cytoplasmic incompatibility), and two Rickettsia species, R. bellii and R. limoniae. FISH analyses revealed that in both M. pygmaeus and M. melanotoma, females Rickettsia species are found in the germarium, the apical end of the ovarioles within the ovaries, a location that suggests vertical transmission. In both Macrolophus species, the two Rickettsia species mostly occupied separate epithelial cells both in the mid-gut and its unique outgrowth, caeca-like organs, and in the Malpighian tubules. Yet, each Rickettsia species had a unique distribution along the digestive system, a pattern that differed between the two Macrolophus species. These species-specific Rickettsia distribution patterns may suggest a different roles in host nutrition, allowing it to derive nutrients from both prey and plant materials.

Deciphering moth sex pheromone biosynthesis pathways and biotechnological production in yeast

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Abstract: The larvae of moths (Lepidoptera) are key agricultural pests, causing significant economic loss on major and valuable crops such as rice, soybean, tomatoes and apples. There is a pressing need to find alternatives to conventional insecticide control, because of human and environmental toxicity, governmental restrictions and resistance development. The use of insect sex pheromones is a sustainable method with a growing market within integrated pest management, working to control moth population in a species-specific manner by either trapping and eliminating male moths in the crop area or preventing them from locating females and thereby achieving mating disruption. This method is already successful at large scale in organic fruit farming, vineyards and in control of certain deciduous forest pest, and to a smaller extent in the production of cotton, rice and cabbage. Chemical synthesis of these pheromones can be complicated and involve harmful chemicals and waste products, whereas with biotechnological production in yeast or plants we can take advantage of enzymatic specificity and cheap renewable feedstocks. With the discovery of pheromone biosynthesis pathways and -genes in the pest insect, “cell factories” can be engineered to produce insect pheromones in the same way we use microbes for production of for example drugs, enzymes, biofuel and industrial chemicals and food additives. We have demonstrated yeast production of pheromones for pests on maize, rice, cotton and cruciferous crops, including the rapidly expanding fall armyworm (Spodoptera frugiperda) and the globally distributed diamond back moth (Plutella xylostella).

Incompatible Insect technique feasibility to control Aedes invasive mosquitoes in Europe

Authors: Damiani Claudia[1], Moretti Riccardo[2], Calvitti Maurizio[2], Fabbri Giulia[3], Lampazzi Elena[2], Serrao Aurelio[1] and Lombardi Giulia[3], [1]BiovecBlok srl and University of Camerino, [2]ENEA Biotechnology and Agroindustry Division, [3]University of Camerino, Italy

Abstract: Incompatible Insect Technique (IIT) is a genetic control strategy based on the exploitation of a natural phenomenon of egg inviability induced by an opportune infection of the endosymbiotic bacterium Wolbachia. Establishing an artificial Wolbachia infection in a species that is uninfected, or naturally infected by a different Wolbachia strain, enables to mass produce and release mosquito males that may sterilize wild-type females without the recourse to any preliminary treatment. Thus, this strategy assures full preservation of male fitness and simpler mass rearing protocols compared to other genetic control strategies as like SIT.

Biovecblok S.r.l., in collaboration with ENEA and the University of Camerino, is exploring the feasibility of proposing IIT as a suppression tool against Aedes albopictus and other Aedes mosquitoes. The present work reports on preliminary studies addressed to test efficiency, safety, and sustainability of applying this strategy on a large scale both in the European context and in Tropical regions where arboviral diseases are endemic. Obtained results are encouraging and allow to be optimistic regarding the future development of this approach.

Plant phenological sensitivity to warming elevates herbivory

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Abstract: Species interactions can drive ecosystem processes and are thus a major focus of global change research. Some of the most consequential interactions expected to shift with climate change are between insect herbivores and plants, both of which are highly sensitive to temperature. Historically, insect herbivores and their host plants display varying levels of synchrony that could be disrupted or enhanced by climate change. Here, with herbarium specimens of 26 plant species collected from 1900 to 2015, we show that plant species whose phenology is more sensitive to warming are more likely than co-occurring, insensitive species to incur elevated levels of insect damage or ‘herbivory’ in warmer years. Our results point to a scenario in which warming lengthens growing seasons for phenologically sensitive plant species, exposing their leaves for longer periods of time to herbivores. Mounting evidence indicates that, in the short-term, plant species that are able to track changing temperatures have a fitness advantage over coexisting species that are less sensitive. However, we show that plants that are sensitive to warming are also exposed to elevated herbivory when temperatures are warmer, which may affect plant fitness and thus community composition and ecosystem function over longer timescales.

Hemoglobin genes are present and expressed throughout Hexapoda

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Abstract: The tracheal system of insects, comprised of intricate cuticular invaginations branching within the body, provide direct access to tissues for gas exchange. Although notable exceptions exist, such as the well-known reddish hemolymph of chironomid midges and recently discovered hemoglobins in a handful of taxa, insects have long been thought to not require respiratory proteins and thus lack hemoglobins. Hemoglobins, however, have been shown to be ancient in origin and are ubiquitous among animals and plants. A comprehensive analysis of transcriptomes across Hexapoda has revealed the expression of hemoglobin genes in all 32 orders of hexapods, including all 29 recognized orders of insects. Discovery and identification of 1333 putative hemoglobins was achieved with target gene BLAST searches of the NCBI TSA database, verification of the presence of functional residues, secondary and tertiary structure predictions, and machine learning-based localization predictions. While the majority of these proteins are intracellular, extracellular hemoglobins were also recovered in a handful of specimens. Hemoglobin gene trees were constructed via multiple-sequence alignments and phylogenetic analyses. These investigations into sequence evolution indicate probable duplication events and adaptive function/significance. Future work involving genome comparisons to transcriptome results and comparative investigations of morphology and ecology will further illuminate the possible roles of these hemoglobins in insects.

Can artificial diets support cost-effective mass production of omnivorous predators?

Authors: De Clercq Patrick, Laboratory of Agrozoology, Department of Plants and Crops, Belgium

Abstract: The use of arthropod predators in augmentative biological control programs necessitates the availability of cost-effective mass rearing systems, allowing the production of large numbers of beneficials at the lowest possible price. Many of these predators are polyphagous to some degree, but it does not necessarily follow that they can be produced on a wide choice of easily reared prey. In addition, several species are omnivores and benefit from or need plant materials to acquire moisture or supplementary nutrients, or they may require plant substrates for oviposition, complicating their mass rearing and shipping. Good success has been obtained with the use of factitious (unnatural) prey for the commercial production of some predatory heteropterans, coleopterans, and neuropterans (e.g. lepidopteran eggs, brine shrimp cysts), as well as several species of predatory mites (e.g. various storage mites). In contrast, despite several decades of research, artificial diets have hardly been used in the commercial mass production of polyphagous predators, with a diet for lacewings being one of the few exceptions. The reasons for the limited success with artificial diets for the production of predatory arthropods as well as potential research avenues will be discussed.

Managing stink bugs on soybean/maize crop systems in the Neotropics

Authors: de Freitas Bueno Adeney, Researcher in Entomology of Embrapa Soybean, Brazil

Abstract: Alternating cultivation of soybean (summer crop) and maize (fall/winter crop) favors population growth and permanence of some stink bug species feeding on crop plants, mainly due to the constant food supply ("green bridge"). Among these species, Euschistus heros and Dichelops melacanthus stand out with their high abundance and injury potentials. Although E. heros causes lower damage on maize than D. melacanthus, growers frequently control both species in these crops. The most important control strategy is the use of insecticides. However, these should only be applied when economic thresholds are reached. Moreover, other control strategies such as the mass release of the egg parasitoid Telenomus podisi should be adopted. Studies have shown that this parasitoid has high parasitism rates on both E. heros and D. melacanthus eggs, and high field performance. In addition, research results indicate that D. melacanthus does not develop well when feeding only on maize seedlings. Therefore, crop remains (soybean seeds dropped on the ground, dry pods, volunteer soybean) and the presence of invasive plants (such as Commelina sp.) play an important role in the development and reproduction of these pests in the production system and should be avoided in order to manage stink bugs in the soybean/maize crop systems. In fact, only a combination of different stink bug management strategies in soybean integrated pest management (IPM) as a whole can be effective against the pest. In the state of Paraná, Brazil, where IPM is adopted, growers are able to successfully manage these pests with a greatly reduced use of insecticides (around 50%).

Quis custodiet ipsos custodies? Hesperomyces virescens, a potential biocontrol agent against the invasive ladybird Harmonia axyridis

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Abstract: Harmonia axyridis is an invasive alien ladybird in North America and Europe. Studies show that natural enemies are starting to use Ha. axyridis as a new host. No studies have focused on the effects of simultaneous infections of multiple natural enemies on Ha. axyridis. We hypothesized that high thallus densities of the ectoparasitic fungus Hesperomyces virescens on a ladybird weaken the host's defenses, thereby making it more susceptible to infection by other natural enemies. We examined mortality of the North American-native Olla v-nigrum and Ha. axyridis co-infected with He. virescens and an entomopathogenic fungus – Beauveria bassiana or Metarhizium anisopliae. Laboratory assays revealed that He. virescens-infected O. v-nigrum are more susceptible to entomopathogenic fungi, but not Ha. axyridis. In another experiment, both fecundity and hatchability were significantly lowered in female ladybirds when co-infected with Spiroplasma bacteria and He. virescens. Considering these results, we can start asking how He. virescens affects survival against other pathogens that previously had little impact on Ha. axyridis.

Citizen science records to complete global distribution patterns of both Harmonia axyridis (Coleoptera, Coccinellidae) and its parasite Hesperomyces virescens

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Abstract: Harmonia axyridis (Coleoptera, Coccinellidae) is a globally invasive ladybird. It was intentionally introduced in many countries as a biological control agent and it has been unintentionally released in many other countries. For a long time, no published reports were known from Central America. Searching through online photographs available from the citizen science project iNaturalist and the photo-sharing platforms Flickr, we reported Ha. axyridis from Costa Rica, Guatemala, Honduras, Panama, and Puerto Rico. The biotrophic microfungus Hesperomyces virescens causes mortality of its ladybird hosts, which makes it a potential biological control agent of Ha. axyridis. Again, photographic records have been obtained from iNaturalist, Flickr, and BugGuide.Net to map the distribution of He. virescens associated with Ha. axyridis in North America and Europe. A social media campaign is in progress to encourage European citizen scientists to contribute photo-records. A dedicated He. virescens–Ha. axyridis project was launched on iNaturalist and distribution maps of curated records will be made available through https://beetlehangers.org/. We stress the need for citizen science projects to assess the presence of alien invasive species and their natural enemies.

Why Open Biodiversity Data matter for equitable and fair share of benefits defined by the Nagoya Protocol

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Abstract: The Convention of Biological Diversity (CBD), and its supplementary agreement of the Nagoya Protocol which has now been ratified by 113 UN member states and the EU, firmly established the territorial sovereignty over all genetic resources and conditioned the rights of scientists to use such resources without the permission of the relevant government authorities. The Protocol was agreed in 2010 and the entomological community has to comply with the fair access and benefit sharing regulations defined by the Protocol and to learn to work in different ways, with different thinking and different reasoning. Despite the guidelines being clear, the implementation of the legislation and the translation of the Nagoya Protocol into laws is a very slow, complicated and diverse process, full of legal and practical uncertainties. Furthermore, a deep and non-consensual split along North-South governmental lines is formed for meeting the benefit-sharing obligations defined by the Nagoya Protocol. Though all parties acknowledge that knowledge sharing and exchange in the form of Open Access that document successes and failures is one of the best practices, it does not solve the goals of benefit sharing defined by the Nagoya Protocol. The recently (10 May 2019) adopted Code of Conduct and annexed best practices of the CETAF, uniting the major European Insect Collections and depositories, has the intention to show a way of successful development of community-based approaches and non-monetary sharing of benefits inside the European Union.

Global Biodiversity Information Facilities aggregates biodiversity data on a global scale and strongly focuses on the integration of a variety heterogeneous data into a synergetic framework of biodiversity data across different domains. Here it is suggested that the global non-monetary, free and open access to biodiversity data, through sharing of datasets under open licence and aggregation through intergovernmental collaborative network composed of governmental bodies and international organizations from countries of all global regions and of all income levels, could be helpful in the context of the current discussions within CBD. The GBIF community is dedicated to the vision of free and universal access to biodiversity data, for science, society and a sustainable future. The opening of primary biodiversity data obtained globally and processed by FAIR principles can assist to remove barriers that prevent institutions and individuals from sharing data, due to a wide range of factors including professional, cultural, institutional, legal and economic concerns. The non-monetary sharing of biodiversity data via global mega data aggregators such as GBIF can serve as a common ground to solve the disagreements related to the benefit-sharing applications between biodiversity rich and economy rich countries as well as stimulate the international cooperation on biodiversity research beneficial for all parties involved.

Medication in monarch butterflies: the role of plant toxins and host microbes

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Abstract: Parasites pose major threats to their hosts' fitness, and hosts can protect themselves against infection through innate immune responses, anti-infection behaviors and microbial defenses. Monarch butterflies are specialist feeders of milkweed host plant species, which vary in their toxicity of secondary chemicals called cardenolides. Monarchs are commonly infected with a protozoan parasite, and infected females preferentially lay their eggs on high-cardenolide species of milkweed, which reduce infection in their offspring. While previous work suggests that these cardenolides directly interfere with parasite infection, current studies also indicate that milkweeds alter the monarch gut microbiome, and that the altered microbiome contributes to parasite resistance. I will summarize the medication behaviors of monarchs and discuss the role of plant chemicals and the gut microbiome in determining parasite resistance.

Management of Plant-Parasitic Nematodes by The Use of Three Saturated Hydrocarbons

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Abstract: The plant parasitic nematodes (PPNs) cause major loss in food production globally. According to an estimation it is 12.3% annually. Among PPNs, Root-knot nematode (RKNs), Meloidogyne spp, group is a problematic soil pest which is distributed worldwide. Presently no full proof strategy is available for control of this pest. Practices that are commonly prioritized by farmers to check the population of these RKNs are chemical based. Thus, the concept of integrated pest/crop management includes a threshold concept for the application of pest control measures and reduction in the amount/frequency of pesticides applied to an economically and ecologically acceptable level. Therefore, research is focused on how to use of straight chain hydrocarbons presents in plant extracts with hexane solvent. In vitro analysis, two concentrations of pure hydrocarbons were applied over a counted number of nematodes. In this study Undecane, dodecane, tridecane were used to check the mortality of Meloidogyne spp. at 1 PPM and 10 PPM. Mortality status of nematode population by counting the live as well as dead individuals after applying a 500 µl of extract was recorded at different time durations i.e., 24h, 48h, and 72h. Undecane seems a promising source for eco-friendly management of Meloidogyne spp.

Nutritional composition, growth and development performance of black soldier fly (Hermetia illucens) prepupae reared on seaweed-enriched substrates

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Abstract: Larvae of the black soldier fly (BSF) are able to convert organic waste such as animal feces and kitchen waste into high-quality biomass, which can be processed into animal feed. However, the influence of marine substrate on BSF life cycle traits, as well as nutritional composition of deriving prepupae have not been thoroughly investigated. Accordingly, the aim of this study was to evaluate the effect of inclusion of brown algae (Ascophyllum nodosum) in BSF growing substrate on nutritional composition of deriving prepupae and insect life cycle traits.

The larvae were reared on two different substrates: i) Gainesville diet used as control substrate (CTR) and ii) Ascophyllum nodosum diet (AN30%) in which Ascophyllum nodosum meal was included in substitution of alfalfa meal (300 g·kg-1 of dry substrate).
Eggs collected from a stable colony of BSF were placed for hatching on two experimental substrates CTR and AN30%. All experiments were carried out under dark condition, at 25°C with 70% relative humidity, and repeated for three consecutive generations. Both rearing substrate and deriving prepupae were analyzed for proximate and fatty acid composition. Results were expressed on dry matter basis (DM). Percentage of mortality in each stage, development period (days required to reach pupa stage), larvae weight, percentage of adult formation, percentage of adult emergence were also recorded.
With regard to nutrient composition mean protein content was 536 g·kg-1 DM in CTR and 446 g·kg-1 DM in AN30% group. Considering fatty acid composition of both CTR and AN30% prepupae were dominated by saturated fatty acids (74.76±2.72% and 83.04±0.48%, respectively). Despite the inclusion of seaweed in the rearing substrate, the concentrations of unsaturated fatty acid were not incremented in AN30% prepupae compared to CTR prepupae. However, a slight increase in eicosapentaenoic acid in in AN30% prepupae compared to CTR ones has been observed. Considering early stages survival, during the larval and pupal stages, no significant differences in mortality were observed between larvae reared on CTR and AN30% substrate. In contrast, BSF development period was lower ($P<0.05$) in CTR than in AN30% group (29.5 vs 43 days, respectively). Finally, no differences were observed between CTR and AN30% pupae in term of weight. Combining obtained results BSF larvae can be grown on media containing up to 30% Ascophyllum nodosum with limited detrimental effect on growing performances. However, further investigations are required for understanding the effect of the composition of the feeding media on the nutritional value of deriving larvae in order to produce BSF meal more suitable for specific feed or food purposes.

Effect of propagule pressure and temperature on establishment success of Bactrocera zonata

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Abstract: The peach fruit fly, Bactrocera zonata (Diptera: Tephritidae) is a major pest of mango, peach and guava. It is of Asian origin, and is currently present in southern Asia, the Middle East and north eastern Africa. It is of concern to areas where it is not yet established, and is listed as a quarantine pest in Europe, Australia and the Americas. Preventing the establishment of B. zonata in new areas relies on understanding the factors influencing its population establishment potential. The two most influential factors for successful establishment of new populations has been shown to be environmental suitability and propagule pressure – that is, the number of founding individuals, and the timing and frequency of introduction events.

This study aimed to determine the influence of, and interaction between, the size of the founding population, number of introduction events and environmental temperature on the establishment success of B. zonata colonies in a laboratory experiment. Bactrocera zonata colonies were initiated by introduction of founding individuals to 3L plastic containers providing ample space and food for colony growth. Five different founding population sizes (n=2, 4, 8, 16 and 20) introduced at four different introduction rates (all at once or incrementally) were tested. This was repeated at three different temperatures (20°C, 25°C and 30°C) to determine the influence of ideal (25°C) or adverse (20°C and 30°C) temperatures on establishment success. We considered establishment to be successful if adult emergence in the F1 generation was greater than the number of founding individuals. We found that adverse hot and cold temperatures resulted in significantly increased mortality and decreased establishment success of B. zonata colonies. Increasing the number of introduction events and the size of founding population also increased successful establishment, especially at adverse temperatures.

The results obtained highlight the factors important for establishment of B. zonata, and give insight into factors and interactions that may be important for establishment and invasion of fruit fly pests in general.

Interspecific interactions between a new invasive Tephritid fruit fly, Bactrocera dorsalis, and other resident species in an insular context

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Abstract: The impact of biological invasions of insects considered as pests has important negative impacts on the economy and the environment, partly because invaders can affect the structure of the community through direct and indirect effects on resident species.

Since the detection, in April 2017, of one of the most harmful pests of fruit and vegetable crops worldwide, Bactrocera dorsalis, Reunion island counts nowadays nine pests species of Tephritid fruit flies of economic importance. Despite the presence of a biological control agent, Fopius arisanus (Braconidae) originally introduced for controlling Bactrocera zonata, B. dorsalis was found to have a high infestation rate and an extreme polyphagia (over 50 host-plant species). Since its invasion, the structure of the fruit fly community has changed: the most abundant species on the island, B. zonata, has almost disappeared, and the host range of other polyphagous species (C. capitata and C. quilicii) has been modified.

To understand the invasion process of B. dorsalis and the impact of this newly introduced fruit fly on the community structure of the resident Tephritid species, and the parasitoid, F. arisanus, it is necessary to study interactions experimentally. We assessed both direct and indirect interactions among polyphagous fruit flies and F. arisanus: i) by analysing interspecific competition among fruit flies, considering competition among female adults for oviposition, and competition among larvae for food resources; ii) by observing host species preference of F. arisanus according to plant species; and iii) by testing the effects of indirect interactions among fruit fly species mediated by F. arisanus.

Bark beetles, drought and tree mortality: Examples from California and Southwest Germany

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Abstract: Bark beetles (Coleoptera: Curculionidae, Scolytinae) are important disturbance agents in conifer forests of temperate and boreal ecosystems, and several notable species are capable of causing significant amounts of tree mortality. Trees of all species, ages and size classes may be colonized and killed, but each bark beetle species exhibits unique host preferences, life history traits and impacts. Mechanisms contributing to outbreaks are complex, poorly understood, and include density-dependent and density-independent factors. In recent years, climate change has contributed to some bark beetle outbreaks in North America and Europe due to shifts in temperature and precipitation that influence both the beetles and their hosts.

Applying anchored hybrid enrichment to study gene flow in the Himalopsyche martynovi species complex (Trichoptera: Rhyacophilidae)

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Abstract: The caddisfly genus Himalopsyche contains 56 species, including 3 species complexes which show variation on both genotype and phenotype within species complex. In the Himalopsyche martynovi species complex there is striking phenotypic diversity among groups of individuals, but previous phylogenetic data was unable to resolve relationships within this clade. We use a comprehensive dataset (791 loci, 655,236 bp, average locus length of 750 bp) generated from anchored hybrid enrichment to study the phylogenetic relationships among individuals of H. martynovi species complex (H. martynovi: 5 males; H. epikur: 2 males, 1 larva; H. viteceki: 2 males) and 1 male of H. immodesta as outgroup. The phylogenetic reconstruction based on the filtered dataset presents highly consistent gene and species trees with strong node support. The concatenated analysis reveals that H.viteceki is sister to H. martynovi + H. epikur. H. martynovi and H. epikur are not fully resolved: H. martynovi species complex splits into two lineages (from hereon group 1 and group 2), where group 2 forms a clade with H. epikur. Groups 1 and 2 also differ slightly in male genitalia, but group 2 is morphologically distinct from H. epikur. To better clarify the species delimitation, we apply D-statistics and DFOIL to detect the introgression among clades. The results indicate a high probability of gene flow among all three nominal taxa.

Molecular and functional characterization of masculinizer gene in Helicoverpa armigera

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Abstract: Bombyx mori Masculinizer(BmMasc) gene is known to control sex development and dosage compensation in B. mori. It remains unclear whether its orthologues also exist and play the same roles in Helicoverpa armigera. To address this question, we used BmMasc protein sequence to blast against the reported transcriptome datasets of H. armigera and retrieved a partial sequence of Masc from H. armigera (HaMasc). Subsequent 5’/3’ RACE, full-length RT-PCR cloning and BLAST search against the male genome of H. armigera showed that HaMasc contains 12 exons and transcribes into two alternative transcripts that differ in the transcription start site and splicing of its 1stintron. Genomic qPCR showed that HaMasc copy number was 2.24-2.40 fold greater in males than in females. RT-qPCR analysis revealed that HaMasc transcripts were significantly more abundant in the embryonic stage, head, and males than in the other stages, other body parts and females, respectively. Transfection of a mixture of 3 siRNAs of HaMasc into aH. armigera male embryonic cell line resulted in reduction of HaMasc transcripts, appearance of the female-type transcript of doublesex gene, and greater transcription of 13 out of the 15 tested Z chromosome genes. Feeding male neonates with the mixture of the 3 HaMasc siRNA for 3 days caused HaMasc knockdown, upregulation of Z chromosome genes, and reduction in the sizes and weights of male pupae testes and male pupae body. These results demonstrate that HaMasc also locates on Z chromosome and regulates sex determination and dosage compensation in H. armigera.

Can the genetic structure of Malus sylvestris impact the feeding behavior and fitness of the rosy apple aphid pest Dysaphis plantaginea?

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Abstract: Apple production can be highly impacted by one of its major aphid pest, the rosy apple aphid (RAA, Dysaphis plantaginea). Surprisingly, the trophic interaction between the RAA, the domesticated apple tree Malus domestica and its crop wild relatives remains unexplored. The European crabapple Malus sylvestris has been one of the main genetic contributors of the apple tree domestication therefore representing a potential source of interesting genetic traits. We assessed the potential resistance of M. sylvestris to RAA by measuring life history traits (aphid weight, daily fecundity and survival of aphid adults) and recording the aphid feeding behavior (electropenetrography technique) within three European populations of M. sylvestris (intraspecific comparisons). Interspecific comparisons were also performed using a Malus domestica pool of seedlings.

Regarding life history traits, there was no or little intraspecific or interspecific differences. Aphid feeding behavior emphasized that M. sylvestris resistance was exclusively linked to phloemian factors and highlighted varying levels of resistance between M. sylvestris populations. Interspecific comparisons showed that one population of M. sylvestris was as sensitive as M. domestica, thus being able to act as RAA reservoir. Depending on the chosen populations, M. sylvestris, could therefore represent an interesting genetic source to confer RAA resistance in apples.

Wing morphological disparity to better understand the patterns of odonate biodiversity in Paris region

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Abstract: The recent alarming loss of species induced by human activities is regarded as the premises of a sixth mass extinction, in reference to the past five major crises evidenced by the fossil record. However, formal comparisons of the Recent with the Fossil remain very few due to analytical limitations. The fossil datasets are subject to sampling biases, and the metrics of diversity are particularly difficult to compare. We propose to apply morphology-based metrics to investigate anthropic pressure on diversity and to compare its effects to past mass extinctions.

Although differing in their respective, underlying causes, the past five major mass extinctions share similar properties, including a major drop of taxonomic richness affecting all types of ecosystems at a global scale. Several studies suggest a change in extinction selectivity during these events. While extinction risk of a given taxon is related to its ecology and to changes in environmental conditions, selectivity decreases during mass extinction events. All types of ecology undergo extinction but, in surviving groups, ecological diversity is often preserved. A measure of morphological diversity can be used to summarize ecological diversity of a group and to test selectivity of diversity loss.

Initiated by S. J. Gould and further developed by M. Foote and colleagues, metrics aiming at quantifying morphologic diversity (disparity) have been developed and tested on the fossil record. The notion of disparity is used to express morphological diversity and body plan variety, as opposed to taxonomic diversity. The corresponding metrics are expected to be much less sensitive to sampling heterogeneity than species richness. The contrast between morphological and taxonomic diversity has been used to describe the properties of extinction events in the fossil record.

To test the proposed approach we analysed diversity and disparity patterns of odonates in several sites, from pristine to highly artificialized environments in the Ile-de-France area, including Paris. Assessment of taxonomic richness is based on standardized data from the Steli, a citizen science program for odonate diversity monitoring in France. Disparity was measured based on selected morphological features of odonate wings which could be taken into account using morphometric approaches. A morphospace encompassing all odonate species recorded in Ile-de-France was derived. Disparity values were computed for each individual site.

Our results have shown a correlation between disparity and diversity. More importantly, they highlighted sites of interest, in the most artificialized areas, with really low diversity but high disparity. However there is no evidence of more tolerant species and there is no clear impact of artificialization on odonate disparity. Streams have been found to be more conductive to odonate disparity. In the case of the disappearance of threatened species, the loss of diversity linked to a constant disparity support a scenario of non-morphologically selective extinction.

Extreme genome reduction in the minute tomato pest Aculops lycopersici

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Abstract: The tomato russet mite, Aculops lycopersici, is an extremely small metazoan species, with a length of merely 150 micrometer. This specialized mite belongs to the Eriophyoideae (Arthropoda: Chelicerata: Acari: Acariformes) and is a destructive priority pest on tomato and able to manipulate the defense response of its host. The tomato specialist A. lycopersici has the smallest genome yet reported for an arthropod, together with the lowest total number of genes. Along with a reduction of intergenic distance and transposable elements, we report extraordinary intron loss, with more than 80% of coding genes having no introns. As compared to a generalist mite herbivore, the two-spotted spider mite Tetranychus urticae, gene families associated with detoxification - cytochrome P450 monooxygenases, carboxyl/cholinesterases and glutathione S-transferases - and chemosensory perception, which are known or implicated in the interaction of herbivores with their plant hosts, are extremely reduced. However, reductions in nearly all gene families were observed. Our work provides a unique insight into the genomic changes associated with arthropod host specialization, as well as that associated with extreme physical miniaturization in metazoans. Furthermore, it provides a molecular basis for investigating the interaction between A. lycopersici and its Solanaceae host.

Does dim Artificial Light At Nigh affect physiological, life-history and behavioural traits in a parasitoid wasp?

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Abstract: Artificial Light At Night (ALAN) is a widespread phenomenon impacting nocturnal species, mostly in a negative way, at several biological levels. Insects are not spared, with potential dramatic consequences on many species, some of them being involved in ecosystem services such as pollination or biological control. However, the impact of ALAN on diurnal species is still rarely studied. Yet, lengthening of the photophase due to ALAN is likely to modify the activity patterns of diurnal organisms, with potential consequences on their behaviour and fitness.

We investigated the effects of ecologically relevant ALAN intensities on the diurnal parasitoid Venturia canescens. First, we examined if ALAN modified the diel activity patterns of insects in terms of foraging for hosts and food, and thus impacted their lifetime reproductive success. Recording the daily survival and offspring production also allowed us to have an insight into both actuarial and reproductive senescence in this species, and to determine if it differed between different light pollution regimes. Secondly, we studied more specifically the behavioural responses of parasitoid females to ALAN in relation to their energetic reserves, at both intra- and between-generation levels. We focused on the decision to search for hosts (immediate fitness gain) or food (delayed fitness gain) that is involved in the state-dependent trade-off between current and future reproduction. The decision-making was modified by ALAN, but without involvement of the energetic reserves.

Our results clearly demonstrate that ALAN has consequences on a diurnal parasitoid species, and therefore raise the question of the effects of light pollution on biological control efficiency.

Influence of bacterial symbionts on host niche and ecological diversification: an integrative approach in a whitefly model

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Abstract: Symbiosis has been associated with major evolutionary innovations. For instance, the acquisition of nutritional obligate symbionts allowed phytophagous insects to feed on plant sap. The whitefly Bemisia tabaci (Hemiptera: Aleyrodidae) is a major economic pest forming a species complex with many biotypes. In addition to the nutritional primary symbiont Portiera aleyrodidarum, most individuals are infected by secondary symbionts (S-symbionts). Symbiotic composition is biotype-specific and may be associated with biological and ecological features such as plant range adaptation. This raises the possibility that S-symbionts play a role in the adaptation of their host to the ecological niche, and in B. tabaci diversification. Genomic studies suggest that S-symbionts could profoundly influence their host metabolism acting as sources and/or sinks of metabolites, and contribute to niche specificity in a nutrient-contrasted environment. To investigate B. tabaci niche exploitation abilities, we first analyzed the amino acid content (by HPLC) of plants this insect is adapted to, and pointed out that they represent a nutritionally-contrasted environment. We then used B. tabaci biotypes harboring different S-symbionts to determine: (i) their free amino acid content and (ii) their life-history traits as physiological state indicators. Our results reveal significant plant-dependent variations in the insects' traits suggesting that plant nutrient properties could be critical for their development. A biotype-dependant plant utilization was also observed. To decipher whether plant utilization is S-symbiont-mediated, efforts are now focused on producing genetically-homogeneous individuals harbouring differents S-symbionts. Investigating the adaptive value associated to symbionts will contribute to elucidate mechanisms of diversification and speciation of insects.

Experience, brain maturation and cognitive flexibiliy in honey bees: from plasticity to metaplasticity

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Abstract: Learning allows individuals to make reliable predictions about connected events in their environment, and is thus a crucial factor for behavioural plasticity. While the honey bee is a model species for understanding learning and memory processes, most studies dedicated to their neural bases have focused on elemental olfactory learning tasks, whose simplicity contrasts with the complexity of the situations to which honey bees are likely to experience while foraging, particularly due to the time-limited availability of food provided by flowers and the complexity of their aromas. Importantly, the ability to solve such complex tasks, as assessed under controlled laboratory conditions, depends on the maturation of specific brain circuits that are required for such tasks, particularly in the mushroom bodies. In addition, mushroom body circuits are shaped by experience at different moments of the bee's lifetime. Recent results showed that the experience-dependent maturation of mushroom body synaptic organization is correlated to the animal's capacity to display complex task abilities, in particular cognitive flexibility.

Challenges for the field-ready deployment of new vector surveillance and control tools

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Abstract: Entomological monitoring is an obvious requirement of vector control programmes but the techniques that we use for these purposes are unwieldy, inaccurate and were never designed for application to an ever increasing number of target environments and vector complexes. New trap types and automated counting and species identification systems that offer alternatives to human landing catches and traditional taxonomy would be of tremendous value. Similarly, an ability to characterise the age of mosquito populations could provide compelling entomological evidence for the risks of transmission and the likely epidemiological impacts of vector control tools. We'll discuss why, despite considerable activity around their development, few of the myriad iterations of these tools are field-ready.

The vector-control management agenda is formidable, involving billions of humans at risk, countless stakeholders and a multiplicity of landscapes, mosquito behaviours and ecologies. Despite substantial research efforts, the key elements of most control programs have changed little over the past 50 years. Particularly for arboviral diseases, the lack of innovation is in part due to issues of governance, the acceptance of poor efficacy among existing tools and a failure to co-opt communities into the decision making and deployment process. It is also true that the tremendous costs of epidemiological trials for new tools, which are required to gain a WHO recommendation and subsequent endorsement from National Control Programs, slow the rate at which new techniques and products can be prioritised and tested. To illustrate this point, we'll look at the development of two new paradigms in vector control; spatial repellents and the release of Wolbachia-infected Aedes aegypti.

Changes in Stonefly (Plecoptera) Assemblages in the Midwest of USA Using Museum and Contemporary Specimen Data

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Abstract: The Midwest USA region suffers from agriculture and urbanization so that as much as 75-95% of total landcover is occupied by agriculture and urban areas. Because of this, the use of contemporary samples from reference quality streams is insufficient to characterize the stonefly fauna of the region. We must depend upon museum specimens to set the baseline of distribution across the region. Early (the 1860s through 1950s) work on stoneflies in the region resulted in significant holdings of stonefly specimens at 25 institutions. Our collection efforts and those of others continued through the 20th and into the 21st centuries, adding many more specimens to museums. We have identified all these specimens to the current taxonomic state of the art, digitizing and georeferencing nearly 40,000 specimen records. Sampling strongly suggests that species richness (156 species) is saturated across the region. Eastern, wooded, and unglaciated drainages hold the greatest species richness. Northern drainages suggest a wrap-around the Great Lakes recolonization pattern. Prairie drainages hold many fewer species. Cluster analysis suggests three assemblages that are mainly governed by proximity to eastern post-glacial dispersal pathways and glacial history. Two species have been extinguished from the region, another 4 are nearly extirpated, and 30 have severe range reductions compared to historical distributions. Data are now being used to conduct state and national conservation status assessments. This study demonstrates the usefulness of museum specimen data for answering broad ecological and conservation questions.

Pitfalls and progress in Collembola phylogeny

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Abstract: Among the three entognathan classes of hexapods (Protura Diplura and Collembola), springtails are arguably the most important both in terms of diversity and ecology. However, traditional views on collembolan relationships based on morphology and taxonomy has had a turbulent history. Their relationships have been debated since the early 20th century and despite recent attempts to solve their phylogeny, both from morphological and molecular data analyses, relationships among the main lineages and the very position of Collembola within Hexapoda remain unclear. Multiple molecular loci for a broad taxonomic sampling are analysed to address the phylogeny of the four orders Neelipleona, Symphypleona, Entomobryomorpha and Poduromorpha, along with the familial relationships within the orders. Ambiguities and lack of resolutions will be discussed.

Adaptive and maladaptive contemporary evolution of thermal tolerance and performance within cities

Authors: Diamond Sarah, Case Western Reserve University, United States

Abstract: Cities have expanded globally over the last century. These replicated urban heat islands provide an unprecedented opportunity to explore how populations cope with rapid increases in temperature. Within-generation phenotypic plasticity is one possible coping strategy, but there is growing evidence that contemporary evolution of temperature-sensitive traits is more common than previously appreciated. Here, I examine the evolution of thermal tolerance and performance in response to urban heat islands using an acorn-dwelling ant species. In a majority of cities, but not all, acorn ants have evolved higher heat tolerance, but lost their tolerance of cold temperatures. These changes were not due to indirect effects of body size, which showed no evolutionary divergence between urban and rural populations, nor maternal effects, as the phenotypic patterns of population divergence persisted from F1 to F2 generations. The evolution of higher heat tolerance appears to be adaptive owing to evidence of positive directional selection on heat tolerance coupled with evidence of local adaptation. In particular, urban populations produced more sexual reproductives under warmer laboratory rearing temperatures, whereas rural populations produced fewer under these conditions. Despite these adaptive shifts, other traits including whole-colony metabolic rate exhibit potentially maladaptive evolutionary divergence, with urban populations exhibiting a higher metabolic rate compared with rural populations. The results of this work highlight how cities can be used to explore contemporary convergent evolution of thermal traits in response to a common agent of selection, the urban heat island effect, but also potential constraints on thermal adaptation.

In a nutshell, a reciprocal transplant experiment reveals fitness trade-offs in response to urban evolution in an acorn-dwelling ant

Authors: Diamond Sarah[1], Martin Ryan[1], [1]Case Western Reserve University, United States

Abstract: What is the evidence for adaptive evolution over contemporary timescales? Although there is widespread evidence for local adaptation in response to environmental variation, how these responses play out over more rapid, recent timescales is unclear. Cities provide an unparalleled opportunity to explore local adaptation in response to contemporary environmental change. Acorn ants (Temnothorax curvispinosus), inhabiting forested urban patches have evolved greater heat tolerance but lower cold tolerance when compared to nearby rural populations. These earlier findings led us to ask how these relatively rapid evolutionary changes have affected fitness and local adaptation. We performed a multi-year reciprocal transplant between replicated rural and urban habitats located in and near Cleveland Ohio, USA across an urbanization gradient to explore local adaptation in response to urban heat in acorn ants. In the case that local adaptation is present, we expected urban ants to have the highest fitness in their 'home', i.e. urban environment, and rural ants to have highest fitness in their 'home', i.e. rural environment, with crossed pairings of the 'away' environment for each population to have relatively low fitness. We broadly find evidence for local adaptation, however, the magnitude of the response appears to be dependent on the season under which fitness is assessed. While rural populations appear to have a relatively equal probability of colony failure throughout the year, urban populations appear to have a much higher probability of colony failure during the coolest portions of the year. Previous evidence of evolved increases in heat tolerance and losses in cold tolerance might leave urban populations vulnerable to cold temperature stress events, even in relatively warmer urban environments. Although a few other urban evolution studies in plants have explored the potential for local adaptation in cities, the acorn ant system appears to be one of the first systems to demonstrate evidence for local adaptation to city life, albeit with some potential maladaptive shifts in cold tolerance responses.

Two new species of Dentigaster Zettel, 1990 (Hymenoptera, Braconidae, Cheloninae) from Brazil.

Authors: Dias Manoel[1] and Dias Angélica[1], [1]Federal University of Sao Carlos

Abstract: Dentigaster Zettel, 1990 has nine neotropical species described. Two new species from Brazil are presented here. Dentigaster sp. nov. 1: type material,16 females from Atlantic forest; this new species has the color pattern similar to Dentigaster erythrothorax Zettel, 1992, but it's morphologically different; has metasoma noticeably narrower, longer and first tergite with anterior prominent median knob. Dentigaster sp. nov. 2: type material, 12 females from savannah and caatinga; yellow and dark brown color, with more or less expanded yellow in different individuals; yellow head with brown spot on face and vertex; brown mesoscutum with two yellow longitudinal bands; brown metasoma with yellow sides, which may be reduced or absent in the second and third tergites in some individuals.

Financial support: FAPESP, CNPq

Endosymbionts of members of the third trophic level manipulate chemical ecology among four trophic levels

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Abstract: Parasitoids harbour a diversity of microbial symbionts including viruses, bacteria, and fungi. In contrast to symbionts of herbivorous and hematophagous insects, parasitoid symbionts do not provide nutrients. Instead, they are involved in parasitoid reproduction, suppression of host immune responses, and manipulation of the behaviour of herbivorous hosts. Moreover, our data show that parasitoid symbionts such as polydnaviruses may also influence plant-mediated interactions among members of plant-associated communities at different trophic levels such as herbivores, parasitoids and hyperparasitoids. This implies that these symbionts have a much more extended phenotype than previously thought. I will highlight this with recent data on the chemical ecological effects of endosymbionts in plant-herbivore-parasitoid-hyperparasitoid interactions and the effects on direct and indirect species interactions and the consequences for community ecology.

Honeydew from aphids feeding on plants whose seeds were coated with neonicotinoids enhances mortality of beneficial insects

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Abstract: Soybean is a major crop worldwide and its seed is commonly treated with neonicotinoids to control the soybean aphid Aphis glycines. It has been recently demonstrated that neonicotinoids, either sprayed or applied via the irrigation system, reach and kill beneficial insects when they feed on honeydew. Here, we tested whether honeydew excreted by A. glycines under field conditions contained the neonicotinoid thiamethoxam and whether it was toxic for the dipteran predator Aphidoletes aphidimyza and the parasitic wasp Aphelinus certus when the aphids fed on soybean plants grown from: i) untreated seeds, seeds treated with ii) thiamethoxam or iii) thiamethoxam + three fungicides.
A. glycines honeydew was collected 30-43 days after sowing (DAS) in July 2019. Honeydew collected in plots seed-treated with thiamethoxam or thiamethoxam + three fungicides contained 10 times higher levels of thiamethoxam than honeydew collected in the untreated plots. In addition, honeydew collected in plots seed-treated with thiamethoxam or thiamethoxam + three fungicides reduced the longevity of the dipteran predator and parasitic wasp compared to control honeydew. The results show, for the first time, that neonicotinoids can reach beneficial insects via honeydew when they are applied as seed coating. This route of exposure is likely to affect a much wider range of beneficial insects and crops.

Mass rearing insects as mini-livestock: effects of environmental factors

Authors: Dicke Marcel, Laboratory of Entomology, Wageningen University, Wageningen, Netherlands

Abstract: With the expected growth of the human population towards 9-10 billion people by 2050, an increase in global food production of at least 60 percent above 2006 levels is required. However, the food system is a major driver of climate change, reason that dietary changes are needed as well as reductions in food loss and waste. A major challenge is to produce sufficient animal proteins in a sustainable way. Several insect species, such as the yellow mealworm (Tenebrio molitor), the buffalo worm (Alphitobius laevigatus), the house cricket (Acheta domesticus) and the black soldier fly (Hermetia illucens) are now reared as mini-livestock. The mealworm, buffaloworm and cricket are especially used as food for humans and the black soldier fly but also the yellow mealworm as feed for livestock.
For a novel circular and sustainable approach to protein production, insects provide excellent opportunities because various species can be reared on organic waste streams. Insects are now reared in large volumes by big companies as well as in smaller volumes by smallholder farmers across the globe. The new insect sector provides animal proteins through a sustainable production process, with low-value input, high-value output and low environmental impact. Insect production can, therefore, become an important component of a circular economy, by closing nutrient and energy cycles, fostering food security while minimising climate change and biodiversity loss.
Important questions in developing the production of insects as source of protein include effects of substrate quality, densities, competition, pathogens and ethical aspects. These aspects influence insect health and welfare as well as economic value in the context of sustainable and circular agriculture. In this contribution I will focus on such aspects of insect rearing. I will conclude on the opportunities for rearing of insects as mini-livestock.

Plant-microbe-insect interactions at the roots

Authors: Dicke Marcel, Laboratory of Entomology, Wageningen University, Wageningen, Netherlands

Abstract: Plants are members of complex communities, both aboveground and belowground. They are exposed to a wide diversity of insect herbivores that are in turn attacked by a wide diversity of carnivorous enemies. Plant responses to herbivore attack modify plant phenotype and, consequently, interactions with community members and community composition. Microbes in the rhizosphere, especially plant-growth promoting rhizobacteria (PGPR), influence both direct and indirect induced defence of plants against insects. These PGPR are supported by plants through root exudates. Upon insect herbivory, plant hormone profiles and subsequently root exudate profiles are altered. Modified root exudation may influence the community of rhizobacteria that colonize plant roots, with consequences for insects herbivores feeding on the roots or shoots. Here, I will present recent developments focussing on insect-plant-microbe interactions at the roots including underlying mechanisms. Such knowledge is instrumental for novel developments in sustainable crop protection strategies.

Pollinator decline – a case study of the need for transformative change to avert biodiversity loss

Authors: Dicks Lynn, University of Cambridge, United Kingdom

Abstract: Decline in pollinating animals has become a prominent example of how biodiversity loss can affect humanity, usually with reference to the potential impacts of pollinator decline on food production. This talk will provide an overview of the state of knowledge on pollinators, including their conservation status, drivers of pollinator declines, and the policy responses underway through national and international strategies and action plans. I will present a global assessment of the relative importance of direct drivers of pollinator decline and ten consequent risks to human well-being, based on a formal expert elicitation process. Our results indicate that policy responses should focus on reducing pressure from changes in land cover, land management and pesticides. We reveal how the risks from pollinator decline differ among regions, with perceived risks substantially higher in the Global South. I will argue that the focus on food production, while providing an important economic argument for looking after some pollinators, does not address all aspects of the problem. Rather, addressing and reversing pollinator declines requires a multi-scale, hierarchical response that tackles both direct and indirect drivers of decline, and takes into account the many values of pollinating animals, beyond their direct contributions to food production.

When management facilitates invasion: the case of Nipeacoccus viridis in Florida citrus

Authors: Diepenbrock Lauren, University of Florida Citrus Research and Education Center, United States

Abstract: Human movement and trade routes are well documented in the spread of invasive species. As such, regulations regarding movement of people and goods are monitored and precautionary measures taken to minimize risk while at the same time, agricultural and trade related organizations continually assess risk of unwanted species to arrive.

Anthropogenic disturbances in the form of land use changes can further exacerbate the potential for adventive species to gain a foothold once introduced. Such is the case for a recently established invasive mealybug, Nipaecoccus viridis Newstead in Florida citrus. N. viridis is a common pest in many citrus-producing regions of the world where it is often managed with minimal chemical input due to ability of natural enemies to suppress the pest before populations reach damaging levels.

After nearly two decades of intense chemical management for Diaphorina citri Kuyawama, the primary vector for citrus greening, many growers in Florida are now reducing their chemical inputs from 14+ applications a year to 6-8 applications targeted at periods where research has shown the greatest potential for management success. In the years since D. citri was found in Florida, followed soon after by citrus greening, citrus habitats have experienced 2 abrupt shifts: (1) focus on IPM with primary reliance on biological control to intense management, and more recently (2) a swift reduction in chemical inputs. These and other changes in management have opened the door for adventive species to successfully establish and cause damage in part due to the lack of abundant generalist predators present in the system.

Why honeybees are poor pollinators of a mass-flowering plant

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Abstract: Honeybees dominate the flower-visitor assemblages of many crops and natural plant communities, yet their efficiency in terms of quality of pollen delivered is largely unknown. Honeybees are very frequent visitors to flowers of this species and cumulatively deposit as much pollen on stigmas as do birds. Yet, flowers from which birds but not bees were excluded seldom set seed. We captured honeybees and used half of them to pollinate virgin flowers on the plant on which bees were caught and the other half to pollinate virgin flowers on different plants. This “split-pollinator” method revealed that the pollen deposited on Aloe ferox flowers by honeybees is mostly low quality self pollen that that leads to substantial ovule discounting and depressed seed set. Lack of movement among A. ferox plants during individual honeybee foraging bouts is the most likely explanation for their deposition of low quality self pollen on stigmas. This study sheds light on why honeybees are often poor pollinators of mass flowering self-incompatible shrubs and trees, and introduces a simple new method to evaluate the quality of pollen delivered by pollinators in both natural and agricultural systems.

Bumble bee queens exploit microrefuges to survive a late summer cold-snap

Authors: Dillon Megan[1] and Dillon Michael[1], [1]University of Wyoming, United States

Abstract: With climate change, frequency and intensity of extreme weather events are expected to increase. Extreme temperatures associated with these weather events may significantly harm some insect populations, particularly during lifecycle milestones. Fall and spring are key milestones for bumble bees; new queens emerge and leave the natal colony in the late summer, mate, and then overwinter underground before starting new spring colonies. Queens may be especially vulnerable to extreme weather events during these milestones as they lack colony or hibernaculum refuges. However, behavior and microhabitat selection of queens are not well documented for these unprotected, solitary periods. Further, whether queens seek environments that would allow them to survive extreme weather is unknown. To assess queen microhabitat selection and survival during an unusual cold weather event, we measure the responses of wild Bombus huntii queens to a late summer snowstorm, during which temperatures fell 16°C in six hours and stayed below 5°C for three days. Only one of 26 queens did not survive the storm. The remaining queens retreated underground or found other cover, often clustering together. These findings show that bumble bee queens behaviorally adapt to sudden temperature drops and have remarkable cold tolerance during an active life stage.

Body condition predicts timing of spring emergence for queen bumble bees

Authors: Dillon Michael E.[1], Keaveny Ellen[1], [1]University of Wyoming, United States

Abstract: For insects, the timing of life history events (phenology) often depends on temperature cues. Body size often mediates insect responses to temperature, so body size may also play an important role in phenology. The determinants of spring emergence of bumble bee queens are not well understood, but body size is likely important for several reasons. In fall, queens accumulate energy stores to fuel overwinter survival. Accumulation of fat stores prior to and depletion of fat stores during overwintering are size-dependent: larger queens accumulate relatively more lipids and have lower mass-specific metabolic rates, suggesting delayed depletion of energy stores and potentially leading to later spring emergence. To address whether timing of spring emergence correlates with body size, we captured 237 Bombus huntii queens in Laramie, WY, during the 2020 and 2021 growing seasons, weighed them, and measured intertegular width (a size metric less affected by variation in feeding and hydration state). Early emerging queens were smaller than later emerging queens across years. Mass relative to intertegular width increased as the season progressed, suggesting, as predicted, that body condition influences the timing of spring emergence for these crucial pollinators.

Shifts in the thermal sensitivity of metabolism for overwintering bumble bee queens

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Abstract: Insects display various strategies for dealing with temperature, especially cold. Two common metabolic methods are compensation and depression. Diapausing animals exhibit metabolic depression as a means of overwintering. While during the cooler temperatures of the active season, they may show higher metabolic rates to compensate for their environment. Metabolic rates of diapause and post-diapause Bombus impatiens queens were measured between approximately 1 and 11°C. We found metabolism shifts for diapausing queens relative to the same individuals 1 week after diapause termination. However, contrary to the expectation of metabolic suppression, diapausing queens tended to have higher and more variable metabolic rates, at least at the intermediate temperatures at which we measured them. These queens showed significant metabolic elevation at temperatures 4, 6, and 8°C (paired t-test, $P = 0.006$, $P = 0.047$, and $P = 0.002$, respectively), but not at 2 and 10°C (paired t-test, $P = 0.884$ and $P = 0.139$, respectively). This may suggest that active post-diapause queens more tightly regulate CO2 emission, particularly at temperatures 8°C and below.

Transgenic dissection of the Aedes siRNAi pathway in antiviral defense and cross-talk with antibacterial immune pathways

Authors: Dimopoulos George, Johns Hopkins University, United States

Abstract: Arboviruses remain an immense public health threat despite vector control efforts, causing yearly large epidemics. The major arbovirus vector Aedeses aegypti utilizes its innate immune system to defend against microorganisms including human pathogens. The RNA interference pathway-mediated antiviral defense system is known to act against a broad range of viruses. However, despite the RNAi pathway's emergence as the major pan-antiviral defense system it remains understudied in mosquitoes, and its utility for vector-borne disease control has not been extensively explored. We have developed the first RNAi pathway engineered mosquitoes that show resistance against multiple human pathogens including dengue and Zika virus. Transgenic over-expression of Dicer-2 (Dcr-2) and R2D2 poses only mild fitness costs and, interestingly, also renders the mosquito more resistant to bacterial infections. The influence of the RNAi pathway on antibacterial defense appears to involve the induction of several antimicrobial peptide genes and other effectors, suggesting a cross-talk with antibacterial immune pathways such as the Toll and Immune deficiency (IMD) pathways. We are also investigating tissue-specific action of the RNAi pathway in antiviral defenses, as well as inter-tissue signaling using state-of-the-art genetic and molecular tools.

Invasive gall-forming wasps threatening non-native plantation-grown Eucalyptus: diversity and invasion patterns

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Abstract: Gall-forming hymenopterans on Eucalyptus species are highly successful invaders causing significant damage to non-native plantation forests. About 80% of the invasive species have emerged over the past two decades and fewer than 10% of these were known from Australia beforehand. Two species, Leptocybe invasa and Ophelimus maskelli, are global invaders that have become established since 2000 in 45 and 25 countries, respectively. There are a number of Hymenopteran groups that cause similar damage and that could become invasive in the future, most of which very poorly studied. The small number of taxonomists able to identify these insects slows accurate and effective diagnoses. Even when initial identifications have been made, these are frustrated by the existence of morphologically similar, but distinct cryptic species, which may differ in their ecology, including host and climatic range, and natural enemy interactions. This lack of information impacts management because breeding for resistance and biological control require accurate identification of the target pest. Given the global nature of invasions by these insects an international and collaborative research approach is required, to inform pre-emptive quarantine, monitoring and potential management options

Molecular tools fast track identification of insect pests in plantation forestry

Authors: Dittrich-Schroder Gudrun[3], Hurley Brett P[2], Wingfield Michael J[2], Slippers Bernard[1], [1]FABI, University of Pretoria, South Africa, [2]University of Pretoria, [3]University of Pretoria, FABI & Department of Zoology and Entomology, South Africa

Abstract: Accurate identification of invasive insect pests is a crucially important first step towards effective management. The rapid increase in invasive insects pests in plantation forestry require rapid and accurate tools for specimen identification. This is complicated by the growing shortage of specialist taxonomists and the shortcomings of morphological comparisons for to identify cryptic insect lineages. Sequence databases can be used to help address these challenges, but these are often poorly curated and incomplete. To address this challenge with reference to the identification of invasive insects pests of Eucalyptus plantation forestry, a forest insect mitochondrial (FIMT) online barcode tool was developed. This database and its associated tools facilitate the identification of unknown specimens through sequence comparisons with a curated database of identified insects pests. It also provides a platform for researchers and practitioners to share information before it is published in public databases, which often take years after the work is started. The information that FMIT can provide is essential in the management of these invasive species using tree breeding or biological control, where the accuracy of identification of the pests and their natural enemies are fundamentally important.

Vicia sativa contains A1b like entomotoxin; biopesticide of plant origin

Authors: Diya Fatima, INSA Lyon, Lebanon

Abstract: To date, crop protection relies almost exclusively on chemical treatments, which cause environmental pollution and lead to the emergence of pest resistance. Societal and public policy considerations create the need for ecologically friendly new solutions. In this perspective, biopesticides are effective alternatives to chemical insecticides for the control of various insect pests. Legume seeds contain numerous insecticidal proteins aimed at protecting their high nitrogen content from animal/insect predation. PA1b (Pea Albumin 1, subunit b), a 37 amino acid is an entomotoxin extracted from pea seeds and is of great interest for the control of cereal weevils (sitophilus spp.), a major pest of stored cereals. Investigating on such a protein family in seed of legumes of the Middle East origin, we discovered insecticidal activity of seed extracts, from different species belonging to the papilionoideae subfamily. We uncovered 12 sequences of amino acids that are homologues to PA1b. Our discovery shows that PA1b-like peptide found in Vicia sativa displays an outstanding insecticidal activity against Sitophilus oryzae WAA42. Besides, it shows cytotoxic effect against insect Sf9 cells (Spodoptera frugiperda). Mass spectrometry is in progress to determine the amino acid sequence of this interesting peptide through a biochemical approach. Moreover, binding assays of the newly discovered homologue to the receptor found in the sitophilus oryzae's proteinaceous tissue will be carried out to determine its affinity. Such observations pave the way for the development of bioinsecticides, with PA1b like peptides as lead compounds.

TaxonWorks: World Auchenorrhyncha Database (Hemiptera)

Authors: Dmitriev Dmitry, Illinois Natural History Survey, United States

Abstract: Suborder Auchenorrhyncha is abundant group of plant-feeding insects. This group consists of leafhoppters, planthoppers, treehoppers, cicadas, and spittlebugs and together with other suborders, Heteroptera, Sternorrhyncha, and Coleorrhyncha, it forms one of the largest insect order Hemiptera. World Auchenorrhyncha database provides information on the nomenclature of the group. At the present time the groups includes 70 valid families, 6,851 valid genera, 47,695 valid species, and >50,000 synonyms and subsequent combinations. The original version of the database could be accessed from http://dmitriev.speciesfile.org. Recently, the database was migrated into TaxonWorks (http://taxonworks.org). Besides nomenclature, the website provides information on species distribution, type material, biological associations, bibliography as well as tools for species identification (dichotomous keys, interactive matrix based keys, and pictorial keys). The data from the database are shared with global aggregates like Catalogue of Life and GBIF.

Higher-Level Phylogeny of the family Cicadellidae and related groups (Hemiptera: Cicadomorpha) based on DNA evidence

Authors: Dmitriev Dmitry[2], Lu Lin[3], Dietrich Christopher[1] and Zhang Yalin[3], [1]Illinois Natural History Survey, Prairie Research Institute, University of Illinois at Urbana-Champaign, United States, [2]Illinois Natural History Survey, United States, [3]Northwest A&F University, China

Abstract: The family Cicadellidae belongs to the most diverse superfamily Membracoidea (Insecta: Hemiptera: Cicadomorpha). It is spread worldwide consisting of about 25,000 described species of 40 subfamilies in the world, including 24 in China (sensu Oman et al., 1990). All being plant-feeders, these leafhoppers include many species that are very harmful pests on trees, fruits, vegetables and other economic crops. Because of their species diversity and morphological differences, and higher-level classification system has been a controversy among leafhopper taxonomic workers and is an urgent issue to resolve. Taxonomy and phylogeny have certain limitations because previous analyse of phylogeny have not consistently parse the relationships of leafhopper based on the morphological characters.
We reconstruct the higher-level phylogeny of the family Cicadellidae and related groups based on five molecular marker genes to test the monophyly of this family and further clarify the relationships among the genera, tribes and subfamilies, using the phylogenetic ML analysis with 237 representative taxa of all major lineages, including 218 cicadellid representatives out of 86 tribes among 34 leafhopper subfamilies (sensu Oman et al., 1990) and 18 species among four superfamilies of related groups. We gained the relationship of Cicadomorpha with bootstrap support at least 90% which is in agreement with previous research (Cryan & Urban, 2012; Dietrich, et al., 2017; Johnson et al., 2018; Skinner et al., 2019) on the phylogenetic relationship of Cicadomorpha and outgroup taxa. The family Cicadellidae is paraphyletic with the two families Membracidae and Aetalionidae, which is consistent with Dietrich et al. (2001, 2017). The largest subfamily Deltocephalinae is also evidenced to monophyly, and 10 related subfamilies are merged into Deltocephalinae,corroborating Zahniser & Dietrich (2010, 2013). Meanwhile, it is worth mentioning that the subfamily Typhlocybinae, the monophyletic group of the second largest group of Cicadellidae is first verified with 27 species of six tribes based on the above genes.

Aposematism and chemical defense in chrysomelid beetles and the physiology behind it

Authors: Dobler Susanne, Molecular Evolutionary Biology, Universitaet Hamburg, Germany

Abstract: Chrysomelid beetles are often shiny and display striking colors, that are usually assumed to represent aposematic warning colorations. Many of these beetles are actually reknown for their chemical defenses which may either be autogenously produced or sequestered from their host plants. Using Chrysolina, Oreina and Chrysochus species as model system I here review evidence for colors as defensive signals and discuss the value of cardiac glycosides and pyrrolizidine alkaloids as defense compounds. Both types of defenses necessitate intricate physiological adaptations to avoid autotoxicity and to transport defensive compounds into specific storage compartments while on the other hand excluding them from sensitive organs. These physiological adaptations are the current focus of my group and our recent results on the role of target site insensitivity and ABCB transporters will be presented.

The making of the monarch: A constrained adaptive path to toxin resistance

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Abstract: Identifying the genetic mechanisms of adaptation requires the elucidation of links between the evolution of DNA sequence, phenotype, and fitness. Convergent evolution can be used as a guide to identify candidate mutations that underlie adaptive traits, and new genome editing technology is facilitating functional validation of these mutations in whole organisms. We combined these approaches to study a classic case of convergence in insects from six orders, including the monarch butterfly (Danaus plexippus), that have independently evolved to colonize plants that produce cardiac glycoside toxins. Many of these insects have evolved parallel amino acid substitutions in the a subunit (ATPa) of the Na+/K+ ATPase, the physiological target of cardiac glycosides. We found substitutional paths involving three ATPa amino acids (111, 119 and 122) that are associated with cardiac glycoside specialization. Using CRISPR/Cas9 genome engineering, we edited the native ATPa gene in Drosophila melanogaster and retraced the substitutional path taken across the monarch butterfly lineage. We could show in vivo, in vitro and in silico that the path confers resistance and target site insensitivity to cardiac glycosides, culminating in triple mutant “monarch flies” as resistant as the monarch butterflies. We also demonstrated that the order in which the substitutions evolved ameliorated, but did not eliminate, antagonistic pleiotropy through epistasis. In our current work, studying natural populations of Drosophila carrying the “monarch” genotype in the three ATPa amino acids (111,119 and 122), we aim to elucidate whether convergent compensatory substitutions have evolved in the monarch and other insect specialists to eliminate the fitness costs of the resistance substitutions. Overall, our work illuminates how the monarch butterfly evolved resistance to cardiac glycoside toxins and reveals rules that govern the evolution of novel adaptive traits.

Large-scale population suppression of wild Aedes Aegypti by release of Wolbachia-infected males

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Abstract: The range of the mosquito Aedes aegypti continues to expand, putting over 2 billion people at risk of arboviral infection. Novel, scalable mosquito abatement tools are needed as chemical insecticides and source-reduction have failed to prevent the proliferation of this species. The sterile insect technique (SIT) has been used to successfully combat agricultural pests at large scale, but not mosquitoes - largely due to challenges with consistent production and distribution of high-quality male mosquitoes. We developed automated processes to rear and release millions of competitive, male-only, sterile (Wolbachia) mosquitoes and conducted a large-scale suppression trial in Fresno County, California. In 2018, we released 14.4 million males across three replicate neighborhoods encompassing 293 hectares. At peak mosquito season, the number of female mosquitoes was 95.5% lower (95% CI: 93.6 - 96.9) in release areas compared to non-release areas, with the most geographically isolated neighborhood reaching a 99% reduction. We speculate that immigration of mosquitoes from neighboring untreated areas prevented higher suppression in release sites. Collectively, our work demonstrates a viable path to effective, large-scale mosquito SIT, re-energizing the prospects for area-wide control of Ae. aegypti.

Exhibition of ant-lepidopteran commensalism is not only for honeydew tending but the similarities of cuticular hydrocarbons also power the attraction

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Abstract: In ant-lepidopteran commensalism, the myrmecophilous grass moth, Parotis marginata, Hampson, 1893 (Lepidoptera: Crambidae) exhibits commensals with Asian weaver ant, Oecophylla smargdina (Hymenoptera: Formicidae). Several weaver ant nests (n=340) of variable sizes were examined from different fruit (n=310) and non-fruit trees (n=30) from West Bengal, India for one year. The lepidopteran caterpillars (n=246) and/or its pupae (n=152) were noticed in almost 24% (n=80) of the studied nests. In understanding of 'cuckoo strategy' behind the commensal association between the moth and the ant, we performed cuticular hydrocarbon (CHC) profiling of the associated commensals. It was found that nearly 33 different CHCs were present in attendant worker ants from decane (C10) to tritetracontane (C43), where the mature ant larvae had only two and half of it (CHC, n=13). In compare to ant's CHC diversities, the hydrocarbons were noticed very limited to the matured caterpillar (CHC, n=7) or absent in its pupae (CHC, n=0). The CHC profiles of caterpillars were fully shared by either the adult workers or the ant larvae. It was well hypothecated that the ants were likely to tend the caterpillars by the attraction of honeydews secreted from the myrmecophilous organs of the caterpillars, but our study indicates that, in addition to attraction of honeydews, CHC alikeness of lepidopteran larvae also excites the ants to attract the caterpillars as a case of exhibiting chemical mimicry.

Evolution of circadian clock genes in insects

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Abstract: Circadian clocks are time-measuring devices that were identified in almost all organisms. The molecular mechanism of clocks in animals relies on several interlocked transcription-translation feedback loops, the majority of which conserved between vertebrates and Drosophila. However, several important differences in the clock setup exist. Here, we will present our systematic analyses of clock setup in all major insect lineages, point to important Drosophila-specific idiosyncrasies, and highlight the conserved and variable components. Furthermore, we will present our functional reverse genetic data on the linden bug Pyrrhocoris apterus, a hemipteran insect in which we have tested the function of the majority of clock components. In addition to recently published data, we will present new phylogenetic analyses and a functional description of novel genetic components identified by RNA-mediated interference.

Photoperiodic timers, diapause and circadian clock genes in the linden bug, Pyrrhocoris apterus (Heteroptera)

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Abstract: Organisms synchronize their behavior to daily changes of environmental conditions and restrict activity to certain periods of the daily cycle. Exogenous cues inform about the time of a day, but mechanisms which control activity rhythms are controlled by endogenous circadian clock. In addition to daily changes of environment we observe also seasonal differences. Many organisms evolved time measuring device which counts the ratio of light to dark (photoperiod) which enables surviving adverse conditions arising from seasonal changes.

The understanding of how photoperiodic calendar works on a molecular level is still not clear, several authors proposed connections between circadian and photoperiodic clock since both rely on similar architecture, but this hypothesis is dismissed by others. The major complication in interpreting functional involvement of circadian gene in photoperiodism is pleiotropy of many factors.

In Drosophila melanogaster cytoplasmic acumulation of PER is delayed by the activity of a DBT kinase which promotes phosphorylation and turnover of PER. dbt mutants of Drosophila melanogaster have altered period of the rhythm. In the linden bug, Pyrrhocoris apterus, RNAi works systemic. After the dbt knock-down we observe lengthened circadian periods but also altered photoperiodic response curves. In the same time, the animals are still able to be reproductive or undergo diapause under specific conditions. We propose dbt involvement in photoperiodic time measurement. The influence of long or short photoperiods on Pyrrhocoris behavior is in consistency with our results from geographic field lines, where animals from different latitudes show great variability in circadian behavior.

Sex determination in the linden bug Pyrrhocoris apterus: identification and functional analysis of doublesex and transformer genes

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Abstract: A variety of sex-determining mechanisms have been described and are fairly well understood in some insect groups. However, data on sex determination in basal insects are mostly lacking. The cascade of genes regulating the sex determination involves two transcription factors – doublesex (dsx) and transformer (tra). The latter is known for its conserved function, playing a role of the dsx's splicing regulator, and has been found in all studied insects. Here we describe the discovery of dsx and tra genes in the linden bug Pyrrhocoris apterus (Heteroptera). We created detailed gene models, identified multiple isoforms in silico, and confirmed them using PCR and Sanger sequencing. Our results show that the observed tra splicing pattern seems to differ from other insect species. We also discovered a clear, sex-specific alternative splicing pattern for dsx, as there are three unique exons present in both female and male transcripts. Further, we analyzed the predicted gene function using maternal RNAi-mediated knockdown. All the progeny of tra dsRNA injected mothers developed into males with clear male-specific morphological structures, while dsx knockdown seemed to have no effect on the offspring's sex determination.

Enhancing khapra beetle detection technology

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Abstract: The khapra beetle is the only stored product insect quarantine pest in the US, feeds on variety of grains. There has been increasing frequency of interceptions at US ports of KB making improved detection crucial for food security. To improve trapping we have examined the surfaces the insects can most easily move upon and made improvements to traps where appropriate. We have also examined how insecticide coated surfaces affect behavior in relation to trapping. Trapping might be improved by design improvements that consider the ability to move on substrates. Insecticide-impregnated materials in traps are likely to affect behavior by disrupting semiochemical responses, but not movement.

Sugar Beet De-Icing Liquid Exposure Perturbs Salt and Water Balance in Mayfly Nymphs

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Abstract: Mayfly nymphs are established bio indicators of freshwater (FW) quality. This study examined the ion/osmoregulatory physiology of Hexagenia limbata nymphs following exposure to beet juice de-icing (BJD) liquid, an alternative to rock salt. The LC50 of BJD liquid was determined to be 4%, therefore a sub-lethal dose of 3.2% was selected for a 7 day exposure and following this ion (K+, Na+, Cl-, NH4+ and H+) concentrations in nymph hemolymph were examined as well as ion fluxes across tracheal gills and rectum. The presence of 3.2% BJD liquid in FW distinctly elevated environmental Na+, Cl-, K+, and NH4+ levels as well as pH, but all remained well below their individual LC50. In the hemolymph, Na+, Cl- and pH were higher in 3.2% BJD-exposed nymphs compared to FW nymphs, but other ions did not significantly differ. Na+ was absorbed at the rectum regardless of treatment, while the gills in nymphs exposed to 3.2% BJD excreted Na+, which was in contrast to the Na+ uptake observed across FW nymph gills. Observations of systemic perturbations in Na+, Cl- and pH balance indicate that these mayfly nymphs attempt to deal with 3.2% BJD liquid exposure, in part, by excreting sodium via the gills.

Genome-wide gene birth-death dynamics are associated with diet breadth variation in Lepidoptera

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Abstract: Both the duplication and loss of genes have been shown to facilitate the evolution of novel and adaptive traits. Thus, quantifying gene duplication and death across a lineage can potentially reveal gene families that have critically shaped morphological, behavioral, or physiological variation. In this study, we explored patterns of gene duplications and deaths among the Lepidoptera and linked gene family sizes with host plant repertoire sizes. We first generated de novo annotations for 30 publicly available reference genomes and then used the complete predicted protein sets to estimate instances of gene family expansions and contractions across Ditrysia. These results were correlated with host plant repertoire data in a multilevel Bayesian model that enabled us to detect significant differences in gene family size along a specialist-generalist feeding axis. We discovered that the sizes of several important gene families (e.g., those linked with detoxification and digestion) are significantly correlated with diet breadth. Our findings highlight significant genomic differences between generalist and specialist Lepidoptera species and demonstrate the value of pairing gene birth-death analyses with life history data to identify repeated patterns of evolution in distantly related clades.

Novel bee viruses - insights into pathogen evolution and conservation impacts

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Abstract: Many viruses infect multiple host species. Such multi-host pathogens can show considerable variation not only in their degree of virulence in different host species, but also in their degree of infection and transmission specificity, which has important implications for potential disease emergence. Using multi-host viruses that infect wild and managed bee species but vary in their degree of specificity, we investigate how ecological changes such as the acquisition of a novel vector affects pathogen prevalence and infection strength in contrasting viruses. We discuss the potential relevance of host-species specific variation in pathogenicity for control and conservation measures. As horizontal transmission of infectious diseases is determined by the hosts' contact networks, these measures in turn need to be informed by the host's contact networks. We combine ecological network data with virome sequencing approaches to study the impact of plant-pollinator interactions on virus dynamics. Together, this evidence on pathogenicity, specificity and interactions can inform how best to control pollinator diseases and improve pollinator population health.

Relationship between entomological indices, climate variables and dengue seroconversion rates in northeastern Thailand and southern Laos

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Abstract: Dengue is the most rapidly spreading mosquito-borne viral disease in the world. About 390 million people are infected per year, and 96 million are clinically apparent. Asia records 70% of the global dengue disease burden. Currently, there are no effective drugs for treating dengue and a recent licenced vaccine confers only partial protection. Although dengue virus infection induces a long-lasting protective immunity to the same homologous serotype, subsequent infection with a heterologous serotype is associated with increased risk of developing severe disease. The detection of clinical cases enables us to measure the incidence of dengue infection, whereas serological surveys gives insights into the prevalence of infection, including those infections that are asymptomatic. In addition, determining factors associated with mosquito abundance is central to predicting the risk of dengue virus transmission. However, it remains unclear whether any consistent association exists among dengue incidence or prevalence and the various entomological indices. This study is, therefore, designed to investigate the relationship among dengue seroconversion and entomological indices, climate variables and socioeconomic factors. Study areas were selected for urban and rural areas of 4 provinces in northeastern Thailand and southern Laos along the Mekong River where dengue is highly endemic. The study regions have a tropical climate with a dry season from October to April and a rainy season from May to September, and dengue transmission occurs mainly in a rainy season. A total of 720 households (HH), 90 households per site, were randomly selected. Baseline socioeconomic and demographic data were collected from all selected HH at the beginning of the study. Two cross-sectional seroprevalence surveys were carried out in May and November 2019. Blood samples were collected from all participants in the selected HH to assess previous exposure to dengue. Monthly entomological collections have been conducted for the whole year of 2019 from the all randomly selected HH. The entomological data include; the number of total containers, number of dry and wet containers, the number of mosquitoes-positive containers and their types and location (indoors/outdoors) and the identification/speciation of all mosquitoes. At the beginning of the study, weather stations were set up in all 4 study sites. Daily max. and min. and total rainfall, max. and min. temperatures, diurnal temperature range, and humidity data were collected. All these variables will be used for the logistic regression univariate and multivariate analyses to examine the relationship among seroconversion rates, socioeconomic characteristics, and entomology indices. The significance of individual coefficients in the logistic regression models will be determined. The results of this study aim to help to establish improved guidance for disease surveillance and vector control strategies.

Pest status and life history of the Afrotropical subterranean scale insect Stictococcus vayssierei (Hemiptera: Stictococcidae) in the Congo Basin

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Abstract: Stictococcus vayssierei is a major pest of root and tuber crops in central Africa. However, data on its biology and ecology are lacking. Here we provide an updated estimate of its distribution and and abundance, and we evaluate its life history in response to a range of temperatures on two common host plants, with the aim of facilitating the sustainable control of its populations. Surveys conducted in nine countries encompassing thirteen ecological regions around the Congo basin showed that ARTS was present in Cameroon, Central African Republic, Congo, Democratic Republic of Congo, Equatorial Guinea, Gabon and Uganda. The scale was not observed below 277 m asl. The pest occurred in the forest and the forest-savannah mosaic as well as in the savannah where it was never recorded before. However, percentage occurrence was higher in the forest (43.1%) where cassava was the most infested crop, compared to the savannah (9.2%) where aroids (cocoyam and taro) were the most infested crops. Scale cohorts reared on cassava cuttings and cocoyam cormels (females) and in plastic tubes (males) in environment chambers at six constant temperatures showed a significant decrease of development time with an increase in temperature in both sexes. The pest can tolerate a broad range of temperature (13-29°C). Females survived better and developed faster on cassava than on cocoyam. At 21°C – the highest survival rate observed – females developed in 15-17 days regarding the host plant and males developed in 12 days. The lower threshold temperatures were estimated to be 7.4°C and 9.8°C for female development on cassava and cocoyam respectively, and 7.6°C for male development. While good regulatory measures within and between countries are required to control the exchange of plant materials and limit the spread of the pest, the study provides information for niche modeling and risk mapping.

The starry sky provides compass information during long-distance nocturnal navigation in the Australian Bogong moth

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Abstract: The Australian Bogong moth Agrotis infusa is a remarkable nocturnal navigator. Following its emergence in early spring, millions of moths migrate over enormous distances (~1000 km) from various regions of southeast Australia to a geographically restricted assemblage of high alpine caves in New South Wales and Victoria. Once in these caves, moths enter a dormant state over the summer ("aestivation"). Towards the end of the summer, the same individuals that arrived months earlier emerge from the caves and begin the long return trip to their place of birth. Once there, these moths mate, lay their eggs and die. The next generation of moths – hatching in the following spring – then repeat the migratory cycle afresh. How do these moths find their way to the mountains? Upon which external compass cues do they rely for navigation while migrating through previously uncharted territories or environments?

In our earlier studies, we found that moths turned predictably when visual landmarks and a correlated natural Earth-strength magnetic field were turned together, but that they became disoriented when these cues were set in conflict. To test whether celestial (stellar) cues might be important as visual cues for migrating Bogong moths, we tethered moths in a flight simulator housed within a 3D array of Helmholtz coils to annul the magnetic field and occlude the magnetic sense. We also projected an image of the starry sky onto a circular screen above the moths in an otherwise visually featureless arena. We found that spring and autumn migratory moths, viewing a seasonally natural starry sky, flew in their seasonally appropriate migratory directions. Moreover, moths turned predictably in the opposite direction when the projection of the sky was rotated by 180°. When stars were randomly and evenly scrambled in the projected night sky stimulus, moths became totally disoriented. Our results suggest that Bogong moths (1) use a stellar compass for long-distance navigation, and (2) can rely on a navigational strategy whereby visual cues in conjunction with a magnetic compass create a robust system for holding a migratory bearing.

In addition to our behavioural experiments we conducted electrophysiological recordings from orientation related brain regions of intact animals while we exposed the animals to the same stimulus configuration as described above (projection of the natural starry sky and a nulled magnetic field). We were able to record directional neuronal responses to the rotation of the projection of the starry sky, but not to the rotation of a control. After the recordings, a neural tracer was injected in these neurons, allowing a subsequent morphological classification of several types of neurons encoding star compass information.

Estimates of real arthropod density in bryophytes

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Abstract: Bryophytes provide an ideal environment for a range of bryobionts and a food source for bryophages. As climate change alters the cover of bryophytes in the environment, these changes have an impact on invertebrate communities. Density of arthropods in mosses can be difficult to evaluate, since unbiased estimates cannot be made by any standard sampling method, including the sieving. Manual inspection is the only way to do it, although it is referred to as “dirty hard work”. Our aim was to quantify the attractiveness of individual bryophytes species for bryophages and bryobionts. At 42 localities, we collected 633 quadrates of moss layer with a size of 0.25 m^2. We gathered data for > 60 species of bryophytes and obtained > 7,500 invertebrates, including > 800 bryophages. We analyzed data for the 20 most common bryophytes (area > 1 m^2, occurrence in ≥ 10 quadrates) using GLMMs. Campylopus introflexus was the most preferred bryophyte for bryobionts but hosted low densities of bryophages. Bryophages and bryobionts densities did not correlate. The exception was Pohlia nutans preferred within both groups. Our results provide the first quantified comparison of the attractiveness of individual bryophyte species for arthropods.

Transcriptome response to early EHDV-2 infection in Culicoides sonorensis: insight into viral dissemination and potential modification of midge sensory function

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Abstract: Female Culicoides sonorensis midges are vectors of epizootic hemorrhagic disease virus (EHDV), an orbivirus which causes morbidity and mortality in wild and domesticated ruminants. We used a comparative transcriptomics approach to identify key gene expression changes in female midges 36 h after ingesting a meal containing EHDV serotype-2 (EHDV-2). The transcriptomes from EHDV-fed and control (blood fed) midges were comprised of 18,754 unigenes. A total of 2401 unigenes were differentially expressed and ~60% were downregulated in response to the virus (953 up; 1448 down). Differentially expressed genes were analyzed by Gene Ontology (GO) enrichment, KEGG pathway mapping, and additional manual inspections in order to pinpoint the effect of virus ingestion at both the gene and pathway levels. A large number of downregulated unigenes were assigned to pathways related to cell/tissue structure and integrity, such as actin cytoskeleton, adherens junction, focal adhesion, and hippo signaling, which taken together may give insight into the process of early virus dissemination. Surprisingly, many downregulated unigenes also were associated with GO terms and KEGG pathways for eye morphogenesis and axon guidance. Manual inspection assigned these unigenes to a variety of sensory functions, especially vision, behavior, learning and memory, indicating that EHDV-2 may have a significant phenotypic effect on sensory and neural tissues, and presumably their function. Upregulated unigenes included those coding for innate immune processes, which may be involved in midge antiviral defenses, as well as photoreceptor pigments and odorant binding proteins, which presumably were upregulated in response to alterations of the other sensory systems. Our study presents the first insight into an orbivirus-induced phenotype in its primary vector and further suggests that EHDV-2 may significantly modify midge sensory function and, consequently, host seeking. EHDV-induced behavioral modification in midges is being explored further in order to better understand how virus infection impacts host seeking and feeding, which could have wide-reaching impacts on the design of collection and control methods.

Transcriptome responses of virus-transmitting aphid vectors are shaped by the host plant and the virus mode of transmission

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Abstract: Viral infection often modifies plant phenotypical traits with consequences on insect-host interactions. There is evidence that these changes can improve virus transmission, in which case one may speak of ‘pathogen manipulation’. How viral plant manipulation translates into changes in vector behavior and performance is largely unknown. It is assumed that most of the modifications are indirect, i.e. aphids and other vectors respond to virus-induced changes in the plant. But recent reports are indicating that not only host plant-mediated changes but also direct virus-mediated changes in aphids are to be considered. While virus-mediated effects on aphids and other hemipteran vectors are well documented, we have only a nascent understanding of how viruses are controlling vectors and which genes are involved. In this study, we were interested to see whether the virus mode of transmission (circulative vs. non-circulative viruses) influences the aphid transcriptome changes. Another objective was to highlight common and virus- as well as plant-specific effects on a vector. We first show a strong plant-specific response of aphid transcriptome, likely related to the hosts’ different susceptibilities to the viruses studied. We also found that stress-related aphid genes were downregulated on both infected plants (regardless of the virus). This suggests that viral infections facilitate the colonization of vectors on the plants. Our results also indicate virus-specific gene expression changes, which might be related to the virus mode of transmission. Overall, the circulative virus tended to affect genes involved in the development, whereas the non-circulative virus had a stronger impact on feeding-related genes.

The charismatic praying mantis: A gateway for insect conservation.

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Abstract: Praying mantids (Mantodea) are not only apex predators with a “mystical‘’ status but are also regarded as a kind of oracle and in some cultures as omens associated with bad or good. The cultural, mystical and religious values allocated to mantids over millennia can in future contribute not only to their own conservation but also to conservation of arthropods in general. Historically, Mantodea influenced African, Greek, Egyptian, Japanese and Chinese cultures and they impacted human culture in a variety of ways, for example, coin designs, hairstyles, swords, death rituals, war strategies and even modern music, advertisements and children’s books. Despite human fascination with mantids, this group of arthropods is unfortunately overlooked in terms of conservation and research. Conservation as a mitigation strategy to protect threatened and endangered species is influenced by philosophical and psychological aspects more than a pure scientific approach. This paper highlights the role of praying mantids in human culture and the historical relationships between humans and other arthropods. Acknowledgement of these cultural aspects of the Mantodea may contribute to a positive change in people’s perceptions of arthropods and eventually insect conservation. It is suggested that Mantodea could be used as a flagship or gateway species to further awareness of insect conservation. By building on the existing “global” cultural values, fascination and intrigue of the charismatic mantis, this can be used to generate much needed insect appreciation and wonderment of the small things that run the world we live in.

Resistance of Busseola fusca and Spodoptera frugiperda and other lepidopteran species to Bt maize: implications for IRM in Africa

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Abstract: Many lepidopteran species attack maize in Africa. Spodoptera frugiperda, the fall armyworm (FAW), invaded Africa during 2016 and is now considered the number one maize pest on the continent. The destructive feeding habits of FAW and a wide range of indigenous lepidopteran pests threaten maize production in Africa. Since stem borers and FAW larvae occupy virtually the same ecological niche, and Bt maize is effective against both these and several other lepidopteran pests, this technology provides a tool for their management. Bt maize that express Cry proteins have been used effectively for control of this pest in the United States, Canada, and several countries in South America. Although most Cry proteins provide effective control of the FAW, this pest evolved resistance to Cry1F Bt maize in Puerto Rico, Brazil and United States, and Cry1Ab Bt maize in Brazil. The African maize stem borer, Busseola fusca, also evolved resistance to single- and pyramid events in South Africa. Monitoring of resistant and proactive management of resistance evolution is therefore required. This study reports on the efficacy of single- and pyramid-gene Bt maize against the lepidopteran pest complex of maize in Africa. The efficacy of Bt maize for the control of S. frugiperda, Spodoptera exempta, B. fusca, Eldana saccharina, Leucania loreyi, Helicoverpa armigera and Chilo partellus was determined by means of larval feeding bioassays in which plant tissue of maize expressing Cry1Ab (single-toxin event) or Cry1A.105 + Cry2Ab2 (pyramid-toxin event), were fed to larvae. Results indicated moderate levels of survival of FAW (4-35%) on Cry1Ab maize and very high levels of mortality on the pyramid event. All the other lepidopteran species were highly susceptible to both Bt maize events. This study provides information on the efficacy of Bt maize against most of the lepidopteran species that damage maize in Africa.

The effect of temperature on the development of Spodoptera frugiperda (Lepidoptera: Noctuidae) in South Africa

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Abstract: The fall armyworm, Spodoptera frugiperda, is native to the tropical and sub-tropical regions of the Americas, but also spread to Africa, Asia and Australia. The effect of temperature on the development of S. frugiperda was studied at five different temperature regimes, namely 18, 22, 26, 30 and 32 ± 1 °C. Fertility was found to be high with all eggs that hatched at temperatures ranging between 18 to 32 °C. Development of eggs at a constant temperature of 18 °C was, however, slow and the percentage of eggs that hatched, very low. Continuous low temperature, although above the lower thermal limit, will therefore delay development and reduce population numbers as a result of high mortality. The optimal range for egg, larval and egg-to-adult development of S. frugiperda was between 26 and 30 °C. Development rate of S. frugiperda increased linearly with increasing temperatures between 18 and 30 °C and larval survival was also the highest between 26 and 30 °C. The optimum temperature with the fastest development rate and lowest mortality for larvae was at 30 °C. Pupal development period ranged between 7.82 to 30.68 days (32 – 18 °C) with a mean pupal development time of 17.06 days at 22 °C. Larvae took only 11.43 days to complete their cycle at 26 °C. Development period from eggs to the adult stage decreased from 71.44 at 18 °C to 20.27 days at 32 °C. Based on linear regression analyses of development rate at all temperatures, a minimum temperature threshold of 13.01 °C was calculated for egg development and 12.12 °C for larvae, 13.06 °C for pupae and 12.57 °C for egg-to-adult development. Degree-day requirements for S. frugiperda egg and larval development was 35.68 ± 0.22 and 204.60 ± 1.23 °D respectively. Pupae needed 150.54 ± 0.93 °D for development while for egg-to-adult development (life cycle) 391.61 ± 1.42 °D were required.

Tuta absoluta base line susceptibility and resistance to insecticides in South Africa

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Abstract: Insecticide resistance by Tuta absoluta threatens tomato production worldwide. Heavy reliance on chemical control resulted in resistance evolution to the main insecticides used in South America, Europe and Asia. It was not known if the pest population that invaded South Africa in 2017 carried insecticide-resistance alleles. The aim of this study was to estimate baseline insecticide susceptibility of T. absoluta and to monitor if shifts in susceptibility occurred over the first five years after invasion. Populations were collected from three localities in South Africa in 2019, 2021 and 2022. Susceptibility testing with commercial formulations of insecticides was done according to the IRAC method 022. Data from populations collected in 2019 and 2021 serve as baseline data and are used in resistance monitoring. Two populations sampled in 2022 exhibited high levels of resistance to the diamides, chlorantraniliprole and flubendiamide, and indoxacarb. This rapid evolution of resistance to chlorantraniliprole and indoxacarb and cross resistance to flubendiamide is ascribed to off-label misuse of chlorantraniliprole and indoxacarb.

Biological control in the aftermath of invasion: a case study with an invasive forest pest

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Abstract: The emerald ash borer (EAB) (Agrilus planipennis) was accidentally introduced to North America from Asia during the 1990s. Despite early efforts by U.S. and Canadian regulatory agencies to eradicate and contain EAB, it has continued to spread and cause economic damage to ash nursery stock and the lumber industry, degradation of ash forests, and reduction in ecosystem functions in ash forests in North America. The classical biocontrol program against EAB, which started over a decade ago with the introduction and establishment of co-evolved natural enemies from the pest's native range, has shown the ability to suppress EAB to lower densities, which may allow North American ash species in hardwood forests to recover and regenerate in the aftermath of the EAB invasion. This program has now documented successful establishment of the egg parasitoid O. agrili and the two larval parasitoid T. planipennisi and S. galinae in EAB-infested forests at most release sites in the northern United States, in areas where surveys to document parasitoid establishment have been conducted. While the role of O. agrili in suppressing EAB population growth requires continued evaluation, the larval parasitoids T. planipennisi (from China) and S. galinae (from the Russian Far East) have become the dominant biotic factors suppressing EAB population growth rates and significantly reducing EAB densities in the aftermath forests in Michigan and several northeastern states, where these parasitoids were released between 2007 and 2017. EAB densities at these biocontrol study sites are now sufficiently low (<10 larvae per m2 phloem area) to allow the surviving trees and saplings to recover and grow to canopy trees, reaching the overstory (Duan et al. 2015b, 2017a, 2021b). Here, we examine the ecological premise of EAB natural enemy introductions, and review the development, implementation, impacts, and challenges in conserving native Fraxinus using biocontrol in the aftermath of the EAB invasion throughout North America. We conclude that successful establishment, spread, and impact of three of the EAB biocontrol agents, T. planipennisi, S. galinae, and O. agrili in Michigan and several Northeastern states (Connecticut, Massachusetts, and New York) in the aftermath forests following EAB invasion, have resulted in low EAB densities, which may allow surviving ash trees to gradually recover, regenerate, and grow into the forest canopy.

Colorado potato beetle semiochemistry: new complexity and potential for field application

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Abstract: Demand for intensive production of potato, the world's fifth most important staple food outside the lowland tropics, has led to unsustainable pest management practices (i.e., frequent applications of many insecticides), provoking evolution of spectacular pesticide resistance by the key potato pest, Colorado potato beetle, in many growing regions. The result of such resistance is the near-permanent loss of once-effective insecticides and more expensive and in many cases excessive pesticide use. These impose risks to human health, non-target beneficial organisms, and the non-crop environment.

Sustainable potato culture where the beetle is present should rely on integration of multiple control tactics to reduce pesticide applications to a necessary minimum. Cultural and biological methods have been underutilized, provoking quick adaptation or evolution of resistance by beetle populations to pesticides with new modes of action. This situation has been likened to the pursuit of the “Red Queen” by Alyokhin et al. in a recent review. Moreover, insights by Jermy, Visser, Dickens, and other researchers have elucidated the beetle's behavioral response to plant and insect semiochemicals, offering opportunities for management that have until now gone largely untapped.

Here we investigated whether male mate-finding behavior was altered based on previous exposure of potato plants to female, male, or no adults. We found that in no-choice tests, virgin males walked for a longer time, undertook more transitions between walking and stopping with antennae up, visited more leaves, and departed more slowly from female-exposed plants than from male-exposed or unexposed plants. When presented leaves from female-exposed, male-exposed, and unexposed plants simultaneously in a three-way choice test, virgin males exhibited behavior consistent with that in no-choice tests. In particular, virgin males spent more time overall, and undertook more transitions between walking and stopping with antennae up, on the female-exposed plants than on male-exposed or unexposed plants. These results indicate a preference for plants containing female-specific residues, which can increase the probability of mate-finding by male beetles. These findings therefore provide insight into which chemical cues mediate attraction and retention of male beetles on potato plants.

With prior knowledge of the male-produced aggregation pheromone, as well as new discoveries by our laboratory concerning female-produced pheromone altering male beetle searching behavior, we propose to develop a new sustainable Colorado potato beetle management strategy that integrates cultural and behavioral controls with infrequent applications of selective chemical or microbial controls. This strategy would control this key potato pest while minimizing resistance selection and conserving natural enemies.

Effects of landscape vegetation productivity and managed pollinators on avocado (Persea Americana Mill.) fruit set in Muranga, Kenya

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Abstract: Insect pollinators provide a critical ecosystem service, yet there is mounting evidence of a global pollinator decline. The effect of interactions between managed and wild pollinators on crop production is inadequately investigated. Avocado, Persea Americana, is an important pollinator-dependent crop grown mainly by smallholders in East Africa. Managed avocado pollination could contribute to closing yield gaps present in African smallholder agriculture. We conducted a study in smallholder avocado farms in Muranga, Kenya to assess effects of managed honeybees on local wild pollinators and fruit set across the three classes of vegetation productivity, viz., low, medium at a landscape scale. The normalized difference vegetation index (NDVI) which is the greenness indicator was used as a proxy for the vegetation productivity. Multi-date Sentinel-2 satellite data were used to estimate the index. Two types of treatments (presence and absence of honeybee (Apis mellifera) hives) were implemented each in distinct avocado farms at the beginning of the blooming period in August 2019 and repeated six-fold within each vegetation productivity class. Flower visitors were sampled during the peak bloom (September 2019). The number of fruits was recorded three weeks after flower marking and counting.

Flower visitors distributed into 21 families, one superfamily and 54 species were captured during the peak bloom period. The most abundant visitors were represented in Apidae (55%), Syrphidae (13%), Muscoidea (10%), Calliphoridae (8%) and Halictidae (1%). The abundance of wild visitors (i.e. excluding honeybees), honeybees, and species richness were compared between vegetation productivity classes and treatments. There was a significant interaction ($P = 0.023$) between vegetation productivity class and treatment on the abundance of wild visitors. Wild visitors were relatively more abundant in medium and high vegetation productivity classes supplemented with hives than in the low class with hives. Landscape vegetation productivity significantly influenced ($P = 0.0099$) species richness of flower visitors. The abundance of honeybees did not vary significantly across vegetation productivity classes and treatments ($P = 0.14$). Species richness was higher in high and medium NDVI than low NDVI. A mixed beta regression showed that only vegetation productivity significantly influenced fruit set ($P = 0.0019$). Fruit set was higher in high vegetation productivity (13%), followed by that in medium (10%) and low (9%) classes. Wild visitors seem to play a role in avocado pollination and seem not affected by managed honeybees. An increase in landscape vegetation cover should be adopted to support wild pollinators and optimize avocado pollination.

Bacillus thuringiensis Spores and Cry3A Toxins Act Synergistically to Expedite Colorado Potato Beetle Mortality

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Abstract: Bacillus thuringiensis (BT) is a widespread bacterium that has been developed as a biopesticide to control insect pests attacking crops as well as disease vectors such as mosquitoes. The insecticidal activity of Bt is primarily due to proteinaceous crystal endotoxins (Cry), which are produced during sporulation and activated by the host's gut fluids. BT virulence factors also include enterotoxins, hemolysins, phospholipases and metalloproteases, which are transcribed in the vegetative cells and play an important role in the infection process. At the same time, the midgut microbiota may be an additional factor enhancing the virulence of the bacteria BT. The Colorado potato beetle Leptinotarsa decemlineata (CPB) is an important pest that can be control with biological preparations based on BT bacteria. Uncovering of BT virulence factors activity in midgut, as well as the participation of host defense systems is necessary for further improvement of biological preparations and their field application strategies. The BT enters the insect host via the mouth and must thwart the gut-based defences to make its way into the body cavity (haemocoel) and establish infection. We sought to uncover the main antibacterial defences of the midgut and the pathophysiological features of Bt in a notable insect pest, the Colorado potato beetle. Exposing the beetles to both Bt spores and their Cry3A toxins (crystalline δ-endotoxins) via oral inoculation led to higher mortality levels when compared to either spores or Cry3A toxins alone. Within 12 hours post-exposure, Cry3A toxins caused a 1.5-fold increase in the levels of reactive oxygen species (ROS) and malondialdehyde (lipid peroxidation) within the midgut – key indicators of tissue damage. When Cry3A toxins were combined with spores, gross redox imbalance and 'oxidation stress' were apparent in beetle larvae. The insect detoxification system was activated when Bt spores and Cry3A toxins were administered alone or in combination to mitigate toxicosis, in addition to elevated mRNA levels of candidate defence genes (pat-tern-recognition receptor, stress-regulation, serine proteases, and prosaposin-like protein). The presence of bacterial spores and/or Cry3A toxins coincided with subtle changes in microbial community composition of the midgut, such as, decreased Pseudomonas abundance at 48 hours post inoculation. Both Bt spores and Cry3A toxins had negative impacts on larval health, and when combined, likely cause metabolic derangement due to multiple tissue targets being com-promised. This work was supported by the Russian Science Foundation grant No. 22-16-20031.

Moving like a model: high-speed videography reveals locomotor mimicry of hymenopterans by clearwing moths- novel morphological mimicry features

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Abstract: Clearwing moths (Lepidoptera: Sesiidae) have long been known for their physical resemblance to hymenopterans, which was, due to their elusive nature, described mainly from pinned specimens. We studied new species of clearwing moths in their habitat – lowland dipterocarp rainforests of Southeast Asia – using high-speed videography in the field to reveal novel behavioural and morphological features. After having observed that clearwing moths in flight are nearly indistinguishable from their hymenopteran mimicry models, we filmed flight trajectories of both bee and wasp mimics, as well as those of sympatric species of bees and wasps. Trajectories' digitization and comparisons revealed that bee mimics have slower, more zigzaggy and irregular flight paths, whereas wasp mimics fly faster, less erratically and in a straighter trajectory, as do wasps. These findings represent the first experimental evidence for behavioural mimicry in clearwing moths. Additionally, slow motion filming allowed us to determine the body posture of insects in flight: bees and bee mimics hold their hind legs hanging downwards in flight, whereas the studied wasps and wasp mimics kept their legs folded against their body. Some bee-mimicking Melittia Hübner species use their strongly tufted, long hind legs to maneuver in flight and to stabilize their body when perching on a surface with their front legs to reach liquids with their proboscis. Finally, high-speed videography shows that a newly described spider wasp mimic, Melanosphecia paolo Skowron Volponi, has an illusion of a narrow wasp waist formed by matching white colouration on the abdomen, inner side of hind legs and inner margin of the hindwing, on the otherwise metallic blue sesiid. Modern filming techniques can thus reveal a number of remarkable adaptations in insects, serving e.g. as a tool to broaden our understanding of the complex mimicry systems in the family Sesiidae.

Mechanistic insights for prostate disease: Lepidoptera sp' actives targeting human cells' inflammation and oxidative balance impairment

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Abstract: The concept of natural drug design has valuable, but less capitalized resources in entomological compounds, based on the structural similarity between insects' active substances interacting with human receptors. Our studies have pointed out therapeutic solutions in an interrelated „in vitro" screening encompassing vascular and prostate inflammation and oxidative processes. Human standardized cell line (PWR-1E - ATCC® CRL-11611™ from prostate dysplasia and vascular endothelial cells HUVEC-C- ATCC® CRL-1730™) and positive controls (Dutasteride 10mM, Dexamethasone 200ng/ml, N-Acetyl-Cysteine 0.5mM) were used, in order to confirm the mechanisms of action for two types of entomological compounds extracted from Lepidoptera sp.: polypeptides and hormone-like compounds. The pro-inflammatory status was induced by a cocktail of TNFa, a powerful, systemic stimulus, and PMA, a pro-inflammatory and pro-oxidative inducer, creating the premises of simultaneous oxidative stress induction. On prostate cells were investigated processes directed by IL6, IL8 cytokines release, concurrent with changes in intrinsic and extrinsic oxidative status: reactive oxygen species and the first defense enzymes catalase / superoxide-dismutase balance, as well as glutathione, the key – molecule for the cellular self- antioxidant protection. Considering the role of the vascular network in the appropriate functionality of prostate, our studies applied on HUVEC cell line focused on effects of entomological compounds on cellular oxidative homeostasis (H2O2 / O2- and intracellular glutathione) and inhibition of inflammation trigger (expression of ICAM-1 and VCAM-1, monocytes – endothelium adhesion molecules and IL6 / IL8 signaling). The accuracy of results was assured by the convergent mechanisms investigated, as well as the specificity and reliability of antigen – antibody binding combined with flow cytometry. Studies have led to the identification of new therapeutic targets for prostate dysfunctions, modulated by entomological water-soluble complex: catalase and H2O2 re-balance (106-240% catalase; 30-83% H2O2); and hormone-like liposoluble compounds: intracellular glutathione recovery (34-64%); superoxide-dismutase activation and O2- decrease (66-80% for SOD and 10-46% for O2-); IL8 inhibition (6-27%). The therapeutically impact is augmented by their vascular action: intrinsic antioxidant system stimulation (increase of glutathione) and inflammatory processes inhibition through reduced release of IL6 (21-56%) and expression of both soluble and membrane forms of ICAM-1 (10-17%). Research project SMIS 122180 - contract no. 256/2020

Genetic diet specialisation in phytozoophagous and zoophytophagous mirids

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Abstract: The Miridae have a true omnivorous diet that includes varying proportions of animal and plant resources. Species belonging to this family can therefore be classified on a spectrum varying from phytozoophagy to zoophytophagy according to the relative proportion of plant and animal resources in their diet. The differences in diet composition can be as important within the species, than between species. Genetic variability in omnivorous populations generate diet specialization (individuals of the same population may consume different proportion of available resources). Here, we compare genetic diet specialisation among two North American species of Miridae, namely the tarnished plang bug Lygus lineolaris and Dicyphus hesperus. These species form a spectrum from phytozoophagous to zoophytophagous. The consequences of genetic diet specialisation in these economically important species in agricultural environments is discussed.

Efficiency of indigenous Nabis americoferus against tarnished plant bugs and aphids in greenhouse

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Abstract: The damsel bug, Nabis americoferus (Carayon) (Hemiptera: Nabidae) is a polyphagous predator indigenous to North America and commonly found in many crops. Nabis species can feed on several important agricultural pests such as the tarnished plant bug (TPB), Lygus lineolaris (Palisot de Beauvois) (Hemiptera: Miridae) or aphids such as Myzus persicae (Sulzer) and Aphis gossypii (Glover) (Hemiptera: Aphididae). Both insect groups are pests of greenhouse crops and can impede high economic damage. The objective of this study was to evaluate the efficiency of this indigenous predator against TPB and A. gossypii in cucumber in greenhouse. This species is one that have been targeted for the development of new biological agent for Canada greenhouses. Experiments have been done in cages in greenhouse. Five cucumbers have been grown in cages, and 3 adults N. americoferus were introduced in cages with cucumber plants initially infested with: 1) 5 TPB/plants, 2) 25 A. gossypii/plants or 3) a mixture of both. A control with the mixture of preys but without the predator was also prepared. After six weeks, the three populations were evaluated. First results showed that at an introduction rate of 3 Nabis per 5 plants failed to control TPB or aphids. Nabis population was highest in presence of both type of preys, suggesting that this predator benefits from a mixture of preys. This predator could be a good biological control agent, but further experiments are needed to evaluate properly the introduction rate and the timing of introduction in greenhouse.

Evaluation of Tarnished plant bug responses to the risk of predation in the presence of Nabis americoferus

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Abstract: The Tarnished plant bug (TPB), Lygus lineolaris (Palisot de Beauvois) (Hemiptera: Miridae) is a major pest in North America. This species threats more than 120 economically important plants, possesses a high reproduction rate and shifts from phytophagy to zoophagy according to the situation. Overall, the presence and high complexity of this species prevents growers to convert to organic agriculture. Currently, to control this pest, the potential of the polyphagous predator naturally present in TPB host crops, Nabis americoferus (Carayon) (Hemiptera: Nabidae), is being evaluated. The effectiveness of predation can be affected by several factors such as handling time, presence of alternative preys or pest response to the risk of predation that needs to be also considered for an optimal biological control strategy. Pest responses to the risk of predation can imply changes in diet preferences, location or resource investment. Then, the objective here is to assess TPB responses to the risk of predation in the presence of N. americoferus.

First results on the effectiveness of the predator have shown that N. americoferus is able to predate on every stage of TPB, is highly voracious and follows a functional response type III that saturates with the ingestion of 13 preys when 20 TPB are offered for 24h. This saturation is much lower when feeding on aphids. On the other side, a greenhouse experiment on cucumber plants has revealed, that after 6 weeks, TPB may invest producing high offspring in the presence of the predator, especially when other preys are not available. Experiments to assess TPB trophic choices, location and number of offspring in the presence of the predator and alternative preys are currently being conducted in controlled arenas. It is expected that in the presence of Nabis, TPB will adapt his choices to evade the risk of predation. Fresh results will be presented during the conference.

Aedes aegytpi and the use of natural molecules for its control

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Abstract: To impact on the suppression of diseases like the Chagas, Zika, dengue, and chikungunya are necessary that all activities of vector control converge in a system smart and exclusive for this goal. That means that many people, like scientific, politics, sociologists, environmentalists, and ordinary people, must be contributing to joining forces to get the goal of mosquito suppression. According to this philosophy, here are we wish to present information focused on our understanding of the discovery of natural molecules to be used by many people implicated in the world of mosquito control. In this sense, this presentation will have information not only understandable to the specialist in the topic, but also for the regular people who suffer from the problem and have no knowledge of how to protect themselves against mosquitoes in their homes.

Product development with entomological application in collaboration with industrial designers

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Abstract: Objective.Show the Importance of transdisciplinary work to create new technologies of scientific interest in entomology. Case: Devices for pest control in public health with input from entomologists and industrial designers. Materials and Methods.We use the scientific method as a line of thinking with students of biology, chemistry and industrial design, as well as PhD in entomology, chemistry and Ms.C in industrial design. In “Trap for capture and monitoring of Aedes aegypti 2011 (WO / 2014/167553) hypotheses were tested with functional models made by industrial designers to determine the mosquito’s preference for oviposition. Trap models with circular, square and triangular section shapes, materials, input characteristics, color, size, capture system and leakage reduction were tested. Following the scientific method treatments and replicas were located, periodic readings, review of results and statistical analysis were made, to make incremental changes until traps with product attributes were reached. Results. For the oviposition of Aedes aegypti it was observed that the shape and size of the trap is not important. The mosquito prefers the red color for the body of the trap. The entrance has color contrast between red and black. The trap allows live mosquitoes to be taken to the laboratory. In the field the trap has a red color and in the laboratory it is translucent. In “Household trap for insects” (2013) WO / 2016/075624, the mosquito has a 78% preference for red traps. Translucent windows with holes allow mosquito to remain in it. In the “Trap for capture and death of culicides” (2016) (patient pendin), it was discovered that a large funnel-shaped entrance facilitates entry and prevents the escape of mosquitoes. Discussion.The publication Desing and Testing of Novel Lethal Ovitrap to reduce Populations of Aedes Mosquitoes. https://doi.org/10.1371/journal.pone.0160386.g001, helps to know the design of the trap. They do research involving entomologists, epidemiologists, social scientists and design engineers. They Built prototypes and experimented in the laboratory. Is a process similar to ours, however, in the design of the trap the aesthetic factors, size and shape, determined them according to community opinions. In our case, the characteristics of the traps are subject to experimental verification, to avoid subjectivity in decision making. In this process is no participation of Industrial Designers. The publication Exacta –EP, São Paulo, v. 15, n. 3, p. 515-526, 2017. ISSN: 1678-5428 of Brazil, identifies the articles published on the Web of Scienci since 1980 to 2014, there is no evidence of collaborative work between Entomology and Industrial Design. Conclusions. Works of devices for pest control in public health with a collaborative approach to Entomology and Industrial Design is little known. The Industrial Design contribution determine in the products the functions practices, aesthetics and symbolic.

Enzymatic defense responses of aphids and their host plants to stress caused by an increase in air temperature

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Abstract: It has been observed in recent years that climate change can affect plants and herbivorous insects. An increase in temperature can indirectly affect insects by changing quality of host plant tissues or directly affecting their biology. So far, little research has addressed the problem of the interactive impact of abiotic and biotic stress on the defense mechanisms and effectivity of a plant, and the direct effect of a rise in temperature on herbivorous insects. The work is aimed at explaining how the plant reacts to abiotic stress caused by elevated temperature and additional biotic stress caused by feeding aphids and also explains how the aphid responds to abiotic stress caused by temperature rise.

Experiments in climatic chambers at three temperatures: 20, 25 and 28 °C were carried out to detect changes in developmental stages, demographic parameters and insect fertility. The activity of enzymatic markers (SOD, CAT, GST, ß-glucosidase, PPO, POD) in the tissues of the host plant and tissues of aphids Aphis pomi were determined.

An increase in air temperature to 28 °C significantly negatively affects the biology of A. pomi, with a shortening of the reproduction period, total lifespan; reducing population demographic parameters and fertility by half. The increase in temperature and foraging of sucking insects, act additively, causing a synergistic defense effect on the plant. Both the plant defense responses and the aphid’s defense responses differed significantly depending on the temperature.

Novel Functions of Ammonia Transporters During Mating and Reproduction in the Adult Aedes Aegypti Mosquito

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Abstract: In the present study, we explored the function of ammonia ($NH3$ and $NH4+$) transporters during blood meal digestion, reproduction, and egg laying in mosquitoes. Shortly after emergence of adults of the disease vector mosquito, Aedes aegypti, a female will pair with a male in flight for copulation whereby the male inseminates the female with sperm and seminal fluid. The female will then imbibe a large protein-rich blood meal for egg development and will excrete unutilized digested protein as nitrogenous wastes. Whilst terrestrial animals typically excrete nitrogenous wastes as uric acid and/or urea because ammonia is toxic at low concentrations, A. aegypti excrete ammonia as their primary nitrogenous waste. The organs and molecular mechanisms involved in ammonia transport and excretion during blood meal digestion and egg development in the adult mosquito are not fully understood. A. aegypti possess at least four specific ammonia transporters; two Rhesus glycoproteins (Rh proteins), AeRh50-1 and AeRh50-2, which are vertebrate homologs and two ammonium transporters (Amts), AeAmt1 and AeAmt2 which are plant, fungal, and bacterial homologs. In blood-fed females, we show that hemolymph $NH4+$ levels and $NH4+$ transport rates by the renal Malpighian tubules (MT) are significantly elevated up to 48 hr post blood meal (PBM), measured using ion-selective micro-electrodes and the Ramsay assay for analysis of MT secretions. We also show that the MTs, hindgut, and fat body most abundantly express Rh and Amt in non-blood fed adult females determined using immunolocalization and qPCR. AeAmt1 is almost exclusively localized in the flagella of the sperm during all stages of spermatogenesis, including mature sperm stored in the spermathecal organs of the inseminated female. Using immunohistology and RNA in-situ hybridization, we demonstrate that AeRh50-1 mRNA and protein is expressed within the nurse cells and follicular epithelium surrounding the developing oocyte during egg development, as well as having high expression in the hindgut epithelium. RNAi studies employing dsRNA injections of adult mosquitoes targeting Amt and Rh protein knockdown suggest integral roles of ammonia transporters in sperm viability and fecundity demonstrated by significant decreases in egg laying and larval hatching, with no effect on blood-fed adult female survival, as a result of Amt and Rh protein knockdown.

Nature conservation considering vector ecological burdens – an interdisciplinary view on cases studies from Germany

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Abstract: This research project focuses on one of the conflicts in wetland management. On the one hand conservation measures can benefit biodiversity. On the other hand, these measures may create stagnant water pools, which can offer suitable habitats for mosquito immatures. Mosquitoes are well known as nuisance species and carriers of infectious diseases. If nuisance mosquito species disperse numerously from wetlands to residential areas and health concerns arise, the public could then demand systematic mosquito control. Systematic mosquito control, principally control with insecticides, can affect non-target organisms and interfere with conservation goals. Knowledge about present mosquito species, their nuisance potential and the effects of wetland conservation on mosquitoes is important. However, particularly in Central Europe, this knowledge is still missing. Therefore, we studied mosquitoes before and after the implementation of conservation measures in selected wetlands in Germany from 2019 to 2021. We evaluated if and to what extent mosquito abundance, development and composition change after wetland conservation measures in wetlands along the river Danube in southern Germany and the Müritz national park in eastern Germany. In one of the four study areas at the river Danube, we noticed a marginal increase in mosquito numbers. While in other areas at the Danube and the Müritz, numbers maintained the same as before the measures. Derived from our observations, we cannot entirely exclude that conservation measures in wetlands benefit mosquitoes. Mosquito control, especially in Central Europe, usually means applying Bacillus thuringiensis var. israelensis (Bti). Bti has lethal effects on the mosquito immatures and is regarded to be the most specific agent. The impacts of Bti on non-target organisms such as chironomids and the ecosystem itself are still discussed in science. Establishing an expertise on mosquito species-specific reactions to conservation measures, can support targeted mosquito control. Additionally, the wetland type and local conditions might play an eminent role for this species-specific control and help future wetland conservation projects.

Latitudinal gradients in tritrophic interaction diversity.

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Abstract: Latitudinal gradients in diversity and specialization have revealed strong patterns of increased diversity and specialization towards the equator. Depending on the strength of these two gradients, interaction diversity and associated ecosystem function may exhibit nonlinear changes along latitudinal gradients. For example, interaction diversity may decrease as specialization increases towards the tropics, but then as diversity increases more rapidly around the tropics, interaction diversity may increase. We present analyses from our long-term plant-caterpillar-parasitoid networks collected using the same methods at sites across the Americas. Our data suggest complex but predictable relationships between diversity, specialization, and interaction complexity for plant-consumer interactions, and these relationships are changing rapidly with global change parameters, particularly increases in extreme weather events. Understanding these relationships provides unique insights into the origin and maintenance of tritrophic diversity as well as a deeper understanding of the consequences of potential global insect declines.

The invasion history of the ambrosia beetle Xylosandrus germanus, an important pest in Europe and North America

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Abstract: Xylosandrus germanus is an economically significant invasive pest in various artificial and natural ecosystems in North America and Europe. Originally from Eastern Asia, X. germanus has managed to successfully colonize novel areas thanks to its peculiar biology, specifically haplodiploidy, inbreeding and fungal mutualism typical of all ambrosia beetles in the tribe Xyleborini. In Europe, it was recorded for the first time in 1951 in Germany, and throughout the rest of the 20th century, its spread to neighboring countries was a relatively gradual process. Its spread seems to have accelerated post-2000 and presently, it is found in most European countries. The expansion of X. germanus also occurs altitudinally, with numerous recent reports from much higher elevations than previously recorded. Genetic data reveal that non-native populations are highly uniform and point to their origin in Japan. However, different haplotypes occurring in Europe and North America indicate that these continents were colonized separately, with a single introduction in Europe and multiple introductions in North America. These findings are in contrast with the inferred invasion histories of some other closely related species, and highlight the diverse pathways by which xyleborines spread around the globe.

Flight of the alfalfa bee: determining limiting microclimatic factors affecting first flight

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Abstract: Unfavorable environmental conditions may potentially limit flight in insects, which in turn may limit reproduction and pollination. Temperature and light provide cues that regulate flight. However, it is unknown how other environmental factors, including wind, humidity, and air pressure, can affect flight in combination with light and temperature. Megachile rotundata, a managed pollinator for alfalfa and other crops, is used across a wide range of latitudes; however, unfavorable conditions in northern latitudes limits farmers from using M. rotundata to pollinate early season crops. The purpose of this study was to determine how environmental conditions, including nest microclimate, stimulate first flight in M. rotundata. To test the hypothesis that multiple environmental factors regulate flight initiation, a weather station was constructed around a nesting block to measure 7 different weather variables. GoPros were programmed to capture videos of the nest blocks from 7-11am daily to capture the first flight of individual M. rotundata. First flight of individual bees was measured for a total of 34 days. Temperature was shown to be important, although on three days, bees flew when ambient temperature was below 15?C. Temperature inside the nesting block for those days was around 5?C warmer than ambient and was at least 10?C at the face of the nesting block. Other variables, including light intensity, also appeared to affect flight incidence. Differences in temperature around and within the nesting block may be important factors that influence M. rotundata flight. Our results demonstrate the complexity of environmental variables affecting pollinators in northern latitudes.

Eight years with Drosophila suzukii (Diptera: Drosophilidae) in SW Germany - current state of knowledge on biology and pest control

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Abstract: The cherry vinegar fly, Drosophila suzukii, was first reported for Germany in 2011. In the invaded areas this polyphagous species occupies a previously empty ecological niche due to its capacity to infest healthy, ripe, soft skinned fruits. Eight years of laboratory and field research resulted in extensive information on its biology, ecology and potential means of control. Since 2012 we continuously monitored the abundance of the flies in orchards and wild habitats in relation to temperature and availability of host fruits. We followed the phenotypical colour variation in D. suzukii throughout the year as well as changes in the developmental stage of ovaries in field caught females. In laboratory experiments we screened natural plant compounds for toxicity and behavioural modifications in D. suzukii. The importance of landscape structures with wild host plants for the migration of the flies into orchards and the level of damage caused was evaluated at different field sites. Cultivars of its main hosts were tested for differences in their susceptibility under laboratory and field conditions. Several larval and pupal parasitoids were identified and tested for their potential use as biocontrol agents.

Our results showed that the yearly dynamic of D. suzukii population growth in SW Germany was determined by the fluctuations of temperature and humidity during spring and summer. Populations reached their peak abundance in late summer and fall. During winter and early spring flies were mostly caught along forest edges and on wild host plants. Moreover, all year long flies were most abundant in those habitats. Cherries and soft fruits are main commercial hosts in SW Germany, differences among cultivars were found to have little impact on the probability of infestation. In laboratory assays we identified plant compounds with contact toxicity, compounds that mediated feeding activity, and compounds that reduced oviposition. Migratory behaviour into orchards was mainly affected by the chronological sequence of ripe fruits. Orchards in close vicinity to hedges and wild host plants did not present a higher number of infested fruits compared to more distant or isolated orchards. A comparison of orchards with and without insect netting indicated an increased level of protection through fly exclusion netting. Behavioural experiments and studies on cultivated fruits under insect nets identified potential candidate parasitoid species (i.e. Trichopria drosophilae) for biological control of D. suzukii. The results will be discussed in terms of their potential applications in strategies of integrated pest management.

Consumption rate of different Stethorus gilvifrons Mulsant (Col, Coccinellidae) stages feeding on Tetranychus turkestani (Acari: Tetranychidae) eggs

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Abstract: The strawberry spider mite, Tetranychus turkestani Ugarov & Nikolskii (Acari: Tetranychidae) is on the most important serious pests of field and glasshouse crops in Khuzestan Province, southwestern Iran that cause massive damage to them. The ladybird beetle, Stethorus gilvifrons Mulsant (Col; Coccinellidae), an acariphagous predator, is a native and active predator in Khuzestan province that voraciously fed on different stages of T. turkestani. The purposes of current research were evaluation of consumption rate of adults and larvae S. gilvifrons feeding on T. turkestani eggs on leaf discs the cowpea, Vigna unguiculata L. Walp at the base of Petri dishes (60 mm × 16 mm) under laboratory conditions at 25+ 1 °C, 65+ 5%RH, and a photoperiod 14:10 h (L:D). The results indicated that the consumption rates of larvae and adults of S. gilvifrons were different statistically significant. Consumption rate of the 1st, 2nd, 3rd, 4th, and adult stages of S. gilvifrons on T. turkestani eggs were 18.50, 26.94, 41.75, 69.71, and 75/72 eggs/days, respectively. Likewise, the net predation rate (C0), the stable predation rate (?), the finite predation rate (?), and Qp of S. gilvifrons were 1827.86, 79.73, 89.29 eggs, and 18.19 eggs/ days, respectively. According to these findings, it can be concluded that S. gilvifrons is used in management programs of T. turkestani in field and greenhouse.

Molecular Detection of Bacterial (Anaplasma, Brocella) and Protozoan (Babesia, Theileria) Pathogens from Ticks Collected on Livestock in Northwest of Iran (2017-2018)

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Abstract: Introduction and Objectives: Ticks are among the most important obligate blood-feeding parasites of vertebrates causing transmission of numerous infections, including viral, protozoan, and bacterial and other diseases. The most important diseases transmitted by ticks include the tick-borne relapsing fever, the Crimean-Congo hemorrhagic fever, ehrlichiosis, anaplasmosis, theileriosis, babesiosis and brucellosis. These agents are firstly multiplied in the ticks' body by blood-feeding and are transmitted to the host animal and then to healthy animals or humans by ticks from the infected livestock. Brucella agents are also transmitted to humans directly and through the consumption of unprocessed livestock products such as milk and cheese contaminated with bacteria. This study was conducted to determine the infection of livestock ticks with Anaplasma, Theileria, Babesia and Brucella pathogenic agents using a molecular method in Ahar and Kalibar Counties of East Azerbaijan Province, northwestern Iran.

Materials and Methods: The Ahar and Kalibar Counties are placed in East Azerbaijan, where agricultural and animal husbandry are common. The specimens were collected using crooked pin heads so that the ticks were not damaged and transferred to special tubes. Next, they were inoculated into the test tubes and transferred to the laboratory by placing them in a special flask and were categorized using valid identification keys at the genus and species level. Nested-PCR and single-step PCR techniques were also implemented for the molecular determination.

Results: In this study, 2022 hard ticks were collected from Ahar and Kalibar Counties. Samples were identified including four genera and nine species of Hyalomma anatolicum, Hy. marginatum, Hy. asiaticum, Rhipicephalus sanguineus, Rh. bursa, Haemaphysalis sulcata, Hae. concinna and Hae. punctata. In this study, two agents of Anaplasma sp and Ehrlichia sp. were detected with the Nested-PCR and sequencing methods, also the Brucellaceae was detected in the trapped ticks with rate of 15.04%.

Conclusion: In this study, in addition to the presence of Anaplasma, Ehrlichia, and Brucellaceae in the livestock in the region, four genera of hard ticks were collected and identified as the vector and reservoir, thus, due to the critical role of ticks in the transmission of bacterial and other pathogens, as well as their close relationship with humans and livestock, especially in rural areas, the officials and staff of health centers, veterinary clinics and livestock breeders must consider the status of dissemination and spread of ticks and associated infections to the necessary measures for prevention and control of them and related diseases.

A Study on Species Composition on Mosquito Larvae in Khorramabad County,Western Iran (2018-2019)

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Abstract: Introduction and Objectives: Mosquitoes are the most important diptera not only responsible for transmission of diseases but also nuisance for humans and animals. They cause more human suffering than any other vectors and they are responsible for millions death. Therefore, more information on mosquito vectors and their activities essentially need for each specific area particularly where with traffic of passengers of migrants. The aim of current study is to obtain more details about breading places of Culicidae larvae in khorramabad country, Lorestan Province, Iran.

Materials and Methods: A cross sectional study was done on breading places of larvae of Culicidae mosquitoes biweekly from May 2018 - April 2019 in 12 villages of khorramabad Country, Lorestan Province, Iran. The sampling was performed in mountainous, slope and plain areas. Breading places were identified in each area and the larvae collected using dipper and counted. The 3 and 4 larvae stages were kept in conservative solution for 24 hours and then used to identify species. In addition, physiochemical characters of water in breading places was analyzed and recorded.
Results: In the current study, 5770 mosquito larvae were collected which categorized in 4 genus and 10 species including: Anopheles superpictus, An.stephensi, Aedes caspius, Ae. vexans, Culex theileri, Cx. perexicus, Cx. pipiens, Cx.molestus, Cx. mimeticus,Culiceta longiareolata. Among all collected mosquitio larvae, Cx. theileri and Cs. longiareolata were the dominate species.
Conclusions: This is the first official biodiversity survey conducted in Khorramabad as a region with a history of native and incoming malaria. The study of biodiversity in this region is recommended on a continuous basis.

The role of behaviour in inseciticide resistance

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Abstract: Insecticide resistance can be developed by insect pest populations as an evolved preference for nontoxic hosts over toxic hosts, thus conferring resistance to insecticides through behavior. Previous studies have shown evidence for behavioral traits that may help an insect avoid a toxin. However, it is not clear whether such behavior is heritable and, conclusive proof for increased resistance as a result of behavior is rarely shown. We performed choice bioassays to test the feeding and oviposition preferences of two strains of the insect pest Leptinotarsa decemlineata, also known as the Colorado Potato Beetle, which exhibits different levels of susceptibility to the neonicotinoid insecticide imidacloprid. While the first choices data did not indicate any feeding preferences, the oviposition and movement data suggest that the susceptible D01 strain prefers to inhabit and lay eggs on insecticide-free plants while the resistant E06 strain did not have a preference between insecticide-free or insecticide-treated plants. In later experiments involving crosses and whole genome sequencing, we aim to find out if these differences have a genetic background to show unequivocal proof for the role of behaviour in resistance.

Ten years after the first catch – overview of the recent records of Bactrocera spp. (Tephritidae, Diptera) in Austria

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Abstract: Fruit flies belonging to the genus Bactrocera (Diptera: Tephritidae) are among the most serious pests worldwide. Within the framework of the survey for the occurrence of Ceratitis capitata in Vienna (Austria), a specimen of the Bactrocera zonata was caught in a trap in 2011. This finding, as well as the frequent reports of introductions of tropical fruit flies at EU entry points (EUROPHYT reports: https://ec.europa.eu/food/plants/plant-health-and-biosecurity/european-union-notification-system-plant-health-interceptions-europhyt/interceptions_en), initiated increased survey efforts for Bactrocera species in Austria since 2012. From 2012 - 2016 these activities focused on sites in Vienna (urban area), where traps with specific lures were employed in allotments, often in close proximity to fruit markets. From 2016 onwards, the survey was gradually extended to eight of nine Austrian federal provinces. In addition, comparisons of the samples by sequence alignment were carried out in order to reveal details about the potential origin of the captured fruit flies.

In total more than 40 individuals belonging to Bactrocera spp. were caught in traps in Vienna (only urban area) in the past decade. Originally, the caught specimens were identified either as B. zonata or as belonging to the B. dorsalis complex. However, recently available diagnostic tools allowed identifying the latter as belonging to B. dorsalis s.l. and one specimen as Bactrocera kandiensis.

The winter conditions unfavourable for the survival of Bactrocera species in Austria and the results of the sequencing support the theory that the captured fruit flies derived from recurrent introductions, most likely by means of transport of infested fruits from various origins.

Fungal and bacterial pathogens threaten mass rearing of the edible grasshopper Ruspolia differens (Orthoptera: Tettigoniidae)

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Abstract: Although significant strides have been made to develop protocols for domestication of the edible grasshopper Ruspolia differens (Serville) (Orthoptera: Tettigoniidae), high mortality is still a big challenge due to obscure reasons. In this study, fungi and bacteria were isolated from R. differens collected from Mbarara, Masaka, Hoima, Kampala and Kabale districts in Uganda in 2018, cultured on standard microbial media, identified using molecular techniques and screened for virulence against the insect. Thirteen and nine species of fungi and bacteria were isolated from R. differens, respectively, with the number of isolates varying based on collection site. The most prevalent species of fungal pathogens of R. differens were Aspergillus flavus Link (27.3%), Fusarium equiseti (Corda) (24.2%), Mucor fragilis Fresen (12.1%), Clonostachys rosea (Link) (6.0%) and Aspergillus tamarii Kita (6.0%); whereas those of bacteria were Serratia marcescens Bizio (38.1%), Bacillus thuringiensis (Berliner) (14.3%) and Enterobacter cloacae (Jordan) (14.3%). Nine fungal species namely Clavispora lusitaniae Rodrigues de Miranda, Lichtheimia corymbifera (Cohn), Trichoderma koningii Oudem, F. equiseti, M. fragilis, Aspergillus niger van Tieghem, Epicoccum sorghinum (Saccardo), C. rosea, Penicillium commune Charles Thom; and five bacterial species (Proteus penneri Hickman, S. marcescens, B. thuringiensis, Staphylococcus sciuri Kloos and Enterococcus faecalis (Andrewes and Horder)) were ~5–7-fold and ~4–5-fold, more lethal to third instars of R. differens than untreated controls, respectively. Some of the pathogens of R. differens namely C. lusitaniae, Exserohilum mcginnis Padhye and Ajello, E. sorghinum, P. penneri and E. cloacae have never been reported as insect pathogens. These findings highlight a need to integrate management of these pathogens in the protocols for mass rearing of R. differens.

Potential of edible insects for improved nutrition and livelihoods in East Africa

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Abstract: Entomophagy is widely accepted among various communities in East Africa. The occurrence of edible insects is highly seasonal, and they are largely obtained through wild harvesting. However, to ensure year-round availability of these insects, icipe and partners have made significant progress towards the development of technologies for indoor mass rearing of 16 edible insect species. We have carried out nutritional profiling of over 28 edible insect species with 92% of the insects having crude protein levels (35 – 73%) that are comparable or superior to that of beef, fish and soya bean. We showed that many of these insects were also rich in amino and fatty acids, flavonoids, vitamins and associated with high Iron and Zinc. Based on the nutrient-rich benefits of these insects, we developed several ways of processing (such as boiling, roasting, bleaching, frying, stewing and curing) to improve their nutritional qualities and sensory attributes. High-quality oils extracted from 10 processed insect species were evaluated for their nutrient quality. Whole insects or insect-based flours were used as ingredients in safe insect-based food formulations such as cookies and other snacks flavoured with ginger, chocolate, lemon, vanilla and strawberry to entice consumers. Consumer acceptability and marketability of some of these products were tested. Our findings revealed that edible insects present unique opportunities for use as ingredients in food fortification to boost the nutritional status of human populations globally. Edible insects also provide opportunities for income generation and employment for youths and women along the value chain (wild harvesting, indoor domestication, processing technologies and marketing).

Pre-release evaluation of Dolichogenidea gelechiidivoris (Hymenoptera: Braconidae), a potential biological control agent of Tuta absoluta (Lepidoptera: Gelechiidae) in Africa

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Abstract: Tuta absoluta Meyrick (Lepidoptera: Gelechiidae) is native to South America, but has invaded the Afro-Eurasian supercontinent, where it is currently the most devastating invasive arthropod pest of tomato. As a part of the first classical biological control programme against T. absoluta in Africa, a larval parasitoid, Dolichogenidea gelechiidivoris Marsh (Hymenoptera: Braconidae) of T. absoluta was imported from Peru into the quarantine facility of the International Centre of Insect Physiology and Ecology, Kenya. Here, we report on the host larval preference of D. gelechiidivoris and the host suitability. Also, aspects of the parasitoid's reproductive strategy, including life-time fecundity, and egg maturation dynamics are documented. Dolichogenidea gelechiidivoris females preferentially oviposited into early larval instars (1st and 2nd) of T. absoluta but parasitized and completed development in all four instars of the host. Host instar did not affect D. gelechiidivoris sex-ratio but females reared on the first instar had significantly fewer eggs than when reared in late larval instars (3rd and 4th). Females of the parasitoid emerged with a high mature egg load which peaked 2 d post eclosion. Females of D. gelechiidivoris survived 8.51 ± 0.65 d and produced 103 ± 8 offspring per female at 24 ? 4?C and 50 – 70 % relative humidity (RH) with males present and fed honey-water (80% honey). Increasing maternal age decreased the proportion of female offspring. For laboratory conditions Gross and Net reproductive rates were 72 and 39.5, respectively, while the mean generation time was 20 d. The potential intrinsic rate of natural increase was 0.18 under laboratory conditions. Dolichogenidea gelechiidivoris is a potential biological control agent of T. absoluta, and should be considered for release in Kenya, and across Africa following host specificity testing and risk assessments.

Susceptibility of Black soldier fly, Hermetia illucens L. (Diptera: Stratiomyidae), to entomopathogenic nematodes

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Abstract: Black soldier fly (BSF), Hermetia illucens L. (Diptera: Stratiomyidae) have been widely used to process biowaste and the larvae are high-quality alternative protein to fishmeal in animal feed. Thus, BSF larvae can be an excellent cash flow for smallholder farmers given that the insect-based feeds are more sustainable than conventional fishmeal feeds. Despite the economic importance, relatively little work on factors that might hinder their development has been undertaken. Entomopathogenic nematodes (EPNs) are of potential interest for inhibiting the efficiency of BSF larvae as it feeds on waste organic substrates mixed with soil. Specifically, the larval stage of BSF may present a unique window for attack by EPN, thus threatening their proliferation. For the first time, we tested the capacity of two EPN species with different foraging strategies, Steinernema pwaniensis and Heterorhabditis sp. to cause larval and pupal mortality in BSF across a range of EPN concentrations (50, 100, 200, 500 and 1000 infective juveniles IJs cm-2), substrate moisture (10, 15, 20 and 25% w/v) and temperatures (15, 20, 25 and 30°C). We found that all EPN species tested caused density dependent mortality in the fourth larval instar while pupae were not affected. Steinernema pwaniensis caused significantly higher mortality across different IJ concentrations and over a wider moisture and temperature range than Heterorhabditis sp. High mortality caused by S. pwaniensis and Heterorhabditis sp was more limited to high IJ concentrations with an optimal temperature of 30°C. Our findings highlight the potential of EPNs to negatively impact the efficacy of BSF larvae under different environmental conditions. The implications of EPNs in emerging waste treatment technologies are discussed.

Thermal differences and the potential for sexual conflict in spiders

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Abstract: The behavior of ectotherms, animals that can cannot generate metabolic heat, is intimately tied to temperature. We explored how shifts in biologically relevant temperature ranges affected both male signaling and female choice in spiders. We found large effects of temperature. Interestingly, temperature affected male and female behavior differently suggesting different thermal optima for males and females in regards to mating behavior. Thermal preferences may be an important, often overlooked, aspect of mate choice and sexual selection in ectotherms.

Population dynamics of winter moth in the northeastern US before and after biological control

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Abstract: Winter moth (Operophtera brumata L.) is a newly invasive species from Europe to the northeastern United States, which caused widespread defoliation of a wide variety of deciduous trees from 2003-2016. Introduction and establishment of Cyzenis albicans (Tachinidae) collected from Vancouver Island, Canada beginning in 2005 has converted winter moth to a non-pest and ended widespread defoliation. Here we present the results of experiments and Life table analyses that show that predation by pupal predators in the soil now regulate the low-density populations of winter moth, much as they do in Canada and England. Fluctuations in high density populations prior to biological control introductions were caused by asynchrony of winter moth hatch with bu-dburst of oak and maple host trees These high-density populations were regulated by density-dependent dispersal of larvae from partially defoliated hosts.

Cascading effects of insect decline on insectivorous birds

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Abstract: Declines in the abundance and biomass of insects and other invertebrates could have profound impacts on insectivorous species and disrupt population processes at higher trophic levels. Many birds feed on insects throughout their annual cycle, especially during reproduction when invertebrates provide necessary protein for chick rearing.
It is, perhaps, no surprise then, that concurrent with declines in insect abundance and diversity over the past half century there have been parallel declines in insectivorous birds. Through a systematic review and meta-analysis, we investigated the potential for insect decline to result in parallel declines in insectivorous birds through the proximate mechanisms of reproductive success and chick body condition, the latter of which is linked to annual survival and juvenile recruitment. We found a strong positive effect of insect food availability on bird body condition and reproductive success, providing strong evidence for what has long been assumed: protein food is limiting for many songbirds during the breeding season. The results of our meta-analysis suggest that recent downward trends in insectivorous bird populations can be partially attributed to insect declines, and that future declines in insect abundance and diversity could cause severe consequences for insectivores.

Analyzing Psylliodes chrysocephala periodicity and abundance in Sweden over 50 years

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Abstract: The univoltine cabbage stem flea beetle, Psylliodes chrysocephala, is a major pest of winter oilseed rape in Europe. P. chrysocephala adults feed on emerging plant leaves in the fall, and the larvae mine leaf petioles in the winter moving in to the stem the following spring. Sweden is on the northern edge of the distribution of this insect. A 50 year data set collected in the south of Sweden is analyzed for periodicity and explanatory environmental factors. The stems of 20-30 winter oilseed rape plants were dissected and larval abundance was recorded in over 3,000 fields in five regions across Skåne, Sweden between 1969 and 2018. Using wavelet analysis and a measure of autocovariance (ACF) it is clear that P. chrysocephala exhibits very strong periodicity in eight-year cycles. An autoregressive model is used to account for density dependence though the mechanism driving the periodicity in this system remains unclear. There is also a trend towards greater larval density in the past five years. Prior laboratory research demonstrated a negative effect of cold temperatures on larval survival, and the field-relevance of this negative effect is supported by a negative relationship between cold winter temperatures and larval densities. The implications of these results are discussed in the context of pesticide-use restrictions, integrated pest management and climate change.

Extraordinary flight performance of miniature Coleoptera

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Abstract: The flight of the smallest insects is of special interest for general biology, biomechanics and aerodynamics, but until recently it was barely researched. It has been shown that the smallest insects are capable of active flight, but for many microinsects it is not known how fast they fly especially compared to larger related species. Ptiliidae and other Staphylinoidea present a convenient range of related species with high variety of body size for this task.

We recorded flight of 17 species of Ptiliidae, Staphylinidae and Silphidae by two synchronized high-speed cameras. The beetles were flying in spacious transparent boxes. It allowed beetles to maneuver freely and reach the maximum possible speed. Infrared LED lighting, invisible for insects, made it possible to achieve the necessary exposure for high-speed recording and keep the light level close to natural for beetles. The flight trajectories were reconstructed frame by frame and triangulated. After smoothing, the speeds and accelerations were calculated.
Ptiliids, like the other studied beetles, show continuous maneuverable flight with complex trajectories. The average flight speed is from 5 to 44 cm/s, depending on the species, the maximum speed is up to 98 cm/s; the beetles are capable of accelerating up to 2.4 g. These measurements indicate the ability of active migration in the absence of wind. We have performed regression analysis of speed and acceleration on body length and shown that among staphylinoids with membranous wings speeds and accelerations allometrically increase with increasing body size, but ptiliids fall out of the trend: their flight characteristics are higher than in the other studied beetles of comparable size.
Unlike miniature hymenopterans, thrips and dipterans, flight mechanics of miniature coleopterans have not been studied. To find out what adaptations determine flight performance of Ptiliidae we performed macro high-speed video recording and 3D reconstruction of morphology and kinematics in Paratuposa placentis and explored its flight aerodynamics by using new high precision numerical simulation method with a resolution down to individual setae. Wingbeat cycle of P. placentis and other Ptiliidae is unique to insects. The wings follow a pronounced figure-of-eight loop that consists of subperpendicular up and down strokes followed by claps at stroke reversals above and below the body. The elytra act as inertial brakes, halving the excessive body pitch oscillation. Computational analyses suggest functional decomposition of the wingbeat cycle into two power half strokes, which produce a large upward force, and two down-dragging recovery half strokes. In contrast to membranous wings of the same size, bristled wings produce slightly smaller aerodynamic force due to air permeability. But the motion of light bristled wings requires much less inertial power that significantly reduces cycle-averaged and peak power consumption. Muscle mechanical power requirements thus remain positive throughout the wingbeat cycle, making elastic energy storage obsolete. These adaptations explain how Ptiliidae and other miniature insects could preserve good aerial performance during miniaturization.

This study was supported by the Russian Science Foundation (project number 22-14-00028), Russian Foundation for Basic Research (project no. 18-34-20063), JSPS KAKENHI (grant numbers 18K13693 and 19H02060), Deutsche Forschungsgemeinschaft (project numbers LE905/16-1 and LE905/18-1).

Nutritional endosymbionts' Shikimate pathways are susceptible to glyphosate inhibition

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Abstract: Glyphosate is widely used as a herbicide, but recent studies begin to reveal its detrimental side effects on animals by targeting the shikimate pathway of associated gut microorganisms. However, its impact on nutritional endosymbionts in insects remains poorly understood. Here, we sequenced the tiny, shikimate pathway encoding symbiont genome of the sawtoothed grain beetle Oryzaephilus surinamensis. Decreased titers of the aromatic amino acid tyrosine in symbiont-depleted beetles underscore the symbionts' ability to synthesize prephenate as the precursor for host tyrosine synthesis and its importance for cuticle sclerotization and melanization. Glyphosate exposure inhibited symbiont establishment during host development and abolished the mutualistic benefit on cuticle synthesis in adults, which could be partially rescued by dietary tyrosine supplementation. Furthermore, phylogenetic analyses indicate that the shikimate pathways of many nutritional endosymbionts likewise contain a glyphosate sensitive 5-enolpyruvylshikimate-3-phosphate synthase. These findings highlight the importance of symbiont-mediated tyrosine supplementation for cuticle biosynthesis in insects, but also paint an alarming scenario regarding the use of glyphosate in light of recent declines in insect populations.

Experimental evolution as a tool for improving entomopathogenic fungi as biocontrol agents

Authors: Erdos Zoltan, University of Exeter, United Kingdom

Abstract: Experimental passage has been used to successfully increase virulence of entomopathogens such as baculoviruses. Passage experiments with entomopathogenic fungi are relatively unexplored and showed mixed results at improving virulence. Here, we adopted an approach based on social evolution and evolution of virulence theory using the pathogen Akanthomyces muscarius and an aphid host Myzus persicae, selecting for virulence at different scales of competition within host, between host and between population. The within host and between host treatments resulted in significant increases in virulence. Gains in virulence were dose specific but also led to more rapid killing of an additional aphid species (Brevicoryne brassica) suggesting the achieved changes are robust and not specific to the host used in passage. Sporulation is a key trait of fungal species for biocontrol, however maintaining sporulation throughout passaging has historically been challenging. We observed significant changes to sporulation between treatments, with the between population selection preserving levels of spore production matching the ancestor. Furthermore, we carry out population genomic analysis to identify genetic variants that show convergence within treatments. The current study contributes to the field of virulence evolution and highlights the potential of theory based experimental passage as a tool for improvement of biocontrol agents.

Spatial and Temporal Substrate Dynamics - Critical factors for Saproxylic Forest Biodiversity

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Abstract: During the last century great changes have taken place in the forest landscape with an ever more focused industry optimized for high yields. In Sweden, forests have become more homogenized and dominated by young, dense tree stands that are thinned and harvested at regular intervals. These changes has happened at the expense of many previously common forest habitats and often disrupted century long stand continuities. The effects of these changes on forest biodiversity have historically been challenging to examine, to a large extent due to laborious survey methods for many saproxylic insect species. Utilizing pheromone-based trapping methods it is however possible to conduct efficient, systematic surveys over both large spatial and temporal scales.

During the last few years we have used pheromone baited traps to compare populations of different taxa of threatened saproxylic longhorn beetles on over 200 localities across southern Sweden. By combining systematic trap catches, mark-recapture studies with GIS analyses of landscape data we found stark contrasts in the responses to modern forestry by different groups of longhorn beetles. Transient species, relying on thinner and freshly dead wood, seem to exist on a landscape scale where they quickly can utilize available substrate, i.e. after forest management actions, and then move on with little regard for forest continuity. Other more perpetual species, specialized on later succession stages, are more dependent on long-term habitat persistence in their immediate vicinity and seem to quickly disappear after a breach in continuity. These different responses will require different conservation approaches if we are to maintain a rich forest biodiversity in the future.

Larval odour and social immunity in honey bees

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Abstract: Disease-associated hygienic behaviour is a well-known defence mechanism of honey bees. Detection and removal of diseased individuals are central tasks. Candidate substances or odorant signature mixtures have been studied intensively, however mainly for Varroa mite and fungi (Ascosphaera sp., causing chalkbrood) infected brood. For all diseases, olfactory cues (brood pheromones, signature mixtures, and diagnostic substances) emitted by diseased individuals are key factors for larvae-worker communication to discriminate healthy from infected brood.

Here, we used coupled gas chromatography-mass spectrometry (GC-MS) to measure changes in cuticular hydrocarbon (CHC) and brood pheromone (BEP) profiles of larvae artificially infected with Melissococcus plutonius, the causative agent of European foulbrood. Although chemical profiles did not differ extensively, and no diagnostic substances were found in significant quantities, infection-specific differences were detectable for CHC and BEP profiles. Furthermore, β-ocimene was present in all larvae with highest quantities in healthy young larvae, whereas the necromone oleic acid was present only in old infected larvae. The variable amounts of each substance may shape the characteristic mixture, which is supposed to trigger EFB-associated hygienic behaviour in specialized worker bees. The degree of hygienic behaviour has to be evaluated in future studies to draw conclusions from artificial laboratory infections to in-field relevance.

Study of olfactory response of Cotesia Plutellae towards ten straight chain saturated hydrocarbons

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Abstract: Plutella xylostella (Linnaeus), a major pest of economically important cole crops, causes approximately more than 50% loss in crop production. Cotesia plutellae (Kurdjumov), the braconid, endoparasite of diamondback moth, P. xylostella is an important natural enemy of this pest. Application of semiochemical cues especially optimised for the concentrations of straight chain hydrocarbons may be an effective means in enhancement of this parasitoid's efficiency. Keeping these all facts, the proposed study is planned to discern the impact of olfactory response of C. plutellae towards ten straight chain saturated hydrocarbons viz, icosane, henicosane, tricosane, tetracosane, pentacosane, octacosane, nonacosane. For this, two concentrations of all saturated hydrocarbons i.e. 10 ppm and 100 ppm were prepared. Y-tube bioassay method was utilized for the assessment of olfaction capacity. Amongst the targeted hydrocarbons, three hydrocarbons, namely, icosane, octacosane and nonacosane with their percentages being respectively 1200%, 534.93%, 105.78% were observed as highly significant efficient attractant for C. plutellae for both the concentrations. These hydrocarbons may be utilised for preparation of alkane based commercial environmental friendly formulation for efficient management of Plutella xylostella (Linnaeus) in cole crop ecosystem.

Aleyrodid fauna of Eastern and Western ghats of India

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Abstract: Whiteflies are economically important group of insects infesting a wide range of host plants that cause damage by piercing and sucking the phloem sap and transmitting 19 viruses and numerous virus like agents. Severe infestation may thus adversely affect the hosts, both by excessive sap loss and through sooty-mould interfering with photosynthesis (Marting et al., 2001). These are regarded to be primary pests of vegetable crops, citrus, sugarcane, cotton, ornamental plants, fruit trees like guava, papaya, banana and are also found to infest many more forest trees in India. There are 1556 described whitefly species grouped in 161 genera in the world compared to more than 6000 coccids, 4400 aphids and 2500 jumping plant lice (Martin, 1999) and from india 10 percent of world aleyrodid is reported (Ragupathy, 2018), emphasizing the need for a study of this group of insects particularly in the biologically rich areas of India such as Eastern and Western ghats. Aleyrodid collections were made along the Western ghats from Tamil Nadu (about 8 degree N) and extended up to Gujarat (21 degree N) and up to Orissa in the eastern ghats. The surveyed forest areas include tropical dry ever green forests, tropical forests, evergreen forest and agroecosystem of the ghats region. The study revealed that many economically important crops, medicinally valued herbs and timber yielding trees have been severely infested by whiteflies in addition to endangered and vulnerable flora.

Survey along the Eastern and Western ghats has been carried out during 2000 to 2018 and leaves bearing nymphs of whitefly were observed using a hand lens, collected and secured in specially designed covers containing blotting papers in order to avoid fungal growth due to moisture content of the leaves. The identity of host plants of whiteflies was determined by Botonical survey of India, Coimbatore and Department of Botany, Madras Christian College, Chennai. The whitefly pupal cases were studied using Nikon Alpphaphot YS 2 Microscope.

The present investigation of aleyrodid fauna in the Eastern and Western ghats revealed approximately 950 species which belong to 66 whitefly genera viz.,

Aericerus, Acanthaleyrodes, Acanthobemisia, Acaudaleyrodes, Africaleurodes, Aleurocanthus, Aleuroclava, Aleurocryptus, Aleurolobus, Aleuromarginatus, Aleuroparvus, Aleuroplatus, Aleuroputeus, Aleurothrixus, Aleurotrachelus, Aleyrodes, Arunaleyrodes, Asialeyrodes, Asterochiton, Cohicaleyrodes, Crenidorsum, Crescentaleyrodes, Davidiella, Dialeurodes, Dialeurolonga, Dialeuronomada, Dialeuropora, Distinctaleyrodes, Dumbletoniella, Editaaleyrodes, Fippataleyrodes, Himalayaleyrodes, Icfrealeyrodes, Indica, Indoaleyrodes, Keralaleyrodes, Lipaleyrodes, Martiniella, Massilieurodes, Milleraleyrodes, Minutaleyrodes, Narendramodiella, Neomaskellia, Orientaleyrodes, Paraleyrodes, Parabemisia, Pealius, Psuedcockerelliella, Pseudozaphanera, Pushpasleyrodes, Rabdostigma, Rhachisphora, Rusostigma, Rutaleyrodes, Setaleyrode

I'll have what she's having: Unraveling ant trophic interactions using next-generation sequencing and isotope tracers

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Abstract: Trophic interactions largely influence the abundance and distribution of a species, but they can be difficult to assess, particularly in small, difficult-to-observe taxa such as insects. We examined the utility two techniques to quantify trophic interactions: high-throughput sequencing molecular gut content analysis (HTS-MGCA) and stable isotope tracers. We applied both techniques to the red imported fire ant (Solenopsis invicta; hereafter fire ant), a highly aggressive species that has invaded many parts of the world. We used HTS-MGCA to identify specific taxa that fire ants consumed in several different habitats, and then we used an isotope tracer to examine the effect of queen number on food-sharing between colonies. Because adult fire ant workers rely on their larvae (brood) to digest prey and share it via trophallaxis with the rest of the colony, we sequenced the gut contents of ant brood instead of adult workers to better capture colony diet. Using the Illumina HiSeq, we analyzed the diets of field-collected fire ants and co-occurring arthropod predators. We detected a total of 89 predation events from 16 samples collected across five different sites. Approximately 94% of all predators showed evidence of intraguild predation. All fire ant samples contained sequences from both detritus-based food webs and plant-based food webs. Conversely, only 30% of all arthropod predator samples contained sequences from both food webs. We also fed 15N-labeled glycine to fire ant colonies that varied in queen number to quantify food-sharing between colonies. The current hypothesis is that colonies with multiple queens readily share food with neighboring colonies, whereas, single-queen colonies do not share and are instead highly territorial towards conspecifics. We found that there was very little sharing between colonies in the field, regardless of queen number, even between colonies that were less than 0.5m away from each other. Our results suggest that both HTS-MGCA and stable isotope tracers are broadly applicable techniques that can be used to unravel insect trophic interactions.

A new Massive Open Online Course (MOOC): Bugs 101, Insect-Human Interactions

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Abstract: Bugs 101 is a Massive Open Online Course (MOOC) that was launched on the Coursera platform in June 2019. The content of the course focuses on insect-human interactions, and also introduces learners to insect evolution, biology and ecology. The course has 12 modules each containing several lessons and culminating in a quiz on the material at the end. The first four modules introduce insect diversity, morphology, biology and locomotion. The next four modules focus on ecosystem functions provided by insects including decomposition, herbivory, pollination and disease vectors. Each module has lots of examples on how these functions directly impact human society. The final group of four modules focuses on ways that humans directly interact with insects through sustainable management of insects considered to be pests, conservation of threatened insect populations, and insects as inspiration in music, art, science and literature. Throughout the course, there are 26 interviews with experts on a range of topics from forensic entomology to insects in art. Several interactive learning objects are incorporated into the course so that students can actively interact with the course material. The course is available for free to a wide range of learners from around the world. There are >5500 students enrolled in the class from over 120 countries 2 months after its launch. Here, we explain the process of building a MOOC, highlight the course content and delivery methods and introduce the learning tools that are used to reinforce and assess student learning.

Using an invertebrate's response to low temperature as a criterion for assessing establishment potential

Authors: Everatt Matthew, Department for Environment, Food and Rural Affairs, United Kingdom

Abstract: Augmentative invertebrate biological control agents are defined as mass produced natural enemies that are periodically introduced into a specific environment to suppress pest populations over short periods. These agents were first used in Europe in the 1920s, when the parasitoid wasp, Encarsia formosa, was released to control whiteflies in glasshouses, and are now a common feature of integrated pest management programmes in commercial horticulture. These agents are often polyphagous, and there is a concern that their introduction will lead to permanent establishment outdoors, with undesirable impacts on native species through predation or parasitism. Applications for the release of polyphagous agents cannot usually be based on their specificity to a target pest, and their safety must, instead, be demonstrated by other means. In England, the potential impact of an augmentative agent is commonly assessed by evaluating whether it is likely to establish outdoors in the country and therefore whether any impact it has on non-target hosts will be limited and transient.

Establishment potential is assessed using a number of criteria, including abiotic factors of low temperature and humidity, and biotic factors of host distribution, alternative hosts and other essential species, and competition and natural enemies. Of these, low temperature is often the most important factor, either because the agent is unable to complete its lifecycle or because it is unable to survive the UK winter. In this presentation, the methods for assessing an agent's low temperature tolerance, including the measurement of an agent's thermal budget, lower lethal temperature and lower lethal time, are described, and then discussed in relation to an agent's safety for release in England.

Global patterns of field-evolved resistance to Bt crops

Authors: Fabrick Jeffrey[2] and Carrière Yves[1], [1]University of Arizona, [2]USDA ARS, U.S. Arid Land Agricultural Research Center

Abstract: Crops genetically engineered to produce insecticidal proteins from Bacillus thuringiensis (Bt) have revolutionized control of some key pests, but their benefits are reduced by evolution of resistance to Bt toxins by pests. The global monitoring data reviewed here reveal at least 22 cases of practical resistance to Bt crops, which is field-evolved resistance that reduces Bt crop efficacy and has practical consequences for pest control. Each case represents the responses of one pest species in one country to one Bt toxin. The 22 cases of practical resistance involve resistance of some populations of nine major pests (seven lepidopterans and two coleopterans), six countries, and nine crystalline (Cry) toxins. Field outcomes confirm predictions from theory that abundant refuges of non-Bt host plants can delay evolution of resistance to Bt crops. Also, multi-toxin Bt crops can most effectively delay resistance to Bt crops when each of the toxins is highly effective against the target pest.

Insecticide resistance increases dissemination of West Nile virus in mosquito vectors

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Abstract: Insecticide resistance has been reported to impact the interactions between mosquitoes and the pathogens they transmit. We investigated whether insecticide resistance mechanisms selected in the mosquito Culex quinquefasciatus would impact vector competence for two arboviruses, Rift Valley Fever (RVFV) and West Nile viruses (WNV). Three Cx. quinquefasciatus lines sharing a common genetic background were used: two insecticide-resistant lines, one homozygous for amplification of the Ester2 locus (SA2), the other homozygous for the acetylcholinesterase ace-1 G119S mutation (SR) and the insecticide-susceptible reference line Slab. Statistical analyses revealed no significant effect of insecticide-resistant mechanisms on vector competence for RVFV. However, both insecticide resistance mechanisms significantly influenced the outcome of WNV infections by increasing the dissemination of WNV in the mosquito body, therefore leading to an increase in transmission efficiency by resistant mosquitoes. These results showed that insecticide resistance mechanisms enhanced vector competence for WNV and may have a significant impact on transmission dynamics of arboviruses. Our findings highlight the importance of understanding the impacts of insecticide resistance on the vectorial capacity parameters to assess the overall consequence on transmission.

The next arboviral threat: Yellow fever

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Abstract: Yellow fever virus (YFV; Flavivirus, Flaviviridae) is mainly circulating in Africa and South America, causing approximately 29,000 – 60,000 deaths annually. Even though the vaccination against YFV is the primary strategy for controlling this disease, the spillover of the virus from sylvatic cycle to immunologically naïve population is still responsible for several outbreaks, recently in Brazil and in Africa (Angola, Democratic Republic of the Congo and Uganda). YFV is still absent in Asia despite the overall favorable conditions, such as presence of mosquito vectors Aedes albopictus and Aedes aegypti, and majorly unvaccinated populations. However, the rapid growth of international commerce and exchanges between Asia and several YFV epidemic African countries have increased the risk of disease introduction. In 2016, 11 Chinese workers exported YFV into China from Angola during the massive outbreak. Although these incidents did not cause any autochthonous cases, the threat is still there underlining the probability for YFV to be introduced in Asia. Using experimental infections, we have evaluated the vector competence of Asian Ae. aegypti and Ae. albopictus populations to YFV. The results are discussed in the light of potential emergence of yellow fever in Asia.

Worldwide invasion dynamics of Aedes albopictus shaped the vector competence of its populations for chikungunya virus

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Abstract: The mosquito Aedes albopictus is among the 100 most dangerous invasive species. Its worldwide spread has created public health concerns as it is the main vector of arboviruses of public health significance such as chikungunya (CHIKV).Dynamics of different genetic backgrounds and admixture events may have impacted competence for CHIKV in adventive populations. Linking the genetic structure of populations across the expansion areas with their competence for different CHIKV genotypes, we found that: the demographic history of Ae. albopictus populations is a consequence of the rapid complex pattern of historical lineage diversification and divergence and it influenced their ability to transmit CHIKV. Indeed, the history of adventive populations was found associated with the CHIKV genotypes in a genotype-by-genotype interaction which impacted their vector competence. Thus, the knowledge of the demographic history and vector competence of invasive mosquitoes is pivotal for assessing the risk of arbovirus outbreaks in newly colonized areas.

Bioinformatic analysis of antimicrobial peptides identified in the Black Soldier Fly (BSF) Hermetia illucens (Diptera: Stratiomyidae)

Authors: Falabella Patrizia[4], Falabella Patrizia[3], Giglio Fabiana[3], Rinaldi Roberta[3], Boschi Andrea[3], Sgambato Alessandro[1], Scieuzo Carmen[3], Vogel Heiko[2] and Salvia Rosanna[3], [1]Catholic University of the Sacred Heart, [2]Department of Insect Symbiosis, MPI for Chemical Ecology, Jena, Germany, [3]University of Basilicata, Italy

Abstract: Antimicrobial and antineoplastic resistances represent two of the most urgent therapeutic worldwide challenges underlining the need to develop novel alternative treatments. Antimicrobial peptides (AMPs), small molecules ranging from 10 to 50 amino acids, play a key role in the innate immunity, the first line of defence against bacteria, fungi and viruses. They are promising molecules potentially lacking toxicity to healthy cells and unaffected by common mechanisms of resistance. Numerous insect-derived AMP have been reported in the literature and the Diptera Hermetia illucens is one of the most promising sources, since larvae thrive in hostile environments rich in microorganisms. To identify AMPs, we generated de novo transcriptome assemblies from larval and adult specimens. All sequences putatively encoding for AMPs were bioinformatically analyzed to predict their physico-chemical properties (by Antimicrobial Peptide Database Calculator and Predictor (APD3)) and their putative activity. AMPs were analysed on the CAMP database to predict their antimicrobial activity, and by iACP, the AVPpred and the Antifp servers to predict anticancer, antiviral and antifungal activities. These analyses allowed us to identify 57 putative active peptides. These preliminary results will allow the selection of the most promising candidates for heterologous expression/chemical synthesis to obtain peptides for in vitro studies.

African horse sickness virus transmission in Senegal: past and current status

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Abstract: In Senegal the horse has long been used as a draught animal for work in the farms and for transporting people and goods by horse-drawn vehicles and carts. With the development of horse breeding, African horse sickness (AHS) becomes endemic and constitutes a major constraint to the development of this breeding. AHS, a vector-borne viral disease, affects equids and causes very high mortality rates. To control the disease, mass vaccination remains the only means of prevention implemented by the public authorities in Senegal. Many effective vaccines have been developed and made available to horse owners. Before the 2007 AHS epizootic, the monovalent vaccine against serotype 9 was the only one used in mass vaccination campaigns. This recent epizootic, due to the new introduction of serotype 2, led to the use of a polyvalent vaccine with nine serotypes of AHS virus for control and mass vaccination campaigns. However, vector-borne diseases control couldn't be effective through vaccination alone; integrated control measures taking into account vector control would be required. In contrast to studies carried out in South Africa on AHS vectors, knowledge of West African vectors has been very limited, making difficult the implementation of effective control measures.

This study presents the state of art of AHS transmission in Senegal based on existing literature and entomological and serological surveys carried out after the 2007 epizootic. To determine the circulating serotypes two serological surveys were carried out on donkeys and unvaccinated horses in 7 out of 14 regions and 10/14 regions with high equine densities in 2008 and 2013-2014 respectively. The sera were analysed by the virus neutralisation test using the known serotypes of AHSV1 to AHSV9 with the exception of AHSV6 which is known to cross-react with AHSV9. For vectors collection, two nationwide surveys were carried out in 2012 and 2018-2019 respectively using Onderstepoort Veterinary Institute OVI-light traps to identify vectors potentially involving in AHSV transmission and their relative abundances.

In 2008 a total of 278 sera were collected from donkeys and analysed with the neutralisation test (VNT). The results showed the presence of two serotypes with an overall seropositivity of 56% for AHSV9 and 49% for AHSV2. Whereas in 2013-2014, out of the 987 sera (444 donkeys and 543 horses) collected, all the serotypes tested were detected with spatial variability of serotypes and seroprevalence (seroprevalence for donkeys = 28.5 SD 11.8%; seroprevalence for horses = 33 SD 11.4%). Serological results from 2013-2014 suggest a vectorial transmission of vaccine strains to unvaccinated animals. The abundance of Culicoides imicola and C. oxystoma was determined and their likely role in AHS virus transmission discussed. Also the study highlighted through a regression model, the relationships between age, animal species and vectors abundance and the presence of serotypes.

LIFE PollinAction: Actions for boosting pollination in rural and urban areas in northeast Italy (LIFE19 NAT/IT/000848)

Authors: Fantinato Edy[1] and Buffa Gabriella[1], [1]Ca' Foscari University of Venice, Italy

Abstract: Pollinator populations are negatively affected by the increasing use of agrochemicals, parasites and diseases, local and global environmental degradation and by the loss of natural and semi-natural habitats. The destruction and fragmentation of these habitats and the consequent reduction in wildflowers cause the loss of nectar and pollen as well as breeding, nesting and overwintering habitats for pollinators, triggering population declines and isolation of populations. The project is creating a green infrastructure network, made up of natural and semi-natural areas, in rural and urban landscapes in North-East Italy and Spain. Actions include conversion of arable land to grassland, improvement of species-poor grassland, and the creation of wildlife corridors for pollinators along road infrastructure, riverbanks, public places, and gardens. The project is collecting seeds from native species in the region to produce seedlings to improve foraging habitats for pollinators.

The State of Mosquito and Vector Control in the United States: A Perspective from a Local Mosquito Control District

Authors: Faraji Ary, Salt Lake City Mosquito Abatement District, United States

Abstract: This presentation will cover the current state of mosquito surveillance, control, and research at the local level. The perspective will be provided through a local government agency providing vector control services in Midwestern United States. Highlights will be given to methods of surveillance, control, research, and interaction with other agencies and organizations across the globe.

Host detection by ticks and effect of repellent exposure

Authors: Faraone Nicoletta[1] and Hillier Neil Kirk[1], [1]Acadia University

Abstract: Ticks are obligate blood-feeding ectoparasites of many hosts and are second only to mosquitoes as the most common arthropod pathogen vectors. Ticks use many different strategies to detect suitable hosts for a successful blood meal. Being almost totally blind, ticks rely on chemosensation to identify and locate hosts for a successful blood meal, and the tick chemosensory system represents a new frontier compared with that of insects. We identified key odorants/ blends by collection and chemical characterization of volatile compound (VOC) from hosts (e.g., humans, cats, dogs, etc.). Because no studies have investigated potential long-term disruption and inhibition of tick abilities to detect hosts, we assessed the effects on tick chemosensory system of long-term exposure to repellents, and investigated whether pre-exposure to repellents impact the chemosensory system of ticks. Through a novel electrophysiological approach, we recorded tick responses to host VOCs alone and to butyric acid pre- and post-exposure to repellents using gas chromatography linked electrotarsography. We validated these findings through behavioural bioassays. Understanding the mechanisms behind tick host selection/acceptance and chemical cue perception will provide means to prevent tick bites and thus infections in humans and animals and to develop effective tick repellent products.

Validation of In2Care® EaveTubes as a new malaria intervention paradigm for controlling insecticide-resistant anophelines

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Abstract: Malaria remains a serious public health threat as the efficacy of contemporary vector control tools is hampered by insecticide resistance. In2Care® EaveTubes are under evaluation at WHO as a new malaria vector control paradigm. EaveTubes create point-sources in house walls that passively funnel occupant odours and lure anopheline mosquitoes. The innovative static netting inserts block and kill resistant vectors by transfering lethal doses of powder-formulated insecticide through polarity.

A large Phase III two-armed, cluster Randomized Controlled Trial was conducted in 40 village clusters in central Côte d'Ivoire between 2017 and 2019 to evaluate the public health impact. In total, 3069 houses in 20 intervention clusters received window screening and on average 10 beta-cyfluthrin-treated In2Care® EaveTubes per house, with a median village coverage of 73% (range 32% - 100%). All 40 clusters received Long-Lasting Insecticide-treated Nets (LLINs) and in each cluster 50 children (aged 6 months to 10 years) were followed up for two years to monitor clinical malaria incidence via active case detection.

Entomological monitoring results show a 61% reductions in indoor-collected anopheline densities and a 39% reduction in outdoor densities. There was a 73% reduction in the indoor Entomological Inoculation Rate. Epidemiological results show that children living in the intervention villages had a 38% lower risk of having a malaria case (Hazard Ratio 0.62 (95% CI 0.51-0.76; $P<0.001$)). There is evidence of a community effect with significant reductions in malaria case incidence in villages with >60% InCare® EaveTube coverage.

Malaria infection prevalence was measured in two cross-sectional surveys . Results showed similar prevalences between baseline and endline in the control villages, whilst the intervention villages saw a 21% drop in malaria case prevalence between baseline and endline. Comparing the two trial arms directly at endline showed a significant reduction in malaria prevalence risk: OR 0.56 (95% CI 0.45 - 0.71 $P<0.001$).

Experimental hut studies were conducted to gather additional entomological evidence on the results of In2Care EaveTubes as a stand-alone method. Results showed that 90% more mosquitoes were attracted to In2Care® EaveTubes than to open windows and that 87% of the highly resistant malaria mosquitoes were killed within 4 nights.

These results indicate that In2Care® EaveTubes provide protection against malaria on top of universal coverage with LLINs in an area with intense pyrethroid resistance. Future trial designs for validating public health value in a second setting are being discussed with the Vector Control Advisory Group, including smaller non-inferiority and interrupted time series studies, and less expensive RCTs that use malaria prevalence and and passive incidence as outcomes.

Shrub contributes to the follicular cell integrity in the panoistic ovary of Blattella germanica

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Abstract: Cytokinesis is the physical process of cell separation in the cell division, in which the cytoplasm of a parental eukaryotic cell divides into two daughter cells. To be carried out the integrity of the cytoskeleton is crucial. shrub encodes a filament-forming subunit of ESCRT-III (Endosomal Sorting Complex Required for Transport) essential in the abscission, the last step of cytokinesis. In female germline stem cells of Drosophila melanogaster, Shrub controls the timing of cell division by recruiting ESCRT-III complex in the midbody before the abscission and its absence stops germinal stem cells division. The current knowledge of the function of Shrub in insect oogenesis is limited to germinal stem cells, and its role in ovarian somatic cells is still unknown. Our objective is to unveil the function of Shrub in the oogenesis of the cockroach Blattella germanica paying attention to the ovarian somatic cells. shrub expression was depleted by RNA interference (RNAi) in young adult cockroaches resulting in sterile females. Basal ovarian follicles didn't grow in shrub-depleted females due to a failure in cytoskeleton proteins assembly. Results obtained show that Shrub-like protein participates in the follicular epithelia integrity during ovarian maturation in B. germanica.

Finding the needle in a haystack: molecules that elicit butterfly egg-killing in plants

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Abstract: Plants can defend against insect eggs deposited on their leaves by e.g. the formation of necrotic tissue underneath the eggs. Several brassicaceous plants, including the annual weed Brassica nigra, respond with an egg-killing necrosis to cabbage white butterfly (Pieris sp.) eggs in nature. Knowledge on egg-associated molecular patterns (EAMPs) or elicitors inducing egg-killing is limited and no bonafide egg receptor has been found so far. We aim to isolate and identify the EAMPs that triggers egg-killing necrosis in B. nigra. First, we show that a wash of Pieris eggs elicits a similar response as the eggs themselves. Dissection of eggs from the ovaries of P. brassicae showed that the active compound is only present on fertilized eggs that have passed the oviduct and its associated gland containing egg glue. These results suggest that the elicitor is in secretions covering the eggs or in the egg glue released with eggs. In addition, this induction was shared between four tested Pierid species. To identify the elicitor, we analysed the chemistry of egg washes by LC/MS, and compared inducing and non-inducing washes. Furthermore, active washes were fractionated. Seven compounds are shared between all inducing washes and are present in an active fraction, and are thus good candidates as necrosis-inducing EAMPs. Validation of these compounds is still ongoing and when accomplished will further aid us in identifying the corresponding plant receptor of this egg-killing response.

The evolutionary history of Sternorrhyncha

Authors: Favret Colin, University of Montreal, Canada

Abstract: The Sternorrhyncha, a monophyletic suborder of Hemiptera, is itself composed of four monophyletic infraorders: Aleyrodomorpha, Aphidomorpha, Coccomorpha, and Psyllomorpha, the whiteflies, aphids, scale insects, and jumping plant lice (or psyllids), respectively. Sternorrhynchs are among the most host-specific of insects, their evolutionary history intimately tied to the plants they colonize. Many species are plant pests, vectors of plant diseases transmitted directly to the phloem elements on which the insects feed. Whereas the aphids and scale insects have long been uncontroversially considered sister taxa, the relative phylogenetic positions of the psyllids and whiteflies are variable depending on the types of data and analyses used. Morphological (including fossil) analyses usually group psyllids and whiteflies as sister taxa, mitochondrial genomes place psyllids as sister to the rest of the sternorrhynchs, but transcriptomes put the whiteflies in that position.

As a whole, the phylogenies of each of the four infraorders are poorly resolved. Whitefly phylogenetics has focused almost exclusively on the <i>Bemisia tabaci</i> species complex. Only a couple scale insect phylogenies have been attempted, although there is agreement on the monophyly of the neococcoid families. There is relative congruence among the several psyllid analyses and mitochondrial and nuclear loci largely agree, thus providing a preliminary but useable backbone phylogeny for the group. In contrast with the other infraorders, there has been a disproportionately larger amount of attention paid to the aphids, partly because they are used as models in a number of research domains (e.g., speciation, microbiomics, host-associated evolution). However, apart from the first branching event separating the obligate egg-laying and cyclically viviparous families, a credible aphidomorphan phylogenetic hypothesis has yet to be accepted.

The presentation will describe the current knowledge of sternorrhynchan evolution, including biological, morphological, and fossil data, and with a particular focus on molecular phylogenetics. It will compare the various datasets and methods used, and suggest possible ways forward, including deeper collaboration between researchers working separately on the four infraordinal taxa.

Gene-flow levels differ between the bumblebee Bombus pascuorum and the hoverfly Melanostoma scalare, two pollinators of isolated forest herbs in agricultural landscapes

Authors: Feigs Jannis Till[1] and Kramp Katja[2], [1]Leibniz Centre for Agricultural Landscape Research (ZALF), Germany, [2]Senckenberg German Entomological Institute (SDEI), Germany

Abstract: Two groups of important pollinators are hoverflies and bumblebees. In intensively used agricultural landscapes they can connect populations of isolated forest herbs found in semi-natural forest remnants. Their dispersal during foraging causes pollen-mediated gene flow among plants. The insects' dispersal behaviour and distribution differs depending on both the species-specific effects of the landscape structure and dispersal distances. Dispersal of a species can thereby be estimated via the analysis of the population genetic structure and gene flow.

Here, we study the population genetic structure of the main insect pollinators of two early-blooming herbs characteristic for old, deciduous forests in temperate Europe. Three landscape windows in South Sweden, Western and Eastern Germany, respectively, with at least six remnant old forests per window with populations of the forest herbs Anemone nemorosa and Polygonatum multiflorum were therefore selected. With a pollinator exclusion experiment we collected information about the dependency of the plant species on the pollinators. We established the main pollinators by observation of pollinator species and their visitation rates as well as species proportions in Malaise traps. Based on microsatellite markers we analysed the population genetic structures of the main pollinators sampled in the old forests with Malaise traps and net catches.

The hoverfly species Melanostoma scalare and the bumblebee species Bombus pascuorum were identified as main pollinators of A. nemorosa and P. multiflorum, respectively. We expect the population genetic structure of the two pollinator species to show differences in the degree of gene flow. Thereby, M. scalare is assumed to cover shorter distances than B. pascuorum. Accordingly, a higher genetic differentiation in the population genetic structure of the hoverfly species is expected in contrast to the lower genetic differentiation in the population genetic structure of the bumblebee species.

The study design allows not only generalising conclusions for the species' interaction with the agricultural landscape structure, but also substantiates hypotheses about particular effects of landscape elements. To further study the plant-pollinator interaction we will use the level of gene flow among the forest remnants detected for the pollinator to infer the expected level of gene flow among the plants. Furthermore, this may help to understand how the pollinator contributes to the chance of long-term survival of the plant species.

Why gene flow levels differ between the bumblebee Bombus pascuorum and the hoverfly Melanostoma scalare - a landscape genetics approach

Authors: Feigs Jannis Till[1], Kramp Katja[2], [1]Leibniz Centre for Agricultural Landscape Research (ZALF), Germany, [2]Senckenberg German Entomological Institute (SDEI), Germany

Abstract: For insect pollinators, intensively used agricultural landscapes are challenging in terms of available habitat and its distribution. The landscape structure has species-specific effects on the insects' dispersal behaviour and distribution, thereby affecting the gene flow. Here, we apply a landscape-genetic approach to assess the species-specific influence of landscape structure on population genetic structure patterns of two pollinators, the hoverfly Melanostoma scalare and the bumblebee Bombus pascuorum. They are main pollinators of two early-blooming herbs characteristic for old, deciduous forests in temperate Europe. The level of pollinator dispersal is assumed to affect the plants' gene flow and thus the survival of isolated plant populations.

Three landscape windows in South Sweden, Western and Eastern Germany, respectively, with at least six old forest remnants per window with populations of the forest herbs Anemone nemorosa and Polygonatum multiflorum were selected. Based on microsatellite markers we analysed the population genetic structures of the main pollinators sampled in the old forests. We determined locations of nesting sites of bumblebees outside the forests with a "mean centre" approach based on sibling identification. To characterise the landscape structure we quantified landscape composition and configuration in buffers around and strips among the sampled forests. We then assessed their effects on the respective population genetic structures of the hoverfly and the bumblebee species using GLMMs.

We expect that the landscape structure shaped the population genetic structure of the hoverfly species more distinct than that of the bumblebee species. For M. scalare, the landscape structure in smaller radii around forests should be stronger correlated to genetic diversity due to the relatively smaller dispersal distances covered by the hoverfly. Moreover, a gene-flow facilitating effect of the amount of grassland and hedgerows should be detectable for both pollinator species. In contrast, mass flowering crops should affect only bumblebees, indicating stronger gene flow and lower genetic differentiation near the resources.

Can generalist predator food webs provide stable aphid control in the future?

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Abstract: In general, increased biodiversity is expected to provide more resilient ecosystem processes. This is because in diverse communities there are more species that can contribute to the functions (functional redundancy), and because different species are likely to respond differently to environmental variation (response diversity). Attempts to empirically assess resilience of ecosystem processes in relation to relevant disturbances are few, not least in agricultural landscapes. We will present results from a study investigating functional redundancy and climate resilience of generalist predators predating on pest aphids and a range of other prey types in Swedish barley crops. To assess functional redundancy we developed a new method linking interaction metrics with metabolic theory that allows for a quantification of redundancy at the level of ecosystem processes. To assess response diversity in relation to global warming we investigated the activity niches of a large number of actively hunting generalist predators in relation to temperature and combined them into a metric of climate resilience. Applying these methods to our generalist predator food webs, we found that both redundancy and climate resilience of aphid predation was significantly reduced in simplified landscapes. Thus landscape simplification will likely reduce the reliability of aphid control in the future.

Polydnavirus Mediates Fitness of Parasitoids, Caterpillars, and Plants

Authors: Felton Gary W., Department of Entomology Pennsylvania State University University Park, PA, United States

Abstract: Many parasitic wasps of caterpillars possess obligate mutualistic viruses called polydnaviruses. Along with eggs, wasps inject polydnavirus inside their caterpillar hosts where the hatching larvae develop inside the caterpillar. Polydnaviruses suppress the immune systems of their caterpillar hosts, which enables egg hatch and wasp larval development. Using two parasitoid species including the specialist Microplitis croceipes and the generalist Cotesia marginiventris, we show that the parasitoids and their associated polydnavirus are able manipulate the salivary enzymes of their host caterpillars and consequently impact the expression of plant defenses. These impacts on plant defenses can even extend to impacting fitness of the caterpillar's host plant.

Salivary Glucose Oxidase Mediates the Intersection of Insect and Plant Immunity

Authors: Felton Gary W., Department of Entomology Pennsylvania State University University Park, PA, United States

Abstract: Glucose oxidase is a widely occurring salivary enzyme in caterpillar species and plays a multifunctional role. Through its production of hydrogen peroxide, glucose oxidase (GOX) can provide antimicrobial protection for caterpillars during feeding. Because hydrogen peroxide serves as a secondary messenger in mediating many plant responses to biotic and biotic, GOX has the potential to also drive a number of plant physiological responses to the environment. We have utilized CRISPR-Cas9 genome editing of GOX in the caterpillar to examine the impact of GOX on both insect and plant immunity. Two mutant lines of GOX caterpillars have been developed which are providing the tools to examine the important role of this salivary enzyme in mediating plant-insect-microbe interactions.

Asymmetric responses to climate change: Temperature differentially alters an herbivore salivary elicitor and host plant responses to herbivory

Authors: Felton Gary W.[1], Tomasula Jewe[2] and Rajotte Edwin[1], [1]Department of Entomology Pennsylvania State University University Park, PA, United States, [2]United States

Abstract: Using experimental warming and a combination of biochemical, molecular and herbivory bioassays, we investigated the effect of elevated temperatures on tomato (Solanum lycopersicum var. Better boy) and a generalist herbivore (tomato fruit worm, Helicoverpa zea). We identified a very novel mechanisms of how climate warming may impact the activity of caterpillar salivary elicitor, Glucose oxidase (GOX) and the ability of insects to trigger plant defense responses. GOX activity on caterpillars reared at a warmer temperature was significantly reduced resulting in a low level of induced plant defensive chemicals. In addition to the warming-mediated changes in caterpillars to elicit plant defenses, temperature directly affected induction of temperature-sensitive defensive chemicals and plant resistance. Herbivore growth was significantly reduced when fed on previously damaged leaves compared to undamaged leaves from plants grown under the above-optimum temperature range, emphasizing the importance of induced plant resistance to estimate the impact of climatic changes on insect-plant interactions, which has generally been overlooked in the past studies. Overall, results from our study produced an asymmetric effect between an herbivore and its host plant, illustrating the complexity of changes in insect-plant interactions that could result as the climate warms. We, therefore, assert that any future predictions under climate change that do not take this complexity into consideration will be unconvincing.

microRNA regulation in an ancient obligate endosymbiosis

Authors: Feng Honglin, Boyce Thompson Institute for Plant Research, United States

Abstract: Aphids harbor a nutritional obligate endosymbiont in specialized cells called bacteriocytes, which aggregate to form an organ known as the bacteriome. Aphid bacteriomes display distinct gene expression profiles that facilitate the symbiotic relationship. However, the mechanisms that regulate these patterns of gene expression are unknown. While microRNAs (miRNAs) have been recently identified as regulators of host/pathogen and host/facultative endosymbiont interactions, the role miRNAs may play in mediating host/obligate endosymbiont interactions is virtually unknown. In my study, I identified conserved miRNAs that potentially mediate symbiotic interactions between aphids and their obligate endosymbiont, Buchnera aphidicola. Using small RNA sequence data and reference genomes of Myzus persicae and Acyrthosiphon pisum, I annotated 93 M. persicae and 89 A. pisum miRNAs, among which 69 were shared. I found 14 shared miRNAs that were either highly expressed or differentially expressed in bacteriome (the Buchnera-housing tissue) vs gut (a non-Buchnera-housing tissue). Strikingly, 10 of these 14 miRNAs have been implicated previously in other host/microbe interactions. Then using a custom computational pipeline, I identified 103 miRNA::mRNA interactions shared between M. persicae and A. pisum. Functional annotation of the shared mRNA targets revealed only two over-represented cluster of orthologous group categories: amino acid transport and metabolism, and signal transduction mechanisms. Furthermore, using a dual luciferase assay in mouse NIH/3T3 cell culture, I experimentally validated the computationally predicted interaction between Mpe-miR-92a and the predicted target region of M. persicae bacteriocyte-specific secreted protein 1 (SP1) mRNA. Those results support a role for miRNAs in mediating host/symbiont interactions between aphids and their obligate endosymbiont Buchnera.

Pest insect monitoring in China: Going automatic and smart

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Abstract: Benefited from rapid development of computer science, artificial intelligence and internet technology, traditional pest insect monitoring technologies are going automatic and smart. With success of deep learning in image analysis and popularization of smart phone, onsite insect species identification and counting small insects, such as aphids, plant hoppers, whiteflies and so on, became instant. Catches of insects in light-traps could be killed with infrared heating killer and identified timely. The image of insects and number of each species counted were sent to a cloud server, and users could view the light trap results with a computer in office or a smart phone anywhere. The accurate rate of species identification was above 80% for common agricultural pests. A national wide network of smart pheromone traps was established in 2009. The smart pheromone trap counter used double or triple layer of infrared counters to count number of trapped insects accurately and send results to a cloud server. Scanning and vertical looking radars were upgraded and new dual-mode radar was developed for insect monitoring. The comparison of radar monitored data with light trap data indicated that the entomological radar could identify common insect species and record the population dynamics accurately. Long-term monitoring indicated insect pests migrated towards north in May, June and July, but towards south in August and September. The modern insect pest monitoring system was used to monitor newly invaded fall armyworm Spodoptera frugiperda and provided satisfied information.

Observing mass migrating insects on marine research ship

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Abstract: Although much is known about the movements of insects across the sea on land for many decades, the migration patterns of most species, the impacts of seasonal weather on annual movements across the sea are poorly known. Here we used high altitude light-trap to monitor the adult dynamics of mass insect migration from Huanghai and Bohai sea for three years. The ovarian development of main lepidoptera female adult captured on the sea ie, Helicoverpa armigera, Mythimna separata,Dichocrocis punctiferalis, etc were dissected.Our results showed that about 69 insect species were captured. According to the capturing time, site, and the weather conditions at that time, using the trajectory analysis to estimate the insect origin and flight destination, some of lepidoptera moths might migrate from Taiwan province of China, Japan or South Korea . Ovarian development level of main lepidoptera female adults combined with insect migration was also discussed.

Invasion asymmetry: origins or opportunities for introduction?

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Abstract: Certain world regions are overrepresented as donors of alien species, while others are overrepresented as recipients. It has been suggested that asymmetric patterns of establishment are due to regional selection for traits promoting invasiveness, but this has rarely been tested empirically. Insects are among the most widespread and problematic alien organisms, and are largely introduced unintentionally by the movement of commodities. This suggests that varying opportunities for introduction through trade and travel may explain invasion asymmetry in insects. However, the selective pressures filtering species differ throughout the invasion process. It is possible that species introductions could be largely determined by trade flows, while insects from certain regions are indeed more likely to establish once introduced. Here we aim to disentangle the impacts of region of origin, and opportunities for introduction, on species flows during different stages of the invasion process. We used border interception records, comprehensive lists of established insects, and global ant distribution data to quantify flows of species between regions. While certain regions supply more species than others, import value had a significant impact on both the number of species transported between regions, and the number of species which subsequently establish. Our results suggest that while species' origins influence their invasion success, the regional asymmetry in insect establishments can to a large extent be explained by differing opportunities for introduction through human-mediated dispersal. Understanding the mechanisms that drive species introductions, establishment and spread outside their native range is crucial for managing biological invasions.

Vectors of Xylella fastidiosa in Spain: distribution, life cycle and dispersal

Authors: Fereres Alberto[1], Moreno Aranzazu[1], Lago Clara[1] and Cornara Danele[1], [1]ICA-CSIC Madrid, Spain

Abstract: Xylem-feeders insects belong to various families of Auchenorryncha, the most common and widespread in Europe being the superfamily Cercopoidaea, whose members are commonly known as spittlebugs or froghoppers. During the period 2016-2019, we surveyed the potential vectors of X. fastidiosa in the main olive, almond and grapevine-producing regions of the Iberian Peninsula. Our survey shows that Philaenus spumarius and Neophilaenus campestris occur in olive groves in spring and early summer on the ground vegetation but very few are present on the tree canopy. In almond groves and vineyards, spittlebugs were found both in the tree canopy and on the ground vegetation. The sharpshooter Cicadella viridis was also found in vineyards but only on the ground vegetation. The occurrence of spittlebugs is mainly concentrated in cold and humid regions where ground vegetation is present most part of the year. Other factors such as the presence of livestock, riparian and grassland vegetation are suitable for spittlebug profusion.

In addition we conducted a study on the life cycle of the monovoltine P. spumarius to set up the best environmental conditions for indoor rearing and artificially reach up a maximum number of generations per year. Our goal was achieved by disrupting both the ovarial and overwintering diapause, shortening its life cycle and obtaining both nymphs and adults, several months before they become available in the field.

Finally, we have set-up a capture-mark-recapture methodology in combination with flight mills to study the dispersal of spittlebugs. We found that they migrate from their spring hosts (eg olive groves) to their oversummering hosts (eg pine trees) and are able to fly at least 2.5 km in 35 days.

All these studies show that vectors of X. fastidiosa are widely present in the Iberian Peninsula in olive, almond and vineyards although mainly associated to specific climatic conditions and cultural practices.

Contributions to improve current environmental risk assessment procedures of GABCAs in Argentina

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Abstract: Argentina has over 100 years of experience in classical biological control, mostly based on the importation of GABCAs against arthropod pests and weeds. Historically, introductions were requested by provincial or national ministries of agriculture and the National Institute of Agricultural Technology (Instituto Nacional de Tecnología Agropecuaria, INTA), and only a few, if any, risk or non-target effect analyses were made prior to entering the organisms. Since the late 1990s, the process for requesting, evaluating and making decisions to import, quarantine, release and post-release monitoring of exotic biocontrol agents is carried out by the the Animal and Plant Protection Service (Servicio Nacional de Sanidad Animal y Vegetal, SENASA) at national level. Safety of introductions is also regulated at international level, by the Plant Protection Committee (Comité de Sanidad Vegetal, COSAVE) formed by Argentina, Brazil, Chile, Peru, Bolivia, Uruguay and Paraguay to accomplish the International Standard for Phytosanitary Measures (ISPM 3). As a part of the process, the evaluation of environmental risks and potential non-target organisms threatened of importing such exotic agents is requested to specialists from academic and scientific sectors. Experts usually face the lack of published information or previous research work done on the biology of the invasive pest, the native natural enemies communities, and at larger scale, the effects on non-target species; thus, they are mostly reluctant to inform positively on those petitions. Lastly, this situation creates tensions among scientists, producers and decision makers to import exotic GABCAs. In this paper, we present the state of the art of the procedures and regulations for the importation of GABCAs in Argentina during the last two decades, summarizing main classical or commercial biocontrol initiatives and discuss the potential risks involved in such introductions. To cope with that, we focused our analysis on the petition to import 18 GABCA species (15 parasitoids and three predators) done from 1996 to date, reported by SENASA and COSAVE websites. We summarized their host/prey range, biogeographical origin, target crop and pest, year of requested importation, experimental or commercial purposes, and denied or approved request (year) by searching information on the species in Google Scholar, CABI and other biological databases as well as that published in primary literature sources, non-peer review papers (technical reports, etc.). We also ranked the species following the ERA-GABCA categories for Likelihood of Establishment (LE) for the exotic agents and Adverse Effects (AEi) on non-target species. We are aimed to provide, from this study, indications and recommendations for scientific researchers, agricultural producers, practitioners and decision makers to improve the current evaluation for GABCA introductions, in a social, environmental and economic safer productive context.

Biological control of Bemisia tabaci biotype B in protected tomato cultivation: dynamics of mortality factors and predation potential of Amblyseius tamatavensis

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Abstract: The whitefly Bemisia tabaci (Gennadius) (Hemiptera: Aleyrodidae) biotype B is one of the main agricultural pests in Brazil and worldwide. The objective of this study was to evaluate the predation potential of Amblyseius tamatavensis Blommers (Acari: Phytoseiidae) in protected tomato cultivation, as well as the dynamics of whitefly mortality factors. Experiments were carried out in laboratory and greenhouse. Initially, the predation preference for eggs and nymphs of B. tabaci was evaluated. Subsequently, the functional and numerical response of A. tamatavensis on immature B. tabaci was determined. The efficiency of A. tamatavensis to control B. tabaci on tomato plants was also evaluated. Finally, the dynamics of natural whitefly mortality factors were compared between B. tabaci infested tomato crops in the presence and absence of the predator A. tamatavensis. The results showed that A. tamatavensis has a preference for early stages of B. tabaci (eggs, first- and second-instar nymphs). The functional response is type II and the mite feeding upon B. tabaci eggs can oviposit 1.4 eggs/day. The release of 26 or 78 predatory mites/m2 soon after whitefly infestation are efficient to keep whitefly population under control. Individuals of the predaceous mites were observed after 4 weeks of release confirming they could develop and remain in the crop. Also, predation is an important mortality of whiteflies regardless the release of A. tamatavensis. This work established the foundation for a whitefly biological control program in tomatoes.

The genome sequence of the iconic pest grape phylloxera.

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Abstract: Although native to North America, the invasion of the aphid-like grape phylloxera (Daktulosphaira vitifoliae) across the globe altered the course of grape cultivation. For the past 150 years viticulture relied on grafting resistant North American Vitis species as rootstocks, thereby limiting genetic stocks tolerant to other stressors such as pathogens and climate change. Limited understanding of the insect genetics resulted in successive outbreaks across the globe when rootstocks failed. In the scope of the International Aphids Genomics Consortium, we report the 294-Mb genome of D. vitifoliae, and its annotation, available at the BioInformatics Platform for AgroEcosystems Arthropods (BIPAA. http://bipaa.genouest.org), as a basic tool to understand host-plant manipulation, nutritional endosymbiosis, and enhance global viticulture.

As a result, our study, supported by a highly complete genome and an uncommon community effort on curated annotation revealed that phylloxera (like aphids) has a high number of coding genes compared to other arthropods, metabolic pathways are similarly represented in phylloxera and aphids, despite the absence of obligate bacterial symbiosis, and we identified an extraordinarily large expansion of a novel gene family of putative effectors. Finally, a large genome-wide sequencing of phylloxera samples from both the native (North America) and introduced populations (Europe and New World vineyards) shows that phylloxera populations of the upper Mississippi River basin, feeding on the wild species Vitis riparia, are likely to be the principal source of the invasion to Europe. Subsequent invasions of South America and western Australia were the result of secondary introductions, from European sources.”

Selection following gene duplication shapes recent genome evolution in the pea aphid Acyrthosiphon pisum

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Abstract: Ecology of insects is as wide as their diversity, which reflects their high capacity of adaptation in most of the environments of our planet. Aphids, with over 4,000 species, have developed a series of adaptations including a high phenotypic plasticity and the ability to feed on the phloem-sap of plants, which is enriched in sugars derived from photosynthesis. Recent analyses of aphid genomes have indicated a high level of shared ancestral gene duplications that might represent a basis for genetic innovation and broad adaptations. In addition, there is a large number of recent, species-specific gene duplications whose role in adaptation remains poorly understood. Here, we tested whether duplicates specific to the pea aphid Acyrthosiphon pisum are related to genomic innovation by combining comparative genomics, transcriptomics, and chromatin accessibility analyses. Consistent with large levels of neofunctionalization, we found that most of the recent pairs of gene duplicates evolved asymmetrically, showing divergent patterns of positive selection and gene expression. Genes under selection involved a plethora of biological functions, suggesting that neofunctionalization and tissue specificity, among other evolutionary mechanisms, have orchestrated the evolution of recent paralogs in the pea aphid and may have facilitated host-symbiont cooperation. Our comprehensive phylogenomics analysis allowed to tackle the history of duplicated genes to pave the road towards understanding the role of gene duplication in ecological adaptation.

Effect of entomopathogenic fungi and pyrethrum combinations on pests and beneficial insects

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Abstract: Entomopathogenic fungi (EPF) and botanical pesticides, such as pyrethrum, are recognised as promising tools for pest control in sustainable agriculture. They are favoured for their low impact on the environment and human health, however, the short period of activity for pyrethrum and the delay from application to effective control for EPF have limited their utility for growers. A combination of both pyrethrum and EPF could overcome these limitations by creating an environmentally benign pesticide which is fast acting through the activity of the pyrethrum, and long lasting through the sustained control from the EPF. Furthermore, it is hoped this multimodal approach may enhance efficacy and challenge the development of insecticide-resistant pest species.

We present findings of our studies of combinations of pyrethrum with EPF strains of Metarhizium anisopliae and Beauvaria bassiana on the mortality of aphids, Aphis fabae, and fall armyworm, Spodoptera frugiperda. Additionally, we explore the impact of a combination treatment on mortality and oviposition behaviour of an important pollinator species, the hoverfly Eupeodes corollae.

Oviposition strategies of container breeding mosquitoes: an investigation into the site search and internal site behaviour of gravid Aedes aegypti.

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Abstract: Aedes aegypti (Diptera: Culicidae), vector of the yellow fever, dengue, chikungunya and Zika viruses, oviposit in a variety of man-made containers in urban environments. Some containers (e.g. water storage units and plant pots) have been identified as more productive in numbers of pupae produced, but the extent to which Ae. aegypti actively seek these sites in which to oviposit remains unclear. Many containers in urban environments appear relatively limited in potential resources but still receive eggs. Understanding this fundamental aspect of mosquito behaviour is essential for developing evidenced-based policies for Ae. aegypti control, and for testing theories of whether insects can reliably select oviposition sites which produce the most offspring (the preference-performance hypothesis).

Here, we examined Ae. aegypti oviposition responses to water from plant pot dishes, a common oviposition site in Brazil. It is believed these may be a preferred and productive container due to organic matter from the soil supporting bacterial growth as a larval food source. We tested whether Ae. aegypti chose to lay in this ecologically relevant substrate under cage bioassay and wind tunnel conditions, and if it conferred any benefits for offspring. We also examined if Ae. aegypti modulate how eggs are placed within an oviposition site (on the side of the container or directly on the water) in response to the water contents, and the potential adaptive benefits of such behaviour.

Our initial results indicate that in standard oviposition cage assays, more female Ae. aegypti laid eggs in plant pot water compared to both deionised water and a brewer's yeast suspension. However, larval survival in plant pot water was not higher than in deionised water and was significantly less than in the brewer's yeast suspension. This suggests that, under these standard test conditions, mosquitoes did not choose the most productive oviposition substrate. Furthermore, female Ae. aegypti modulated the placement of eggs within an oviposition site according to the contents of the water. We are currently investigating whether this strategy promotes bacterial growth and larval survival.

In wind tunnel assays, individual females laid more eggs in pots containing plant pot water than deionised water. However, the relative position of plant pot water within the wind tunnel air stream affected the relative number of eggs laid. This may indicate a role for volatile chemicals in locating or discriminating between potential oviposition sites and suggests a more opportunistic behaviour when the preferred pots were in a more cryptic location. Through 3D flight tracking, we are currently investigating the number of visitations per site in relation to the total number of eggs laid, and the order in which sites were visited. Together, these results may indicate how and why Ae. aegypti come to lay more eggs in preferred oviposition sites, even if they are not necessarily the most productive.

Community genomics and comparative behavioural assays shed light on host-specific chemosensory evolution in plant-associated drosophilids.

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Abstract: Host plant shift is a major source of diversification in herbivorous insects implying the evolution of multiple behavioral, physiological and morphological traits. However the evolutionary context of the early stages of host shifts, such as resource availability and escape from competition, remains often unclear. We investigate the recent specialization on the island of Mayotte of the generalist African fly (Drosophila yakuba) on the toxic fruits of Asian noni (Morinda citrifolia). Population genomics suggested D. yakuba to be present on the island 29,000 years ago, far before early human colonizers would have been able to plant noni or inadvently bringing other Drosophila competitors on the islands. We use chloroplast DNA and genome wide polymorphisms (RADseq) to infer the expansion date of noni into the Western Indian Ocean islands. We also use comparative population genomics, behavioural assays (taste preference) and physiological experiments (survival) in multiple Drosophila species that have also been bred from noni on Mayotte. The results suggest that a combination of historical events and ecological interactions facilitates host plant specialization in generalist insects.

Improving monitoring and control of black vine weevil (Otiorhynchus sulcatus) in soft fruit and ornamental crops

Authors: Fezza Eugenia, Harper Adams University, United Kingdom

Abstract: The black vine weevil, Otiorhynchus sulcatus (Coleoptera: Curculionidae) is one of the most economically important pests of soft fruit and ornamental crops. To develop an effective and reliable monitoring system for vine weevil adults a series of experiments were completed under laboratory condition in order to determine the influence of colour, height and entrance position on the efficacy of a model monitoring tool. Results indicate that dark, tall refuges with entrances around their base were preferred by vine weevil adults.

Additional experiments have investigated the behavioural responses of vine weevil to a range of olfactory cues associated with host plants or conspecifics. The aim, here, was to understand which olfactory cues stimulate positive behavioural responses in vine weevil adults in order enhance the efficacy and reliability of monitoring tools for this species through inclusion of a semiochemical lure. Results indicate that response olfactory cues are determined by the time of the day when the experiment was completed.

This study improves our understanding of the visual and olfactory preferences of vine weevil. Improved understanding of these behavioural responses can be exploited in the design of more effective and reliable monitoring tools for this species that may be used within IPM programmes.

Key lessons learned from recent insect biocontrol programs

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Abstract: The intensification of commercial trade over the last three decades has increased the rate of new pest introductions worldwide. It has also resulted in new pathways in the transportation of pests from countries not traditionally known as suppliers, such as central and south East Asia for North America and Europe, and South America for Europe and Africa. Recently introduced pest case studies will be used here as a baseline for understanding trends that are currently driving classical biological control (CBC). We will attempt to draw guidelines with respect to target selection, host range testing for regulatory approval and risk assessment, and measurement of economic, ecological and social impacts. As per target selection, the choice of pests with rapid expansion and high negative impact varies upon different factors. Pests impacting high-value added crops (spotted lanternfly and spotted wing drosophila on grapevine, the fall armyworm on cropped cereals), or crops having a great natural and cultural value (Asian chestnut gall wasp), or crops with a high demand from the farming industry (Bagrada bug on cole crops, brown marmorated stink bug on various fruits, vegetables, and ornamentals), have been prioritized. In addition, it became common to select targets that have been successfully controlled with known and evaluated beneficial agents in one place, to be introduced in another (Anagyrus kamali on the pink hibiscus mealybug, Mastrus ridens against codling moth, Neodryinus typhlocybae against the citrus planthopper). Thus, biocontrollers reduce the number of species for host range testing and maximize their chance of success and avoiding adverse impacts. Over 140 years of records in CBC, only 1.5% of worldwide programs had one or more non-target effect record. However the trend is to reduce this ratio for getting approval for release, and the most suitable species are selected for testing and that the resulting data provide the most rigorous test of the risk hypothesis of no adverse effect. Filtering on main criteria such as, spatial, temporal and morphological attributes on one hand, and species availability on the other hand, typically leads to a short list of species that may be tested (case studies of Bagrada bug and Brown marmorated stink bug). The test list is also based on phylogenetic relatedness, sympatry of target and non-target species (spotted-wing Drosophila). Finally, measurements of economics and ecological impacts show an extremely positive feedback on cost-effectiveness of CBC (Clover root weevil in New Zealand, mealybugs in agricultural systems). As a result, although the rate of new biocontrol agents introduced has been decreasing since the 1980s, a better success in the rate of success and establishment of BCAs has been observed. This trend could be partly due to all factors detailed above, like a better selection of non-target species to test, reducing the ecological risks that were the center of discussions in the 1990s.

Are eggs of Hermetia illucens L. (Diptera: Stratiomyidae) suitable for mass rearing predatory mirids?

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Abstract: The black soldier fly (BSF) Hermetia illucens L. (Diptera: Stratiomyidae is mass produced for biowaste conversion, protein meal, insect oil and fertilizer. BSF production is expected to increase after the European Commission authorized the use of insect-based protein in aquaculture feed. Higher market demand and production may reduce the cost of BSF products, including eggs, in the next years.

The market of commercial biological control agents is growing worldwide. Mass production of many generalist predators is dependent on the use of factitious prey like insect eggs. The eggs of Ephestia kuehniella Zeller (Lepidoptera: Pyralidae) and Sitotroga cerealella (Olivier) (Lepidoptera: Gelechiidae) are currently the staple food source used in commercial production of many natural enemies.

Mirid bugs (Hemiptera: Miridae) are among the most important natural enemies in protected crops. In order to reduce the cost of E. kuehniella eggs, the production of mirid bugs (mostly species in the genera Dicyphus, Macrolophus and Nesidiocoris) uses a mix of E. kuehniella eggs and Artemia sp. (Anostraca: Artemiidae) cysts.

BSF based diets have been previously studied on vertebrates like fish, pigs and poultry. However, there are few studies that evaluate the effect of H. illucens diet on other insects.

In this study we assessed the suitability of BSF eggs as factitious prey for predatory mirids. We chose the mirid Dicyphus cerastii Wagner (Hemiptera: Miridae) that is found from Portugal to Turkey on differerent crops.

Nymphal development time, nymphal mortality, adult longevity, weight and progeny were compared between D. cerastii nymphs reared on: 1) eggs of BSF; 2) eggs of E. kuehniella; 3) eggs of E. kuehniella + Artemia sp. cysts. Nymphal development time was not different between diets containing E. kuehniella eggs. However, it was significantly longer when reared on BSF eggs, suggesting it may be a lower quality diet compared to E. kuehniella.

Protecting processing tomato crop against Tuta absoluta (Meyrick) in Ribatejo region

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Abstract: Tuta absoluta (Meyrick) has been a key pest of tomato processing crop in the Portuguese region of Ribatejo since 2011, causing significant losses in some seasons.

In order to develop friendly to use tools for decision-making process to protect this crop a partnership bringing together growers' organizations, universities, technological centres and industrial companies) developed a plan supported by the project - PRODER 4.1 "Protomate" - Development of a new tool to support the management of the tomato crop to guarantee the quality of the final product". We aimed at improving risk assessment methods and the timing of the treatments and decreasing its number with better efficiency. A partnership network was built allowing a permanent interchange with knowledge, results and experience sharing routines in time during the crop cycle. In 2013 and 2014 crop seasons, adults of T. absoluta were monitored with delta pheromone traps and plants were checked for eggs and larvae according to a stablished protocol. Insects were collected for laboratory observation. Damage risk factors were identified at farm and regional scales. Risk maps were performed based on development parameters and temperature registered by satellite. The risk assessment program was applied in each field taking into account these maps, the adults in the delta traps, crops in the vicinity and their harvesting dates. The success of control methods was monitored. A diagram for decision-making in processing tomato is presented.

Critical role of the food K:Na ratio for ecology and evolution of herbivorous and detritivorous insects

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Abstract: The functioning of herbivorous and detritivorous insects is affected by nutritional limitation originating from general trait of plant tissues and products, i.e. low concentration of sodium (Na), required by consumers in high proportions. Therefore, Na availability influences survival, fitness, and abundance of consumers feeding on plant matter as well as shapes ecological interactions, and food webs. However, considering only one nutrient at a time is neither physiologically nor ecologically relevant, and the effect of Na on consumers may be regulated by the K:Na ratio. Sodium and potassium (K) are physiologically bound and excessively high K:Na ratio in food have detrimental effect for consumers even if Na concentration is high. Our preliminary studies on Apis mellifera have shown that, contrary to common knowledge, bees prefer specific K:Na ratio, not solely Na concentration in food and water. However, the concentrations of the two elements in pollen eaten by bees are closely linked and the K:Na ratio in pollen is stable and high. Moreover, the K:Na ratio in pollen is too high regarding the bee needs and Na must be supplemented from other sources to allow for adequate overall food K:Na balance. We therefore propose use of the K:Na ratio in studies considering ecology and evolution of bees and other herbivorous and detritivorous insects to broaden our understanding of plant-insect interactions and lay the grounds for better understanding of: (1) general ecology and evolution of insects, (2) evolution of bees, especially regarding trade-offs experienced when evolving from carnivory to herbivory, and (3) the role of soil-plant-consumer pathway in nutrient cycling in ecosystems.

How to really help bees: nutrient demand and supply in a changing environment

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Abstract: Wild bees often cannot access the optimally balanced diet required for their survival because local and global changes affect which pollen varieties are available to them in the environment. Understanding how the nutritional quality of various pollens affects bees could help us determine whether and how floral diversity and composition shape bee communities and populations. Therefore, to study how the nutritional quality of pollen influences wild bee fitness-related traits (survival, cocoon development and body and cocoon sizes), we asked questions about bee functioning in environments offering various nutrient diversities and compositions via available pollen species. Utilizing a feeding experiment, we show that the nutritional quality of the pollen diet eaten by bee larvae is shaped not by pollen diversity per se but by a specific pollen species composition that results in specific nutrients being scarce or sufficient and affects bee fitness-related traits. Suboptimal concentrations of certain nutrients in pollen produced by specific plant species resulted in increased mortality, decreased size and underdeveloped cocoons, and the strength of the observed negative effect was sex dependent and alleviated if scarce nutrients were added to the pollen diet. Therefore, nutritional stress caused by habitat loss and transformation and further alterations due to global changes, e.g., pollen nutrient dilution associated with rising atmospheric CO2 levels, may be direct drivers of observed wild bee declines. Accordingly, we propose that the functioning of bee populations and communities may depend on the floral diversity of the local habitat, which determines whether a nutritionally balanced pollen diet obtained from certain species can be provided to bee larvae. Considering bee fitness and health holistically in this manner could reveal important interactions between bees and other parts of the food web as well as lead to new ways of conserving bees and the critical roles they play in ecosystems.

Efficacy of neem and coconut oil for treatment of Tungiasis in Kilifi County, Kenya

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Abstract: Background: Tungiasis is a neglected tropical skin disease caused by female sand fleas (Tunga penetrans) which burrow into the skin causing immense pain, itching and debilitation as they grow. There is currently no simple, effective and affordable method of treatment available in Kenya. However, communities in Kilifi County have been successfully using a locally made blend of neem and coconut oil.

Methods: Ninety six school children aged 6-14 years with at least one clear viable, embedded flea at Fortaleza stage 3 were enrolled. They were randomized to be treated with either the study product, a blend of 20% virgin neem (Azadirachta indica) seed oil in virgin coconut (Cocos nucifera) oil or with the current standard of potassium permanganate (KMNO4) followed by vaseline. All embedded fleas were treated. Up to two viable fleas were selected for each participant and were monitored every other day for 7 days after treatment using a digital handheld microscope for signs of viability and abnormal development. Acute pathology was assessed on all areas of the feet. The children were asked to assess their level of pain and itching using visual analogue scales. The trial was approved by KEMRI-SERU, PPB-ECCT and registered on PACTR.

Results: The study product only left 22% of the fleas fully viable by Day 7, compared to 48% of the fleas treated with KMNO4 (OR 0.29, 95% CI=0.10-0.88, $p=0.029$) and a significantly higher proportion of fleas (62%) were rapidly aged by day 7, than those treated with KMNO4 (26%, OR 4.7, 95% CI: 1.6-13.9, $p=0.005$) The neem and coconut oil also significantly reduced the tungiasis-associated acute pathology ($p<0.005$), and the proportion of children reporting no pain or itching doubled (pain OR2.2, $p=0.05$, itching OR2.15, $p=0.007$). On the other hand, the acute pathology of children treated with KMNO4 did not decrease and significantly more children reported increased pain and itching on Day 7 (OR3.6 more pain and OR2.6 more itching). Conclusions: The 20% neem in coconut oil is a very promising treatment for tungiasis. Further trials are needed to assess what dosage will completely kill the majority of embedded fleas within 7 days.

Beyond consumption: Rethinking the role of multi-species wasp assemblages in aphid suppression

Authors: Finke Debbie, University of Missouri, United States

Abstract: Predator–prey interactions have traditionally focused on the consumptive effects that natural enemies have on prey. However, enemies can also reduce the abundance of prey through behaviorally-mediated non-consumptive effects. Furthermore, non-consumptive effects of natural enemies can also extend to non-prey herbivore populations (i.e., suppression by non-enemies). We investigated the relative contributions of consumptive and non-consumptive effects to aphid suppression by a multi-species wasp assemblage containing both enemies and non-enemies. We examined the response of two aphid species with different defensive strategies, pea aphids (Acyrthosiphon pisum) that drop from their host plant to the ground and green peach aphids (Myzus persicae) that remain on the plant and walk away, with the expectation that riskier defensive behaviors would result in larger non-consumptive effects. We found that, despite differences in defensive strategies, the non-consumptive effects of wasps on aphid abundance were more than twice the consumptive effects for both aphid species. Additionally, we found that non-consumptive effects arise from interactions with both enemy and non-enemy wasps and that both contribute to aphid control when part of a broader community. In fact, the presence of non-enemy wasps prevented aphid outbreaks and contributed to population stability over multiple generations. We conclude that the presence of non-enemy species in a multi-species assemblage may contribute directly to aphid suppression and provide insurance against fluctuations in the size of consumptive enemy populations.

Plant primacy in the effect of drought on aphids and their natural enemies

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Abstract: Climate change is increasing the frequency and intensity of drought events. More extreme and variable precipitation patterns are predicted to have widespread impacts on productivity, species interactions, and ecosystem processes. Water limitation affects the quality and quantity of plant resources for herbivorous insects, leading to cascading effects for higher trophic levels. Physiological changes in response to water stress may make plants more nutritious for insect herbivores, but it comes at the cost of increased plant defensive responses, declining biomass, and restricted access to the phloem. These changes in the plant have direct effects on natural enemies by changing the attractiveness of the habitat, and indirect effects by changing the quality of their prey. Our study examined the response of an arthropod community to water limited wheat (Triticum aestivum L.) in a field setting, with a focus on the response of aphids and their natural enemies. We used rainout shelters to exclude precipitation and irrigated raised bed plots to create three levels of water availability. Any amount of water limitation negatively affected the abundance of arthropods detected in weekly surveys, including aphids and their natural enemies; however, the composition of the arthropod community was reliant on the magnitude of water stress the plants were experiencing. Through structural equation modeling, we determined that aphids were more affected by stress induced changes in plant properties other than plant biomass, whereas natural enemies were strongly affected by changes in plant biomass. This effect was exacerbated as plant stress intensity increased. Interestingly, the reciprocal response of aphids and natural enemies was not significant, indicating that the contribution of top down effects were dampened by the strong bottom up effects driven by plant water limitation. By incorporating multiple levels of drought stress and assessing the response of the whole arthropod community into this study, we are better able to predict field scale responses of aphids and natural enemies to drought. Understanding such impacts is critical to predicting the consequences of altered precipitation patterns for the sustainable provisioning of ecosystem goods and services.

Impact of feeding strategies on venom composition in aquatic Heteroptera

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Abstract: True water bugs (Nepomorpha) are mostly predacious insects occurring in aquatic habitats around the world. Their venomous saliva facilitates capture and extra-oral digestion of prey animals. In Germany, various nepomorphan species from different families co-occur in the same habitat, however, their feeding ecology including venom composition and deployment is largely unknown. Using an integrated-proteomic-transcriptomic approach, we could show that the ecological niche strongly determines venom composition in four water bug species sharing the same habitat. We found considerable species-specific differences in the composition of digestive enzymes and identified venom components that likely evolved as adaptations to a particular food source, foraging strategy, or microhabitat. The outstanding differences of Corixa punctata venom to strictly predatory species, and the high abundance of herbivory-associated proteins suggest a mostly plant-based diet for C. punctata. Our study shows that the venom composition in Heteroptera is a dynamic trait that can differ considerably between species even though they share the same habitat and ecological niche. However, further research is required to confirm diet-associated patterns, since reliable conclusions cannot be drawn based on saliva composition alone.

Principles of Insectary Design

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Abstract: Preliminary considerations for designing an insect-rearing facility include understanding the rearing requirements for the species of interest, recognizing the functions of an insectary, identifying design elements that will satisfy both the requirements and functions, and creating a preliminary design that incorporates those elements. Rearing requirements consist of the biological and environmental needs of the insects; customer expectations for insect quantity, quality, and delivery; procedures such as diet preparation, handling insects, and collecting and packaging insects; program scale-up requiring additional facilities, equipment, and automation; prevention and management of microbial and arthropod contaminants; sanitation and disposal of waste products; potential health and safety hazards for employees; and familiarity with other insectary operations. The facility functions to achieve the following: 1. Contain insects. The type of larval and adult containment devices, whether reusable, single-use, or a combination of both significantly impacts facility design, utilities, flow plan, equipment, and cost. The type should be determined early in the design phase. 2. Control insectary contaminants. Microorganisms, natural enemies, arthropod competitors, and nuisance species can adversely impact product quality and production efficiency. Principles of control consist of preventing contaminants from entering the facility, maintaining conditions that inhibit their growth, keeping them from spreading, and installing barriers that prevent their transfer to succeeding cohorts. 3. Provide a hygienic environment. Incorporate "clean" construction materials and methods into the design such as smooth wall, ceiling, and floor coatings; coved floor/wall junctions; solid ceilings in holding rooms; and smooth door thresholds. 4. Isolate critical rooms and activities. These include insect-holding room(s), a dirty workroom designed to contain and remove contaminants, a clean workroom that excludes contaminants, and a quarantine area that is physically separated from the primary cultures where arthropods from anywhere outside the insectary are received and held. 5. Establish a logical flow plan. The route that insects, materials, and employees move within the facility determines the location of insectary rooms and eliminates the backflow of contaminants. Flow-plan success depends on the thorough understanding of all activities performed in each room. 6. Provide optimal conditions for the insects. These include temperature, humidity, airflow pattern, airflow rate, air-pressure differential between rooms, ventilation, and air cleanliness. Avoid temperature stratification and buildup of heat, CO2, and moisture in high-density vertical racks. Experienced insect-rearing personnel play a significant role within the design team, particularly during the initial phases of the process.

Chickpea pod borer, Helicoverpa armigera IPM in Ethiopia

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Abstract: Helicoverpa armigera (Hubner) (Lepidoptera: Noctuidae), is a destructive pest of chickpea that has proven difficult to control using conventional methods. It is considered as the main production constraints of chickpea under field condition in Ethiopia. We evaluated botrack lure with funnel type efficient and specific pheromone trap for H. armigera. Population build up starts in September and climbing up for the highest peak during February. Besides, we identified five species of hymenopteran and dipteran larval parasitoids on H. armigera in chickpea. Moreover, we developed a management options including botanicals (Azadirachta indica and Milletia ferruginea) extracts and bio-pesticides (Beauveria bassiana, Metarhizium anisopliae and Bacillus thurengiensis) for the management of H. armigera under field conditions. Molecular characterization of H. armigera indicates high haplotype and low nucleotide diversity in six populations of H. armigera in Ethiopia with high gene flow. High percentages of variation between within populations were also evident. Selective and low dose synthetic insecticides can be used at peak time followed by bio-pesticides and botanical extracts.

The role of insulin signaling in shaping life-history variation

Authors: Flatt Thomas, Department of Biology, University of Fribourg, Switzerland

Abstract: The insulin/insulin-like growth factor signaling (IIS) pathway provides an excellent example of how mechanistic and evolutionary insights might be combined to gain a more comprehensive understanding of the ultimate and proximate determinants of life-history variation, including plasticity. Since the 1990s a great deal has been learned about the genetic, developmental and physiological effects of this pathway on fitness-related traits, especially in model organisms. This work has shown that loss-of-function mutations in the IIS pathway have major, often evolutionarily conserved effects on growth, size, reproduction, lifespan and stress resistance in insects (e.g., Drosophila), the nematode worm C. elegans, and the mouse. The functional characterization of this pathway thus promised an opportunity for evolutionary biologists to identify naturally occuring, segregating variants in IIS that might be involved in life-history adaptation. Today, we have indeed growing evidence that variation in IIS can make an important contribution to life-history evolution (and plasticity) in flies and other insects (as well as in worms, fish, reptiles and mammals). The aim of my talk is to give a brief overview of some of this work.

The impact of viruses on honey bees at the individual and cellular levels

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Abstract: Honey bee colony losses are influenced by multiple abiotic and biotic factors, including viruses. To investigate the effects of RNA viruses on honey bees, we infected bees with a model virus (Sindbis-GFP) in the presence or absence of dsRNA. In honey bees, dsRNA is the substrate for sequence-specific RNAi-mediated antiviral defense and is a trigger of sequence-independent \ antiviral responses. Transcriptome sequencing identified more than 200 differentially expressed genes, including genes in the RNAi, Toll, Imd, JAK-STAT, and heat shock response pathways, and many uncharacterized genes. To confirm the virus limiting role of two genes (i.e., dicer and MF116383) in honey bees, we utilized RNAi to reduce their expression in vivo and determined that virus abundance increased. To evaluate the role of the heat shock stress response in antiviral defense, bees were heat stressed post-virus infection and virus abundance and gene expression were assessed. Heat stressed bees had reduced virus levels and greater expression of several heat shock genes compared to controls. To determine if these genes are universally associated with antiviral defense, bees were infected with another model virus (flock house virus) or deformed wing virus and gene expression was assessed. Dicer expression was greater in bees infected with either FHV or Sindbis-GFP compared to mock infected bees, but not in deformed wing virus infected bees. To further investigate honey bee antiviral defense mechanisms and elucidate the function of key genes (dicer, ago-2, MF116383, and Hsps) at the cellular level, primary honey bee larval hemocytes were transfected with dsRNA or infected with Lake Sinai virus 2 (LSV2). These studies indicate that MF116383 and Hsps mediate dsRNA detection and that MF116383 is involved in limiting LSV2 infection. Together, these results further our understanding of honey bee antiviral defense, particularly dsRNA-mediated antiviral responses, at both the individual bee and cellular levels.

Bridge or interlude: the role of the insect egg stage in symbiotic interactions with bacteria

Authors: Florez Laura V., University of Copenhagen

Abstract: Many insects engage in symbiotic associations with bacteria, ranging from flexible interactions with environmentally acquired microbes to highly specific partnerships involving stable and dependent co-existence. The establishment of a reliable transmission route from parents to offspring involving the egg stage can be a turning point in the evolution of increasingly dependent symbiosis. However, there can be different selective pressures and constraints influencing the evolution of symbiont transmission via the insect egg. As other extracellularly transmitted symbionts, bacteria smeared on the egg surface by Lagria beetle females must survive this environmentally exposed stage. Then, the bacteria must re-colonize the insect host making their way to the symbiotic organs where they are housed throughout larval development. Using manipulative assays with a culturable symbiont strain, we determined the timing of re-entry in the host and the bacterial population bottleneck during colonization. Also, we used random mutagenesis to predict candidate colonization factors. Notably, in Lagria beetles the egg is not only a key stage for bacterial transmission, but is also a relevant scenario for interactions with other microbes. Microbe-microbe competition is likely important to warrant symbiont colonization in this insect, and at the same time benefits the host by hindering pathogen infections.

IPM of stable fly populations affecting beef cattle production in North America

Authors: Foil Lane[1], Hogsette Jerome[2], [1]Louisiana State University Agricultural Center, United States, [2]USDA–ARS, Center for Medical, Agricultural and Veterinary Entomology, Gainesville, FL, United States

Abstract: The stable fly, Stomoxys calcitrans, is considered to be the second most important economic pest of livestock in the United Sates. Stable flies also are considered to be mechanical vectors of many livestock disease agents worldwide. Adult stable fly management has been challenging because of the fly's dispersal behavior and its tendency to remain on the host only a few minutes each day while feeding. Different types of traps have been used to survey adult stable fly populations and in some cases reduce population levels. Durable insecticide-treated targets made from blue and black cotton fabric developed for tsetse fly management in Africa have been found to be attractive to stable flies. The results of target evaluations and toxicant studies that have been conducted in Louisiana and Florida will be presented.

For many years, the stable fly was not considered to be a problem with pastured cattle because of the lack of habitats for larval development. However, following the advent of large, round hay bale use in livestock agriculture, larval habitats of hay trodden upon by cattle, and mixed with dung and urine are now plentiful. A summary of studies conducted on larval habitat management will be presented; and finally, the elements of potential IPM programs for stable flies will be summarized.

The role of an abundant male nuptial gift protein in sexual conflict in the decorated cricket

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Abstract: Sexual reproduction is a cooperative endeavor, but the interests of the sexes frequently diverge, leading to sexual conflict, which is common among insects. Males often attempt to manipulate female behavior and physiology to increase their share of paternity. One hypothesis posits that males of some species use a nuptial food gift, comprised of materials other than sperm and offered to females at copulation, to achieve this. In the decorated cricket, Gryllodes sigillatus, nuptial food gifts take the form of a spermatophylax, a gelatinous mass forming part of the male spermatophore and consumed by the female after mating prior to her removing the sperm-containing ampulla. Spermatophylax feeding deters females from prematurely terminating sperm transfer, thereby enhancing the paternity share of the male, and may be a route through which the male further manipulates females to their own fitness benefit. In this study, we focused on the effect of SPX1, which is the most abundant protein in the spermatophylax of male decorated crickets. We used RNA interference to generate a knockdown of SPX1 expression, and tested its effect on spermatophylax feeding duration and the latency to remate in females. We found that females fed for a shorter time on spermatophylaxes generated by SPX1 knockdown males, and that these same females fed longer on the spermatophylax offered to them during a second mating with a control male. As such, SPX1 seems to play an important role in mediating sexual conflict in this species, enhancing paternity by increasing a male's sperm transfer time, while decreasing that of a competitor in the next mating.

Tales from the Crypt: A parasitoid manipulates the behavior of its parasite hosts

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Abstract: Sand live oaks (Quercus geminata) and Southern live oaks (Quercus virginiana) in the United States harbor a community of manipulators. This community is comprised of cynipid gall wasps, which manipulate the trees into producing galls that protect the wasps from natural enemies. These manipulators can also be manipulated. For example, the crypt gall wasp, Bassettia pallida, manipulates live oaks into producing "crypts", in which the wasp undergoes development before excavating an emergence hole and escaping as an adult. The crypt gall wasp is susceptible to manipulation by the crypt keeper wasp (Euderus set). This parasitoid manipulates its host into excavating a small emergence hole out of the crypt and then dying with its head plugging the hole. The crypt keeper wasp then consumes it host, and emerges through the host's head. This manipulation benefits the parasitoid, as crypt keeper wasps who have to excavate emergence holes themselves are three times more likely to die trapped in the crypt. E. set was recently found to manipulate at least six additional, taxonomically diverse gall wasp species. While more work is needed to confirm the range of hosts E. set infects and manipulates, it appears that the gall wasp host's extended phenotype (i.e., the structure of the gall it induces oaks to produce) is an important factor dictating the host range of this master manipulator.

Integrating heterogenous data sources to assess the status and risk of butterflies to Anthropogenic threats in the western United States

Authors: Forister Matthew[4], Halsch Christopher[4], Grames Eliza[4], Burls Kevin[8], Carroll Cas[4], Bell Katherine[4], Jahner Joshua[7], Bradford Taylor[4], Zhang Jing[5], Cong Qian[6], Grishin Nick[5], Glassberg Jeffrey[1], Shapiro Arthur[3] and Riecke Thomas[2], [1]North American Butterfly Association, [2]Swiss Ornithological Institute, [3]University of California Davis, [4]University of Nevada Reno, United States, [5]University of Texas Southwest Medical Center, [6]University of Washington, [7]University of Wyoming, [8]Xerces Society for Insect Conservation

Abstract: Ongoing declines in insect populations have led to calls for action. However, even for relatively well-studied groups, like butterflies, information relevant to species-specific status and risk is mostly scattered in field guides, the scientific literature, and agency reports. Thus much attention and resources have been spent on a vanishingly small fraction of insect diversity, including a few well known butterflies like the monarch (Danaus plexippus). Here we bring together heterogenous sources of information for 396 species to provide what is, to our knowledge, the first regional assessment of butterflies for the 11 western US states. For 183 species, we use observational data (e.g., from monitoring programs) to characterize historical and projected trends in population abundance; for another 213 species (for which observational data is not available), we use exposure to climate change, development, geographic range, host breadth and other factors to rank species for conservation concern. We also organize information relevant to subspecific risk and prioritize a top 30 subspecies for further attention. Notably, many of these species have broad geographic ranges, which perhaps highlights a new era of insect conservation in which small or fragmented ranges will not be the only red flags that attract conservation attention.

Do host plants influence the evolution of sexually selected weaponry?

Authors: Forthman Michael[2], Miller Christine[2] and Kimball Rebecca[1], [1]Department of Biology, University of Florida, United States, [2]Entomology & Nematology Department, University of Florida, United States

Abstract: The weapons of sexual selection are surprisingly diverse across taxa and even within groups of closely related species. A major hypothesis for weapon shape diversity is changes in selection via fighting styles. As fighting styles diverge, so should weapon shapes. Yet, we know little about the ecological factors that might start this process of divergence. Here, we investigate the evolution of diverse weapon shapes in leaf-footed bugs and allies (Hemiptera: Coreoidea) using phylogenetic comparative methods. We performed a molecular phylogenomic analysis with ultraconserved elements, with weapon shape reconstructed at ancestral nodes. We then investigated how changes in habitat (i.e., host plant use) have selected for altered weapon forms. Our results showed that weapon morphology (e.g., femur enlargement, presence of spines, tibial expansions) exhibits convergent evolution throughout the evolutionary history of Coreoidea, which suggests ecological factors are promoting weapon diversity. Understanding ecological correlates in shaping trait morphology are critical in the present time of anthropogenic change, where modifications to habitats may alter the evolutionary trajectories of populations.

Bioassays to evaluate bednet performance in the laboratory and field

Authors: Foster Geraldine[1], McCall Philip[1], [1]Liverpool School of Tropical Medicine, United Kingdom

Abstract: Long-lasting insecticidal nets (LLINs) are essential for sustainable reduction and eventual elimination of malaria in Africa. Widespread pyrethroid resistance in vector populations and reduced performance of standard LLINs has driven substantial investment into the search for novel insecticides suitable for delivery on bednets. So far, a small number of new LLINs are being evaluated in the field, with unknown numbers of additional insecticides, both new and repurposed, further upstream in development pipelines. To accelerate these efforts, we have developed a suite of bioassays suitable for use at initial screening of chemistries for insecticidal properties to evaluating performance of the final LLIN product in situ in Africa.

Previously, testing efficacy relied on World Health Organization (WHO) recommended bioassays that measured immediate knock down or mortality after 24 (and 48+ hrs) hours, in non-blood fed adult female mosquitoes exposed in a suitable way to the active ingredient. The new suite of 3 tests generates data on knockdown, mortality at 24, 48+ hrs, repellency, contact irritancy, duration and location of LLIN contact, blood feeding (duration, volume, rate, inhibition) and temporal changes in these responses. Maintaining mosquitoes post-exposure allows detection of delayed or sub-lethal effects e.g. refeeding ability, oviposition and hatching rates, and longevity until natural death. As the tests simulate exposure under natural conditions during all stages, they are also suitable for characterising responses to LLINs in targeted vector populations targeted, before and after control.

Results will be presented from studies on a range of standard pyrethroid and next-generation combination LLINs, from initial developmental work performed in the UK to field implementations in East and West Africa. Laboratory studies on various novel treatments demonstrate that the new combination LLINs provoke a range of behavioural responses which, in most cases, are dependent on the presence of a host attractant during exposure. Additionally, responses are frequently strain-specific, further compounding the complexity of determining the ‘correct’ LLIN to deploy, especially in locations where more than one vector population may be present.

Our assays permit the relatively rapid characterisation of behavioural modes and post-exposure effects in vector populations exposed to single- and multiple-active ingredient LLINs. Together with data from experimental hut trials, detailed predictions regarding the likely success of an LLIN product against specific vector populations can be generated, creating a ‘performance index’ of products. This characterisation provides the key evidence necessary for decision-making when selecting the most appropriate LLIN for any location, and therefore should be fundamental to any pre-deployment LLIN evaluations.

Optimum placement for Drosophila suzukii (SWD) control approaches

Authors: Fountain Michelle[1] and Walker Adam[1], [1]NIAB EMR, United Kingdom

Abstract: Drosophila suzukii (SWD) remains a challenging pest to control in a arrange of fruit crops and has jeopardised Integrated Pest Management practices used for other pests. Although some crops are gaining adequate SWD control through a mixture of efficient crop hygiene and insect excluding mesh, the majority of crops are reliant on routine sprays of insecticides from a restricted range of modes of action. In addition, insecticide resistance is beginning to occur in some cropping systems.

The winter form of SWD is not reproductively active in the UK in the winter. However, it remains mobile in woodlands and native hedgerows adjacent to fruit crops on mild days, and continues to be attracted into baited traps . Whilst many studies have focussed on mass trapping inside crops during the growing season this study exploits SWD physiology and behaviour in the winter form. This is an ideal opportunity to reduce overwintering numbers to supress spring invasion into crops the following season.

Using a large number of trapping devices we have continued to trap SWD through replicated woodlands compared to untreated woodlands on the same farms. Results will be presented on the populations trapped and the optimum location for placing traps, through habitat scoring. In addition, we aim to present results on numbers of eggs laid in fruit from emerging overwintered SWD in adjacent crops in the spring.

It is vital that non-insecticidal methods are incorporated for SWD control on farms to slow the occurrence of insecticide resistance, reduce residues in fruit, and damage to the surrounding environment. This optimised integrated control method could have season long impacts for reducing fruit damage.

Drosophila suzukii resistance monitoring: results from South East England

Authors: Fountain Michelle[3], Shaw Bethan[1], Deakin Greg[2] and Wijnen Herman[4], [1]NIAB EMR, East Malling, Kent; University of Southampton, Biological Sciences, Southampton, United Kingdom, [2]NIAB EMR, East Malling, Kent, United Kingdom, [3]NIAB EMR, United Kingdom, [4]University of Southampton, United Kingdom

Abstract: Since its global dispersal, insecticides have played a vital role in supressing D. suzukii (SWD) populations in susceptible crops. However, in 2018 the first report of insecticide resistance was published by researchers based in The USA. Within the UK we are also concerned with detecting whether resistance could be developing in conventional cropping systems. Within this presentation, we will discuss the results from resistance monitoring in South East England, United Kingdom to commonly used insecticides over the past 4 years. These results are vital for early detection of resistance in cropping systems and should be used to raise awareness of insecticide resistance development. Direct spray of formulated products were applied to field collected strains and tolerance recorded. There were significant differences in mortality between strains treated with the same dose of three commonly used insecticides over time and between collection sites. In addition, within season susceptibility was assessed with further incidences of variation in mortality between sites.

Exploitation of interspecific signals to deter oviposition by spotted wing drosophila (Drosophila suzukii, SWD)

Authors: Fountain Michelle[4], Harte Steven[5], Bray Daniel[1], Tungadi Trisna[3], Shaw Bethan[2], Hall David[5], Farman Dudley[5], Powell Glen[3] and Wijnen Herman[6], [1]Chemical Ecology and Plant Biochemistry Group, Natural Resources Institute, University of Greenwich, United Kingdom, [2]NIAB EMR, East Malling, Kent; University of Southampton, Biological Sciences, Southampton, United Kingdom, [3]NIAB EMR, East Malling, United Kingdom, [4]NIAB EMR, United Kingdom, [5]University of Greenwich - Natural Resources Institute, United Kingdom, [6]University of Southampton, United Kingdom

Abstract: The worldwide invasive fruit pest, Drosophila suzukii; commonly known as spotted-wing drosophila (SWD), lays its eggs in soft- and stone-fruit before the fruit can be harvested. It has spread from Southeast Asia to Europe and the US and has become the most serious pest threatening the future of horticulture industries in these countries (Asplen et al., 2015). SWD is one of two species of drosophilids that can lay eggs in pre-ripened fruit. Larvae degrade fruit rapidly as they feed on the pulp and the oviposition holes allow entry of fungal and bacterial pathogens. Currently growers rely extensively on increased numbers of applications of insecticides but increased regulatory restrictions on pesticide usage, ecological impacts and likely emergence of insecticide resistance make this strategy unsustainable in the longer term. Extensive pesticide usage may also compromise other pest management programmes that growers use, which often involves using beneficial natural enemies of the insect pest.

This project aims to exploit the strong natural interspecific interactions between SWD and its sister species within the Drosophila melanogaster species group to develop novel approaches to control SWD. We found that SWD females are deterred from laying eggs (ovipositing) on artificial media where eggs have been laid by D. melanogaster previously (Shaw et al., 2018). This suggest that SWD detect a signal released by D. melanogaster and that this signal deters SWD from egg laying.

The first aim of this project is to determine the origin of the oviposition deterrent to SWD, and whether the signal originates from D. melanogaster adults, larvae, or eggs. Secondly, to identify the mechanism through which SWD detect the oviposition deterrent (i.e : through olfaction or gustation). This will be critical to its exploitation as field-based oviposition deterrent in the future. Thirdly, to identify the chemical compound or composition of the chemicals that deter SWD from ovipositing. Lastly, we will investigate if other drosophilid species beside D. melanogaster exhibit a similar inhibitory effect on SWD oviposition .

The highs and the lows: an overall economic analysis of classical weed biocontrol in New Zealand

Authors: Fowler Simon[1], Groenteman Ronny[1] and Paynter Quentin[1], [1]Landcare Research, New Zealand

Abstract: Research and development costs across all weed biocontrol programmes in New Zealand (NZ) from 1926 to 2019 were US$75 million PV (Present Value, 8% discount rate). Net Present Value (NPV) analyses for the five most successful programmes produced results ranging from a US$2.3 billion benefit for St John's wort (an agricultural weed) to a US$1.9 million loss for heather (an environmental weed). The overall benefit:cost (b:c) ratio for productive sector weeds was a strongly positive 72:1, but for environmental weeds it was -0.9:1; a negative return of -US$0.9 for every US$1 invested. Environmental weeds in NZ are usually targeted for biocontrol when other forms of weed control are being abandoned because of expense, ineffectiveness, and/or non-target impacts. Hence, successful biocontrol of environmental weeds in NZ resulted in a saving in other weed control costs of just US$0.16 million in 2019. In contrast, the annual benefit from biocontrol of productive sector weeds in NZ was US$67 million in 2019, largely due to increases in productivity of large areas of low value grazing land cleared of St John's wort, and to reduced control costs for ragwort in the dairy sector. Annual investment in research and development for all weed biocontrol programmes in NZ was US$1.4 million in 2019, only 2% of the current annual benefit. Several other biocontrol programmes against productive sector weeds in NZ are showing promising results, so annual benefits and b:c ratios are likely to increase substantially in future. For environmental weed biocontrol in NZ, biodiversity and ecosystem benefits are more important drivers than monetary benefits or b:c ratios.

Fifty years of Lepidoptera monitoring in Great Britain: trends and drivers of change

Authors: Fox Richard, Butterfly Conservation, Sustainability Institute, University of Exeter, United Kingdom

Abstract: British butterflies and macro-moths are among the most comprehensively monitored insect taxa in the world, with spatially-extensive data on species distribution and population abundance dating back to the 1970s. These data, contributed mainly by citizen scientists, enable the calculation of robust long-term trends for c.450 species and provide a detailed and balanced assessment of biodiversity change. I will introduce the data sources and analysis techniques, before summarising the results of 50 years of monitoring Lepidoptera in Great Britain. The findings present a complex picture of winners and losers, challenging the contemporary narrative of insect armageddon, while remaining consistent with overall patterns of global biodiversity loss.

Much progress has been made in elucidating the drivers of change among Britain's Lepidoptera and I will review the evidence from 20 years of research, highlighting individual and synergistic effects, as well as the remaining key knowledge gaps.

Indirect effects of predators on herbivore host switch: an eco-evolutionary experiment

Authors: Frago Enric[1], Tighiouart Karim[2], [1]Centre for Biology and Management of Populations, Montpellier, France, [2]CIRAD - UMR PVBMT, Réunion

Abstract: Most herbivores are plant specialists and depend on certain chemical and morphological plant characteristics to thrive. A little explored question is whether plant specialization depends on the presence of natural enemies or competitors. We hypothesize here that an insect herbivore will switch from its host plant to a plant of suboptimal quality based on the density of its interspecific competitors, and on the presence of its competitors' natural enemies. In a long-term laboratory experiment, we found that the thrips Echinothrips americanus switched to a plant of suboptimal quality at large densities of its competitors. This switch, however, did not occur when natural enemies of these competitors were introduced in the community. Further experiments revealed that host plant switch led to the evolution of particular traits that may allow development on a suboptimal nutritional source. The presence of the natural ennemy induced changes in adaptive traits of the thrips by reducing survival rate and development time. This experiment is an example of an eco-evolutionary dynamics triggered by indirect effects of natural enemies. Our study has implications for biological pest control and for the emerge of novel pests. The species we worked with, Echinothrips americanus, is an important and polyphagous pest, and we show here, that predator indirect effects can lead to this species to become pest of a novel plant.

The effect of natural enemy diversity on herbivore suppression and community stability

Authors: Frago Enric[1], Tighiouart Karim[2], Sanders Dirk[4], Montoya Daniel[5], Montoya José[5] and Nibouche Samuel[3], [1]Centre for Biology and Management of Populations, Montpellier, France, [2]CIRAD - UMR PVBMT, Réunion, [3]CIRAD-3P, UMR PVBMT, Saint Pierre, La Réunion, France, [4]Environment and Sustainability Institute, University of Exeter, United Kingdom, [5]Theoretical and Experimental Ecology Station (SETE-CNRS), UMR 5321, Moulis, France

Abstract: In diverse natural enemy assemblages, herbivore suppression is usually stronger and community stability (i.e. temporal variation in species density and persistence) larger. This has been demonstrated in natural arthropod communities, and by means of theoretical modelling. However, the mechanisms underlying these effects, in particular on stability, are still poorly understood, and experimental demonstrations are lacking. In addition, it is not yet clear whether these positive relationships can be dampened when natural enemies engage in antagonistic interactions like intraguild predation (i.e. when two predators feed on each other, but also on a shared resource). To explore this question, we worked with a community that can be found in greenhouse agroecosystems, and which is composed of four herbivores and four natural enemies. The natural enemies included both generalist and specialist species, some of them engaging in intraguild predation. This assemblage of species was manipulated to create eight different communities along a gradient of natural enemy diversity. These communities were replicated in population cages and their long-term dynamics monitored over several months. We hypothesise that network parameters like the number of predatory links will relate positively with herbivore suppression and with community stability, but this effect will be dampened when a large amount of intraguild predation links are present. Our results revealed that herbivore suppression and community stability was mostly driven by few, highly-influential species, with strong impacts on overall community dynamics. In this talk I will particularly focus on the conditions that allowed the long-term persistence of the aphid parasitoid Aphidius colemani. Our work reveals experimentally that the structure of natural enemy networks can determine the dynamics of terrestrial ecosystems, and the services these communities provide, particularly pest biocontrol.

Microbial brokers of plant-insect interactions: a facultative endosymbiont modulates the response of pea aphid to rhizobacteria-harboring plants

Authors: Francis Frederic[1], Barrera Andrea[3], Quaghebeur Celeste[1], C. Ramirez Claudio[5], Serteyn Laurent[1], Molina-Montenegro Marco[2] and Cabrera Nuri[4], [1]Functional and Evolutionary Entomology, Gembloux Agro-Bio Tech, University of Liege, Gembloux, Belgium, [2]Laboratorio de Ecología Vegetal, Instituto de Ciencias Biológicas, Universidad de Talca, Talca, Chile Centro de Estudios Avanzados en Zonas Áridas (CEAZA), Univ, [3]Laboratorio de Ecología Vegetal, Instituto de Ciencias Biológicas, Universidad de Talca, Chile, [4]Laboratorio Interacciones Insecto-Planta, Instituto de Ciencias Biológicas, Universidad de Talca, Chile

Abstract:
- The effects of microorganisms on plant-insect interactions have been usually underestimated. While plant growth-promoting rhizobacteria (PGPR) are known to induce plant defenses, endosymbiotic bacteria hosted by herbivorous insects are often beneficial to the host. Here, we aimed to study whether PGPR-induced defenses in broad bean plants could impact pea aphid reproduction and probing behavior, depending on the presence of a facultative endosymbiont.
- We estimated aphid reproduction, quantified defense- and growth-related phytohormones by GC-MS, and measured different plant growth and physiology parameters, after PGPR treatment. In addition, we recorded the feeding behavior of aphids by electropenetrography.
- We found that PGPR treatment of broad bean plants reduced the reproduction of the pea aphid that did not harbor the endosymbiont H. defensa. We highlighted a phenomenon of PGPR-induced plant defenses priming, but no noticeable plant growth promotion. Main changes in the aphid probing behavior were related to salivation events into phloem sieve elements.
- Endosymbiont H. defensa played a key-role in plant-insect interactions, possibly helping aphids to counteract plant induced resistance and allowing them to develop normally on PGPR-treated plants. Our results suggest that plant- and aphid-associated microorganisms add greater complexity to the outcome of plant-centred multitrophic interactions.

Food webs in vineyard landscapes: optimizing the delivery of natural pest control services.

Authors: Franck Pierre[7], Rusch Adrien[8], Barraquand Frederic[2], Sauve Alix[1], Mouden Charlotte[4], Aluome Christelle[6], Vacher Corinne[4], Papura Daciana[5], Thiéry Denis[5] and Roux Pascale[3], [1]University of Bordeaux, Integrative and Theoretical Ecology, LabEx COTE, France, [2]CNRS - University of Bordeaux - Institute of Mathematics of Bordeaux, France, [3]Ecole Normale Superieure of Lyon - UMR Institute of functional genomics, France, [4]INRA - UMR Biodiversity, Genes and Communities, France, [5]INRA - UMR Health and Agroecology of vineyards, France, [6]INRA - UMR Interactions Soil Planet Atmosphere, France, [7]INRA - UMR Plants and horticultural systems, France, [8]INRA, UMR SAVE - Villenave d'Ornon, France

Abstract: Predicting the delivery of pest control services based on farming system intensity and landscape context is necessary to support the expansion of agroecological farming systems. However, the optimal food web structure that maximized pest control services remain largely unknown. Organic farming and semi-natural habitats in the landscape are expected to increase the diversity of both predator and prey species. However, increasing the diversity of natural enemies could lead to higher complementarity between species and enhance the level of pest control but could also dilute the effect of natural enemies to control pest species due to intraguild predation for instance. To explore this question and test these hypotheses, we sampled a large set of natural enemies of pests on 21 pairs of vineyards (one organic and one 'conventional') selected along two orthogonal landscape gradients. We described their diet using a meta-barcoding approach and estimated the level of biological pest control potential by exposing sentinel preys (eggs of Lobesia botrana) in the field. Such approach provides a mechanistic understanding of the relationships between the structure of the natural enemy community and the delivery of pest control services and suggest opportunities to predict these services in other contexts.

Genetic structure of codling moth populations from worldwide to farm spatial scales

Authors: Franck Pierre[1], Gauffre Bertrand[1] and Olivares Jérôme[1], [1]INRAE

Abstract: The genetic diversity and structure of codling moth (Cydia pomonella L.) populations at several spatial scales were carried out with a panel of microsatellite markers. First, the codling moth evolutionary history based on the genetic differentiation between 25 worldwide populations sampled in apple and walnut orchards was analyzed to sheds light on the main centers of diversification, the routes of colonization, and specialization to host plants. Secondly, key population demographic parameters (dispersal, reproduction) and their variations depending on agricultural practices and landscape characteristics were estimated from the comparison of the genetic variability between individuals. Dispersal was assessed from spatial autocorrelations of the genetic structure (isolation by distance) at the scales of the European continent, a production basin (lower Durance valley, France), and a cluster of orchards in a farm. All these works confirmed the low dispersal of the codling moth in spite of the ability of the pest to move on long distance and to attack various fruits.

Hedgerows and flower strips differentially support predator abundance and predation in organic apple orchards

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Abstract: Management of plant diverse habitats surrounding crop area can promote the occurrence of natural enemies and have suppressive effects on the pest populations. Each year, growers experience yield losses due to pest damage in organic apple orchards in Denmark. This means that there is a present need for developing sustainable pest control strategies enhancing pest natural enemy abundance and diversity. We examined the impact of hedgerows and flower strips on the predation contribution to control of the rosy apple aphid, Dysaphis plantaginea Passerini (Hemiptera: Aphididae) by the predator complex in organic apple orchards in Denmark. Sampling of the most abundant predators in the orchards was conducted at the beginning of flowering of the apple trees, after flowering and at June drop (the second fruit fall). This was done in the apple row near the hedge, the row near the flower strip and in the middle row of apples with equal distance to these two habitat structures. Abundance of D. plantaginea was assessed visually, and abundance of the predator species was assessed by beating samples. Predators sampled were primarily spiders (Linyphiidae, Tetragnathidae, Philodromidae, Theridiidae), flower bugs (Deraeocoris flavilinea, Atractotomus mali), anthocorids (Anthocoris nemorum), nabids (Himacerus apterus), coccinellids (Coccinella septempunctata), and earwigs (Forficula auricularia). A molecular gut contents analysis was used to detect if predators had remains of D. plantaginea DNA in their gut. Spiders were more abundant early in the season, both spiders and insects were abundant after flowering, while flower bugs were more abundant at June drop. Preliminary results suggest that there were more insect predators screening positive for DNA of D. plantaginea in the row near the flower strip, than in the middle row and in the row near the hedge, after flowering, while the proportion were more evenly distributed at June drop. The highest proportion of insect predators screening positive for DNA of D. plantaginea was D. flavilinea, followed by F. auricularia. Flower bugs were more abundant near the flower strip, while anthocorids were more abundant near the hedge, and more anthocorids from the middle row screened positive for DNA of D. plantaginea. The preliminary results suggest that an orchard can benefit from both hedgerows and flower strips for increasing the natural enemy community, and thereby encourage the natural regulation of D. plantaginea and other pests in organic apple orchards.

Population genetic structure of the Codling Moth in Chile and Argentina: implications for area wide management programs

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Abstract: The codling moth, Cydia pomonella (L.), is an invasive pest of pome fruits introduced to the Americas during the 19th century. In the southern cone of South America this pest is widespread at both sides of the Andes range separating Argentina and Chile, where the largest area of pome fruit production of the southern hemisphere is located. We performed an analysis of the population genetic variability and structure of C. pomonella in Argentina and Chile using microsatellite markers. We sampled C. pomonella from apple as the main host-plant along its distribution area (approx. 1,800 km) in both countries. Significant genetic differentiation among samples from Argentine and Chile (FSC = 0.045), and between all localities (FST = 0.085) was found. Significant isolation by distance (IBD) was found for each country and also when samples from both sides of the Andes range were pooled, although with a lower correlation coefficient. By using a Bayesian individual assignment method (Structure) we found different populations in the Chilean and Argentinian sides of the Andes, which suggest independent invasion events and subsequent genetic isolation between countries. In summary, our results indicate a high genetic exchange of C. pomonella within countries, but with significant genetic differentiation between countries. Our results could be explained by C. pomonella dispersal mediated by human activities related to fruit production in each country with little exchange between them, because the Andes range is a significant barrier for dispersal by flight and quarantine barriers prevent the movement of plant material or infested fruit between countries.

The evolution of an underwater tape: uncovering the genomic basis of caddisworm (Insecta: Trichoptera) silk

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Abstract: Caddisflies (Insecta: Trichoptera) are among the most diverse freshwater insects, both in terms of species number and ecological diversity. Caddisfly larvae, or caddisworms, inhabit most freshwater habitats with one family existing exclusively in marine tidal pools, an anomaly among insects. Caddisflies are reciprocally monophyletic with Lepidoptera (moths and butterflies) and share the ability to spin silk from modified salivary glands. Caddisworms use underwater silk to construct a variety of underwater architectures, including portable tube cases, silken capture nets that resemble spider webs, and underwater funnels. These innovations, made possible through their use of silk, are thought to be central to their diversification underwater. Caddisworm silk consists primarily of two proteins, the heavy and light fibroins (h-fibroin and l-fibroin). The h-fibroin protein consists of n and c termini with a large repeating sequence in between and is thought to be the primary component of caddisworm silk. Early efforts to sequence the h-fibroin gene using short-read sequencing resulted in partial assemblies. However, recently, the full gene was sequenced for the first time using long-read sequencing of whole caddisfly genomes. Here, we combine proteomics, SEM-EDS imagery, TEM protein imagery, and whole-genome? sequencing to shed light on silk use in Trichoptera. By linking phenotypic data with genomic data, we are beginning to uncover some of the secrets of this remarkable underwater bioadhesive.

Connecting Taxa: How does nonnative vegetation affect arthropod diversity and biomass in urban forest fragments?

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Abstract: As human populations grow and development expands, urban forests are threatened by habitat loss and fragmentation. Forests contribute to the preservation of native species and habitat, carbon sequestration, and atmospheric cooling. Increased urbanization of forest fragments lead to invasions of nonnative plant species, which changes ecological communities and alters forest function.

We studied urbanization effects on forest communities in 24 forest research fragments in two cities along the eastern coast of the United States. We sampled two cities to understand if interactions change under different temperatures, providing insight to how a warming climate may affect urban systems. Newark, Delaware represented a high latitude city and Raleigh, North Carolina represented a mid-latitude city. Sites ranged from 1 to 25 hectares and in level of urbanization. Within each forest, we established 10 locations to sample plants, soils, and arthropods. In 2017, we quantified the vegetation community using metrics of vegetation density, canopy cover, and species abundance. Soil samples were collected to determine pH, organic matter, and micronutrients per site. Ground arthropods were sampled in 2017 and 2018 using pitfall traps. Arthropods on understory vegetation were sampled in 2019 using a bug vacuum.

We sampled two categories of arthropod taxa to understand how nonnative plant invasion and forest structure influence arthropod communities. We sampled carabid beetle (Coleoptera: Carabidae) species, model organisms to track community change, to determine how urban vegetation affects ground-dwelling arthropods. Canopy openness correlated with increased nonnative plant invasion and understory density, and nonnative plant invasion in turn reduced forest specialist species and increased open area specialist species. All carabids declined with increased understory vegetation density, ground cover vegetation, and leaf litter volume. These results support conserving forests with intact canopies to reduce long-term nonnative plant invasion, while removing dense nonnative vegetation, especially nonnative ground cover, to manage forests short-term.

We then expanded our scope of inference to all arthropods on understory vegetation, and investigated relationships between total, nonnative, and native vegetation structure and arthropod abundance, biomass, richness, and diversity. Arthropod abundance and biomass increased with greater total, nonnative, and native structure, while richness and diversity declined with greater nonnative structure. This suggests urban forests invaded by nonnative plants may provide adequate arthropod biomass as food for other taxa, like birds, but may fail to provide unique ecological services required in forests, as the number of species filling unique niches declines.

Urban forests are not negligible ecosystems and support diverse, native biotic communities. However, nonnative plants reduced urban forest arthropods and forest specialist species. Forest specialist arthropods are likely not the only organisms negatively affected by nonnative plant invasion in urban forests. These results outline the need to establish regional invasive management plans to strategically remove invasive species from urban forests and improve forest quality for native communities.

Drivers of insect biodiversity in urban green spaces: A review and meta-analysis

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Abstract: Urban forests provide critical ecosystem services by capturing carbon, mitigating pollution, reducing energy costs, improving human health, and providing habitat for wildlife. However, urbanization increases heat and pollution, fragments natural habitats, and alters the composition of the urban biota through the introduction of exotic species. Such stressors threaten the services urban forests provide and may alter the ability of these green spaces to support biodiversity. In this study, we use review and meta-analysis to synthesize the recent literature on the effects of urbanization on urban forest arthropods. We characterize published studies by spatial scale (between city, rural-urban gradient, within-city), taxonomic resolution (whole-assemblage, order, family, species), taxon, environmental variable (city size, distance to urban center, impervious surface cover, temperature, tree diversity, patch size, edge effects), and response variable (survival, fecundity, abundance, species richness, herbivory, predation, parasitism). When possible, we also quantify the magnitude of the difference in arthropod responses between high and low levels of urbanization and calculate effect sizes for meta-analysis. Through these two complementary methods, we identify key patterns of altered urban forest structure, including changes to the density, diversity, and geographic origin of trees and the ubiquity of the urban heat island effect. We tie these changes to arthropod demographic parameters, abundance, diversity, and rates of interaction. Notably, only a few taxa, including Lepidoptera and Carabidae, are well studied historically in cities, and our knowledge remains limited regarding the responses of many other groups. For the studies reporting comparable quantitative data, increasing urban pressures (such as higher impervious surface cover, lower vegetation cover, and small patch sizes) generally lead to declines in arthropod species richness, though effects on abundance are more variable and depend on the taxon and taxonomic resolution reported. Similarly, the increased proportion of exotic species in cities has led to a variety of outcomes, including reduced tree health, outbreaks of herbivores, loss of arthropod diversity, or no discernable effects. We propose that the outcome of potential novel plant-herbivore interactions, in which plants and herbivores without co-evolutionary history encounter each other, is often influenced by a combination of abiotic conditions, defense-free space, herbivore host-switching ability, and the potential for enemy escape. Our study highlights the major trends in the study of arthropod responses to urbanization, quantifies the relationships between particular urban environmental variables and arthropod responses, and points to the need for targeted future studies and the preservation of biodiversity in urban green spaces.

Human health risks of pine processionary caterpillars increase with urban warming

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Abstract: Urban warming may alter organisms' development or survival. For organisms that are hazardous to people, these changes in development or survival may magnify or reduce the risks the organisms pose to people. Larvae of the pine processionary moth (Thaumetopoea pityocampa; Lepidoptera: Notodontidae; "PPM") are covered in urticating setae that cause allergic reactions in humans and other vertebrates. Though PPM larvae are common in urban areas, they have primarily been studied in forests, where human population density is low. Here, we report the results of a field study conducted in Orléans, France, to determine whether PPM colonies in cities have altered phenology and/or survival compared to PPM colonies in forests. We find that PPM larvae in the city spend a longer time in the fifth, most dangerous instar than larvae in forests because urban warming causes unequal shifts in the beginning and end of the fifth instar. In addition, urban warming indirectly increases winter survival by advancing larvae to later, more cold-tolerant instars before the winter cold period. These results indicate that the risks PPM pose to people are currently underestimated in cities. As PPM continues to expand its range with climate change, cities may alter the effects of this expansion for people.

Latitude and habitat affect herbivore density on urban trees

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Abstract: The effects of urbanization, particularly high temperatures, can harm urban trees by increasing herbivory by arthropod pests. However, benefits for herbivore fecundity, survival, and population growth depend on background temperature of a site and the extent of urban warming. We predict that herbivores living at high latitudes or in cool forest fragments will exhibit lower fecundity, density, and population growth than those in warmer locations. Moreover, we predict that herbivores from northern latitudes will thrive when moved to warmer southern latitudes, a simulation of how they may be affected by climate change. The scale insects Melanaspis tenebricosa and Parthenolecanium quercifex are common pest of urban trees that reach higher densities due to the urban heat island effect. In a mid-latitude city, Raleigh, North Carolina, US, trees in forest fragments were 1.3° cooler and had significantly less M. tenebricosa and P. quercifex than trees in ornamental landscapes. However, there was no difference in scale density between forest and landscape trees in Newark, Delaware 4 degrees of latitude north. When P. quercifex were moved from Newark south to Raleigh their population growth was higher and they reduced tree growth more than scales from Raleigh. Our results suggest that relatively innocuous herbivores can become damaging pests as climate change and urbanization position them closer to their thermal optimum.

ABC transporters and target-site mediated resistance to Bt toxins

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Abstract: Spodoptera frugiperda, fall armyworm (FAW), is a major lepidopteran pest and recently invaded the Eastern Hemisphere. FAW pest management strategies are based on synthetic insecticides and transgenic crops expressing Bacillus thuringiensis (Bt) insecticidal proteins. Continuous selection pressure resulted in populations resistant to Bt crops, e.g., transgenic corn expressing the Bt toxin Cry1F, particularly in Brazil. Our group recently characterized the molecular mechanism of Cry1F resistance in Brazilian FAW populations and it was shown to be linked to mutations in the ATP-binding cassette transporter C2 (ABCC2). Here, we employed a cell-based assay to study the interaction of recombinantly expressed ABCC2 transporter variants and Bt insecticidal proteins to elucidate mechanisms of resistance in noctuid pests. Our study confirmed the importance of indels in the ABCC2 extracellular loop 4 (ECL4) for Cry1F resistance in S. frugiperda. Whereas Cry1A toxins seem hardly affected by most of the ABCC2 mutations in ECL4 detected in Brazilian field populations of FAW.

Adult learning, rather than larval experience or transgenerational acclimation, affects female host plant preference in Pieris butterflies

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Abstract: Traditionally, the overwhelming majority of specialized phytophagous insects has been explained by the preference-performance hypothesis, which poses that females that prefer to oviposit on plants that maximize the performance of their offspring are favored by selection. Often, however, the female preference hierarchy among potential hosts deviates substantially from the larval performance on these plants, indicating that alternative selection pressures and phenotypic plasticity affects the female host choice. Recently, several studies have found evidence for an impact of larval experience on adult female host preference. These findings have led to a resurged interest in a potential general importance for Hopkins' Host Selection Principle, and it has been hypothesized that HHSP is particularly adaptive in combination with transgenerational acclimation, so that females both allocate and adapt their offspring to the same type of host they experienced as larvae. Such a scenario could facilitate host shifts and thus promote diversification. Here, we use Pieris butterflies as model to test the impact of larval host plant, female adult learning and transgenerational effects on the willingness to oviposit on two alternate host plants of different nitrogen content. A previous study has indicated that these butterflies alter their within-species host choice depending on the nitrogen content of the host individual they were feeding upon as larvae. Our study shows that adult learning, rather than HHSP or transgenerational effects affects female host preference, and reports negative transgenerational effects on larval performance. The larval offspring of mothers developed on a suboptimal host grew slower on both host plant species, and especially on the suboptimal host. Our results thereby contrast to previous studies.

Genomic signatures of adaptation to Bt-expressing transgenic crops in the agricultural pest, Helicoverpa zea

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Abstract: Insect adaptation to management tools, or resistance, is common in agricultural landscapes. Loss of efficacy of insect management tools has economically significant consequences for growers. An ability to detect emerging adaptive changes prior to widespread resistance-associated crop damage by insects would benefit the agricultural community. It has been hypothesized that new genomic approaches could track molecular signals of emerging resistance and trigger efforts to pre-empt widespread damage. We tested this hypothesis by quantifying genomic changes in the North American pest, Helicoverpa zea, over a 15 year period concurrent with commercialization and subsequent loss of efficacy of transgenic Bt-expressing crops. Our results demonstrate the complex nature of adaptation in agricultural ecosystems and provide insight into the potential and pitfalls of using genomic approaches to track emerging resistance.

Herbivore abundance and species-level network characteristics can predict their apparent competitive effects on other herbivores

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Abstract: Apparent competition is an important indirect interaction mechanism that structures host-parasitoid communities. In several applied scenarios it would be useful to be able to use traits to predict which host species will cause and be affected by apparent competition. Using temperate forest plant-caterpillar-parasitoid quantitative food web data I tested whether there are traits, including trophic traits related to network position, which can predict species' involvement in apparent competition. Host abundance and network generality and vulnerability (both binary and quantitative) were related to the strength and direction of apparent competition between pairs of host species. Host body size was not. These results could have great utility in the provision of alternative hosts for conservation of natural enemies for biological control, in predicting food-web impacts of invasive species, and in modeling community-wide responses to disturbance.

Fungal endophytes mediate insect pest control and shape trophic networks

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Abstract: Current research highlights plant-associated microbes as key players shaping multi-trophic interactions in terrestrial ecosystems. For example, microbially mediated plant-herbivore interactions can have both bottom-up and top-down cascading effects in food chains. Here we focus on systemic and vertically transmitted fungal endophytes of cool-season grasses, which mediate plant defense by the production of toxic and deterring alkaloids. Due to the obligate dependence of the fungus on its plant host, we hypothesized a close chemical crosstalk between the partners, where herbivory can shape the chemical profile of the plant by inducing the production of specialized metabolites. Besides an herbivore-species-specific induction of fungal origin alkaloids, we found that plant age and seasonal timing strongly modifies the amount of alkaloids produced in a grass-endophyte symbiotum.

To be able to predict the plants benefit of microbe-mediated plant defenses it is necessary to include their effect on higher trophic levels. Feeding on endophyte-infected grass decreased the fitness of several herbivorous insects but further several predatory insect species experienced fitness losses. Applying modern chemical-analytical methods, we showed the stability of endophyte derived alkaloids within the food chain being responsible for fitness disadvantages in aphids and aphid predatory insects. Interestingly, we found that predatory insects considered to be especially resistant to environmental pollutants were unaffected by potentially cascading alkaloids within the food chain.

Besides the deterring effects of alkaloids we found first results indicating that olfactory foraging predatory insects may prefer endophyte-infected over uninfected plants exposed to aphid herbivory, likely caused by an endophyte-mediated manipulation of herbivore-induced plant volatiles (HIPVs).

Applying plant-associated microbes in sustainable pest control has a great potential circumventing the heavy use of pesticides but may additionally shape entire insect communities in grassland ecosystems.

Comparing the efficacy of various aerial spraying scenarios using Bacillus thuringiensis to protect trees from spruce budworm defoliation

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Abstract: Large-scale aerial spray operations against the spruce budworm (Choristoneura fumiferana (Clemens)) (SBW) with the biological insecticide Bacillus thuringiensis ssp. kurstaki (Btk) aim at maintaining trees alive during outbreaks. This objective is thought to be achieved when=50% of current-year foliage is preserved until the end of the outbreak. This protection target is associated with low balsam fir (Abies balsamea [L.] Mill.) mortality. However, it is unknown whether this approach is always needed or whether less frequent interventions could provide similar results at a lower cost. Between 2010 and 2016, we conducted field experiments in Quebec's Côte-Nord region to determine the efficacy of five different Btk spraying scenarios for protecting balsam fir, white spruce (Picea glauca [Moench] Voss) and black spruce (P. mariana [Mill.] BSP) in mixed stands. We used the residual photosynthetic capacity (RPC) to evaluate the efficacy of the five scenarios. RPC makes it possible to take into account the impact of SBW defoliation on foliage contribution to tree photosynthetic effort over several years, and can be used as a proxy of the risk of tree mortality. We hypothesized that less frequent Btk applications could maintain the required RPC level to keep trees alive. Our results show that areas not protected resulted in great losses of RPC in balsam fir and white spruce. Btk applications every 3 years kept RPC above 50% for 2 years in balsam fir and 4 years in white spruce. RPC losses were above 62% after 4 years in both species. The strategy currently employed in Quebec (spraying every year after a first year of moderate-severe defoliation) and the intensive protection scenario (Btk applications every year) meet the protection goals for these hosts. However, their cost prevents their application at a large scale. Btk applications every 2 years seems a relevant alternative to the current strategy to protect balsam fir and white spruce stands given the adequate level of protection provided (RPC above 39%) and the reduction in the number of Btk applications required (36% fewer applications over 7 years, resulting in 36% lower cost), particularly if the objective is to maintain trees alive. Black spruce maintained at least 54% of its RPC, even without protection. Btk applications every 3 years might be a valid alternative to reduce growth losses in black spruce-dominated stands. The use of different spraying scenarios may allow us to develop cost-efficient treatment strategies to protect Quebec's forests.

Nordic conquest: Evolutionary history of lunar-rhythmic and lunar-arrhythmic reproduction in marine midges may identify candidate genes for the enigmatic circalunar clock

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Abstract: The intertidal midge Clunio (Chironomidae, Diptera) has a synchronized reproduction to the lowest low-tides around new moon and full moon, by combining circadian and circalunar clocks. After the last glacial period, Northern Europe was colonized by lunar-rhythmic Atlantic Clunio populations. In adaptation to the tide-free habitat in the Baltic Sea and to constant daylight above the Arctic Circle, two lunar-arrhythmic ecotypes have evolved.

We established seven Clunio laboratory strains from the Baltic Sea, Norway and the West European Atlantic coast and characterized their lunar-rhythm ecotypes under constant conditions. In order to investigate their evolutionary history, we sequenced 168 individual genomes from the same locations. Analysis of a set of > 700,000 SNPs showed strongest genetic differentiation according to geographic location. The data indicate that the Baltic Sea and the high Arctic were colonized in two independent events, suggesting that the two lunar-arrhythmic ecotypes evolved convergently. Near Bergen (Norway) a lunar-rhythmic and a lunar-arrhythmic strain co-exist in sympatry. There is strong gene flow between the two strains, indicating that ecotype is not a strong isolation barrier.

Molecular mechanisms and evolution of self-sacrificing gall repair in the social aphid, Nipponaphis monzeni

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Abstract: Aphids contain more than 80 social species with individuals altruistic to their colony mates, called soldiers. Their primary social role is colony defense, but some gall-forming social species also perform altruistic tasks such as gall cleaning and gall repair. Gall repair is a unique social behavior reported from the social aphid, Nipponaphis monzeni, that forms a completely closed gall on the host tree. Since the plant tissue of the growing gall is soft and thin, gall-feeders such as lepidopteran larvae often invade the gall by tunneling through the wall. When a hole was bored in the gall wall, the soldiers immediately gathered around the hole, discharged a large amount of body fluid from their cornicles on the damaged area, and mixed the fluid with their legs. The discharged fluid soon became viscous and solidified, whereby the hole was filled up completely. Here, we uncovered the molecular and cellular bases of this social behavior, especially the mechanisms of body fluid solidification. The body cavity of soldiers is filled with peculiar soldier-specific “large globular cells (LGCs)” that accumulate a large amount of phenoloxidase, a key enzyme involved in melanization and scab formation in insects, and lipids, whereas their hemolymph contains high levels of tyrosine and a unique repeat-containing protein (RCP). After discharge of the body fluid, the LGCs rupture and release phenoloxidase and lipids to the hemolymph. The lipids form a soft clot immediately, whereas the activated phenoloxidase oxidizes tyrosine to dopa, which is followed by generation of highly-reactive quinones through the melanin synthesis pathway. The reactive quinones crosslink surrounding proteins including RCP, whereby the clot is solidified and hardened. Transcriptome analyses of N. monzeni and its allied species revealed that they possess at least five paralogous phenoloxidase genes, one of which shows fast molecular evolutionary rate and highly up-regulated expression especially in soldiers of N. monzeni. These results indicate that the soldiers of N. monzeni enhance their innate immune and wound healing mechanisms and co-opt them for colony defense.

Development of microsatellite markers for the endangered butterfly, Leptidea amurensis (Lepidoptera: Pieridae)

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Abstract: The eastern wood white butterfly, Leptidea amurensis (Lepidoptera, Pieridae), is an endangered butterfly species in East Asia. In Japan, this species inhabits semi-natural grasslands but available habitat is declining owing to the rapid loss of grasslands, including farmlands, pastures and riverbanks, and the abandonment of regular grassland management. Here, we developed 16 microsatellite loci for L. amurensis based on de novo genome sequence data and observed that nine loci exhibited polymorphisms in 16 individuals collected from various habitats in Japan. Using these microsatellite markers, we analyzed 49 individuals collected from five distant habitats, Aomori, Miyagi, Fukushima in Honshu Island, Kumamoto in Kyushu Island, in Japan. The structure analysis based on this genetic information revealed genetic differentiation among four Honshu and one Kyushu habitats. Value of the gene diversity (Hs) was relatively high with 0.46–0.57 in the four Honshu habitats, whereas low with 0.14 in Kumamoto. Similarly, allelic richness (AR) was 2.5–3.2 in the four Honshu habitats, whereas 1.4 in Kumamoto. Our results suggest that genetic diversity of Kumamoto population has decreased due to the habitat fragmentation and isolation and that this population should quickly be targeted for conservation.

Insecticidal property of novel meta-diamide compound TENEBENAL™

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Abstract: TENEBENAL™ (common name; Broflanilide) is a novel di-amide compound invented by Mitsui Chemicals Agro, Inc., Japan. This compound is under global development for the purpose of crop protection, sanitary pest control, vector control and wood protection in collaboration with BASF. In this study, we evaluate insecticidal activity and property of TENEBENAL™.

1. Property for crop protection.
TENEBENAL™ acts on nerve as GABA-gated chloride channel allosteric modulator. It is classed in new group "30" by Insecticide Resistance Action Committee (IRAC). TENEBENAL™ shows insecticidal activity at low dosage rate against important crop pest order, such as Lepidoptera, Coleoptera and Thysanoptera. This compound is effective against existent resistant pests.
The efficacy test using larvae of common cut worm and diamond back moth showed that the insecticidal activity of TENEBENAL™ is stronger in oral ingestion than percutaneous ingestion. Preferable antifeeding effect is observed due to the good insecticidal activity and rapid action of the compound.

2. Property for sanitary pest and vector control
TENEBENAL™ shows good efficacy against sanitary pests and vectors including Hemiptera, Blattaria, Diptera, Siphonaptera and Acari. In particular, the efficacy was observed against cockroaches, mosquitoes and bedbugs which are highly developed resistance difficult to control.

3. Property for wood protection.
TENEBENAL™ shows good efficacy against termites and bark beetle. It controls termites equally or prior to the existent termiticide. It does not show repellency for termites in laboratory tests.
Due to these preferable and good properties, TENEBENAL™ is expected to contribute to the crop protection, hygiene and wood protection.

Rediscovery of a Lost Semi-aquatic Leaf Beetle in the Huleh Valley

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Abstract: Between 1951-1959, most of the Huleh Lake and its surrounding swamps in the Upper Jordan River (Rift) Valley of Israel were drained with the supposed purposes to eliminate Malaria and to reclaim land for agriculture; both reasons later proved to be unnecessary decisions. With the paucity of biological knowledge of the Huleh region, especially its aquatic invertebrates, accurate assessment of the environmental damage from this drainage is still being realized. Based on natural history museum collection records the pre-drainage presence of some aquatic insect species have verified. Among these is Donacia bicolora a member of a semi-aquatic subfamily (Donaciinae) of Leaf Beetles and whose Israeli populations were thought to have gone extinct because of the drainage of the Huleh and other locations. Recently this species was rediscovered in extremely isolated populations. Here this recent re-discovery is detailed and its conservation status discussed. Also new molecular data suggests this is Donacia simplex rather than D. bicolora.

LIFE 4 Pollinators: Involving people to protect wild bees and other pollinators in the Mediterranean (LIFE18 GIE/IT/000755)

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Abstract: A significant proportion of the EUs wild bees are threatened with extinction and data are lacking for over 50%. Information is particularly scarce from the Mediterranean basin which is considered a biodiversity hotspot. Additionally, there is a general lack of awareness about the role of wild pollinators and the importance of conserving their diversity. The project aims to encourage a change of behavior in key stakeholders (farmers, beekeepers and park managers) and civil society, improving the application of pollinator-friendly practices across the Mediterranean region. A series of actions are being implemented, ranging from education to dissemination, information and environmental governance, using a citizen science approach to foster public outreach and engagement. Wild pollinators are monitored in 12 agricultural pilot areas in northern Italy and additional sites in target countries to assess the impact of pollinator-friendly actions, such as reduction in the use of pesticides, planting flower strips, placement of "bee-hotels", but also managers and visitors awareness. Through events, citizen science activities and providing training to key stakeholders, the project is increasing awareness of the importance of, and threats to wild pollinators across Italy, Greece, Spain and Slovenia.

Arthropods as an Experiential Learning Strategy

Authors: Gálvez Rosa[2], Bermejo Angela[2], López de Felipe Marcos[2] and Hidalgo Francisco[1], [2]Universidad Autónoma de Madrid, [1]Insectalia

Abstract: We developed and described the impact of an educational project targeted at schools and designed to introduce living arthropods in the classroom. This project, implemented during the 2021-2022 academic year, arises from a university-company collaboration assembled through a specific collaboration agreement (code number 2021/0293) between the Universidad Autónoma de Madrid and Insectalia, a new generation company dedicated to the sustainable production of insects as animal and human food.

Among the activities offered by this project are the installation of different species of insects in the classrooms (Tenebrio Molitor and Grillo Acheta) and the development of activities of some insects (Messor barbarus, Danaus plexippus and Phlebotomus perniciosus).

Specific objectives are: 1) to recognize animal models far from the classic perspective, 2) to identify the different phases of the scientific method and the skills developed in each of them, 3) to promote attitudes focused on the love for nature, 4) to work science from a STEAM (science, technology, engineering, art y mathematics) perspective

A total of 5 schools participated in the project getting involved a total of 413 students from preschool, elementary, medium and high school. We analyzed the interviews conducted with 20 teachers who implemented these activities in their classrooms.

Gene expression responses to latitudinal clines of stonefly communities in Japan

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Abstract: Environmental heterogeneity continuously produces a selective pressure that results in genomic variation and selected gene expression profile differences among organisms. Although genetic variation in natural populations is common, those expressions at the community level and the genetic basis for this difference is scarce. We aim to unravel the process that dominates the evolutionary adaptation of the organisms by observing gene expression pattern and the potential coevolution of genes within a population shedding the light to local adaptation pathways and physiological responses. We investigated RNA-seq and proteomics dataset of seven stoneflies species from four geographical regions along latitudinal gradient in Japan. We detected 1077 gene distributed among geographical regions principally dominant with cellular process and metabolic functions. We examine physiological changes and community turnover as the underlying mechanisms shaping community adaptation to environmental variation. Here we will present the preliminary results of this analysis.

Sperm with wings: Inbreeding avoidance via male dispersal in a stingless bee

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Abstract: Inbreeding costs are a major driver of dispersal behaviour in animals. In taxa with restricted female gamete dispersal, inbreeding avoidance rests largely on the movement of male gametes. In eusocial bees of the tribe Meliponini (stingless bees), dispersal of reproductive females (queens) is restricted because daughter nests must be within short flight distance of parent nests, on which they initially rely for resources. Here we confirm that in the Australian stingless bee Tetragonula carbonaria, long-distance dispersal of males acts to offset this restricted movement of females. T. carbonaria colonies invest in a constant supply of males, which leave the colony when mature and do not return. To assess the distance males disperse, we manipulated colonies into rearing virgin queens and then sampled the males that formed mating aggregations outside these colonies. Based on genotypes, the distribution of brothers across swarms was relatively homogenous at scales of 400 km2, indicating that males readily disperse up to 10 km from their natal nests (20 times typical flight distance of females). These distances were consistent with mark-recapture studies of males, which indicated that they can travel at least 1km per day, and live for 21 days. The surprising dispersal ability of male T. carbonaria suggests that stingless bees can readily avoid inbreeding, even in fragmented landscapes. Furthermore, we propose that the genetic diversity of mating aggregations can serve as a tool for estimating population health and colony densities of stingless bees, analogous to strategies developed for honey bees (Apis sp.).

Assessing the tissue-specificity of adaptive immunity in Aedes aegypti

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Abstract: A detailed understanding of antiviral responses in insect vectors is crucial to improving surveillance and controls strategies for arboviruses. Recent findings in flies and mosquitoes suggest that the central antiviral pathway, the RNAi pathway, can elicit a form of adaptive immunity. Key to this process if the formation of viral DNA, a product of the reverse transcription of viral RNA carried out by retrotransposons active in the host genome. Whilst detailed studies in Drosophila melanogaster have determined that vDNA is specifically produced in phagocytic immune cells called haemocytes, it is unclear whether similar tissue-specificity is observed in vDNA formation in the mosquito vector Aedes aegypti. To address this, female Ae. aegypti (Puerto Rico strain) were mock infected or infected with 1.25x106 pfu/ml Zika virus (Brazilian strain ZikaSPH2015) by blood feeding. Engorged females were collected at 14 days post feeding and haemolymph was extracted (N=14 mock, N= 16 infected) and mid guts ovaries and carcasses were dissected (N=13 mock, N= 18 infected); tissues from mock and infected individuals were pooled. RT-qPCR done individually using RNA extracted from legs and wings indicated that 88% of individuals used to extract haemolymph and to dissect midguts, ovaries and carcasses had disseminated viraemia. Circular DNA was extracted from pooled tissues either using a miniprep plus RNAse A treatment or by treating RNAse A-treated total DNA with Plasmid Safe DNAse to remove linear genomic DNA. NGS libraries of circular DNA samples were made and sequenced on a HiSeq instrument (Illumina). Preliminary qPCR analysis of NGS libraries using a single primer pair targeting NS5 indicates amplification of Zika vDNA in libraries from infected midguts and in libraries made from Zika-infected Aag2 cells at 48 hours post infection. Ongoing sequence analysis will enable assessment of the tissue-specificity of vDNA production and of the molecular species that predominate including any retrotransposon-vDNA hybrid reads that may provide insight into vDNA biogenesis in Ae. aegypti.

Characterization of egg parasitoids to implement future biological control against native and exotic Pentatomidae in France.

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Abstract: The Pentatomidae family is a large taxonomic group, which includes major pests of agricultural crops. Reduction of pesticide use and biological invasions has caused the emergence of various pests from this family, urging the development of new biological control strategies. In France, these initiatives are implemented against the native pests Nezara viridula in horticultural crops, Eurydema spp. on cabbage and Palomena prasina in orchards. We are also interested in the exotic black marmorated stink bug Halyomorpha halys.

In a first step, the natural biodiversity of captured egg parasitoids was characterized via DNA barcoding. For this we exposed 40 000 sentinel eggs in 16 different locations in France during 2018 and 2019. Although expected, we did not detect the presence of Trissolcus. japonicus, an exotic parasitoid of H. halys that recently established in some European countries. In a second step, we estimated the influence of rearing hosts (N. viridula vs H. halys) on the quality of T. basalis strain. We evidence complex and opposite results while the development in H. halys seems to improve physiological traits but negatively impact the morphological ones with regards to N. viridula. So, we conclude that frozen mass eggs of H. halys could be used as a substitution host for the routine rearing of our Trissolcus strain, even if some vigilance must be kept. In the last step, (semi-) field experiments were carried out to test the effects of number released and frequency of releases on the efficacy of pest control. Two years of trials under compartmented greenhouse highlighted the best control of N. viridula on eggplants with the release of 1 parasitoid/m^2/week.

A new hope for the biological control of Aculops lycopersici (Acari: Eriophyidae) with the predatory mite Typhlodromus (Anthoseius) recki Wainstein (Acari: Phytoseiidae)

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Abstract: Currently, no natural enemy is efficient enough to control Aculops lycopersici at field level. We found interesting predatory ability of the Phytoseiid mite Typhlodromus (Anthoseius) recki in lab conditions. The present study aims to determine the efficiency of this species in semi-field conditions. As this predator is found on mints, we used it as companion plant to introduce T. (A.) recki. Firstly, mints and tomatoes were co-planted in plastic containers, at two ratios (1:1 and 1:2). The mints were inoculated with 20 females of T. (A.) recki, and tomato plants infested or not with A. lycopersici. T. (A.) recki is able to colonise and settle on tomato plants. This dispersal is much higher when tomato plants are infested by A. lycopersici, suggesting that the presence of the prey attracted T. (A.) recki. The second experiment was conducted in greenhouses. Thirty predators were introduced per tomato plant by placing branches of mints in the axil of the first tomato leaf. Tomato plants were artificially infested with A. lycopersici. The introduction of T. (A.) recki significantly reduces the length and the intensity of stem russeting and the number of A. lycopersici on tomato plants. Experiments are needed to investigate strategies of introduction.

Life in a contaminated habitat: How heavy metal contamination effects colony fitness of the common eastern bumblebee, Bombus impatiens

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Abstract: Heavy metal contamination is a byproduct of industrial and urbanization processes that can have negative and prolonged impacts on biota. Cities are oftentimes contaminated with heavy metals (HM), however, also support a diversity of bee species. Currently, little is known about the impacts of HM contamination on bee fitness. Bumblebees are prolific pollinators that are common in cities and whose foraging behavior potentially exposes them to a plethora of contaminants such as HMs. We examined how exposure to environmentally relevant concentrations of the HMs arsenic, cadmium, chromium, and lead within nectar sources influence bumblebee brood survivorship. Using HM concentrations from bumblebee-collected honey in hives located in Cleveland, OH we developed a replicated foraging experiment to measure the fitness effects of these contaminants. We conducted 15 d foraging experiments within 13.5 m3 tents, where nectar treatments were compared: arsenic (0.84 mg/L, n=4), cadmium (0.84 mg/L, n=4), chromium (0.76 m/L, n=4), lead (0.265 m/L, n=4), all HM's (n=4) and an uncontaminated control (n=12). Treatments were arranged in a randomized design. Each tent contained a nectar feeder with respective HM concentrations, a pollen feeder, and one colony with approximately 70 workers, allowed to forage ad libitum. After the exposure period, all colonies were weighed, dissected, and brood and adults counted. We found similar brood abundance across treatments, but a significantly higher proportion of dead brood in HM exposed hives. These data illustrate that even environmentally relevant concentrations of HMs found within cities can negatively influence bee fitness and threaten urban conservation efforts.

Disentangling landscape and local drivers that structure ground-dwelling beetle communities in urban greenspaces

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Abstract: Community assembly is the process by which local communities are organized and maintained from the regional species pool. Urbanization strongly regulates insect community assembly, but the relative importance of landscape and local drivers of assembly are understudied in urban ecosystems. Understanding processes of insect assembly are of interest in 'shrinking' cities where an overabundance of vacant land is being redesigned into alternative greenspaces such as pocket prairies. These greenspaces represent viable conservation spaces for insects such as beetles that contribute to essential ecosystem services including pest suppression, decomposition, and nutrient cycling. The objective of this study was to investigate the landscape and local drivers of ground-dwelling beetle community assembly in greenspaces that vary in habitat design, local management intensity, and landscape context in Cleveland, Ohio using a functional trait-based approach. Functional traits with a strong predictive capacity for ecological functions were measured on beetle species collected via pitfall traps in 2018 and 2019 in four habitat management treatments: 1) vacant lots mown monthly; 2) urban pocket prairies seeded with wildflowers; 3) Metropark forests; and 4) old fields. Understanding how insect communities are structured in urban landscapes will provide context for observed patterns in biodiversity and advance conservation biodiversity efforts.

From potential to practical: balancing the needs of people and pollinators to achieve urban conservation goals.

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Abstract: The documentation of many rare or declining bee species in urban green spaces has led to a recent focus on cities as conservation targets. However, for pollinator conservation to succeed long term, we argue that the opinions and values of local community members must be prioritized more explicitly. In our experience, conservation is difficult to achieve when the aesthetic and safety concerns of urban residents are not reconciled with the goals and habitat designs of conservation practitioners. Similarly, from a bee ecology perspective, many questions concerning optimal design and management practices for pollinator habitats in cities remain unresolved. It is our hope that frank discussion of the challenges associated with urban pollinator conservation in public green spaces will inspire thoughtful consideration of how best to implement new initiatives in cities.

Trophic interactions between native parasitoids and invasive alien species: identification of host shifts and new associations in biological control

Authors: Gariepy Tara, Agriculture and Agri-Food Canada, Canada

Abstract: The establishment of invasive alien species in a new location has the potential to impact species interactions in a given invertebrate food web. Invasive species may provide a new host resource for native parasitoids, resulting in host-shifts or new associations that were previously undescribed. The detection and quantification of these interactions can be difficult using traditional rearing and dissection techniques, particularly when the interaction is non-viable (i.e., unsuccessful parasitoid development). The development and use of molecular diagnostic tools has the potential to provide rapid and accurate identification of hosts and parasitoids, and can provide more complete information on species interactions. In particular, it can provide conclusive evidence of host-shifts and/or new associations that would otherwise have gone undescribed. Case studies in a variety of systems are presented here to outline the utility of molecular diagnostics in the identification of trophic links between native parasitoids and invasive alien insects, and the impact that these interactions may have in the context of biological control.

Can the parasitoid wasp, Trissolcus japonicus (Ashmead) parasitize and develop on stink bugs native to Ontario, Canada?

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Abstract: Trissolcus japonicus (Ashmead) (Hymenoptera: Scelionidae), is an Asian parasitoid wasp known to be an egg parasitoid of Halyomorpha halys (Stål) (Hemiptera: Pentatomidae), the brown marmorated stink bug (BMSB). Brown marmorated stink bug is a serious invasive agricultural pest in Europe and North America, and insecticides appear to be of limited efficacy. Trissolcus japonicus is considered a candidate for classical biological control agent in many regions where BMSB has established. Given the recent discovery of adventive populations of T. japonicus in the US, Europe, and Canada, surveys to determine the establishment and spread of adventive populations in Ontario, Canada are being conducted. Data collected in the summer of 2019 demonstrated that T. japonicus populations persist in London, Ontario, but has not yet been found in other areas of southern Ontario. Results from testing T. japonicus host range suggest that it can parasitize and develop on a subset of native stink bugs, but the extent to which it will attack them is unknown. As a result, a study is being conducted to investigate whether T. japonicus will parasitize and develop on 11 non-target stink bugs native to Ontario.

Ontogeny and defensive induction explain the phloem chemistry of two species of ash (Oleaceae: Fraxinus) in New Hampshire, USA

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Abstract: Since its introduction into North America three decades ago, the invasive emerald ash borer, Agrilus planipennis Fairmaire (Coleoptera: Buprestidae) has spread rapidly across the United States and killed millions of ash trees (Oleaceae: Fraxinus). This has resulted in billions of dollars in economic losses, as well as severe ecological damage to natural and managed forests. In North America, Fraxinus do not share a coevolutionary history with A. planipennis, allowing the beetle to quickly colonize and kill its hosts. While most Fraxinus are susceptible to A. planipennis, smaller diameter trees experience reduced colonization by A. planipennis compared to larger trees. We hypothesize that patterns of colonization by A. planipennis are explained by the chemical profiles of Fraxinus, and predict that ash of different ages have different chemical profiles. Our hypothesis was evaluated with two species of North American Fraxinus across four size classes with three treatments: no colonization, colonization by A. planipennis, or defensive induction with methyl jasmonate. Preliminary analysis identified 115 unique compounds across all samples. Non-metric multidimensional scaling of the four size classes of Fraxinus prior to treatment indicates some compounds are shared amongst size classes, but that there is a large divergence in the chemical composition of ash phloem after defensive induction. Ongoing analyses will identify compounds driving these interactions and evaluate quantitative differences among compounds identified in our study. Our research will increase our understanding of defensive strategies of Fraxinus, informing horticultural or silvicultural strategies to maintain Fraxinus, in light of the current invasion by A. planipennis.

Impacts of a climate-driven range shift of the Southern pine beetle (Dendroctonus frontalis) on gallery-associated arthropod communities

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Abstract: Climate-driven range shifts are increasingly common in today's warming world. Together with biological invasion, distributional change via climate tracking results in the creation of novel assemblages or arthropods, microbes, plant hosts, etc. Species richness and composition the novel communities can have important impacts on population ecology of range-shifting species, and on best management practices in case of pest species. Differences in the identity, abundance, and behavior of key natural enemies, competitors, mutualists, and other associates can have major consequences for equilibrium abundances and/or dynamics (i.e., the frequency and amplitude of population cycles where they exist). Thus, the degree to which these communities differ from those in the core of a species' historical range, could help predict aggressiveness or impacts, among other factors of interest. The Southern pine beetle (SPB), Dendroctonus frontalis Zimmerman, (Coleoptera: Curculionidae), is an aggressive tree killing bark beetle native to southern North America as well as to parts of Central America. SPB, among the region's most destructive pine pests, has recently established in pitch pine (Pinus rigida) barrens in New York and Connecticut, over 100 km to the north of historical range limits. In 2017-18, we intensively sampled SPB-associated arthropod communities in infested pine. Resulting diversity, abundance, and composition estimates were then compared with a parallel dataset collected from 1975-1997 in four forests across three states within the core southern range in the beetle. Rarefied arthropod richness was marginally higher in northern sites when pooling sampling methods. Key community members (i.e., fly and beetle predators and hymenopteran parasitoids as well as Ips engraver and longhorn beetle competitors) were present in both the northern and southern regions, though overall community composition and relative abundances differed markedly. One ecologically important predator, the clerid beetle Thanasimus dubius (Fabricius) (Coleoptera: Cleridae) was present in approximately equal densities across regions. Fly, wasp, Ips engraver beetle richness was also similar between regions, but abundances were substantially lower in northern sites. Low frequency and abundance of Ips avulsus – a dominant, widespread interactor in southern sites – could in part explain patterns of higher bole utilization by SPB observed in the North, as this beetle appears to displace SPB in the tops of trees in southern site. Our results show that despite potentially important differences in abundance and perhaps in behavior, SPB-associated communities are compositionally similar among sites in the south v. the novel northern range. Ongoing research on the community as it relates to SPB dynamics in the North will add to core understanding of key feedbacks and their implications for management.

Effects of exposure to Metarhizium-colonized plants on the cotton leafworm Spodoptera littoralis

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Abstract: It has been recently reported by several researches that exposition of lepidopteran larvae to entomopathogenic fungi-endophytically colonized plants may lead to medium to low mortality rates not related to fungal outgrowth, with the underlaying cause of death not well understood. The aim of the current work was to investigate the effects of the ingestion of M. brunneum EAMb 09/01-Su strain colonized melon plants on S. littoralis survival and reproduction. The fungus was able to colonize melon plants (Cucumis melo var. Galia), with 45.0% leaf colonization at 48 hours post-inoculation. Larvae feeding on fungus-colonized leaves showed a 53.3% mortality and 7.3 d average survival time (AST) that differed significantly from the 16.7% mortality and 6.5 d AST detected in the controls. It was noteworthy that neither signs of fungal outgrowth nor apoptosis related to caspases 1, 3/7 and 8 activities were detected in the cadavers. Meanwhile, fecundity of adult females coming from fungus challenged surviving larvae, 71.2 eggs laid per female, was significant lower than that of the controls, 219.7 eggs laid per female. These results were discussed in terms of their significance to the mode of action of entomopoathogenic fungi when they are offered via colonized plant tissues and on the impact of such colonization of the control of the pest.

A novel high-resolution melt assay for xenomonitoring of Human African Trypanosomiasis

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Abstract: With elimination of Human African Trypanosomiasis (HAT) targeted by 2020 and complete interruption of transmission by 2030, it is increasingly important to identify remaining active cases, foci of transmission and areas of disease resurgence. With declining numbers of cases, active screening programmes are no longer cost-effective and there is a need for a screening tool which can be maintained sustainably post-elimination. Screening vectors for parasites, known as xenomonitoring, provides a low-cost and simple monitoring method which can measure trypanosome transmission dynamics within an area in real time. Traditionally, xenomonitoring of HAT has been reliant on detection of trypanosomes by microscopy or using PCR. High resolution melt (HRM) is a closed tube post-PCR method which is highly sensitive and specific, and has a faster time to result than gel-based PCRs. We have developed a multiplexed HRM assay for the detection of both sub-species responsible for Human African Trypanosomiasis: T. b. rhodesiense and T. b. gambiense. The assay contains novel primers for T. b. rhodesiense designed to target the serum resistance-associated gene (SRA) and previously published T. b. gambiense primers designed based on the T. b. gambiense-specific glycoprotein gene (TgsGP). An additional primer set designed to amplify a single-copy phospholipase-C gene (GPI-PLC) expressed by all members of the Trypanozoon group were included to indicate whether sufficient DNA is present for the amplification of single copy genes. The HRM was found to be highly specific with no-cross reactivity when tested with a range of pathogenic animal trypanosome DNA. The limit of detection was found to be 10^4 tryps/mL. The assay sensitivity was compared to TgsGP PCR and was found to be as sensitive for T. b. gambiense detection and tenfold more sensitive when compared to SRA PCR at detecting T. b. rhodesiense. Further testing of assay performance is being performed on samples of T. brucei s.l. infected tsetse containing confirmed T. b. rhodesiense caught in 2015 from the Serengeti National Park and associated game reserves in Tanzania.

Our results indicate that this novel high-resolution melt assay could provide a highly sensitive and specific method of screening tsetse flies for pathogenic trypanosomes. With tsetse often caught as part of HAT control, this method could be implemented as part of elimination programmes and used within long-term HAT surveillance.

Culicoides Latreille (Diptera: Ceratopogonidae) taxonomy: The tree that hides the forest.

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Abstract: Culicoides Latreille biting midges (Diptera: Ceratopogonidae) cause a significant biting nuisance to humans, livestock and equines, and are the biological vectors of a range of internationally important pathogens of both veterinary and medical importance. Despite their sanitary and economic significance, the delimitation and identification of species and evolutionary relationships between species within the genus remains at best problematic. To date no phylogenetic study has attempted to validate the subgeneric classification of the genus and the monophyly of many of the subgenera remains doubtful. Many informal species groupings are also known to exist but few are adequately described and validated, further complicating accurate identification.

Recent contributions to Culicoides taxonomy and systematics using molecular analyses have revised the systematic scheme of the main subgenera and revealed the existence of cryptic species within important vector groups in the Palearctic region. This communication highlights two recent studies aiming at revising the current taxonomic scheme using species delimitation models: one analyzing the phylogenetic relationships in the Avaritia subgenus in the Afrotropical region (Bakhoum et al 2017) and one characterizing and mapping the cryptic diversity within the Obsoletus/Scoticus Complex at the European level using a multi-marker methodology (Mignotte et al 2020).

Landscape genetics and vector-borne diseases: Culicoides obsoletus (Diptera: Ceratopogonidae), a livestock virus vector species in the Palearctic region, is not a bad flyer!

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Abstract: Since 2006, recurrent and major epizootics of bluetongue (BTV) and Schmallenberg virus (SBV) have been reported in the Palearctic region. They are both transmitted by native hematophagous midges of the genus Culicoides (Diptera: Ceratopogonidae). These viruses affect domestic cattle, sheep, goats and wild ruminants. Culicoides dispersion is referred to as a stratified dispersion. This is a combination of dispersion processes occurring actively at short distances and passively or semi-actively at long distances, allowing dispersion jumps of hundreds of kilometers. Culicoides obsoletus has been identified by previous studies as an abundant and widespread main vector species of BTV and SBV over western and northern Europe. The objective of this work was to identify the meteorological and environmental factors that promote or limit gene flow within and among C. obsoletus populations and infer their impacts on Culicoides dispersal. The study was conducted at two geographical levels (i) country scale (France, 46 sampling sites), and (ii) continental scale (from Scandinavia to Northern Africa, 36 sampling sites). A wide range of meteorological (temperature, rainfall) and environmental (land cover, altitude, host type and density) factors was used together with genetic data obtained using 11 microsatellite markers. Both univariate and multivariate analyses were applied to assess the correlation between differentiation and environmental factors. The latter analyses were performed following two complementary and distinct approaches: a pairwise approach in which genetic distances are compared with environmental distances computed with circuit theory and second a point approach in which local genetic dissimilarity measures are compared with local environmental conditions.

Culicoides obsoletus showed a low genetic structuration level at the national scale, highlighting a high dispersal capacity. Similarly, at the continental level, a low genetic structure is detected. Despite this overall low level of genetic differentiation, three genetic clusters were detected at the continental level: one Mediterranean cluster, one Northern European cluster, and one cluster related to the Canary Islands. The main environmental factors having a significant impact on the genetic dissimilarity of C. obsoletus populations are the host density and the land cover. On the contrary, wind speed and direction are the two main factors having a significant impact on the genetic similarity of C. obsoletus populations. These results will be confirmed by simulation approaches.

In conclusion, we have quantified for the first time the effects of landscape heterogeneity on gene flow of one main Palearctic vector species and identify the wind as a main environmental factor to explain genetic similarity between populations. This result allow to discuss the long distance dispersal of Culicoides and implication for virus transmission, most often underestimated.

Pest Adaptation in a Transgenic Landscape: Western Corn Rootworm and Bt Maize

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Abstract: In the United States, the western corn rootworm, Diabrotica virgifera virgifera (Coleoptera: Chrysomelidae), is among the most serious pests of maize. Current management relies heavily on planting of transgenic maize that produces insecticidal toxins derived from the bacterium Bacillus thuringiensis (Bt). In some regions of the United States, western corn rootworm has evolved resistance to Bt maize. The first cases of Bt resistance involved maize that produced Bt toxin Cry3Bb1. Over time, the magnitude of Cry3Bb1 resistance has increased, and cross-resistance has been found among Cry3Bb1, mCry3A and eCry3.1Ab. More recently, evidence has emerged of resistance to Cry34/35Ab1 maize in some populations, and of widespread resistance to Cry3Bb1 maize. Management of corn rootworm resistance to Bt maize has focused on non-Bt refuges and pyramiding of multiple Bt toxins. However, non-recessive inheritance of resistance, minimal fitness costs of resistance, and use of Bt traits singly before pyramiding have all likely reduced the resistance-management benefit of these approaches. In general, it is clear that better use of integrated pest management, in particular a more diversified approach, will be essential to achieve sustainable management of western corn rootworm with current and future transgenic technologies.

The Evolution of the State-University Partnership in New Jersey Mosquito Control

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Abstract: The State of New Jersey's emergence as a pioneer in mosquito control followed directly from John B. Smith's appointment to Rutgers University in 1889. Stressing that "research must guide the mosquito movement," Professor Smith's studies showing mosquitoes were a statewide rather than merely a local issue resulted in state legislators authorizing and funding the creation of local mosquito control units in 1912. Professor Headlee later established those units as well as state, regional, and national mosquito control associations, all ideas widely emulated nationally and internationally. Drawing on state funding, Headlee further built a world-class mosquito research program. In 1956 the state formed a commission to manage mosquito control efforts previously run by Rutgers. New funding was infused into local programs to support aerial spraying, equipment, biological control, and water management, but state funding for research subsequently withered. In 1976 Professor Crans developed a plan for statewide surveillance of mosquitoes and arboviruses centered on robust local, state and university cooperation and interdependence. The surveillance program has been highly successful and should be a model for re-envisioning other aspects of New Jersey mosquito control.

Over its long history the State-University partnership has often appeared mired in competitiveness and mistrust. New leadership, however, could present new opportunities for sweeping changes in institutions which have been largely refractory to change including: expanding the mission to additional vectors, encouraging applied research in local units, moving the state and local units into health departments, increasing efforts against urban species, promoting professionalism in local units, and joint efforts to aggressively seek new funding across the board.

Digestive mutualism in Nepenthes pitcher plants: role of the 'macrobiota' and its variation among plant species

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Abstract: Carnivorous Nepenthes plants derive essential nutrients from arthropods captured in their pitcher-shaped leaves. The pitchers secrete a digestive fluid and house specific microbiota and 'macrobiota', mostly mosquito larvae, that aid in digestion, breaking the prey down into an easily assimilated form. We tested and measured the occurrence of such facilitation processes among Bornean Nepenthes. In a field experiment, prey items were introduced into the fluid of newly open pitchers of four Nepenthes species and their state was compared one month later between control pitchers and pitchers initially closed by insect screening mesh. The same experiment was performed in water-filled glasses. Metazoan diversity, tank dimensions and fluid pH were then measured in the 150 tanks.

Prey in macrobiota-deprived pitchers experienced lower degradation than in control pitchers in all Nepenthes species but not in water-filled glasses. Macrobiota exclusion impacted less species characterized by narrower pitchers and more acidic fluids. Rate of prey degradation increased significantly with abundance and diversity of inquilines. Therefore, Nepenthes pitcher plants are highly dependent on their 'macrobiota' to decompose prey. Such digestive mutualisms are even crucial in species whose pitchers have large aperture and less acidic fluids, housing a more diverse infauna and secreting presumably fewer digestive enzymes.

Museomics identifies genetic erosion in two butterfly species across the 20th century in Finland

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Abstract: Erosion of biodiversity generated by anthropogenic activities has been studied for decades and in many areas at the species level, using taxa monitoring. In contrast, genetic erosion within species has rarely been tracked, and is often studied by inferring past population dynamics from contemporaneous estimators. An alternative to such inferences is the direct examination of past genes, by analyzing museum collection specimens. While providing direct access to genetic variation over time, historical DNA is usually not optimally preserved, in low quantities and degraded. It is necessary to apply genotyping methods based on hybridization-capture to unravel past genetic variation. We applied such a method, i.e., HyRAD, to large time series of two butterfly species in Finland: Erebia embla and Lycaena helle. We developed a new bioinformatic pipeline that standardizes and optimizes the analysis of HyRAD data. We show in the localities for which the data retrieved has sufficient power to accurately examine genetic dynamics through time, that genetic erosion has increased across the last hundred years, as revealed by signatures of allele extinctions and heterozygosity decreases, despite local variations. In one of the two butterflies, i.e., Erebia embla, isolation by distance also increased through time, revealing the effect of an increase in habitat fragmentation.

Main changes in the genus Plateumaris Thomson in the second edition (2022) of the Catalogue of Palaearctic Coleoptera: Chrysomelidae

Authors: Geiser Elisabeth, NHM Wien, Austria

Abstract: The members of the genus Plateumaris belong to the subfamily Donaciinae, whose larvae develop completely under water with a set of sophisticated morphological and physiological adaptions. They occur in the Nearctic region with 17 species and in the Palaearctic region with – that is the question!
The number of Palaearctic Plateumaris species considered as valid varies in the literature between 9 and 16. In my current update of the Catalogue of Palaearctic Chrysomelidae – Donaciinae I recognize 10 species as valid. However, there remain some doubts, especially in the highly variable Plateumaris sericea, which is also shown by at least 37 synonyms.

Traditionally, the Palaearctic Plateumaris were split into two subgenera: Plateumaris sensu stricto and Juliusina. But it figured out that the two "subgenera" didn't have even a single synapomorphy in common. Further molecular studies showed that the next relatives of many Palaearctic Plateumaris species are Nearctic species. Therefore, the subgenera had to be eliminated.

The Catalogue of Palaearctic Coleoptera also contains distribution information about each species. This will be updated, too. As the countries are only indicated with a short abbreviation in the Catalogue, further publications are edited now with detailed information and the source of it.

The Palaearctic species of the genus Plateumaris Author (Coleopterea, Chrysomelidae, Donaciinae): Who are they and if so how many?

Authors: Geiser Elisabeth, NHM Wien, Austria

Abstract: The number of Palaearctic Plateumaris species considered as valid varies in the literature to a remarkable extent. Askevold (1991) recognized nine species, but Silfverberg (2010) recognized 16. Other authors use other numbers in between. This is NOT due to new detected and new described species but results from the different opinions about species delimitation, subspecies status and synonyms. Some enigmatic species – described 100 years ago, never recorded again, type specimens missing – pop up in literature again and again like the undead.

In my current updating of the Catalogue of Palaearctic Chrysomelidae – Donaciinae I aim to declutter this situation. A very effective method is to compare museum specimens from different locations to study their morphological variety. The problematic species are very rare therefore it would be difficult to recapture them again at sites where they were found 100 years ago. Furthermore, the interesting biogeographical locations of the Caucasus and the countries south are dangerous regions to travel nowadays. Meticulous morphological study is an important step to better understanding of the species delimitation. This is prerequisite for the next step which is molecular analysis of museum specimens. These methods are rapidly developing now and they will be precise and affordable within the next years.

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Metabarcoding Malaise trap plant components enables monitoring the diversity of plant-insect interactions

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Abstract: The declines in insect abundance and diversity over the past decades has also been observed in plants, and these events are most certainly linked. When insects are captured in Malaise traps, they carry traces of plants they have visited, either on the body surface or in the gut contents. DNA metabarcoding offers a promising method for identifying these plant traces, however, this method is not without its shortcomings and DNA metabarcoding of plant traces from Malaise samples types has not yet been tested. To examine the soundness of this method we analyzed 105 samples from sites across Germany with the ITS2 barcode. Here we report on the feasibility of sequencing these sample types, analysis of the resulting taxa, the usage of cultivated plants by insects near nature conservancy areas, and the detection of rare and neophyte species. We will additionally comment on the potential and pitfalls for plant metabarcoding from a variety of insect-mediated sources. DNA metabarcoding has advantages for rapid largescale biomonitoring inefficiency and resolution over microscopic identification of pollen, and we expect that it will have broad utility for future studies of plant-insect interactions when careful consideration is taken in study design and analysis.

Involvement of two secondary metabolites secreted by Serratia marcescens in mosquito-bacteria interactions

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Abstract: Bacteria colonising the mosquito have positive impacts on their host, including protection against infection by pathogens, contribution to larval development and to blood digestion, but negative impacts have also been reported, they notably restrain lifespan and fecundity. We studied a strain Serratia marcescens isolated from our mosquito colony that has pathogenic effects on Aedes aegypti mosquitoes. S. marcescens produces several secondary metabolites in a strain-dependent manner, including prodigiosin, a red pigment known to have microbicidal and larvicidal activities, and serratamolide, a non-pigmented microbicidal and haemolytic metabolite. Our strain is a prodigiosin producer (red) that kills mosquitoes upon oral infection at high concentration and displays proteolytic and haemolytic activities. We produced two white mutants by non-targeted mutagenesis to investigate the role of prodigiosin in host-microbe interactions. We observed that mutant C1 is slightly less virulent than the wild type and that C3 is almost non-lethal. We also show that the culture supernatant of wt and C1 displays proteolytic and haemolytic activities, which are lost in C3. We hypothesized that C1 is deficient for prodigiosine synthesis only while C3 would produce neither prodigiosine nor serratamolide. We confirmed by whole-genome sequencing that C1 has a stop codon in prodigiosine-synthase while C3 has several mutations which are currently under investigation. Moreover, HPLC profiles suggest that serratamolide is present in C1 and absent in C3. Together, these data indicate that prodigiosine has a minor role in the virulence of S. marcescens in Ae aegypti while serratamolide may have strong implications on bacterial virulence and enzymatic activities.

Is biological control a solution for maize crop protection against maize leaf weevil (Tanymecus dilaticollis Gyll) attack in Romania?

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Abstract: Romania has more than 2.5 million hectares as maize cultivation which represents the highest area within the EU. Maize leaf weevil (Tanymecus dilaticollis Gyll) is the most dangerous pest of the maize crops. Favorable area of this pest is located in south and south-east of the Romania. The attack is dangerous when maize plants are in early vegetation stages (BBCH 10-BBCH 14). In case of high T. dilaticollis attack, the maize seedlings could not survive and the farmers have to sowing again their crops, that causing unexpected costs. Spring drought and higher air temperatures are even more favorable conditions for weevils attack. Also, maize monoculture has an increasing effect on pest density associate with higher impact of the attack. Recent studies from the last decades pointed out that chemical treatment of the maize seeds with systemic insecticides was the most effective control method of this pest at maize crops in Romania. However after European Commission Regulations 218/783, 218/784 and 218/785, no chemical alternatives remain available for maize seed treatment against T. dilaticollis in our country. In this paper there were presented results of a three years study, effectuated at NARDI Fundulea, in south-east of Romania, concerning the effectiveness in weevils control of the biological insecticides, used both, at seed treatment and foliar spraying (spinosad active ingredient and neem oil) comparative with chemical seed treatment with imidacloprid active ingredient. Attack intensity of the weevils at maize was evaluated when plants arrive in four leaf stage (BBCH 14), according a scale from 1 to 9 (1-plant not attacked; 9-plants complete destroyed, with stem chafed close to the soil level). Between 2016 and 2018, weather conditions from experimental location, during spring period were atypically for both, maize plants early stages development and weevils attack. The attack intensity of T. dilaticollis at maize untreated plants was 5.91 in 2016, 5.59 in 2017 and 4.61 in 2018. In case of variants treated with neem oil and spinosad active ingredient, the attack intensity of the weevils at maize plants ranged from 4.52 to 6.12. During this research, there weren't ascertained significant statistical differences ($p<0.05$) between weevils attack intensity registered at maize plants from untreated variant and attack intensity registered at maize plants from variants treated with neem oil and spinosad active ingredients, applied both, like seed and foliar treatments. In all years from this research, lowest attack intensity of the weevils at maize plants was registered in case of variant with maize seeds treatment with imidacloprid active ingredient. In this case attack intensity ranged from 3.45 to 3.70. Oil neem and spinosad active ingredients couldn't be an alternative for biological control of T. dilaticollis weevils in conditions of high pest pressure from south-east of the Romania.

Red Flour Beetle Oviposition and Development on Wheat Flour Alternatives

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Abstract: Many ancient and contemporary grains, seeds, nuts and other materials have been ground into flour and serve as alternatives or additions to traditional wheat flour in baking. Increased interest in using other types of flours has been driven by gluten allergies or sensitivities as well as an interest in a variety of texture, flavor and nutritional properties. Stored product insect pests such as the red flour beetle, Tribolium castaneum, can be major pests of wheat flour, but we know less about how susceptible these new flours are to infestation. Here we assess how readily red flour beetles will lay eggs in 17 alternative flour types when compared to wheat flour as a control. We find that there is a significant difference in the number of eggs laid across our tested flours, with wheat and teff having highest numbers of eggs laid and amaranth and cassava having the lowest. In addition, we find differential adult emergence, with teff and wheat having the highest number of progeny and almond, amaranth, cassava, and coconut having no progeny emergence. We find that the number of progeny negatively correlates with manufacturer labeled nutritional content such as total grams of fat and sodium but positively correlates with dietary fiber. Timing of adult emergence of the oviposited eggs was also different by flour with development quickest on wheat and teff with most adults emerging was highest 4 weeks after oviposition; followed by spelt, rye, quinoa, barley, and millet, with peak adult emergence on week 5; oat, corn, and buckwheat, with highest emergence on week 6; and sorghum and rice having the slowest developmental rate, with emergence peaking on week 7. We also evaluated egg to adult development over 4 weeks with a single egg placed in each of the flours. We found after 8 weeks on the flour, almond and amaranth have nearly 90% of eggs with no larval, pupal, or adult activity; cassava, coconut, and garbanzo have 30-40% of eggs that reach at least the larval stage, with some adults in garbanzo flour; potato had 20% of eggs emerge as larvae but no adults; and barley, buckwheat, corn, millet, rye, spelt, sorghum, wheat, and teff all have greater than 60% adult emergence. Together, these results suggest that female T. castaneum discriminate among different types of flour by laying different numbers of eggs. However, females laid high numbers of eggs on several flours, but adult emergence was low, suggesting these beetles may not be able to discriminate fine-scale nutritional profiles that restrict beetle development. In addition, immatures develop at different rates on the flours and have different probabilities of making it to the adult stage, suggesting some inhibiting factors such as a lack of key nutritional components. Future analyses will need to be done to pinpoint these components. The differences in oviposition and developmental rates suggests that some of these flours may not be as susceptible to insect infestations.

The Whitefly Bemisia tabaci is expanding its transmitted viruses to the aphid-transmitted genus polerovirus

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Abstract: The whitefly Bemisia tabaci, is a complex of cryptic species and considered one of the most invasive pests and a major worldwide threat to many agricultural crops. It feeds directly on plants causing weakening and honeydew secretion. The major damage inflicted by B. tabaci is the transmission of plant viruses from different genera, especially begomoviruses. The exceptional invasiveness of B. tabaci is a major factor that contributes to the spread and emergence of new plant viruses. During the last 20 years, new viruses belonging to genera that were not associated with whiteflies, were reported to be transmitted by B. tabaci, majorly the Middle East Asia Minor 1 (MEAM1) and the Mediterranean species (MED), also known as the B and Q biotypes, respectively. Poleroviruses (Luteoviridae) are phloem-restricted RNA plant viruses, which are exclusively transmitted by aphids. Multiple aphid-transmitted polerovirus species commonly infect pepper, causing vein yellowing, leaf rolling and fruit discoloration. Despite low aphid populations, a recent outbreak with such severe symptoms in many bell pepper farms in Israel led to reinvestigation of the disease and its insect vector. This outbreak was caused by a new whitefly (Bemisia tabaci)-transmitted polerovirus, which we coined Pepper whitefly borne vein yellows virus (PeWBVYV). PeWBVYV is highly homologous (>95%) to Pepper vein yellows virus (PeVYV) from Israel and Greece on its 5' end half, while it is homologous to African eggplant yellows virus (AeYV) on its 3' half. By constructing a PeWBVYV infectious clone causing the pepper disease, we were able to fulfill Koch's postulates and show that the B biotype of B. tabaci, but not the Q biotype or aphids, is able to transmit this new recombinant polerovirus. This is the first report of a whitefly-transmitted polerovirus which made a significant leap in its association with insect vectors and further demonstrates the ability of B. tabaci to expand the diversity of its transmitted viruses.

Role of endoplasmic reticulum-associated responses in Liberibacter transmission by psyllids

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Abstract: We have recently identified a novel interaction between Candidatus Liberibacter asiaticus (CLas), the causative agent of the citrus greening disease and transmitted by the Asian Citrus Psyllid (ACP), and Candidatus L. solanacearum (CLso), which causes the carrot yellowing disease and transmitted by the carrot psyllid (CP). This interaction shows that the acquisition of CLso and CLas by CP and ACP, respectively, induced cellular morphological abnormalities in the adult guts of both vector species, but not in nymphs. Further transcriptomic and microscopic analyses from adults and dissected guts in both pathosystems showed similar and unique molecular immune and stress responses to the acquisition of the bacteria. Most importantly, the response of Endoplasmic reticulum (ER)-associated molecular pathways are induced, and ER-associated functions in the cell are recruited for the bacteria persistence and replication. Our hypothesis is that those closely-related bacteria evolved shared and unique mechanisms to establish their interactions with the vectors. Identifying such responses and insect factors that aid in the pathogen transmission is important for devising new control methods to prevent disease transmission.

Plant volatiles modulate immune responses of Spodoptera litura

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Abstract: Plants emit a specific blend of volatiles in response to herbivory and these volatiles, which often attract predators and parasitoids function as an indirect plant defense. The impact of plant volatiles in shaping herbivore defenses is unclear. Here, we report that specific plant volatiles induce immune responses in the polyphagous herbivore, Spodoptera litura. We characterized the hemocyte profile and established their functional significance with respect to ontogeny and exposure to specific plant volatiles. Fifth instar larvae showed the highest number and hemocytes diversity. We characterized seven different types of hemocytes, of which granulocytes performed phagocytosis, oenocytoids showed melanization activity, and plasmatocytes along with granulocytes and oenocytoids were found to be involved in encapsulation. Among the six volatiles tested, exposure to (E)-ß-ocimene caused highest increase in total hemocytes number (THC) followed by linalool and (Z)-3-hexenyl acetate exposure. Although THC did not differ between these three volatile treatments, circulating hemocytes diversity varied significantly. (E)-ß-ocimene exposure showed higher number of plasmatocytes and phenol oxidase activity. The interaction of parasitic wasp Bracon brevicornis with (E)-ß-ocimene exposed larvae was poor in terms of delayed paralysis and lower egg deposition. In choice assay, the wasp showed clear preference towards control larvae indicating (E)-ß-ocimene treatment renders the host unattractive. Hemocyte profiles post-parasitoid exposure and (E)-ß-ocimene treatment were similar indicating cue-based priming. When challenged with Bacillus thuringiensis, linalool exposure caused highest survival as compared to other volatiles. Our results show that specific HIPVs can modulate cellular immunity of S. litura, revealing a new role for HIPVs in tri-trophic interactions.

A role for baculoviruses as vectors of horizontal transfer of transposable elements in lepidopterans?

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Abstract: Horizontal transfer (HT) of genetic material is central to the architecture and evolution of prokaryote genomes. Within eukaryotes, the majority of HTs reported so far are transfers of transposable elements (TEs). Because of the lack of large-scale survey, the amount and impact of HT of TEs (HTT) in eukaryote evolution, as well as the mechanisms and vectors mediating these transfers, are poorly known. Here, I will report the results of our recent comprehensive analyses of HTT in 195 insect genomes. We developed a pipeline to detect and count HTT events which allowed us to infer a minimum of 2,248 independent HTT in insects. We show that DNA transposons transfer horizontally more often than retrotransposons, and unveil phylogenetic relatedness and geographical proximity as major factors facilitating HTT in insects. We also show that host taxa play an important role in shaping HTT by identifying Lepidoptera as a hotspot of transfers. I will also report the results of our search of TEs integrated in the genome of ten vertebrate and insect viruses using ultra-deep sequencing. While we found a large number and diversity of TEs integrated into the genomes of four baculoviruses replicated on six species of Lepidoptera, almost no TE were recovered from the other six viruses. Together, our results establish HTT as a major force shaping insect genome evolution and support the role of baculoviruses as vectors of HTT in Lepidoptera.

A targetted survey for the endemic and little-known bark beetles of the Hawaiian Islands

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Abstract: The insect fauna of the Hawaiian Islands is over 95% endemic and at a heightened threat of endangerment, yet it remains largely understudied. One radiation of endemic Hawaiian insects is the xyleborine bark beetles, consisting of 21 described species of Xyleborus Eichhoff. They are the only indigenous scolytines in the islands, and many species have not been recorded for decades, or since their descriptions. In order to gain insights into the present diversity, distribution, relative abundance, and conservation concerns of these beetles, targeted sampling for bark beetles was undertaken across the Hawaiian Islands. We collected beetles using standardised lured Lindgren-funnel traps, deployed across numerous sites containing predominantly native vegetation, across six islands over the course of three years. We summarise the results of the survey, which confirm the persistence of native beetles at several sites containing well preserved native forest habitat. However, our results also indicate that native bark beetles now persist only as a numerical minority in local scolytine communities, occurring in low relative abundances, accounting for far less of the total trap catches across all sites than introduced exotic bark beetles. However, despite their comparative low abundances, locally, native bark beetles can represent the majority of species-level alpha diversity in native forest sites. The discovery during this survey of species not recorded since their descriptions, together with several new records that represent potentially undescribed species, suggest that much remains to be learned from the insect fauna of Hawaii's threatened forest biotopes.

Behavioral responses of invasive ambrosia beetles to fungal volatiles in mixed hardwood forests

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Abstract: Invasive ambrosia beetles (Coleoptera: Curculionidae: Scolytinae) are serious pests of landscape, nursery, orchard and forest trees worldwide, and are among the most commonly intercepted insects at ports-of-entry in the United States. Early detection of nascent invasive beetle populations is essential to initiate effective management efforts before incurring catastrophic losses. Current detection tactics for these pests utilize traps baited with ethanol lures placed at high-risk areas, such as ports and shipping hubs, but these are often ineffective at detecting incipient, low-level populations. There is a critical need for advanced methods to detect and manage these potentially destructive beetles. Recent studies have demonstrated that volatile compounds produced by symbiotic and co-occurring fungi of ambrosia beetles are behaviorally active and may enhance or reduce the response of beetles to other attractants. In this study, we conducted field-based experiments to determine the extent to which a suite of fungal volatiles influence the attraction of invasive ambrosia beetles to ethanol-baited traps. This information will be useful in establishing effective management programs for invasive ambrosia beetles to sustain the health, quality, and productivity of hardwood forests.

Competition within the parasitoid guild of Halyomorpha halys: Trissolcus japonicus and Trissolcus mitsukurii

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Abstract: The invasive stink bug Halyomorpha halys, originally from East Asia, is a serious agricultural pest of worldwide importance. Its economic impact and failures of chemical pest management led to consideration of biological control as the most effective long-term management approach. Two Asian egg parasitoids, Trissolcus japonicus and Trissolcus mitsukurii, are considered effective candidates as biological control agents. Because these two species can co-occur in the same habitats, interspecific competition could play an important role in the success of natural control. Interspecific competition can potentially disrupt biological control programs, or cause synergism, or it may have no influence at all. We investigated the foraging behavior and mechanisms displayed during interspecific competition between T. japonicus and T. mitsukurii and the way these species exploit common resources. In laboratory experiments using testing arenas, we simulated three different interspecific competition scenarios: i) indirect competition, where H. halys egg masses first parasitized by one species were subsequently offered to the second species after 0, 3, 5, or 7 days; ii) direct extrinsic competition, where both species were tested in arenas with simultaneous introductions, or iii) where half of the host egg mass had already been parasitized by the other species. Both Trissolcus species were able to parasitize H. halys eggs already parasitized by the other species. However, the female of the first-arriving species always produced more progeny. Nevertheless, when simultaneously releasing females in the arena, T. mitsukurii was the more aggressive competitor and spent more time defending host egg masses than T. japonicus. Based on our results, for biological control of H. halys a single-species release appears to be the best strategy. Indeed, the multiparasitism displayed by both species under laboratory conditions might also result in wasted searching time and energy and a reduced reproductive potential in the field.

Update on the fight against Halyomorpha halys with an adventive population of Trissolcus japonicus in New Jersey, USA

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Abstract: Unintended border crossing events by insects raise major concerns, but in some rare cases could speed up the use of a biological control agent to manage invasive insect crop pests. In 2014, an adventive field population of Trissolcus japonicus (Ashmead), an Asian egg parasitoid of the invasive Asian brown marmorated stink bug (BMSB), Halyomorpha halys (Stål) appeared in the USA in Maryland. Populations of T. japonicus have been recorded across the USA, Canada, Switzerland and Italy. Prior to its first detection outside its native range T. japonicus was evaluated in quarantine facilities and extensive studies were conducted to evaluate potential non target effects.

Our work, focused on combining monitoring of BMSB and T. japonicus distribution in various crops across New Jersey for two years and conducting laboratory host range testing (choice/no-choice) on native Pentatomidae. Finally, we supported the national effort of redistribution of the adventive population of T. japonicus across the USA by conducting a propagule pressure experiment in a peach/apple orchard or soybean field.

As expected, the New Jersey T. Japonicus population appears to be more of an oligophagous egg parasitoid with a preference towards BMSB. Parasitism rate of BMSB is around 80% and can be achieved in 1 hour in laboratory conditions. Longer exposure periods do not result in higher parasitism rates. In the field, sentinel BMSB egg masses were exposed to parasitism for one day on various host plants. While low numbers of egg masses were parasitized, various parasitoids were collected and parasitism rates were acceptable. BMSB and T. japonicus field populations were also closely linked to the insect control strategy used at the site and the surrounding habitat.

Entomopathogenic Nematodes: Recent advances in genomic studies

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Abstract: Entomopathogenic Nematodes (EPN) have been used for biological control of insects in the past three decades. However, their expansion and intensification of use is still partial due to some limitation in their incompatibility with environmental conditions as well as relatively short shelf live in storage and transportation. One of the main avenues to enhance EPN performance as biocontrol agents is to use genetic approach for improvement their environmental tolerance, storage survival and efficacy.

Several research teams, worldwide, are utilizing advanced molecular and genetic techniques to explore the genetic foundation of key mechanisms in EPN. That includes transcriptomic and proteomic approaches to identify potential virulence factors produced by the EPN, genomics of longevity and storage survival of EPN infective juveniles, molecular basis of EPN host seeking behavior as well as identification of key survival genes among natural populations.

In the presentation, the recent studies related to these topics and some suggestions for future challenges will be given.

Genetic diversity of non-retroviral RNA virus integrations in the genome of Aedes aegypti mosquitoes

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Abstract: The yellow fever mosquito, Aedes aegypti, is the primary vector of arboviruses, such as yellow fever, dengue, chikungunya, and Zika viruses, that have major impacts on human health. The intimate interactions among viruses and vectors lead to multiple levels of coevolution. Genomic integrations, complete copies or fragments of the virus genetic material that become incorporated into the vector genome, are one way in which viruses can influence their vector. Viral genome integrations are known to be widespread in insects and recent studies have shown that they are present in Ae. aegypti mosquitoes. Characterization of these non-retroviral integrations in a limited number of collections and cell lines indicates that they are predominantly related to insect-specific RNA viruses. We are conducting a screen of 230 Ae. aegypti genomes from across the species distribution to understand the extent and diversity of non-retroviral integrations in this mosquito and shed light into their biogenesis, function, and potential role in disease transmission. We present the results of this survey and discuss the implications of our findings for vector control

Using Selection Analysis to Investigate Gall Induction in Cynipid Wasps

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Abstract: Gall wasps (Hymenoptera: Cynipidae) induce complex galls on oaks, roses and other plants, but the mechanism of gall induction is still unknown. Here we take a comparative genomic approach to revealing the genetic basis of gall induction. We compared the genomes of gall wasps that are capable of different levels of host manipulation to identify genomic changes associated with the evolution of gall induction. We used a novel Bayesian selection analysis, which accounts for branch-specific and gene-specific selection effects, to search for signatures of selection in thousands of single-copy orthologous genes shared by Cynipid species. We then used gene set enrichment analysis to determine which biological process are more strongly associated with gall making.

Spectrum of pests associated with Oyster Mushroom (Pleurotus ostreatus) in Western Kenya and their management

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Abstract: Oyster mushroom is a major source of food and income in western Kenya. The production of oyster mushroom in this region has been hampered by arthropod pests that cause serious production losses in terms of quality and quantity. Development of an efficient pest control measure is based on the identification of pests infesting oyster mushroom in this region. This study aimed at identifying arthropod pests of oyster mushroom in western Kenya and developing an Integrated Pest Management (IPM) strategy to manage the pests. Oyster mushroom Pleurotus ostreatus was established at three sites: on-station, old and new mushroom farm sites. Pests were sampled weekly and identified using taxonomic keys at National Museums of Kenya. Various pest management options locally available to farmers were tested against the mushroom pests. Mites Pygmephorus spp. (Acaridae) and dipterans Megaselia scalaris (Phoridae), Bradysia spp. (Sciaridae), Culicoides spp. (Ceratopogonidae) and Anatrichus spp. (Chloropidae) were identified. All the other pests except Bradysia spp. were reported at the three sites through the three seasons. The incidences of all these pests were reported only during the incubation phase of oyster mushroom. Incidence of M. scalaris was 42% of the total count of the four pests that were sampled followed by Culicoides spp. at 33% with that of Pygmephorus spp. being 17% while that of Anatrichus spp. being 8%. Pygmephorus spp. was vectored by M. scalaris. These pests caused both direct and indirect damage on oyster mushroom. The old mushroom farm reported highest number of these pests. The integrated pest management method consisting of Nylon net + potted T. minuta + High spawn rate had a significantly lower mean number of pests compared to the individual methods. Therefore to effectively manage oyster mushroom pests, one would go the integrated way than using single methods.

In the front line against regulated pests: the work plan of the EURL for insects and mites (Montpellier) during the next two years

Authors: Goldarazena Arturo[1], Taddei Andrea[2], Reynaud Philippe[2], Mouttet Raphaelle[1] and Balmes Valerie[1], [1]EURL, France, [2]European Union Reference Laboratory for insects and mites, France

Abstract: National Reference Laboratories (NRLs) are specialist laboratories responsible for maintaining EU-wide standards for the routine testing of feed, food and plant and animal health. They provide advice and support on methods for official control testing, ensuring the delivery of risk-based and proportionate food enforcement to protect consumers. In the area of Plant Health, NRLs performed thousands of insects and mites identifications every year from samples coming from official interceptions at European ports and airports or from field surveys to confirm the absence of regulated or invasive arthropods on plant commodities. The results of these tests influence important decisions, i.e. refusal, destruction, return of commodities or onsite measures like crops destructions. This requires harmonization, validation, standardization of test methods and coordination of the network of NRLs to ensure accurate identification. In this poster, we describe the activities that will be developed at the European Reference Laboratory of insects and mites (EURL) (Montpellier - France) during the next two years. It will carry out a Proficiency Test on the identification of Spodoptera frugiperda J.E. Smith, based on morphological analysis of the male genitalia structure during December 2019-January 2020. In spring of 2020 it will carry out a proficiency test on the identification of Thrips palmi Karny based on morphological analysis of the adult female. The laboratory will organize a workshop for all the National Reference Laboratories with trainings about quarantine pests. Finally, at the end of 2020, we will organize a proficiency tests on the diagnosis of Popillia japonica Newman based on morphological analysis of the adult. At the same time, we are developing a project to improve NRLs diagnosis capacities of neotropical species of Epitrix that threaten European potato crops. Improving identification capacities of NRLs is a way for the European Union to better anticipate future insect and mite invasions. The EURL is now developing a website that will be for sure an important tool of communication in the next future for all the NRLs.

A new laboratory of entomology is born in Europe to defend us from the invasive plant pests

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Abstract: National Reference Laboratories (NRLs) performed thousands of insects and mites identifications every year from samples coming from official interceptions at European ports and airports or from field surveys to confirm the absence of regulated or invasive arthropods on plant commodities. The results of these tests influence important decisions, i.e. refusal, destruction, return of commodities or onsite measures like crops destructions. This requires harmonization, validation, standardization of test methods and coordination of the network of NRLs to ensure accurate identification. To fulfil this important task, a new European Reference Laboratory (EURL) for Insects and Mites was designated by the European Commission in 2019 (Regulation (EU) 2019/530 of 27 March 2019) as a consortium between the Entomology and Invasive Plants Unit at ANSES Plant Health Laboratory (Montpellier, France) and the Department for Molecular Diagnostics of Plant Diseases at AGES (Vienna, Austria). The EURL work program has the following tasks: (1) to ensure availability and use of high quality methods and to enable high quality performance by the NRL (providing reference methods and reference materials; organizing inter-laboratory comparative testing or proficiency tests; cooperating with NRLs and Commission in all subjects of detection of invasive plant pests); (2) to provide scientific and technical assistance to NRLs (coordinating practical arrangements necessary to apply new methods of laboratory analysis; conducting training courses for NRL staff; providing information on relevant national, Union and international research activities); (3) to provide scientific and technical assistance to the European Commission and other organizations; (4) Reinforce the reference collections and the molecular techniques of the NRLs to facilitate quick detection of quarantine pests. Through this new framework, testing results shall therefore become more reliable and comparable throughout the European Union.

The vagaries of biocontrol of exotic invasive species on exotic plant species in a non-evolved ecosystem; a study of the unexpected from New Zealand

Authors: Goldson Stephen, Bio-Proprotection Research Centre, Lincoln AgResearch, Lincoln, New Zealand

Abstract: New Zealand's intensive pastures, comprised almost entirely introduced Lolium L. and Trifolium L. species are arguably the most productive intensive grazing-lands in the world. However, these areas, because of their inherent lack of species diversity, present very little biotic resistance to destructive invasive pest species. There is a native natural enemy fauna in New Zealand that has evolved over millions of years of geographical isolation, but, it remains confined to indigenous ecosystem remnants. It therefore plays a minimal role in creating biotic resistance in the exotic pastures.

Of New Zealand's pasture pests, three of the most damaging are the Argentine stem weevil (Listronotus bonariensis), the clover root weevil (Sitona obsoletus) and the lucerne weevil (Sitona discoideus). These weevil species have been successfully suppressed by three different introduced koinobiontic parasitoids, Microctonus hyperodae, Microctonus aethiopoides (Irish strain) and Microctonus aethiopoides (Moroccan strain) respectively. Such a biological control result is rare with the chances of success being calculated at 1:1000 based on historical biological control records. Arguably the parasitoids themselves have been highly effective because they, like many of the exotic pest species, have benefited from enemy release in a simplified ecosystem. At the same time the absence of evolved complexity in New Zealand's sown-pastures has probably contributed to unimpeded parasitism of the host species.

Such parasitism has been so intense that, very unusually, the Argentine stem weevil has now evolved resistance to its parthenogenetic parasitoid Microctonus hyperodae. The high selection pressure has combined with the limited (if any) ability of the parasitoid to adapt compared to the sexually-reproducing weevil. Indications are now that the mechanism behind this Argentine stem weevil resistance is based on adaptation that results in enhanced evasion of the parasitoid. That the response is more strongly expressed in weevil populations collected from the warmer parts of New Zealand points to the parasitoid selection pressure being higher in these regions.

Olfactory signalling between flowers and bumblebees

Authors: Gomez Carolina[1], Muktar Iman[1], Schmitt Thomas[2] and Riabinina Olena[1], [1]Durham University, [2]University of Würzburg, Germany

Abstract: Plant-pollinator interactions are complex processes driven by diverse signals such as floral scent (Raguso, 2008). Bumblebees are important pollinators who are confronted with an enormous diversity of floral cues, which they use to make foraging choices (Mertes et al., 2021). Bumblebees are normally thought of as generalist pollinators (Goulson, 2003), although the specific floral and olfactory preferences across bumblebee species are not well known.

In this project we investigate whether bumblebees use smells of flowers to make their foraging decisions, and whether flower smell preferences are species-specific. We conducted collections of bumblebees in summer 2021 in Durham, UK, taking note of the flowers they were found on. Next, we collected floral volatiles using standard traps, and analysed them via gas chromatography-mass spectrometry. This approach allowed us to identify key volatiles of the flowers that were or were not visited by 10 sympatric bumblebee species. We also started to establish the patterns of floral preferences for our species of interest. The behavioural responses of the bumblebees to floral volatiles will be ascertained via dual- or multiple-choice assay with real or artificial flowers.

This work will contribute and expand the knowledge about sensory ecology of bumblebees and their important role as pollinators.

Carrion-feeding blowflies (Diptera, Calliphoridae, and Mesembrinellidae) as an indicator of the anthropogenic disturbance on the landscape in Colombia

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Abstract: Some insect taxa had been recognized as indicators of anthropogenic disturbance in tropical environments. However, studies at different disturbance levels, spatial and temporal scales are required for their practical usefulness. Carrion-feeding flies (Diptera, Calyptratae) were suggested as a restoration and conservation management bioindicator in the tropical rain forest, and also an indicator of the anthropic impact on the Andean landscape. Thirty localities were assessed, from a pristine tropical rain forest to a highly dense urban settlement within all Colombian natural regions. Each locality was categorized and ranked according to the values deducted on the Human Influence Index (HII) raster dataset. A data set (presence/absence) of the carrion feeding blowflies ensembles and the related blowfly fauna is offered as a critical supply to use this taxon as a practical parameter to assess the degree of anthropic disturbance of the landscape involved. Synanthropic preference and ecological category are documented. Finally, a checklist and a discussion of potential key species pointed to a particular landscape conservation status are treated. The study of carrion-feeding flies' ensembles at a low budget will quickly assess tropical landscape conservation status, monitoring, and restoration stage. We claim this taxon be included in Colombian environmental impacts assessments.

Bio-geography, species diversity, and host-specificity of the gall midge Mycodiplosis (Diptera, Cecidomyiidae) feeding on rust fungi (Basidiomycota, Pucciniales)

Authors: Gomez-Zapata Paula[2] and Aime M. Catherine[1], [2]Purdue University, United States, [1]Purdue University

Abstract: Rust fungi are plant pathogens that cause diseases on economically important crops and threaten native species with extinction in natural ecosystems. Although fungicides are the most common option to control rust fungi, their overuse causes severe damage to the environment and selects more aggressive rust strains. Biocontrol is an attractive alternative method for rust disease management. The gall midge, Mycodiplosis, is a promising biocontrol agent of rusts whose larval stage feeds on the spores of several rust species. However, phylogenetics, ecological information on Mycodiplosis and its relationship with rust fungi are scarce. In addition, the species identification of Mycodiplosis is based only on the morphology of adult males, which are rarely found on rusts. This study focuses on the biogeography, species diversity, and host-specificity of Mycodiplosis to rusts worldwide. We screened 6,000 rust collections from the Arthur Fungarium for the presence of Mycodiplosis, including major crops such as coffee, corn, wheat, willows, and species in the Myrtaceae family. Larval species were identified using morphological and molecular data and confirmed with live rearing of adults where possible. These data will provide baseline information to identify fly larvae feeding on rusts and their potential as a biocontrol agent for rust diseases

Bio-geography, species diversity, and host-specificity of the fungivorous insect Mycodiplosis (Diptera, Cecidomyiidae) as a natural enemy of rust fungi (Basidiomycota, Pucciniales)

Authors: Gomez-Zapata Paula[2] and Catherine Aime M.[1], [2]Purdue University, United States, [1]Purdue University Department of Botany and Plant Pathology, United States

Abstract: Rust fungi are plant pathogens that cause diseases on economically important crops worldwide. In addition, they threaten plant species with extinction and disrupt natural ecosystems. Fungicides are the most common option to control rust fungi when disease-resistant cultivars are unavailable. However, the overuse of fungicides is causing severe damage to the environment, and it is selecting new resistant rust strains to the fungicides. Biocontrol is an attractive alternative method for rust disease management. This method uses natural enemies to control the infection and prevent disease dispersion. The fungivorous insect, Mycodiplosis, is a natural enemy of rusts whose larval stage feeds on the spores of several rust species without causing any damage to the plant. Although this insect has potential as a biocontrol agent of rust fungi, we need to understand first how specific they are to the rust species and their distribution patterns before using them in open field essays. This study focuses on the biogeography, species diversity, and host-specificity of members of Mycodiplosis to rust fungi. We screened 6,000 rust-infected plant samples collected worldwide and looked for the presence of Mycodiplosis larvae. We identified larval species using morphological and molecular data. We also analyzed larval distribution patterns through heat maps and studied their preference for rust species through multi-locus phylogenetic analyses. This study covers the most representative sampling data of Mycodiplosis species feeding on rust fungi worldwide. It also provides the baseline for characterization studies of Mycodiplosis as a biocontrol agent of rust diseases.

Evolutionary history and species distribution of New Caledonian Taophila (Lapita) Gómez-Zurita et Cardoso (Coleoptera: Chrysomelidae) suggest their association with habitat transformations

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Abstract: New Caledonia is one of the most important biodiversity hotspots in the world, characterized by a high number of species often presenting a peculiar pattern of microendemicity possibly conditioned by the geological and the climatic history of the archipelago. The leaf beetle subfamily Eumolpinae is coherent with this scenario, showing a remarkable diversity, higher than previously suspected, and the species seem to have small ranges. Here, we put the focus on the diversity and evolutionary history of subgenus Lapita Gómez-Zurita et Cardoso belonging to the endemic genus Taophila Heller through a phylogenetic framework using the mitochondrial markers cox1 and rrnS. Only three species of the subgenus were known, but we increased the number up to eleven based on the analysis of morphological and genetic differences. Distribution data for these species is consistent with a pattern of microendemicity exclusively within the so-called New Caledonian rainforest ecoregion, with most species being allopatric, with the exception of some sympatric and parapatric species in the central part of Grande Terre. The mitochondrial phylogeny of Lapita shows that this linage evolved during the Miocene, originating in the northern part of the island about 30-17 Mya, and immediately separating in two northern and southern lineages possibly following a vicariant or a dispersal model. The expansion of the southern lineage some 15-6 Ma ago into an area with different geological origin and soil composition, and consequently with different plant communities, possibly triggered subsequent diversification. It is possible that climatic changes during the Pliocene and Pleistocene changed the distributions of biomes and evolutionary lineages, leading to secondary contacts of some of these lineages in the central region of the island. This scenario is consistent with hypotheses of the evolution of forest biomes in the major island in relation to the geological and environmental transformations occurred in the upper Cenozoic, which may have driven the evolutionary history of this group.

Stowaways in the Matahourua or the long transoceanic trip of the Eumolpini (Coleoptera: Chrysomelidae, Eumolpinae) to reach New Zealand

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Abstract: The Eumolpinae are a species-rich group of leaf beetles in the tropics, well represented in Australia and SE Asia, that colonized most of the western Pacific archipelagos all the way through to Samoa. Eumolpinae are particularly diverse in old tropical archipelagos such New Caledonia (NC) and Fiji, where they radiated locally and, supposedly, from a reduced number of transoceanic arrivals of Eumolpini in the case of NC and Typophorini in Fiji. However, they are also present in temperate western Pacific islands, including New Zealand (NZ), where they have a reduced number of species, but of highly original groups, which were classified as five essentially endemic genera of Eumolpini. Here, we aim at shedding some light on the origins of this original fauna by investigating its phylogenetic relationships with representatives of neighbouring faunas, including Australia, NC and Lord Howe Island (LH). Several hypotheses have been proposed for the origin of the biota of NZ, including palaeoendemic and recent origins, and the latter from several different sources, typically from Australia because of geographic proximity, but also from other regions. In this respect, it is risky to make generalizations or predictions about the origins of specific NZ groups, and answering the question about these origins needs analyses on a taxon-by-taxon basis. For the study of NZ Eumolpini, we obtained sequences of two mtDNA markers (cox1, rrnS) and three protein-coding single-copy nuclear genes (Wnt, CPS, PABP1) for a representative sample of this tribe from the New World, SE Asia, Australia, LH, NC, and three out of five genera of Eumolpini from NZ. We investigated their phylogenetic relationships using maximum likelihood and their timing of separation using molecular clock approaches in a Bayesian framework. The most remarkable discoveries from these analyses, include: (1) a highly supported (NC+NZ+LH) clade corresponding to current emerged lands of the lost continent of Zealandia, and sister to the remaining Eumolpini; (2) polyphyly of NZ, with each genus nested within a different group of NC Eumolpini, thus representing unrelated origins for each NZ genus; and (3) independent origins of NZ genera occurring during the Oligocene, within a time interval between 15-30 Ma, after the separation of NC and NZ with the opening of the New Caledonian Basin, thus requiring separate transoceanic dispersal events for each genus. Eumolpinae in New Zealand enlarge the pool of recent endemic lineages that refute the Gondwanan hallmark of its original biota, strengthen the relevance of Zealandia as a biogeographic unit, and provide with interesting cases of long-distance dispersal in the Western Pacific. But at the same time, the study underlines the need to consolidate these ideas by expanding it to cover as much of the biodiversity of Eumolpini in NZ but also in Australia and other nearby islands, not sampled here, including Norfolk Island, Tasmania, Fiji or the Kermadec Islands.

Benefit and risk of combining an entomopathogenic virus with parasitoids to control Tuta absoluta

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Abstract: The combination of different biocontrol agents, in particular of micro- and macro-organisms, can contribute to new and sustainable pest control approaches. Tuta absoluta (Meyrick) (Lepidoptera: Gelechiidae) is one of the most destructive pests of solanaceous crops, and an emerging management strategy consists of biological control using the hymenopteran parasitoids Necremnus tutae (Reuter) (Eulophidae) or Dolichogenidea gelechiidivoris Marsch (Braconidae), however with limited efficacy. We evaluated the risks and benefits of combining the parasitoids with the Phthorimaea operculella granulovirus (PhopGV, Baculoviridae) infecting T. absoluta larvae. Due to their host specificity, potential non-target effects of baculoviruses on parasitoids should not result directly from infection. However, impacts can result from the viral infection killing the host before the parasitoid has completed its development, or from overlapping resource requirements of parasitoid immatures and the virus. Benefits arise in particular, if parasitoids discriminate between healthy and infected host, as they can minimize negative interference and control those hosts that have escaped the virus. We evaluated the interaction between the baculovirus and the koinobiont endoparasitoid D. gelichiidivoris and the idiobiont ectoparasitoid N. tutae in the laboratory. We assessed whether ovipositing females discriminate against virus-infected hosts and examined the outcome of within-host competition between parasitoids and virus. Then we evaluated the efficacy of the combined use of the baculovirus with the parasitoid N. tutae in greenhouse experiments. Female D. gelichiidivoris were able to discriminate against virus-infected hosts, whereas N. tutae were not. Depending on the species and the time after virus infection, we found reduced size, emergence, longevity and a longer development time, but in general, the virus had a low impact on parasitoid offspring. Finally, when compared to N. tutae and the baculovirus used solely, their combination improved significantly the control of the pest in the greenhouses. Therefore, both parasitoids seem to be compatible with the baculovirus to control T. absoluta.

Elucidating mechanisms that promote or deter conservation biological control

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Abstract: Although it is widely understood that the dynamic interactions among natural enemies, pests and plants govern conservation biological control, the underpinning mechanisms of such interactions remain largely underexplored. Searching for the underlying mechanisms of such interactions is paramount to gain a new foothold in conservation biological control. Nonetheless, the outcome of these interactions may be context-specific, and their complexity will likely increase with the number of species involved. Thus, carrying out multiple manipulative field experiments and drawing on insightful connections among the variables assessed is essential. For biological control practitioners and researchers, it is specifically important to learn how habitat manipulations in agricultural settings can affect those trophic interactions, and ultimately the control of arthropod pests. In this context, in a series of field experiments we have been investigating the mechanisms that play out in companion planting settings, and how they impact biological control. Specifically, we have examined how companion plantings in a brassica system affect nocturnal vs. diurnal natural enemies, intraguild predation, the numerical response from natural enemies, the attraction of distant natural enemies, as well as their potential to favor key pests. We have found that bearing flowers is not a prerequisite for companion plants to promote conservation biological control. Additionally, companion plants will affect distinct groups of natural enemies in different manners, which may either promote or impair biological control. Lastly, the results suggest that companion plants may be more important for sheltering generalist natural enemies, which tend to arrive early in the growing season as well as to perform better in a more diversified agroecosystem.

The role of natural transposable element insertions in environmental adaptation

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Abstract: Transposable elements are ubiquitous, abundant, and active components of genomes. Although most of the mutations caused by transposable elements are likely deleterious or neutral, adaptive mutations have also been repeatedly identified across species. Drosophila melanogaster is an excellent model species to quantify the role of transposable elements in environmental adaptation as it has recently colonized very distinct habitats. We have generated 32 Drosophila melanogaster reference genomes using long-read sequencing of flies collected in arid, cold and temperate environments. We have discovered and annotated transposable elements in these genomes using a combination of homology-based and de novo approaches. The in depth annotation of these genomes has allowed us to discover three new transposable element families in this well-studied species. We have also generated RNA-seq data for 25 of these genomes that will allow us to elucidate the role of transposable elements in expression quantitative trait loci variation. We are currently investigating the role that the identified transposable elements play in desiccation, oxidative and heavy-metal stress resistance. Our results will allow us to quantify the role of transposable elements in environmental adaptation and to generate testable hypothesis for follow-up functional validation studies.

A novel automated surveillance system which is capable to remote classify target mosquitoes by specie, sex and age.

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Abstract: Mosquitoes are considered one of the deadliest animals worldwide regarding their capacity to transmit several infectious diseases such as dengue, malaria, yellow fever, chikungunya, Zika, West Nile fever and Rift Valley Fever. Entomological surveillance of mosquito populations has been carried out, traditionally, through larval counting, ovitraps and sticky traps. Such methods, however, are notoriously costly, depend on entomology experts and are very time-consuming. These costs can significantly be reduced with remote sensing devices providing real time data effortless.

Here we present VECTRACK, a H2020 European project whose main output is the creation and continued development of an automated optoelectronic sensor which is already capable to distinguish between the specie, sex and age of mosquitoes with promising levels of accuracy.

A total of 5000 tests have been performed in order to train and validate the sensor through deep learning techniques. Three target species (Aedes aegypti, Aedes albopictus and Culex pipiens) have been tested for both sexes and three age categories. Major accuracy levels were obtained for genus and sex classification. Differentiation of species from the same genus was challenging but further samples will be tested to increase this accuracy. Age classification ranged between acceptable levels of accuracy, but it is improvable as well.

Currently, more species and biological conditions are being considered in laboratory experiments in order to increase the applicability of the system in field conditions. The overall final objective of VECTRACK is to provide the first transnational and automated surveillance system for mosquito control, a long-sought objective of public health agencies.

Hunting with catapults: the predatory strike of the dragonfly larva

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Abstract: Odonata larvae are often key predators in their aquatic biotopes. They catch their prey with a unique and highly efficient apparatus, the so-called prehensile labial mask, a strongly modified and extensible mouthpart. However, the main driving mechanism and underpinning biomechanics of this movement remained questionable.

We used various techniques, such as micro computed tomography (µCT), scanning electron microscopy (SEM), confocal laser scanning microscopy (CLSM) and high-speed videography combined with manipulation experiments to gain insights into the biomechanics of the predatory strike of Odonata larvae.

Our results suggest a catapult system as the main driving mechanism for this prey-capturing process. We could identify two resilin-dominated sclerites (T-rod and premental sclerite) and two accessory muscles 0la5 and 0hy7 responsible for the mechanism of fast extension. Here the resilin-containing structure is strained by slow muscle action and thereby energy is stored. To allow for this energy storage in spring-loaded catapult systems, a complex latch mechanism and a trigger muscle (0la15) are present.

Furthermore, the hypothesis that hydraulic pressure is the driving force of the striking process, as suggested by former investigations, could be refuted by manipulation experiments. We suggest that hydraulic pressure is most likely used for recoil-preventing jet propulsion during the prey capturing process. Finally, we provide a proof of concept by a 3D-printed robotic system inspired by the odonate prehensile mask.

Sexual dimorphism in morphology of the raptorial forelegs and the dynamics of the predatory strike in Hierodula majuscula (Insecta: Mantodea)

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Abstract: Raptorial forelegs are prey capturing devices, which evolved convergently in different groups of insects. These predatory appendages are best known and investigated in praying mantises (Insecta: Mantodea), a group that shows strong morphological adaptations towards the lifestyle of an ambush predator. Sexual dimorphism occurs in many species of mantises, causing a difference in size and appearance between males and females. Although morphology and behaviour of adult Mantodea were investigated in the past, yet information about sexual dimorphism in internal and external morphology of the raptorial forelegs, as well as the dynamics of the predatory strike is scarce. We combined morphological methods (micro-computed tomography (µCT) and dissection) with force measurements, to compare male and female individuals throughout the postembryonic development until adulthood. Here, we show a detailed description of the extrinsic and intrinsic musculature of the raptorial forelegs, of male and female Hierodula majuscula (Mantidae) – a species showing noticeable sexual dimorphism only in adult stage. Using this data in combination with force measurements, we analyzed the scaling effect of muscle growth against force output throughout the postembryonic development. We supplemented our results with kinematic information, obtained from high-speed-video analysis, concerning duration, velocity and speed of the different phases of the predatory strike. By highlighting the musculature of the raptorial forelegs, in combination with kinetic and kinematic analyses, our work serves as a starting point for further investigations of the predatory strike, throughout different groups of mantises, differing in their lifestyle, prey preference and therefore eco-morphology.

Numerical flow simulations reveal the eco-morphological adaptations of the prehensile labial masks of dragonfly larvae (Insecta: Odonata)

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Abstract: The larvae of dragonflies and damselflies capture prey underwater using the prehensile labial mask, a fast-moving raptorial appendage. Within dragonflies (Anisoptera) two general shapes of the prehensile labial mask have evolved, differing in their distal segment, which is either flat and slender or concave. While the former (Anax) is a pure grasping device, the latter (Sympetrum) is also capable of scooping up smaller prey items, keeping them inside the cavity by arrays of setae. Fast motion in water usually causes substantial amounts of drag, yet the hydrodynamic properties of these structures have not been assessed previously. Based on high-speed footage and computer tomographic data (µCT), we use computational fluid dynamics (CFD) simulations of the prehensile labial mask to investigate how the different shape of the prehensile labial masks of two dragonfly groups (Anax and Sympetrum) impacts their function. The results suggest that both prehensile labial masks are highly streamlined and generate a low-pressure zone above the distal segment, which is even more pronounced in Sympetrum. We assume that this could be an effect analogous to compensatory suction feeding, as it is known for other aquatic predators. This may prevent the formation of a pressure wave in front of the grasping device, that could displace the prey. Our study provides first insights into the hydrodynamics of the predatory strike in dragonfly larvae and how the eco-morphology of the different shapes of prehensile labial masks impact their functionality.

Anchoring of whitefly eggs on plant leaves

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Abstract: Whiteflies attach their eggs to plants by implanting the egg pedicel (hollow stem) into the fluid-filled epidermis cells of the underside of leaves. While the egg is kept in the gaseous leaf boundary layer, its pedicel slips into a secretion-filled hole, prepared by the ovipositor. During the insertion, the pedicel rotates and deforms, increasing frictional interactions and interlocking with the plant substrate. After implantation, the basal pedicel is clamped between tensile-loaded plant cell wall edges; the distal one is surrounded by the egg secretion released to the fluid plant intracellular matrix. Thus, it works like a wall plug embedded in sealing cement, presenting a smart and strong interconnection. How strong whitefly eggs adhere to plant leaves was comparatively studied with four cultivars of cut roses. To detach the egg from lower young rose leaves, a maximum pull-off force of 5.4 mN was measured, corresponding to maximum 941 times the egg mass and maximum adhesive strength of 12.2 MPa (Voigt et al. 2019). Leaf structural features had no significant impact on egg pull-off forces. A major effect of leaf turgor pressure and swelling of the probably proteinaceous, composite fluid-fibrous egg secretion surrounding the whitefly egg stem is assumed to facilitate the firm bond between egg and plant epidermis by a combination of form closure, friction locking, and adhesive bond by a composite material in the contact region.

Reference:
Voigt D, Schrameyer K, Kiefer J, Zebitz CPW, Gorb, S (2019) Anchoring of greenhouse whitefly eggs on different rose cultivars. Arthropod-Plant Interact 13: 335-348.

Morphological, compositional and mechanical properties of the semi-lunar process (SLP) and their role in power amplification of locust locomotion

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Abstract: Power amplification is one of critical mechanisms for some insects to achieve rapid locomotion like jumping and kicking. As one of typical insects with power amplification, locusts have an impressive jumping and kicking performance that are suggested to be resulted from the storage and release of elastic strain energy in the semi-lunar processes (SLP) cuticle of their femorotibial joints. It is well-known that the amount of elastic strain energy depends on the mechanical properties of the materials. However, the power amplification mechanism of the SLP cuticles remains unclear. In this study adult locusts (Locusta migratoria manilensis) were investigated using some advanced micro-scale imaging techniques, mechanical tests and numerical simulations to reveal the microstructure, material composition and mechanical properties of the SLP cuticle, as well as the power amplification mechanism of the SLP for jumping and kicking. Following results were obtained. 1) The locust femur reveals pronounced stress relaxation behavior with evident displacement-force shift and weak fatigue resistance without cuticle healing. 2) The SLP cuticle consists of five main portions with di?erent microstructural features, material compositions, and mechanical properties. The mechanical properties of these five components are all transversely isotropic and strongly depend on their water contents. 3) The two parts of the core region of the SLP cuticle (i.e., dorsal-core and ventral-core parts) likely make significant contributions to its outstanding strain energy-storage ability. 4) Both of these two key portions exhibit strain rate-sensitive elastic modulus regardless of water content, meaning that the efficiency of elastic energy storage is only 51%-70% in the case of low strain rate. These findings deepen our understanding of the superior power amplification mechanism of locust locomotion and further provide valuable knowledge for design optimization of power amplification apparatus as well as bio-inspired jumping robots.

The stick insect attachment system: functional morphology and the evolution of attachment microstructures

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Abstract: Insects have developed a broad array of specialized structures on their feet to properly attach to the vast diversity of natural surfaces. Stick and leaf insects (Phasmatodea) in particular achieve attachment to the substrate by using two different types of attachment pads: the tarsal euplantulae and pretarsal arolium. The euplantulae are cuticular structures capable of mechanical adaptation to the substrate profile and by this generation of the required attachment. The rapid adaptive radiation of stick and leaf insects caused various specializations to different environments including adaptations of the attachment system. This resulted in a wide range of microscopical functional surface microstructures on the attachment pads, especially on the euplantulae. Our investigation of 116 representative species, covering the major clades recognized in phasmids, their different ecological specializations and the entire distributional range of phasmids, yielded 12 different types of attachment microstructures (AMS) on their attachment pads. To access the phylogenetic context of the AMS distribution, we inferred the phylogeny of Phasmatodea based on molecular data and discussed the pattering of AMS in light of the phylogenetic relationships within Phasmatodea. The distribution of the AMS among phasmids suggests a high degree of independent origins of the same types of AMS, which can be explained by their high dependence of the ecological niche. An ancestral character state analysis yielded smooth AMS as the probable ancestral state. The AMS origin and their developmental background, however, remain largely unknown. To approach the mechanisms leading to different AMS, we applied the mathematical reaction-diffusion-model by Alan Turing. Using the model describing pattern formation in nature by self-organization of two chemical morphogens, we were able to simulate eight principal patterns of the phasmid AMS of phasmids and their transitions. The ease of the transitions between different AMS suggests their remarkable adaptive potential to different ecological contexts and furthermore explains the high degree of convergences between different AMS. We additionally discuss the functional morphology of different microstructures and their assumed advantages in the context of the ecological background of species studied.

Biomechanics of egg adhesion to artificial and natural substrates in Propylea quatuordecimpunctata and Harmonia axyridis (Coleoptera, Coccinellidae)

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Abstract: For predatory insects, such as Coccinellidae, the foraging habitat is predominantly one or several host plant species. The ability to attach firmly to different plant surfaces during all developmental stages is a fundamental prerequisite for these predators. For this reason, the physical and chemical features of plant surfaces can greatly affect egg adhesive performance of predatory insects that face all the mechanical barriers developed by plants against herbivore insects. In this regard, the aim of the present investigation is to clarify the biomechanics of egg adhesion in two common ladybird species, Propylea quatuordecimpunctata and Harmonia axyridis (Coleoptera, Coccinellidae) on substrates with different chemical and mechanical features. P. quatuordecimpunctata is typically mass reared and used as biological control agent, while H. axyridis is considered an invasive species. Using a traction force experiment set up, we tested the egg adhesion to artificial substrates having different wettability (hydrophilic, hydrophobic) and roughness as well as to natural surfaces (plant leaves) with different morphology (smooth, hairy, with cuticular folds, with 3D wax projections). We used characterized artificial and natural surfaces under cryo-SEM and measured their surface free energy. We studied the egg chorion and the glue in TEM and estimated the glue stiffness with indentation measurements. H. axyridis eggs adhere to the different natural and artificial surfaces strongler than P. quatuordecimpunctata . On artificial surfaces, the lower adhesion is shown on the higher roughness and on hydrophobic surfaces in both species. On natural surfaces, the egg glue has to cope with plant mechanical barriers such as trichomes and waxes, which heavily impair egg adhesion to the substrate in both species. The glue is very stiff, comparable with cuticle stiffness showing a Young's modulus of 0.82±0.23 GPa. The results of the present research (1) shed light on the mechanical ecology of evolutionary successfull group of coccinellids ; (2) may aid in development of suitable substrates for coccinellid egg laying, in order to improve the mass rearing technique of species used in biological control; (3) may aid in developing new biomimetic adhesive materials.

Genetic effects of global warming in populations of malaria mosquitoes in the taiga zone of Eurasia

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Abstract: Global warming has led to a change in the ranges of sibling species of Anopheles mosquitoes (Diptera, Culicidae): An. beklemishevi, An. daciae, An. maculipennis, An. messeae. Mosquito An. beklemishevi was driven out of a number of breeding sites in the southern taiga zone. The southern part of the area of this species is currently fragmented. Refugiums of An. beklemishevi are preserved in the subtaiga zone (in the Meshchera lowland, in the swampy territory of the Moscow and Ryazan regions). Mosquito An. daciae advanced north and entered the northern taiga zone in the south of the Komi Republic. This species is now dominant among the malaria mosquitoes of the steppe and forest-steppe zones. It has been shown that An. daciae replaces An. messeae at breeding sites in the south of Western Siberia (Tomsk region). Mosquito An. maculipennis significantly expanded its area in Europe; it spread to the northwest and northeast, to Karelia and to the Komi Republic. At the same time, this species moved east, from the Volga region to the Middle and Southern Urals, overcoming the Ural Mountains. Mosquito An. messeae became the dominant species of malaria mosquitoes in the northern taiga, along with An. beklemishevi. Chromosome composition of An. daciae / An. messeae has changed significantly over 45 years of observation. The first changes in the frequencies of chromosomal inversions were noted in the south of Western Siberia, beginning in 1985 (Gordeev, Ejov, 2004). Inversions XL0 and 2R0 first appeared in populations of the northern taiga, where they were not there before. The frequencies of these inversions increased everywhere in the southern and middle taiga. In our opinion, changes in the chromosome composition of populations are associated with an increase in average winter temperatures and with better survival of adults during diapause. We have shown that the chromosome compositions of populations of polymorphic species An. daciae / An. messeae correspond to certain landscape and climatic zones. Previously, the highest level of chromosomal polymorphism was noted in populations of the subtaiga zone. Currently, the chromosome composition of these populations has become more homogeneous, similar to the composition of steppe and forest-steppe populations. We predict further restructuring of the species composition and genetic structure of populations of malaria mosquitoes and the movement of sibling species to the north of the taiga zone, above the 65th parallel. Changes in the composition of malaria mosquitoes serve as a signal of the initial transformation of the ecosystems of the Eurasian boreal belt as a result of global warming. Global warming increases the risk of malaria recovery due to the spread of southern species of malaria mosquitoes and lengthening the season of transmission of Plasmodium parasites. The reported study was funded by Russian Science Foundation according to the research project 22-24-00183, https://rscf.ru/project/22-24-00183/.

Distribution of invasive species of mosquitoes Aedes albopictus (Skuse, 1895) and Aedes aegypti (Linnaeus, 1762) in the south of European part of Russia

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Abstract: Populations of Aedes albopictus Skuse, 1895, the main vector of a number of arbovirus infections, were first detected in the Greater Sochi region, the Black Sea coast of the Caucasus, in 2011 (Ganushkina and other, 2012). This invasive species has captured a zone of humid subtropical climate on the Black Sea coast of the Caucasus for several years. The species has already crossed the Great Caucasus Range and began to develop the temperate zone in 2017. We have determined that by 2019 Ae. albopictus advanced north to the cities of Timashevsk, Korenovsk, Kropotkin. The northern border of the range corresponds to the isohist of 550 mm per year and air humidity of 60% in the summer. The eastern border of the area passes through the cities of Armavir and Labinsk. The western border of the area passes in the region of Anapa on the Black Sea coast of the Caucasus. Ae. albopictus has advanced 60 km into the Russian Plain over the past year.

Spread of Ae. albopictus was accompanied by a sharp decrease in the number of Aedes aegypti Linnaeus, 1762. This species was re-recorded on the territory of Russia in 2001 and captured the entire zone of humid subtropical climate by 2011. A sharp decrease in the number and habitat reduction of this mosquito was noted in 2012. Ae. aegypti was recorded by us only in the city of Sochi in 2019. This mosquito was found with Ae. albopictus, however, significantly inferior to him quantitatively.. We recorded 5-7 attacking Ae. aegypti females and about 200 Ae. albopictus females in 30 minutes during activity hours. Ae. albopictus is considered a semi-synanthropic species, in contrast to the synanthropic species Ae. aegypti. However, at the beginning of the invasion in Russia Ae. albopictus was recorded exclusively in urban areas with abundant vegetation and in rural settlements. The advancement of this species into the forest zone in the Greater Sochi region, with a rise to a height of 400 m, was noted by us only in 2019. Larvae were found in fallen large leaves and rocky depressions filled with rainwater. This territory is adjacent to the points where the number of the species was maximal (over 200 attacking females in 30 minutes, when counting during activity hours) and is close in climatic parameters to the natural range of this species.

We believe that air humidity is an important limiting factor for imago of Ae. albopictus. This species prefers moist habitats shaded by vegetation. Females of Ae. albopictus is active throughout the daylight hours, with a small pessimum for two hours in the afternoon. In our opinion, dry steppe zones are a natural obstacle to the further distribution of Ae. albopictus to the west and north. Promotion Ae. albopictus in the east will be easier and faster than in the north. The appearance of Ae. albopictus in the Stavropol province, as well as on the Crimean peninsula, is a matter of time.
The reported study was funded by RFBR, project number 19-34-90192.

Foothold matters in omnivorous mirid bugs Dicyphus errans, bridging gaps and contributing to the consolidation of multitrophic networks

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Abstract: Omnivorous predatory mirid bugs Dicyphus errans Wolff and closely related species, belonging to the subfamily Bryocorinae (Heteroptera, Miridae), prefer to live on pubescent plant species, where other entomophagous insects struggle. Thus, the mirid bugs overcome structural hurdles and explore challenging niches, which let them seem to be promising predatory insects for biocontrol strategies. In context with their omnivorous mode of life, they are 'intermediate agents' of food chains, which implicates complex interactions at several trophic levels (Voigt 2005). Foothold matters in the highly complex life of omnivorous D. errans: mirid bugs' foothold increase significantly with plant trichome diameter and length (Voigt et al. 2007). Fecundity, hatching rate, and juvenile development relate significantly and positively with an increased foothold. Stronger attachment on the plant corresponds to a higher consumption rate (Voigt 2019). This study demonstrates that interfacial effects play a crucial role in insect-plant interactions. Insect settlement on plants depends on insect attachment ability (i.e., foothold), which is influenced by plant substrates. Hence, the impact of plant surface structures on mirid bug's, or even wider, on insect attachment ability and interfacial interactions should further be carefully considered when evaluating insect life history, prey consumption, and multitrophic plant-insect associations in the context of evolution, ecology, and sustainable pest management.

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How Japanese pine sawyer beetles hold on arboreal substrates

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Abstract: Most longhorn beetles impress with their considerable body size, long antennae, long legs bearing expanded hairy tarsomeres and well developed paired claws. They have been observed to attach strongly to various surfaces. However, host substrates and attachment system were not considered in detailed studies so far. Exemplarily, host plant surfaces and tarsi of the Japanese pine sawyer beetle (Monochamus alternatus Hope) were visualized in order to shed light on longhorn beetle attachment.

Light microscopic observations, cryo-scanning electron microscopic studies and measurements of free surface energy of host substrates were carried out. Additionally, traction forces of male and female longhorn beetles on glass were measured and set into the context.

Monochamus alternatus may attach to a range of surfaces, including pine needles, twig and stem bark as well as female elytrae, which all vary in texture and free surface energy. Five tarsomeres are densely covered with in total about 23600 ribbon-shaped adhesive setae bearing oval spatula-shaped, tapered terminals. Terminals are dorsally equipped with 5 to 10 setulae. In contrast to numerous leaf beetles and ladybirds, no sexual dimorphism in shape of adhesive setae is observed. The 3rd tarsomere in both sexes appears clearly belobed. Adhesive setae occur anisotropically arranged. On flat glass, up to 102 mN pulling force is generated, whereas up to 206 mN are measured on glass rods (considerably stronger pulling forces compared to those of other insects). We suppose an adaptation of the tarsal attachment system of Monochamus alternatus to rod-shaped structures, such as present in the natural habitat of these longhorn beetles.

Funding: ECOST-STSM-TD0906-010314-040971; JSPS Grant-in-Aid for Scientific Research on Innovative Areas Grant Numbers 24120005 and 24120006

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How tight are beetle hugs?

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Abstract: Sexual selection and mating behaviour in insects are fascinating phenomena, challenging experimental studies of the dynamic interactions. Similar to other leaf beetles, rosemary beetles Chrysolina americana exhibit a distinct sexual dimorphism in tarsal attachment setae. Setal discoid terminals occur only in males, and they have been previously associated with a long-term attachment to the female's back (elytra) during copulation and mate guarding. For the first time, we studied living males and females holding to female's elytra. Pull-off force measurements with a custom-made tribometer featuring a self-aligning sample holder confirmed stronger attachment to female elytra compared with glass in both males and females; corresponding to 45 and 30 times the body weight, respectively (Voigt et al. 2017).
In line with previous studies, males generated significantly higher forces than females on convex elytra and flat glass, 1.2 times and 6.8 times, respectively. Convex substrates like elytra seem to improve the attachment ability of rosemary beetles, because they can hold more strongly due to favourable shear angles of legs, tarsi and adhesive setae. A self-aligning sample holder is found to be suitable for running force measurement tests with living biological samples.

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Associational resistance to exotic invasive pests in forests

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Abstract: Invasive exotic pest species become increasingly important in forests worldwide. Theory and empirical studies suggest that mixed forests are more resistant against pest and pathogens than pure forests. This is generally referred to as associational resistance, summarising mechanisms leading to reduced likelihood of detection and vulnerability of a focal plant species with increasing plant diversity or changing plant species composition in its surrounding. Evidence comes mainly from studies on native insect species while the relationships between tree diversity/composition and exotic invasive species deserve to be better understood. We hypothesise that higher tree diversity and phylogenetic distinctiveness reduces the abundance of exotic pest species in forests. To test this, we compiled existing datasets of standardised assessments of insects in forests along a tree diversity/composition gradient in which exotic invasive insect species were sampled in sufficient numbers worldwide. We further identified key characteristics and functional traits of assessed exotic insect species. This study was conducted within the EU project HOMED. We found that the response of species abundances to tree diversity in terms of effect direction and shape depended on the traits of exotic species (e.g. the degree of host specialisation) as well as on characteristics of the forests (phylogenetic distance of trees) and regions (overall abundance of the exotic pest and regional environmental characteristics) included in a dataset. We discuss possible mechanisms underlying these diverse responses. Overall our study suggests that associational resistance can be important not only for native but also for exotic pest insect species and should be considered in future forest management strategies.

Photoperiodic regulation of insulin and juvenile hormone signalling pathways through the circadian clock in a bean bug

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Abstract: Many temperate multivoltine insects assess photoperiods by a photoperiodic time measurement system, which is assumed to be a function of circadian clocks. Under short days, they activate or inactivate the endocrine organ or cell to enter diapause. However, the molecular elements involved in the axis from the circadian clock to the endocrine organs/cells are poorly understood. To approach this issue, we investigated the insulin-signalling and juvenile hormone (JH) pathways and their control under the circadian clock in the bean bug Riptortus pedestris. One of the insulins, ILP1, which is expressed in 12 cells in the pars intercerebralis in the brain, is upregulated under long days. RNAi targeted to Ilp1 reduced fecundity, but not affected ovarian development and yolk protein expression. A cytochrome P450 Cyp15, which catalyzes the epoxidation in the JH biosynthetic pathway, is also upregulated under long days. RNAi targeted to Cyp15 suppressed ovarian development even under diapause-averting long days. RNAi targeted to per, one of the circadian clock genes, induced Ilp1 and Cyp15 expression as well as ovarian development even under short days. This study clarified the photoperiodic regulation of insulin and juvenile hormone signalling pathways through the circadian clock.

Impact of constant versus fluctuating temperatures on the development and life history parameters of Tetranychus urticae (Acari: Tetranychidae)

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Abstract: The impact of daily temperature fluctuations on arthropod life history parameters is inadequately studied compared with the ample amount of research that has been conducted on the effects of constant temperatures. Fluctuating temperatures are likely to be more realistic, as they are ecologically more similar to what these arthropods cope in nature. In this study, we compared the impact of 11 constant temperatures that ranged from 10 to 35°C with fluctuating temperatures with the same corresponding mean temperature and an amplitude of 10°C between high (12 h) and low (12 h) temperatures on the development and life history parameters of Tetranychus urticae under continuous light conditions. No eggs hatched at constant 10°C, whereas 81.5% of eggs successfully completed development at fluctuating 10°C (15/5°C). Egg-to-female adult development was faster under fluctuating temperatures from 12.5 to 27.5°C than under constant temperatures, whereas the opposite trend was observed at >30°C. The lower thermal thresholds (T) were 11.63 and 8.63°C, and thermal constants (K) were 127.81 and 150.69 degree-days for egg-to-female adults at constant and fluctuating temperatures, respectively. The data were analyzed based on age-stage, two-sex life table theory to take both sexes and different developmental stages in to consideration. The numbers of oviposition days were significantly higher at fluctuating 15°C than at the corresponding constant temperature, whereas the opposite trend was observed from 20 to 30°C. The intrinsic rate of increase (r) was higher at fluctuating than at constant 15°C. The r-values ranged from 0.063 day-1 (15°C) to 0.423 day-1 (30°C) at constant temperature, while they ranged from 0.104 day-1 (15°C) to 0.438 day-1 (30°C) at fluctuating temperature. The net reproductive rate (R0) was also higher at fluctuating than at constant 15 and 35°C, but showed an opposite trend at 20 and 25°C. We conclude that fluctuating temperatures should be considered to accurately predict the population dynamics of spider mite in nature.

Ontogenetic description of Proctolaelaps bickleyi (Bram) (Acari: Melicharidae), newly recorded in Japan from lepidopteran insect cultures

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Abstract: Numerous species of Mesostigmata mites (Arachnida: Acari) have close association with insects. Proctolaelaps bickleyi (Bram) (Melicharidae) is redescribed from females, males, deutonymphs, protonymphs and larvae collected from laboratory cultures of Chilo suppressalis (Walker) and Cossus insularis (Staudinger) (Lepidoptera: Crambidae, Cossidae) in Japan. Mites were directly picked up from insect rearing cultures under stereomicroscope and mounted on glass slides using Hoyer's medium. The ontogenetic changes in idiosomal and leg chaetotaxy are discussed and a key to the Japanese species of Melicharidae is provided.

Local adaptation to seasonal cues in a range-expanding butterfly

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Abstract: Range-expanding populations need to adapt to new environments, but lack of genetic variation in marginal populations as well as maladaptive gene flow from the core range may hinder adaptation. Previous studies on adaptation in expanding populations have mainly focused on dispersal ability, while less is known about important life history traits such as seasonal timing in response to photoperiod. Using controlled laboratory experiments we show that populations of the range-expanding wall brown butterfly, Lasiommata megera, have, on a relatively small spatial scale, adapted locally to photoperiodic seasonal cues. In long day treatments, caterpillars from the northern range margin in central Sweden were more likely to enter diapause than caterpillars from southern Sweden. Although temperature also affected diapause induction, there were no signs of similar differentiation among populations in the response to temperature. Northern range margin populations seem to have rapidly evolved their response to photoperiod to match local season length and photoperiodic conditions. This is a crucial adaptation for correct life cycle timing and is in many insects likely to be important for successful colonization of novel areas during range expansions across latitudes

Convergence of nutritional symbioses in obligate blood-feeders

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Abstract: Symbiosis with intracellular or gut bacteria is essential for the nutrition of animals with an obligate blood feeding habit. Divergent bacterial lineages have independently evolved highly functional interactions with obligate blood feeders, but all have converged to an analogous biochemical feature: the provisioning of B vitamins. Although these symbionts and their hosts coevolve interdependence for millions of years, we emphasize here that their associations are not necessarily stable and permanent. Ancestral symbionts undergo massive genomic reduction that may lead to accumulation of maladaptation. Recently acquired bacteria with similar biochemical features are able to out-compete these ancestral symbionts, leading ultimately to their extinction. Additionally, a streamlined biotin (B7 vitamin) operon experiences extensive transfers across bacterial lineages, favouring the spontaneous emergence of novel nutritional symbioses with blood feeders.

Do Juvenile Hormone and ecdysteroids mediate aggressive behavior in a solitary parasitoid wasp?

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Abstract: In vertebrates, titers of androgens such as testosterone are known to upregulate aggressive behaviors associated with reproduction. In insects, ecdysteroids (ESH) and juvenile hormone (JH) are good candidates to study the mediation of aggressiveness because they have important effects on both reproductive processes and behavior. Both ESH and JH have a gonadotropic effect across a broad range of insect species, increasing ovarian development in females and JH play a role in the regulation of aggressive behavior during competition in different species. To date, inconsistent results have been found with ESH, but only very few species have been studied. In Hymenoptera, the functions of ESH and JH have only been explored in social species. Surprisingly, no work has yet focused on the relationship between these hormones, reproduction and aggressiveness in a non-social Hymenoptera, although it may help understanding how hormone actions have evolved across taxa with different degrees of sociality. The question is also topical because the use of growth regulating insecticides, especially JH agonists, raises questions about their effects on non-target species. Here, we explored whether titers of ESH, JH and one of its agonist, the insecticide pyriproxyfen, influenced female reproductive status as well as aggressiveness and resolution of conflict in Eupelmus vuilleti (Hymenoptera: Eupelmidae). In this solitary ectoparasitoid wasp that can be used as biological control agent to regulate population of the pest Callosobruchus maculatus, females can indeed fight for hosts on which they lay their eggs. By quantifying hormone titers that naturally circulate in females after a contest, we first showed the ESH titers did not correlate with female aggressiveness, but winner wasps had higher titers than losers. Then, by injecting ESH or JHIII or by applying wasps externally with pyriproxyfen, (1) we confirmed that ESH, JH and pyriproxyfen favored egg maturation (i.e., gonadotropic effect) in E. vuilleti and (2) we showed that JH and pyriproxyfen increased female aggressiveness while ESH increased their probability of winning host access. Our results represent an important step in understanding how hormones mediate aggressive behavior during competition and highlights the importance of studying the diversity of possible unintended sublethal effects of pesticides on beneficial insects.

Impacts of a Warming World: Exposure to Simulated Heat Waves Decreases the Upper Thermal Tolerance of Buff-tailed Bumblebees

Authors: Goulson Dave[1], Sepúlveda Yanet[1], [1]University of Sussex, United Kingdom

Abstract: Climate change is one of the most significant challenges in the 21st century and among the main drivers of biodiversity loss. Recent distributional shifts and declines of pollinators seem to be associated with this phenomenon. However, few studies have assessed the upper thermal limits of temperate bumblebees. This study estimates the critical thermal maximum (CTmax) and heat coma temperature (HCT) of the British buff-tailed bumblebee, an important pollinator of wild and agricultural plants. CTmax occurred between 48.98-52.78 °C and was characterised by muscular spasms, disorganised movements, and inability to move forward, while HCT varied between 50.75-53.48 °C and occurred when the ability to move their body, legs, and/or antennae was lost. After measurements, around 23% of bees (n = 30) survived 24 hours or longer and coordination was never recovered, indicating that elevated temperatures may cause irreversible damage. There was no association between thermal tolerance and body mass, which highlights the need to integrate other factors to comprehend the mechanisms behind upper thermal limits. Individuals did not show acclimation capacity after heat wave exposure. In fact, the upper thermal limits of bumblebees decreased significantly after being exposed to a single heat wave of 34-36 ºC, while individuals exposed to a heat wave of 30-32 ºC showed no significant changes in their thermal tolerance. Our study provides novel insights into the upper thermal tolerance limits of Bombus terrestris audax and reveals that heat waves can have cumulative negative impacts on the fitness and survival of individual bumblebees, which is critical to predicting responses to future climate warming and increasing frequency of extreme weather events.

Aspirin-triggered anti-inflammatory eicosanoid-like mediators in Drosophila

Authors: Govind Shubha, The City College of New York and Graduate Center, City University of New York, United States

Abstract: Epidemiological reports have linked the use of aspirin to a drop in cancers and other chronic inflammation (CI)-based human diseases. Aspirin remains one the most effective pain-relieving and life-saving drugs. Its dual biochemical roles in reducing the levels of cyclooxygenase-mediated pro-inflammatory prostaglandins and increasing pro-resolution molecules in mammals are well known. But whether insects produce similar molecules and how these molecules affect their immune health has been an outstanding question in the field. Previous studies have shown that insects are sensitive to aspirin treatment, suggesting that its actions might be realized via anti-inflammatory lipid mediators acting through conserved mechanisms. In mammals, aspirin triggers the production of anti-inflammatory electrophilic mono-oxygenated (EFOX) lipid mediators. We therefore studied aspirin's effects in Drosophila models of CI. Ectopic immune (Toll/NF-kappaB and JAK/STAT) signaling in mutant D. melanogaster larvae leads to an expansion of the hematopoietic blood progenitor population and inflammatory granuloma-like blood tumors. Ectopic immune signaling also results in metabolic inflammation. Aspirin-treated mutant flies exhibit reduction in metabolic inflammation, mitosis, ectopic immune signaling, and macrophage infiltration into the fat body. Moreover, these flies synthesize 13-HODE (an oxygenated PUFA in mammals, associated with pain and inflammation) and aspirin triggers 13-oxoODE (13-EFOX-L2) production. Dietary supplementation of 13-HODE's precursor, C18 linoleic acid, or targeted knockdown of the transcription factor STAT in inflammatory blood cells (without aspirin), boosts 13-EFOX-L2 levels, while decreasing metabolic inflammation. Thus, hematopoietic cells appear to regulate CI in flies, and their effects can be reversed by pharmaceutical or dietary intervention. Aspirin's anti-inflammatory and anti-cancer effects in fruit flies suggest deep phylogenetic conservation in the processes required to resolve inflammation, repair tissue damage, and restore homeostasis. This model system brings the power of Drosophila genetics to bear on immuno-metabolic mechanisms that boost systemic health in humans, with the potential to identify conserved mechanisms across taxa.

Food is life - The effect of plant diet on the susceptibility of Agriotes obscurus towards the entomopathogenic fungus Metarhizium brunneum

Authors: Grabenweger Giselher[3], Reinbacher Lara[3], Praprotnik Eva[2], Razinger Jaka[1] and Bacher Sven[4], [1]Agricultural Institute of Slovenia, Ljubljana, Slovenia, [2]Agricultural Institute of Slovenia, Slovenia, [3]Agroscope, Zurich, Switzerland, [4]Department of Biology, University of Fribourg, Switzerland

Abstract: Entomopathogenic fungi (EPF) have been described as promising biological control agents against wireworms but success in field experiments is inconsistent. An array of abiotic and biotic factors may influence the efficacy of EPF. One of the latter is the fitness of the targeted insect and the ability of the potential host to withstand fungal infection. For the insects' immune defense, nutrition is among the most important determinants.

In this study, we investigated the effects of five plant diets on the development of the wireworm Agriotes obscurus in a greenhouse pot experiment. After living on a specific diet for eight weeks, wireworms were exposed to an environment inoculated with the EPF Metarhizium brunneum ART2825 and monitored for their susceptibility to fungal infection.

The results of this study may help to develop tools for an integrated pest management strategy against wireworms. Plant species which constitute unsuitable nutritional resources for wireworms and compromise their fitness, may be combined with application of EPF and ultimately enhance efficacy of the treatment in the field.

Identifying and integrating diverse datasets to understand insect decline: the EntoGEM project

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Abstract: To fully understand insect population and community trends, it is necessary to identify, integrate, and synthesize datasets representing the diversity of insect taxa and their habitats globally. The literature documenting such datasets is vast and scattered across disciplines, from medical and forensic entomology, to agricultural pest management, to ecology and conservation biology, and more. The Entomological Global Evidence Map (EntoGEM) project is a systematic effort to broadly search for and catalog diverse studies with long-term data that can be used to understand changes in insect abundance and diversity. Though we have screened less than 10% of >130,000 studies that potentially contain long-term insect data, we have already identified more than 270 >10-year datasets and hundreds more shorter time series (2-9 years) documenting insect population and community trends. The datasets identified by the EntoGEM project can be used to estimate global trends more comprehensively, disentangle drivers of decline, and answer a myriad of questions about short- and long-term insect population dynamics.

Who is Knocking on Our Door? Meeting the Challenges of Invasive Species from a Southern Perspective (Tennessee, USA)

Authors: Grant Jerome, Department of Entomology and Plant Pathology The University of Tennessee Knoxville, Tennessee 37996, United States

Abstract: Invasive species pose tremendous threats to agricultural lands, forests, landscapes, natural areas, and urban areas. In Tennessee, some of these threats have been realized as millions of ash trees have died from emerald ash borer and millions of hemlock trees have died from hemlock woolly adelgid. Both of these species arrived unexpectedly and spread rapidly, mainly due to the abundance of hosts and suitability of climate for development and reproduction. The invasion of these species, as well as others (including kudzu bug, brown marmorated stink bug, and crapemyrtle bark scale), have posed challenges to our local municipalities and state government, land managers, federal agencies, etc. The eastern part of the state of Tennessee (USA) is located in the Southern Appalachian Mountain Range; other parts represent at least five other physiographic regions. The climate in these regions is conducive to establishment and reproduction of many invasive species, due to the warmer temperatures in the winters which reduce winter kill of invasive species. This climate, coupled with the diversity in geography, topography, etc. and the diversity of industries (e.g., nursery, agricultural, forestry, etc.), provide unique critical issues/challenges related to invasive species. Located in a southern climate, Tennessee has numerous high-traffic interstates and much international (and interstate) business is conducted. Thus, critical issues related to invasive species become obvious. This paper will address those critical issues and challenges from a southern perspective that relate to invasive species. This paper also will address the challenges faced by local and state governments, universities, and federal agencies in the state from funding issues to politics to natural enemy assessment to management. Because hemlock woolly adelgid, emerald ash borer, and kudzu bug have recently posed (and continue to pose) challenges in our state, this paper also will focus on lessons learned from these invasive species. Lessons learned will focus on importance of early monitoring, public involvement, education of legislators/government agencies, as well as the public, and communication. These experiences have provided insight into the spread, movement, and impact of invasive species and will prove to be extremely beneficial to our state as we face new invasive species ‘knocking at our door.’ These include gypsy moth, Asian longhorned beetle, and spotted lanternfly. Our previous experiences and lessons learned will enable us to better prepare for the establishment of these new invasive species.

Gut content analysis of preserved carabid specimens reveals past trophic interactions

Authors: Graux Yohann, Tours University

Abstract: Significant carabid collections have been built in many research institutes as part of studies focusing on biodiversity assessments or biological control in agricultural landscapes. Often, these specimens are preserved in ethanol. A metabarcoding analysis of these carabids’ gut contents would allow the determination of past trophic interactions and their evolution through time. The Zone Atelier Plaine & Val de Sèvre in Western France has carabid specimens collected yearly since 1995. Although, sample collection and specimen preservation were not conducted specifically for molecular analyses, this collection constitutes a repository of information about prey communities in agricultural landscapes in the past decades.

We analysed more than 200 specimens from two generalist predatory species (Nebria salina and Poecilus cupreus) collected between 2013 and 2021. Specimens were dissected and prey DNA was amplified from the insects’ crop using generalist PCR primers. The diet of carabids was then analysed using a metabarcoding approach.

By using existing collections of ethanol preserved carabids, our method has the potential to inform on the biocontrol services provided by carabids and its evolution through time. When applied to generalist predators, this method can highlight shifts in arthropod communities that may be related to global changes, agricultural practices or land management.

Recent advances on taxonomic status of pentatomid pests in the Neotropics (Heteroptera: Pentatomidae)

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Abstract: Pentatomidae is the fourth most numerous families within Heteroptera including about 5,000 species in more than 940 genera. Pentatomids are represented in all zoogeographical regions although the tropical and subtropical faunas are the widest; they are commonly known as stink bugs. Nine or ten subfamilies are recognized, half of them with restricted distribution. In the Neotropical Region seven subfamilies are present: Asopinae, Cyrtocorinae, Discocephalinae, Edessinae, Pentatominae, Podopinae and Stirotarsinae. From the applied point of view the following four subfamilies should be highlighted. Pentatominae is the most diverse with 3,484 species in 660 genera in the world, and 886 species in 138 genera in the Neotropics. They are all phytophagous; many species are serious pests of crops. The classification within this subfamily has been considered chaotic including from eight to more than 40 tribes according to different authors. Asopinae have predacious habits and its importance as biological control agents is increasing. They are found in all zoogeographical regions with 303 species in 63 genera, and around 100 species in 23 genera in the Neotropics. Discocephalinae is exclusively Neotropical with 325 species in 81 genera. It includes two tribes, Discocephalini and Ochlerini, all phytophagous and some species are important vectors of Phytomonas spp. (Trypanosomatidae) in palms in South America. Edessinae includes the most colored and largest stink bugs, with great diversity in the Amazon region, with around 340 known species in 15 genera. They have in common the strong development of the metasternum. For more than a century the group was treated as a tribe of Pentatominae but studies in the last two decades raised the taxon to subfamily rank and increased the number of genera to fifteen. Recent studies in Pentatomidae have promoted a better understanding of the relationships among and within groups recognized as subfamilies whose impact on the current classification will be discussed, highlighting the pentatomid pests in the Neotropics.

A litmus test for harmonized mosquito monitoring across Europe and Africa

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Abstract: The increasing incidence of mosquito borne diseases is urging the development of effective tools for monitoring insect populations and their larval habitats. The use of harmonized field protocols helps to build a comprehensive picture on species-specific vector ecology, and to implement coordinated mosquito surveillance programs across continents. We sought to test the efficiency and potential drawbacks of harmonized protocols proposed from earlier EU project VectorNet. We specifically aimed to capture the ecoregional variation of breeding site characteristics and population density of five mosquito vectors in Europe and Africa. As expected, the five species show different aquatic habitat preferences. Culex pipiens, Aedes albopictus in Europe and Ae. aegypti in Africa select breeding habitats within specific volume classes, while Anopheles gambiae and An. coluzzii select breeding habitats based on seasonal availability. Population densities in aquatic habitats greatly varied across species and countries, but larval production sites of Ae. albopictus generate populations with higher ratio of pupae compared to the other species. This result underlines the fundamental ecological difference between the selected vector species disregarding of the ecoregion. Mean water temperatures had limited variation across species and higher among countries. Understanding the ecology of native and non-native mosquito vectors is key in evaluating transmission risks for diseases such as West Nile, chikungunya and dengue fevers, zika and malaria. The proposed harmonized field protocols are a valuable tool for achieving homogeneous mosquito surveillance and support integrated vector management programs at various scale and across continents.

Risk-based surveillance of an imminent invader in the EU: the EFSA pest survey toolkit and the emerald ash borer Agrilus planipennis

Authors: Graziosi Ignazio[1], Delbianco Alice[1], Cortiñas Abrahantes Jose[1] and Vos Sybren[1], [1]European Food Safety Authority (EFSA)

Abstract: The emerald ash borer (EAB) Agrilus planipennis is approaching the European Union territory, where the beetle is subjected to mandatory surveillance. We developed three integrated tools for preparing and designing the surveys. The Pest Survey Card on Agrilus planipennis (https://arcg.is/09S94u) helps to define the target population of Fraxinus hosts and the methods for detecting the insect. The survey area is divided in epidemiological units (administrative boundaries and/or land use), risk locations are associated with higher probability of EAB presence, and risk areas identified based on the presence of ash resources. Trapping insects using green funnel traps is the recommended method early detection, and it can be combined with other techniques. The Guidelines for statistically sound and risk-based surveys of Agrilus planipennis (https://www.efsa.europa.eu/en/supporting/pub/en-1983) propose a step-wise approach for designing detection surveys to substantiate pest freedom and delimiting surveys for defining the boundaries of an infested zone. The method sensitivity, the confidence level and an appropriate design prevalence feed into the statistical tool RIBESS+ (https://arcg.is/0vWufj1), which calculates the sampling effort required to survey the target population. The proposed toolkit ensures harmonized survey conclusions that can be compared in time and space, thus providing robust evidence for pest freedom.

Strengthening the firewall against invasive insects: the EFSA plant pest survey toolkit

Authors: Graziosi Ignazio[1], Delbianco Alice[1], Mustapic Luka[1], Camilleri Melanie[1], Cortiñas Abrahantes Jose[1] and Vos Sybren[1], [1]European Food Safety Authority (EFSA)

Abstract: The European Union' Commission Implementing Regulation 2019/2072 lists Union quarantine plant pests (including over 400 insect taxa) for which EU member states are required to conduct surveys. We developed a Plant Pest Survey Toolkit (https://arcg.is/1v99CH) in line with the International Standards for Phytosanitary Measures to assist member states with surveillance activities. Detection (substantiating pest freedom of an area) or delimiting surveys (defining the boundaries of an infested zone) are completed through three-step process: preparation, design and implementation. 1) Pest Survey Cards help gathering relevant information for survey preparation. They are designed to characterize the target population (epidemiological units and risk areas are linked with environmental suitability, host range, and the pest' spread capacity), select an effective detection method, and appropriate inspection units. 2) Guidelines for statistically sound and risk-based surveys of plant pests are used to design the survey by defining the host population size, and setting method sensitivity, confidence level and design prevalence. The required sample effort is calculated through the RIBESS+ statistical tool. 3) Inspection units are allocated to the survey sites and surveys are implemented at member state level according to the design. This approach contributes to a cross-country harmonisation of surveillance activities.

Have residual chemical insecticides devalued urban entomology and can technology restore it?

Authors: Green Matt, Rentokil-Initial PLC, United Kingdom

Abstract: The last thirty years have seen a marked decline in the use of residual insecticide use in urban insect pest control. The role of residual insecticides has, in turn, degraded from: 'eradication solution' to; 'part of an integrated pest management programme' which places more emphasis on the ability of the operator to correctly understand and interpret observations on the biology of the insects they are looking to control. This re-emphasis has been industry driven, rather than through academic led best practice research and publishing.

New technology, particularly in the field of surveillance and remote monitoring can provide entomologists working in urban pest control with pertinent behavioural information that can and should inform the operator. This will necessarily require pest control operators to possess different skill sets than they would have had thirty years ago and will require a significant upskilling of those entering and continuing to work in the field.

This is a review of the discipline of urban entomology and pest control from a historic context, examining the reasons for its relative low status in the broader field of entomology and examines the potential role of technology in its future.

Mating signal evolution via sensory bias: lessons from the acoustic Lepidoptera

Authors: Greenfield Michael, Department of Ecology and Evolutionary Biology ; University of Kansas, United States

Abstract: Pair formation in moths typically involves pheromones, but some pyraloid and noctuoid species use sound in mating communication. The signals are generally ultrasound, broadcast by males, and function in courtship. Long-range advertisement songs also occur which exhibit high convergence with communication in other acoustic species such as orthopterans and anurans. Tympanal hearing with sensitivity to ultrasound in the context of bat avoidance behavior is widespread in the Lepidoptera, and phylogenetic inference indicates that such perception preceded the evolution of song. This sequence suggests that male song originated via the sensory bias mechanism, but the trajectory by which ancestral defensive behavior in females—negative responses to bat echolocation signals—may have evolved toward positive responses to male song remains unclear. Analyses of various species offer some insight to this improbable transition, and to the general process by which signals may evolve via the sensory bias mechanism.

Insulin signaling during overwintering in the alfalfa leafcutting bee, Megachile rotundata

Authors: Greenlee Kendra[3], Yocum George[2] and Cambron Lizzette[1], [3]North Dakota State University, United States, [2]Edward T. Schafer Agricultural Research Center USDA-ARS, United States, [1]Department of Biological Sciences North Dakota State University, United States

Abstract: Insects overwinter in a diapause state to survive unfavorable conditions, including low and fluctuating temperatures. For some species, commercial managers use storage at constant temperatures to mimic the overwintering period. The alfalfa leafcutting bee, Megachile rotundata, is often stored at 6°C during the winter months. Previous work showed that bees stored at constant temperatures had different gene expression profiles when compared to bees overwintered in naturally fluctuating temperatures from field conditions. The differences in genetic profiles included several metabolic pathways, but it remains unclear how the insulin signaling pathway varies during this time period or if it insulin signaling is affected by temperature fluctuations. Megachile rotundata overwinters as a prepupa for up to 9 months and does not feed during this time period, relying on energy stored from the previous summer to support metabolic processes. With fixed energy resources, overall metabolism and insulin signaling are maintained at low levels. Because insulin signaling is thought to regulate energy allocation, and insect metabolism is tightly linked to environmental temperatures, we expected to see differences in expression of genes in the insulin signaling pathway between bees overwintered in constant conditions and in the field. We used nCounter analysis (NanoString Technologies Inc.), a multiplex technique, to measure expression of genes in the insulin signaling pathway and cell cycle. We compared bees overwintered in the lab and field from November to June, spanning the entirety of overwintering stages. Expression of the insulin-like receptor differed by month depending on location, with lab bees having higher expression levels, suggesting the possibility of temperature regulating gene expression. Samui, a putative diapause termination signal, showed a similar pattern, potentially indicating that diapause is dysregulated in lab bees. Together these data suggest a possible connection between temperature and insulin signaling. During overwintering, expression profiles of genes in the insulin pathway did not all change, meaning only key players of the pathway, such as FOXO, PI3K, and MAPK, were being used. These targets connect to the cell cycle, which also showed significant differences in gene expression by location. The use of insulin pathway targets has been shown in other diapausing insects, but further studies are needed to determine how these targets are being regulated and interconnected.

The intestinal microbiota profile of Hermetia illucens larvae is modified by diet and genetic background and is linked to biomass accumulation

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Abstract: Black soldier fly (Hermetia illucens) larvae are detritivores capable of converting large volumes of organic waste into high protein and fat content biomass. In recent years, industrial- and subsistence-level larval rearing systems have been developed to exploit this capability for the renewable production of protein-rich animal feeds, lipids and fertilizers. While much information regarding effective colony management and feed protocols are available in the literature, few studies have explored the relationship between black soldier fly gut microbiome dynamics, host genetics and larval performance traits. In this study, we focused on characterization of bacterial microbiome diversity and structure within late-instar larvae in light of different genetic backgrounds and multiple, industry-relevant diets. Microbiota composition and alpha diversity differed starkly by diet option, with moderate evidence for differentiation by genetic background. Furthermore, a core gut profile - consisting of 30 bacterial genera - was identified in line with what has been reported in prior studies of this species. Bacterial community structure, as inferred from correlation networks, was observed to be dynamic and altered by both feed and genetic background. Additionally, larval biomass metrics (dry mass, protein content, fat content) were found to be significantly linked to microbial community structure. In totality, the data highlights the importance of considering the larval gut microbiome in the development of alternative rearing protocols, as well as emphasizing the complexity which underlies the management of this gut ‘phenotype’.

The beetles bark but the caravan moves on. What do we really know about bark beetle control?

Authors: Grégoire Jean-Claude, Spatial Epidemiology lab Universite libre de Bruxelles, Belgium

Abstract: A few species among the 800+ conifer bark beetles in the world count among the major insect pests of forestry in Europe, North America and Asia. Their devastating outbreaks may, at best, be prevented but, in many cases, the foresters can just attempt to contain them at high costs and with heavy economic losses. The example of the European spruce bark beetle, Ips typographus, will be used to discuss how the management issues raised by these insects have been influenced by our improving knowledge of their biology and ecology, by changing priorities regarding the role of forests and, more recently, by increasing constraints brought by climate change. The species is still increasing its range in Eurasia, following the expansion of spruce plantations, and causes frequent outbreaks, generally after a storm or during a very hot and dry year. For a long time, sanitary thinning and clearfelling, and the peeling or fast removing of attacked stems were the only available options for the managers. About fifty years ago, the development of chemical ecology brought new possibilities for integrated pest management, with the prospect of easier monitoring and even preventive or curative mass-trapping or, possibly, push-pull behavioural manipulations. However, several factors should teach us to remain wary of reductionist solutions. On the one hand, the growing knowledge about bark-beetle dispersal, interactions with host- and non-host trees and with symbionts, competitors and natural enemies, gradually brings in more variables to take into account. On the other hand, the increasing emphasis on the multiple role of forests, beyond the production of wood, as well as a changing view of bark beetles, from simple pests to actors in ecosystem dynamics, also influence decision thresholds.

The role of landscape composition and heterogeneity on the conservation of coccinellid communities and their service

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Abstract: Coccinellids are important natural enemies of pests, with native species playing a crucial role in this important ecosystem service. Their abundance, diversity, and function may be affected by landscape composition and heterogeneity. Nevertheless, very few studies on this topic have been published so far, and fewer have separately analyzed the responses of native and exotic coccinellid species. In this presentation we show empirical evidence that native and exotic coccinellid species differentially respond to landscape characteristics. At local scale, we point out that edges are important structures for coccinellid colonization of crops. At the landscape scale, we provide evidence that i) native and exotic species differentially use cover types depending on their disturbance; ii) natives are favored by more heterogeneous landscapes whereas exotics seems to be less affected; iii) biological control of aphids in alfalfa fields is positively associated with the abundance of native coccinellids; iv) in more urbanized landscapes coccinellid richness and abundance in greenspaces decline, especially of native species; and v) the composition of coccinellid functional groups vary with landscape urbanization. These results highlight the importance of maintaining landscape heterogeneity at different spatial scales in order to conserve the composition and functionality of natural enemies in agroecosystems (Funding: FONDECYT 1180533).

Sow Wild! Citizen scientists find sown mini-meadows increase pollinator diversity in gardens

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Abstract: With increasing urbanisation there is growing potential to support insect populations in urban landscapes. Using citizen science, we investigated the effectiveness of a small 4m^2 mini-meadow in recruiting beneficial insects in UK gardens and allotments. Participants were allocated one of three treatment groups: Seed mix 1 (commercially available ‘meadow mix’); Seed mix 2 (formulated based on pollinator foraging preferences); or Control (no additional wildflower mixes). All participants conducted insect sampling over two years using standardised pan and sticky trap methods May-August. Samples were returned for identification by trained specialists. Mini-meadows provided resource-rich habitats, increasing wild bee richness and supporting on average 111% more bumblebees, 87% more solitary bees and 85% more solitary wasps in the year following seed-sowing, compared to Control. The wildflower mixes were also taxon-specific in their attractiveness, probably due to key plant species in the mix. We used citizen science as a novel and pragmatic approach to access private gardens to survey insects. Participant retention was good, and citizen scientists made an invaluable contribution. Domestic gardens and allotments provide huge potential habitat for pollinators. Small-scale floral enhancements can attract more beneficial insects in fragmented urban landscapes, supporting urban biodiversity, pollination services and biological control.

Immune response and alterations in midgut bacterial community of Galleria mellonella resistant to Bacillus thuringiensis

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Abstract: During selection of greater wax moth Galleria mellonella for resistance to Bacillus thuringiensis (Bt) (R line) the microevolutionary alterations in midgut bacterial community have been detected as compare with insects of susceptible line (S line). Uninfected R line insect had less percentage of genus Enterobacteriaceae than the S larvae, however, upon infection with Bt the percentage were significantly elevated up to 80 % in R line. Unlike the S insects, Bt infection significantly in 2-3 times reduced the percentage of the genus Enterococcus in the R insects but in 2-3 times elevated in S line. As compare with insects of S line we have detected less percentages of potentially pathogenic bacteria genus Serratia and Bacillus in midgut of R line larvae during Bt infection. This tendency has been detected in cadavers of the larvae from R line. In the uninfected state, resistant insects exhibited enhanced basal expression of antibacterial (AMP) genes in the midgut. Following oral infection with Bt, the expression of these genes was elevated in the midgut of S line larvae. RNA interference of Gloverin gene resulted in elevated susceptibility of insects of S line to Bt infection. These observations suggest that the R line not only has a more intact midgut but is secreting antimicrobial factors into the gut lumen which not only mitigate Bt activity but also affects the viability of other gut bacteria. The expresion of Bt genes in cadavers of R and S line insects were detected for the first time. The results will be discussed at conference. This work was supported RSF 19-16-00019, RSF 20-76-00025

Essentials of ecological knowledge that applied biological control urgently needs

Authors: Groot Tom[1] and Calvo Francisco Javier[2], [1]Koppert Biological Systems, Netherlands, [2]R&D Koppert Biological Systems, Spain

Abstract: The call to increase the contribution of biological control in IPM is louder than ever before, but current research efforts are often not geared towards meeting this demand. We argue that more focus on applied problems is needed in order to increase the efficiency of developing new biological control products. Selecting the right species to develop for augmentative biological control is hard and time consuming. There are several known selection criteria that are typically assessed in controlled laboratory and semi-field assays. Such assays typically quantify biological parameters in early phase of candidate screening. Besides these parameters, there is another group of applied criteria that a successful candidate biological control agent needs to pass. Such criteria examine versatile aspects of the candidate's suitability to be mass produced and shipped. Other criteria are related to the complexities of the agro-environmental conditions where the agents are released. We argue that applied problems are not high enough on the agenda of biocontrol research when the selection of candidates is concerned. In this presentation we review these. We discuss how reducing the gap between the current scientific efforts and the realistic field situation at growers' site may increase the efficiency of developing new biocontrol agents.

Phytoplasma infection of apple (Malus domestica) affects the behavior of its vector Cacopsylla picta

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Abstract: The phloem feeding insect Cacopsylla picta Foerster (Hemiptera: Psyllidae) is vectoring 'Candidatus Phytoplasma mali', a small bacterium inducing apple proliferation disease (AP) in apple trees. In their migratory lifecycle, the young adults emigrate to conifers as overwintering sites, before they remigrate into fruit orchards the following spring where mating and reproduction takes place. The females oviposit on fresh green apple leaves. In previous no-choice studies, it was reported that higher numbers of eggs were placed on leaves of healthy apple plants [Mayer et al., 2011]. In dual choice tests, we assessed the behavior of C. picta females when given the chance to choose their oviposition site between a healthy or AP infected apple leave intruding from opposite sites into a small gauze tube. Location and number of eggs were recorded after 96 h. We found that females preferred healthy leaves over AP infected leaves for oviposition. Furthermore, the influence of host plants infection status onto the feeding behavior of the vectoring insect C. picta was assessed. Analysis of 12 hour lasting electrical penetration graph recordings (EPG) from distinct developmental stages of the vector showed changes in feeding behavior influenced by developmental stage as well as by phytoplasma infection of their host plants. In order to link behavioral changes in vectoring insect to alterations in their host plant caused by phytoplasma infection, we studied phloem metabolite composition by collecting phloem sap using the centrifugation technique [modified after Hijaz & Killiny, 2014], derivatization and GC-MS analysis followed by AMDIS analysis according to [Gallinger & Gross, 2018]. Phytoplasma infection resulted in significant physiological changes especially regarding the sugar composition of the phloem.

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Integrative taxonomy of some West Palearctic Trichogramma species

Authors: Groussier Géraldine[2], Marchand Anael[1], Cruaud Astrid[1], Rasplus Jean-Yves[1], Ris Nicolas[3] and Warot Sylvie[1], [2]INRA, France, [1]INRA, France, [3]National Research Institut for the Agronomy, France

Abstract: Trichogramma are minute chalcid wasps that are, altogether, egg parasitoids of various insect orders (mainly Lepidoptera). The genus is extremely diverse with more than 200 described species worldwide and 40 in Europe.
This diversity, their small size as well as the possible presence of species complexes make difficult their identification, in particular by non-specialists. This situation is detrimental not only for basic research but also (and maybe more importantly) for the use of some Trichogramma strains as biological control agents.
Using (i) intensive DNA Barcoding using part of the mitochondrial marker Cytochrome Oxidase I (COI), (ii) multi-locus phylogeny including COI but also other mitochondrial (CytB) and nuclear markers (Wingless, EF1alpha, RpL27a et RpS4), (iii) crossing experiments as well as (iv) additional sources of information (e.g. previous identifications based on morphological characters or GENBANK accessions), we investigated the diversity of Trichogramma strains collected by ourselves or provided by various international colleagues in the Western Palaearctic.
Taken as a whole, we hence identified about 20 Molecular Operational Taxonomic Units (MOTUs), most of them being cross-validated by other sources of information. Among this diversity, some MOTUs were nevertheless not associated with a species' name and required further investigations. Moreover, two species complexes were observed, the first one encompassing T. cacoeciae and T. embryophagum as well as putative new species and the second one encompassing some strains previously identified as T. brassicae and T. euproctidis.
Based on this first dataset, our perspective is to widen our collaborative network not only to have access to new strains/information but also to unite disseminated specialists of this genus. This objective is also supported by the creation and certification (ISO9001:2015) of a Biological Resource Center in France devoted to Egg Parasitoids (BRC EP-Coll – https://www6.inra.fr/crb-eggparasitoids-coll/Presentation).

Invasion theory and natural enemy introductions

Authors: Gruner Daniel, University of Maryland, United States

Abstract: Biological invasions are major drivers of the global biodiversity crisis, causing economic losses and profound impacts to recipient communities and ecosystems. Invasive species successfully colonize novel ecosystems, establish populations, spread geographically, and overcome antagonistic species interactions to impact native communities and ecosystems. Classical or introduction biological control seeks to reproduce these phases, in service towards reduced population growth and spatial spread of invasive species. The defining life history, behavioral and population traits that contribute to invasiveness are also traits we seek in identifying candidate biological controls to arrest their spread. Testing hypotheses for failure or success of biological invasions has been problematic and controversial, however, in part because information is incomplete and research is reactive. Arguably, few advances from ecological theory have advanced the success of biological control, whereas biological control introductions can provide hypotheses testing for invasion theory because variables such as propagule pressure, residence time, climate-matching, and phenological synchrony can be controlled and monitored in experimental approaches.

Using invasion theory to guide natural enemy introductions

Authors: Gruner Daniel, University of Maryland, United States

Abstract: Biological invasions are major drivers of the global biodiversity crisis, causing economic losses and profound impacts to recipient communities and ecosystems. Invasive species successfully colonize novel ecosystems, establish populations, spread geographically, and overcome antagonistic species interactions to impact native communities and ecosystems. Classical or introduction biological control seeks to reproduce these phases, in service towards reduced population growth and spatial spread of invasive species. The defining life history, behavioral and population traits that contribute to invasiveness are also traits we seek in identifying candidate biological controls to arrest their spread. Testing hypotheses for failure or success of biological invasions has been problematic and controversial, however, in part because information is incomplete and research is reactive. Arguably, few advances from ecological theory have advanced the success of biological control, whereas biological control introductions can provide hypotheses testing for invasion theory because variables such as propagule pressure, residence time, climate-matching, and phenological synchrony can be controlled and monitored in experimental approaches.

A root-feeding herbivore uses chemical cues to avoid competition and elevated predation risk

Authors: Grunseich John[2], Hay Allison[1], Grunseich John[1] and Thompson Morgan[1], [2]Texas A&M University, United States, [1]Texas A&M University, United States

Abstract: Plant-produced volatile compounds play essential roles in foraging by both herbivores and their natural enemies. It has been well documented that herbivore feeding damage on plants triggers the production of herbivore-induced plant volatiles (HIPVs) and that these volatiles can protect plants directly by repelling herbivores or indirectly by recruiting natural enemies that kill herbivores. Although the majority of studies have focused on aboveground systems, recent research has demonstrated that herbivore-damaged plant roots also emit HIPVs. Despite growing recognition that plant cues are important for below-ground ecological interactions, however, our understanding of root-produced HIPVs and their ecological functions in soil environments remains limited. In this study, we investigated the role of volatile compounds from roots of cucumber plants (Cucumis sativus) in mediating foraging decisions by specialist cucumber beetle larvae (Acalymma vittatum) and entomopathogenic nematode natural enemies Heterohabditis bacteriophora (EPNs).

Improved monitoring of thrips by the combined use of attractive visual and olfactory cues?

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Abstract: Coloured sticky traps are used worldwide for the monitoring of thrips (Frankliniella occidentalis) in greenhouses. Especially blue sticky traps are used for the monitoring of thrips and can sometimes be used to get informations about the thrips population density on crops. In the last two decades, LED-traps have been tested for attractivity toward thrips in mostly small scale experiments under controlled conditions. Additionally, different semiochemicals that were found to be attractive toward thrips, are nowadays used for an enhanced thrips monitoring. However, the combination of those semiochemicals together with attractive LED-traps has been studied very few. To understand the behavioural ecology of thrips in more detail, it is necessary to proof the promising results from small experiments under more complex conditions. Within a BMEL project, the attractivity of the combination of the olfactory together with a visual cue is studied under greenhouse conditions. It will be investigated if those monitoring tools can improve the detection of thrips in crop stands by an earlier detection of the pest. Besides this, it will be investigated if one can get more informations about the thrips population density on the crop and if it is possible to pull the insect to the trap.

Forensically relevant developmental data for Necrodes littoralis (Coleoptera: Silphidae)

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Abstract: Necrodes littoralis is a necrophagous beetle, that may be useful for postmortem interval estimation. It is frequently found on human cadavers. Unfortunately there are no forensically useful developmental models for this species. Here, we present first full developmental dataset for N. littoralis from ten constant temperatures (14-30°C).
To establish a colony, adult beetles were collected from pig carcasses. Larvae were reared in aggregations (50 larvae per container, eight containers per temperature) at constant temperature and humidity, with photoperiod 12:12. They were fed with pork ad libitum and had constant access to water. Six randomly chosen larvae from four containers were measured at intervals representing no more than 10% of the stage duration. Larvae in all containers were monitored for developmental landmarks. Postfeeding larvae were transferred into smaller containers for pupation. At emergence we measured length and weight of adult beetles and determined their sex. Thermal summation models, isomorphen and isomegalen diagrams and growth curves were derived using the data.
Depending on the temperature, development lasted between about 23 and 89 days. Mortality was high at the extremes of the temperature range. The thermal summation constant for the total development was 434.7 ± 28.86 accumulated degree-days above a developmental threshold of 9.04 ± 0.55°C.

Effect of fungicide on pollen foraging by honeybees differs by fungicide type

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Abstract: Honeybees (Apis mellifera Linnaeus) (Hymenoptera: Apidae) play a major role in the pollination of cranberry (Vaccinium macrocarpon; Ericaceae). However, fungicide applications during cranberry bloom may affect bees foraging behavior. This research reports the amount of cranberry and noncranberry pollen brought back to hives immediately before and after two types of fungicide applications. The amount of cranberry pollen decreased while the amount of noncranberry pollen increased following a fungicide application. However, this relationship differed depending on the type of fungicide applied. Understanding how different fungicides specifically impact bee behavior is essential to minimizing bee exposure to potentially harmful chemicals.

Functional genomic approaches in the cruciferous pest Plutella xylostella

Authors: Guest Marcus[2] and Gonzalez Izquierdo Patricia[1], [2]Syngenta, United Kingdom, [1]Syngenta

Abstract: Forward genetic methodologies provide a non-hypothesis led route to pesticide mode of action and mode of resistance elucidation. Linkage mapping, of either field isolated or lab generated resistance, provides a genetic link between active ingredient and candidate resistance mutation / potential target sites. Reverse genetic studies can be used to validate candidate resistance mutations. Whole genome resequencing and genome editing make such approaches feasible in pest species.

We have been utilising genome editing and linkage mapping techniques in Plutella xylostella to study a range of insecticide mechanisms of resistance / mechanisms of action, as well as to generate strains to assist in developing crop protection products. Plutella is a particularly useful model for lepidopteran pests due to its small size, relatively short life cycle and relative ease of genetic manipulation. In this poster, we discuss some of the methodologies developed and results obtained.

Comparative anatomy of venom glands suggests a role of maternal secretions in gall induction by cynipid wasps

Authors: Guiguet Antoine[2], Tooker John[1], Deans Andrew[1] and Hines Heather[1], [2]Penn State, United States, [1]Penn State

Abstract: Many herbivorous insects are capable of hijacking plant development to induce novel plant organs called galls. In most groups of galling insects, the insect organs and molecular signals involved in gall induction are poorly understood. We focus on gall-wasps (Cynipidae), the second largest clade of gall inducers, for which the developmental stage and organs responsible for gall development are unclear. We investigated female abdomen anatomy in gall-inducing and non-gall-inducing species across each of the major lineages of the Cynipoideae super-family to test the correlation between this lifestyle and the relative size of secretory organs. We confirmed the massive expansion of the venom apparatus size in gall-inducing species. Among these gallers we measured the largest venom gland apparatus relative to body size ever recorded in insects. Non-galling inquiline species are accompanied by reduction of this apparatus. Altogether, the massive expansion of secretory organs specifically in gall-inducing species strongly suggests a role of these secretions in the process of gall formation, and the variance in size of venom glands, accessory glands, and the contents of these glands among gallers, suggests that gall formation across this clade is likely to employ a diversity of molecular strategies.

Advances in Ixodes scapularis Genetics and Genomics

Authors: Gulia-Nuss Monika[4], Nuss Andrew[3], Sharma Arvind[3], Rasgon Jason[1], Pham Michael[3], Harrell 2nd Robert[2] and Yim Won-Choel[3], [4]The University of Nevada, Reno, United States, [3]The University of Nevada, Reno, United States, [1]Penn State University, United States, [2]The University of Maryland, United States

Abstract: Ticks are obligate hematophagous parasites and are important vectors of a wide variety of pathogens. Lyme disease (LD) caused by the spirochete Borrelia burgdorferi and vectored by the black-legged tick, Ixodes scapularis, is the most prevalent vector-borne disease in the United States. Despite their importance, our knowledge of the biology of the ticks on a molecular level is limited. Advances in tick genomics and genetics have mainly been stymied by a lack of molecular tools to carry out forward and reverse genetics. Similarly, genome sequencing has been challenging due to a large (2.1 Gb) genome with long repetitive sequences. The currently available I. scapularis genome comprises of 369,495 scaffolds representing 57% of the genome. The fragmented genome further poses challenges in identifying gene sequences and therefore a high-quality genome sequence is needed for advance genomics and genetics work in this vector.

To fill these gaps, we have developed methods for targeted gene disruption using CRISPR-Cas9 and have utilized both embryo injections and a newly developed ReMOT Control (Receptor-mediated Ovary Transduction of Cargo) strategy for delivery of gene-editing reagents. In addition, we used the 10X sequencing along with chromatin capture Hi C technique to achieve chromosomal level assembly of the tick genome. We successfully assembled the genome in 28 >100Mb sequences that correspond to 28 chromosomes in I. scapularis. The availability of near-complete I. scapularis genome along with gene-editing tools that we developed will advance our knowledge of the biology of this and related tick species.

Cryopreservation effects on drone sperm Apis mellifera L. morphometric parameters and ultrastructure

Authors: Gulov Alexey[2], Bragina Yelizaveta[1], [2]Federal state budgetary scientific institution “Federal beekeeping research cent, [1]A.N. Belozersky Research Institute of Physico-Chemical Biology, M.V. Lomonosov M

Abstract: Long-term cryopreservation is detrimental to sperm function and drone fertility, killing more than 50% of the sperm during the process. Prediction of cryopreservation damage from freezing drone semen remains elusive. The purpose of this study was to assess the impact of long-term cryopreservation in “Kakpakov diluents” (C46) on morphometric measurements of sperm head of the Apis mellifera L. and ultrastructure. For the experiment, sperm samples from the cryobank of the Federal Beekeeping Research Centre (Russia), frozen since 1993, 2011 and 2013 were used. In the present study, it was found out that cryopreservation had a considerable impact on the drone sperm head morphometry. Sperm head measurements of cryopreserved samples were significantly lower compared with the extended sample for morphometric measurements of the nucleus area 3.55±0.12, 4.07±0.1, 4.31±0.04 (5.57±0.03, respectively); nucleus perimeter 10.57±0.11, 11.11±0.13, 11.59±0.05 (11.72±0.06, respectively); nucleus length 4.66±0.05, 4.82±0.06, 5.07±0.02 (5.22±0.03, respectively); nucleus acrosome length 3.72±0.08, 3.65±0.08, 3.96±0.05 (4.24±0.04, respectively). Cryopreserved and thawed spermatozoa revealed changes in ultrastructure such as vacuolation of the axoneme, intranuclear vacuoles, and loss of the derivative’s mitochondria. These details provide valuable data for further experiments on modification of the composition of cryomedium to minimize cryodamage in the semen of honey bee drones.

Environmental sensing, xenobiotic detoxification and digestive capabilities of Halyomorpha halys (Stål), the brown marmorated stink bug

Authors: Gundersen-Rindal Dawn, USDA-ARS European Biological Control Laboratory, Montpellier, France

Abstract: Halyomorpha halys (Stål), the brown marmorated stink bug, exhibits high levels of polyphagy and is a remarkably invasive insect species, having emerged as a top pest in North America and Europe. In addition to causing significant economic losses in agricultural contexts, its overwintering in human habitats makes it a considerable nuisance. To better learn of the genetic elements responsible for some of its behaviors, which in turn may serve as gene targets for use in biopesticide formulations, a genome sequencing and community annotation project was undertaken, led by USDA-ARS. These efforts have generated considerable knowledge about this insect's biology in general and the genic underpinnings of its highly polyphagous feeding behavior in particular. In this presentation, we will emphasize some of the gene families arguably most promising for biological control of this species, including chemosensory, vision-related, defensome constituents (i.e., cytochrome P450s, carboxylesterases and glutathione S-transferases), cathepsins and salivary effectors, among others. We will also discuss challenges encountered and propose means to overcome them in future genomics projects.

Evolution in Isolation: insights on evolution of dung beetles from the atypical Australasian fauna

Authors: Gunter Nicole, The Cleveland Museum of Natural History, United States

Abstract: The evolution of dung beetles (Coleoptera: Scarabaeinae) is contentious, especially the origin of the dung feeding that has been attributed to their ecological success. Today, most of the 6,600 species feed exclusively on mammal dung and the diversity of scarabaeines across biogeographic realms broadly correlates with the diversity and density of mammals in these regions. Australian native dung beetles are unique having evolved in under an entirely different set of selective pressures that the rest of the global fauna, most significantly the absence of placental mammals, and their dung, through most of their evolutionary history. Their feeding biology provide insights into ancestral traits of dung beetles and how they adapted in isolation on the Australian continent. Furthermore, most species from the Australasian endemic clade have restricted geographic ranges, we explore phylogeographic trends to provide evidence in support of a Gondwanan origin that predates colonization of marsupials to Australia.

Increased density of endosymbiotic Buchnera related to pesticide resistance in yellow morph of melon aphid

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Abstract: Many invertebrates develop into different color morphs in response to changes in environmental conditions. Color morphs can differ in their biology and stress tolerance including pesticide resistance, but underlying mechanisms are unclear. In this study, we found that yellow morphs (predominant in hot summer conditions) of an agricultural pest, the melon aphid Aphis gossypii, have higher levels of resistance to the commonly-used pesticides imidacloprid and sulfoxaflor compared to the green morphs (predominant in cooler spring and autumn conditions), while no difference was found in morph resistance to the antibiotic/pesticide avermectin. Transcriptome analysis and biochemical assays of enzyme activities revealed no differences in metabolic processes between the two color morphs except for differentially-expressed genes related to wing development. Microbiome analysis revealed that the endosymbiont Buchnera aphidicola is the dominant bacterium in both morphs, representing 86.76%-99.88% of the microbiome. The yellow morph had a higher density of Buchnera compared to the green morph. When yellow morphs were treated with avermectin and antibiotics, the density of Buchnera was reduced to levels similar to the green morph, and their susceptibility to imidacloprid was simultaneously increased. These results indicate an association between resistance in the yellow morph of A. gossypii and symbiotic bacteria, providing novel insights into pesticide resistance mechanisms and the plasticity of stress adaptation.

Are ecological communities the seat of endosymbiont horizontal transfer and diversification? A case study with soil arthropod community

Authors: Gupta Manisha, Indian Institute of Science Education and Research, Mohali (IISER-Mohali), Knowledge city, Sector 81, SAS Nagar, Manauli, PO 140306, Punjab, India, India

Abstract: Maternally inherited endosymbionts are one of the most abundant bacteria infecting arthropods and show extensive horizontal transfer. Such widespread distribution and extensive recombination among these endosymbionts could be an outcome of horizontal transfer as for such genetic exchanges to occur their hosts should come in contact. One such level of biological organization where different hosts can do that is the ecological community. Despite various studies focusing on known model species and specific ecological interactions among hosts, reports on community wide endosymbiont data are rare. To better understand endosymbiont spread, we investigated the incidence, diversity, extent of horizontal transfer and recombination of three such endosymbionts (Wolbachia, Cardinium and Arsenophonus) in a specific soil arthropod community. Wolbachia strain characterization was done using multiple genes whereas single 16S rRNA gene was used for Cardinium and Arsenophonus. Amongst 3509 individual host arthropods belonging to 390 morphospecies, 12.05% were infected with Wolbachia, 2.82% with Cardinium and 2.05% with Arsenophonus. Phylogenetic incongruence between host and endosymbiont indicated extensive horizontal transfer of endosymbionts within this community. Three cases of recombination between Wolbachia supergroups and eight incidences of within supergroup genetic exchange were also found. Statistical tests of similarity indicated supergroup A Wolbachia and Cardinium to show a pattern consistent with rapid horizontal transfer within the community. However same tests done for super group B Wolbachia and Arsenophonus did not show similar patterns. We highlight the importance of extensive community wide studies for a better understanding of the spread of endosymbionts across global arthropod communities.

Assemblage structure, functional diversity and predation patterns of spiders (Araneae) across landscape complexity gradients in brassica production systems

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Abstract: The accelerating loss of farmland natural enemy diversity due to agricultural intensification and anthropogenic activities can impair the viability and functioning of the agro-ecosystem. To prevent the loss of natural enemies in an agroecosystem, it is necessary to precisely understand the multiple factors involved in shaping the assemblage of species and their foraging patterns. However, there is a scarcity of information on the response of predator assemblages and their predation patterns in highly dynamic agroecosystem such as those that are common in smallholder production systems, especially in response to local management and surrounding landscape composition. Focusing on spiders, essential providers of biological control, we tested the influence of local and landscape factors as the filters of taxa, functional assemblages and prey items in brassica vegetable fields. At the local scale, the crop identity showed a significant influence on all taxonomic and functional diversity measures. In contrast, pesticide regime had a significant influence only on the taxonomic measures of spiders but not on functional diversity. Local and landscape-scale factors interacted such that high proportions of cauliflower crops (a complex plant structure and longer duration crop than Chinese cabbage) and neighboring forest fragments positively influenced the assemblage of both taxonomically and functionally diverse spider assemblages including many web and non-web builders. In contrast, pesticide-treated Chinese cabbage (a simple plant structure and shorter duration crop than Chinese cauliflower) fields surrounded with simple landscape had impoverished assemblages of spiders and were dominated by active hunters (such as ground runners). Next-generation sequencing-based food web analyses confirmed that resource partitioning occurred in terms of abundance and diversity of prey taxa in the gut of spiders. Prey of Araneidae, Lycosidae, Pisauridae, Salticidae and Thomisidae spiders were enriched with dipterans, coleopterans, hemipterans, lepidopterans and orthopterans along with a wide range of other prey groups. These results suggested that in a highly dynamic agroecosystem, the existence of structurally complex crop species and conservation of neighboring forest patches can play a potent role in protecting the loss of farmland biodiversity and lessen the damaging effects of conventional management schemes, which in turn can offer an improved level of pest suppression and decrease the crop damage. The dietary patterns correspond well with the generalist foraging behavior of spiders and making them important taxa in encouraging and strengthening the biological control efforts in agroecosystems.

Working with smallholder farmers in Papua New Guinea to protect sweetpotato crops using habitat manipulation, organic mulches, and Entomopathogens.

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Abstract: Sweetpotato is the major food staple in Papua New Guinea, integral to the culture of its peoples, and key to economic development. The crop is heavily attacked by a complex of arthropod pests yet farmers currently have little knowledge of management options and commonly plant new crops immediately adjacent to older (infested) crops, contributing to large yield gaps. Current efforts to transition sweetpotato production to more intensive production as a cash crop demand the development of effective pest management tactics that are suitable for use in remote areas with poor access to inputs and extension support. Here we report on a project in which a package of low-tech and biologically-based methods is being developed and tested on farms in the Highlands of Papua New Guinea. Habitat manipulation approaches include planting of new crops several meters from other crops, into beds that are free of weeds and residue from the preceding crop, and surrounded by a row of barrier plants to repel adult sweetpotato weevils and potentially provide floral resources to natural enemies of pests. Mulches of locally-available plant materials are being screened in laboratory and on-farm studies to identify those that protect sweetpotato storage roots from attack by weevils, and some of these treatments promote natural enemies. Entomopathogenic fungi, that could be produced in 'cottage industry' enterprises, have been screened in the laboratory and optimal isolates are now being tested on farms in conjunction with mulches that provide protection of the fungus from desiccation and ultraviolet light, and may even constitute a substrate for fungal growth. Together with the use of clean planting material and sex pheromone trapping of sweetpotato weevil adults, these biologically-based strategies have doubled marketable yields in the first year of on-farm trials.

Not just more plants, but the right ones: species richness and traits supporting ecosystem services on East African smallholder farms.

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Abstract: Because smallholder farmers typically do not use expensive agricultural inputs such as pesticides, they are highly reliant on ecosystem services such as natural pest regulation. However, evidence suggests many smallholders do not fully appreciate the benefits they receive from such ecosystem services. Consequently, there is a need to ensure strong evidence-based guidelines on optimal management of field margins and non-crop vegetation, to support beneficial insects like pollinators and natural enemies. We studied 32 smallholder fields of common bean (Phaseolus vulgaris) across Tanzania and Malawi, as beans are an important protein source for communities in these regions. By combining botanical surveys with insect trapping and observational transect walks we were able to build interaction networks and analyse associations between plant species and insect functional groups. We discovered that plant species richness positively predicts beneficial insect abundance and activity overall, and several aspects of network structure (e.g. robustness). Natural enemies of pests such as aphids were significantly associated with fields where herbaceous plant richness was high, but the importance of native species was less clear-cut. Farms with higher tree species richness also had higher levels of carpenter bee visitation on the crop, and trees were overrepresented among those plant species predictive of beneficial insect abundance. Several plant species associated with beneficial insects, such as Bidens pilosa, Ageratum conyzoides and Tithonia diversifolia, also have pesticidal properties when processed by farmers into a spray or drench, and so are promising candidate plants to support multiple ecosystem services on smallholder farms. As fields with plant-rich field margins benefited from more pollinator activity and lower pest damages at the crop edges, establishment of field margins is recommended. However, many of the plant species associated with beneficial insects were non-native to the regions, and the implications of promoting such species should be considered carefully.

Field and landscape management to support beneficial arthropods for IPM on vegetable farms

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Abstract: The colonization of arthropods in an agricultural field depends on the arrangement of land-cover types (landscape complexity) and its effects on the factors that control the exchange of species between the habitats. Landscape complexity almost always increases the abundance and diversity of natural enemies by providing resource subsidies such as shelter, nectar, alternative food sources, and pollen. Many natural enemies are influenced by the non-crop habitats surrounding the agricultural fields. We surveyed 492 focal crops including sweet corn, brassica, carrot, lettuce, capsicum, and beans field, across Australia, to determine if, and at what scale, adjacent land-use types influence the abundance and diversity of pests and natural enemies. We identified and measured the pest and natural enemy populations in the edges of focal crops adjacent to different habitats. We found that the diversity and density of both pests and natural enemies are significantly influenced by the adjacent land-use types. Non-crop vegetation such as riparian strips and shelterbelts tended to be associated with higher numbers of natural enemies and lower numbers of pests in the nearby edges of vegetable crop fields. Field centres, in contrast, had more pests and fewer natural enemies, suggesting that (i) riparian vegetation and shelterbelts are donor habitats for beneficial arthropods and that could be associated with pest suppression and (ii) the spatial scale at which vegetation patterns on farmlands affect in-crop pest and beneficial densities is small, at least for many key taxa. Crops of a given vegetable species planted contiguously tended to have fewer beneficial arthropods and more pests but separating crops by areas of other land uses, including crops of other species, improved the composition of arthropod communities. Notably, pests were similar in number across both organic and conventionally managed crops, whereas natural enemies were significantly higher in organic fields. This suggests that synthetic insecticides may not be essential; natural enemies can adequately check pest outbreaks in the absence of synthetic insecticide use.

Microbial influence in the niche shift of an insect pest: Drosophila suzukii

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Abstract: Insect-microbe interactions provide insights about how the microbes might act as resources for the insects, be it beneficial or non-beneficial. Hence, it is essential to understand whether microbes associated with an insect influence its life history traits. Drosophila suzukii is an invasive insect pest of soft fruits with its origin in South Asia. It infests ripening fruits, unlike the other members of its family Drosophilidae that infest rotten fruits. The fundamentals of D. suzukii in the Netherlands are backed by a limited study of its microbiome. We have characterized the bacterial and fungal communities in D. suzukii in order to address the question of whether its pest status is contributed by its associated microbes.

Demography of the Filbert Aphid, Myzocallis coryli (Goeze) (Hemiptera: Aphididae) on three different hazelnut species

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Abstract: The filbert aphid Myzocallis coryli (Goeze) is a serious aphid pest of hazelnut in North America, Italy, Spain, and Turkey. M. coryli were reared on three hazelnut species including Corylus avellana (L.), Corylus colurna L. and Corylus maxima Mill. under laboratory conditions to assess the resistance of hazelnut species to the aphid. Prolonged developmental times result in longer exposure of the more vulnerable, immature stages of the pest to natural enemies. In addition, the use of host-plant resistance together with biological control has been proposed as a sustainable alternative to chemical control. The developmental times of preadult and adult stages, total longevity, reproduction, and life table parameters were analyzed according to age-stage, two-sex life table theory, in which the stage differentiation and variable developmental rates among individuals could be described. The intrinsic rate of increase (r) and finite rate of increase (λ) varied among the species. The highest values were found for aphids reared on C. maxima (r= 0.2330 d-1, λ=1.2624 d-1), which differed significantly from C. colurna (r= 0.1944 d-1, λ=1.2146 d-1), whereas these parameters were lowest for C. avellana (r= 0.1838 d-1, λ=1.2018 d-1). Based on longer nymphal and preadult development periods, adult longevity together with the demographic parameters, C. avellana provide an unfavorable environment for the filbert aphid than the other species. The results obtained from demographic data together with estimates of pest growth potential generated by computer projection based on age-stage, two-sex life table theory, demonstrate that C. maxima is the most susceptible species to M. coryli among the tested hazelnut species.

Local and landscape effects of bioenergy cropping on arthropod traits and pest suppression

Authors: Haan Nathan[1] and Landis Douglas[1], [1]Michigan State University

Abstract: Bioenergy cropping could transform landscapes in coming decades and have sweeping impacts on biodiversity and associated ecosystem services like pest suppression. The nature of these changes will depend on which crops are adopted, how they are managed, and which ecosystem types they replace. We censused several taxonomic groups and measured pest suppression rates in a long-term experimental array containing ten bioenergy cropping systems including three intensive annual crops, four simple perennial grass systems, and three complex perennial polycultures. Species richness of most groups varied strongly across cropping system types and was usually low in annual systems, somewhat higher in simple perennial systems, and highest in complex perennial polycultures. Functional group composition of ground beetles and ants, which can be important predators of crop pests, also varied among crop types with predatory species often being more well-represented in perennial crops. Predation potential, which we measured by quantifying attack rates on plasticine caterpillars, also varied strongly among cropping systems and usually mirrored biodiversity trends. Expansion of arable bioenergy crops is likely to reduce biodiversity and erode biocontrol services, while replacing marginal annual crops with complex perennial bioenergy habitats could enhance them.

Time-series to study insect decline

Authors: Habel Jan Christian, University of Salzburg

Abstract: Historical data sets show a rapid and continuous decline in insect diversity. Large data sets collected over long time periods and across large spatial scales show a dramatic decline in insect diversity as well as abundance and thus biomass during the past decades. In addition, species communities are changing significantly, proving that numerous species are suffering from agricultural intensification. Here, in particular specialist species are vanishing rapidly acorss landscapes. An assessment of the current situation and an estimation of future trends is only possible by considering historical data sets collected over several decades.

Toward reference quality assemblies of agricultural pest insects, updates from the Ag100Pest Initiative

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Abstract: The Ag100Pest goal is to produce annotated, reference quality genome assemblies for the top arthropod agricultural pests in the United States. The Ag100Pest prioritization team is considering approximately 400 species nominations and establishing selection criteria for arthropod pests of US field crops, livestock, bees, trees, and stored products as well as foreign pest species considered potential invasive threats to US agriculture. The foundation for these genome assemblies will be PacBio single molecule data, from a single insect when possible. This data is further combined with Illumina, 10X Genomics, and HiC data to generate chromosome-scale assemblies to serve as a foundation for these pest species.

Beyond genomes, Ag100Pest teams are developing best practices that will benefit the entire arthropod genomics community. Examples of high quality assemblies created from single insects will be presented, using CLR long reads and compared to HiFi reads. Additionally, standard, low, and ultra-low input methods will be demonstrated, towards creating routine methodologies for high-throughput whole genome assemblies.

A Universal Food Immunomarking Technique (UFIT) for Studying Arthropod Feeding Activities

Authors: Hagler James, USDA-ARS Arid-Land Agricultural Research Center, United States

Abstract: The molecular identification of predator feeding activity relies almost exclusively on the use of species-specific polymerase chain reaction (PCR) assays. However, there is viable alternative to the PCR assay approach. The method consists of tagging potential food items with exogenous protein(s). In turn, the guts of foraging arthropods can be examined for the presence of protein-marked food items by a suite of standardized protein-specific sandwich ELISAs. I will discuss how this universal food immunomarking technique (UFIT) can be adapted to pinpoint life stage-specific predation events, cannibalism, and scavenging.

Does the source matter for SIT? No effects of x-ray vs gamma irradiation on sterilization or sterile male performance in the mosquito Aedes aegypti.

Authors: Hahn Daniel[1] and Chen Chao[1], [1]University of Florida, United States

Abstract: Sterile insect technique (SIT) can be effective as a component in area-wide integrative pest management for multiple insect pests. SIT may be particularly useful for vector mosquitoes like Aedes aegypti that live in close proximity to humans, occupy cryptic larval breeding sites with adults resting in places difficult to reach with insecticide sprays, and that have populations showing resistance to common chemicals. For SIT, males are typically sterilized by exposing them to gamma radiation. However, gamma irradiators are not always available of easily accessible due to restrictions on the radio-isotopes used. One solution to this problem is to irradiate male mosquitoes using x-rays rather than gamma sources because x-ray irradiators are readily available, relatively affordable, and do not require the stringent safety and security restrictions necessary for gamma irradiators. Here we compare an established gamma irradiator heavily used for an operational Ae. aegypti SIT pilot program with that of a new x-ray irradiator for sterilizing male pupae and adults while maintaining male performance after irradiation. Our results show Aedes aegypti SIT programs can successfully transition from gamma to x-ray sources, and new programs can begin using x-ray irradiation sources to avoid regulatory and cost hurdles associated with gamma sources.

Invasion Dynamics, Prediction and Spread of Accidental Introductions of Natural Enemies

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Abstract: In nearly all global regions, various natural enemy species have been accidentally transported with cargo and passengers outside of their natural ranges. In regions where they encounter hosts, several species have established. The ability of accidentally introduced natural enemies to become established and spread depends in part on the biologies of the natural enemy and host. We propose theories to help explain and predict which natural enemies are more likely to be transported and easily established after introduction. For example, entomopathogens and insect-parasitic nematodes causing more chronic infections could be introduced easily along with invasive hosts. More virulent natural enemies, such as parasitoids would have a better chance of becoming established if host populations are already present in invaded areas. Examples of different scenarios will be provided as well as data on interceptions of natural enemies that document their transport.

Large-scale multi-year trends using benthic arthropod COI metabarcodes as bioindicators

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Abstract: Canada holds 20% of the world's total freshwater resources consisting of a large number of river systems, lakes and wetlands. In order to reinforce biomonitoring capabilities of the Canadian Aquatic Biomonitoring Network (CABIN) we began piloting the use of benthic DNA metabarcoding in key areas such as the Peace-Athabasca delta in northern Alberta. Climate change is causing an increase of freshwater evaporation and reduction in the frequency of ice-jam flooding in this region. Through analyzing layers of richness data across 6 years of biomonitoring in the delta, we detected similar biodiversity trends which correlated with recent flooding events in 2011 and 2014. At a local scale, annual differences in benthic arthropod community composition compared to our baseline was driven largely by turnover, whereas at a broader scale, differences were largest when measured over time. Assessing biodiversity change through investigating different levels of richness and function at different spatial and temporal scales is essential for better understanding the effects of global ecosystem perturbations on benthic macroinvertebrates. Since 2018, we began a Canada wide project, STREAM (Sequencing the Rivers for Environmental Assessment and Monitoring) by merging the sampling capacity of community-based monitoring with benthic DNA metabarcoding. This effort will set the stage for routine application of DNA-based biomonitoring across all Canadian watersheds.

Hazard assessment of oak processionary moth (Thaumetopoea processionea L.)

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Abstract: The growing presence of oak processionary moth (OPM), Thaumetopoea processionea L. (Lep., Thaumetopoeinae), in Central Europe since the 1990s and the concomitant consequences for the vitality of the host trees and human/animal health urgently require hazard assessment and control strategies. Regarding climate change, increased intensities of oak tree defoliation and human/animal infections with the urticating hairs (setae) released by the larvae are expected.

For hazard assessment, the online early warning system “PHENTHAUproc“ was generated. This tool comprises six different models, i. a. newly developed, temperature-based phenology models for bud swelling of oak (Quercus robur L.) and for the non-overwintering OPM stages. The prototype of PHENTHAUproc which was created and validated for Germany gives local predictions (for the sites of meteorological stations) and regional predictions (map service). The early warning system provides information on OPM-related hazards for the public and decision support of planning and implementation of appropriate and effective integrated pest management for professionals to protect oak tree vitality and human/animal health in forest, urban and rural areas.

Best management plans for rose rosette disease: A threat to roses worldwide

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Abstract: Rose rosette disease (RRD) is a fatal viral disease of roses. Most infected plants die within 2-3 years. Symptoms include a profusion of thorns, thin elongated leaves, thickened stems and dense witches’-broom growth. The only known vector is an eriophyid mite, Phyllocoptes fructiphilus. These tiny mites spread to other plants by floating in the wind. The populations of P. fructiphilus are forty times higher on tissues collected from rose shoots symptomatic for RRD than asymptomatic foliage on the same plant. The use of miticides has had mixed results in protecting roses from infection. Two other eriophyid mite species have been found on roses infected with Rose Rosette Virus (RRV): Eriophyes eremus and Callyntrotus schlechtendali. It is not known if these mites can vector RRD. The search for host plant resistance is ongoing with rose trials in Tennessee, Delaware, Oklahoma and a few in Texas.

Elevated CO2 alters the effect of plant silicon on aphids and their parasitoids

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Abstract: Many grasses take up large amounts of silicon (Si) which acts as a potent physical defence against insect herbivores. Silicon supplementation has also been linked to the jasmonic acid (JA) signalling pathway, which underpins a wider array of anti-herbivore defences. We recently found that elevated CO2 (eCO2) decreases silicon uptake through the suppression of the JA pathway. Despite this decrease, we found that silicon remained an effective defence against herbivory by a pest caterpillar (Helicoverpa armigera) under eCO2. Aphids, however, are thought to be less susceptible to physical Si defences and in some cases respond positively to eCO2. Si and eCO2 induced changes in phytohormone signalling, and subsequent changes in plant quality may not only affect herbivores but also their natural enemies. To date, only a few studies have investigated the effect of Si uptake on tritrophic interactions and none have linked this to changes in defensive phytohormonal pathways under eCO2. We investigated the effect of Si on a plant-aphid-parasitoid system, using a common pasture grass, Phalaris aquatica, which is known to produce a range of toxic alkaloids. The aphid, Rhopalosiphum padi, and its hymenopteran parasitoid (Aphidius colemani) were reared on plants grown with and without Si under both ambient and elevated CO2. Alkaloid and phytohormone concentrations were quantified in response to Si supplementation, CO2 and aphid infestation. We found that aphids significantly reduced Si uptake due to lower endogenous JA. Host aphid (mummy) size was significantly larger on non-Si plants but only under ambient CO2. While the reverse was true on eCO2 plants, i.e. mummy size was larger on Si plants. Parasitoid size however, was only larger on non-Si plants under ambient CO2. Fewer parasitoids emerged from aphids reared on Si supplemented plants under ambient CO2 while those on eCO2 plants emerged on average two days earlier. The difference in plant quality due to Si supplementation reduced host aphid quality and subsequent parasitoid development but only under ambient CO2. We found that the effects of Si on higher trophic levels depend on CO2-related changes in both host plant and aphid quality.

Laboratory and field studies on leptotriene, a component of the male-produced aggregation pheromone of the western conifer seed bug, Leptoglossus occidentalis, an invasive pest of pine trees in Europe

Authors: Hall David[2], Ponce-Herrero Laura [3], Pajares Juan[3], Millar Jocelyn[1] and Zou Yunfan[1], [2]Natural Resources Institute, University of Greenwich, [3]Sustainable Forest Management Research Institute, University of Valladolid-INIA, [1]Departments of Entomology and Chemistry, University of California, Riverside, CA

Abstract: The western conifer seed bug, Leptoglossus occidentalis Heidemann (Heteroptera: Coreidae) is native to North America but was introduced into Europe in the 1990s, and has since spread rapidly throughout the continent. This species is a specialist feeder on conifer seeds. In both its native and invasive ranges it can be a major pest in conifer seed orchards, and in Europe it is of particular concern to growers of edible pine nuts.

One male-specific component of the volatiles collected from virgin male L. occidentalis elicited a strong electroantennogram response from both male and female bugs in coupled gas chromatography-electroantennography analyses. This was isolated, and identified as a unique sesquiterpene which was synthesised and given the trivial name "leptotriene".

Trapping studies in Spain showed that synthetic leptotriene was highly attractive to both female and male L. occidentalis. Addition of possible minor components did not consistently affect this attractiveness.

In laboratory studies over three years, male L. occidentalis typically produced leptotriene in two periods during February-March and July-August, whereas trap catches in the field were highest in September-October. The reasons for this will be discussed along with the possible roles of potential minor components of the sex/aggregation pheromone.

Friend or foe? Drosophila suzukii interactions with fungi

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Abstract: Interactions between Drosophila and fungi range from mutualistic, such as the "farming" and dispersal of yeasts, to antagonistic competition and parasitism. While most drosophilids rely upon yeast rich fermenting substrates such as overripe fruit, the invasive pest Drosophila suzukii attacks ripe, unspoiled fruit. Despite this unique niche, fungi significantly impact D. suzukii's life history. D. suzukii feed upon a variety of yeast species; in particular, Hanseniaspora uvarum has been recovered from 93% of field collected larvae (n = 56 across 4 sites and 2 states) and 100% of adults (n = 11 across 2 sites and 1 state). Yeasts are critical for D. suzukii larval survival, impacting adult and larval behavior. In addition to yeasts, D. suzukii co-occurs with fruit rot fungi. We are characterizing adult and larval D. suzukii fungal communities, as well as evaluating the nature of their relationship with fruit rot fungi. Understanding how D. suzukii interacts with fungi may lead to the development of novel sustainable pest management strategies for this fruit pest. If D. suzukii influence fruit rot epidemiology, improved insect and pathogen management programs may also be developed.

Managing Natural and Constructed Agricultural Wetlands for Athropod Biodiversity

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Abstract: Wetlands in the agricultural landscape has been the focus of numerous studies where emphasis on arthropod diversity in the light of wetland construction and re-construction is key. However, when considering agricultural wetlands as highly productive ecosystems, where successional transition is incredibly rapid; one must also consider the way in which such a habitat is managed. Its structure will soon change if left to its own accord, and with it, the arthropod community within. Therefore, the aim of this project is to understand what mechanisms drive arthropod diversity in agricultural wetlands, how these mechanisms affect arthropod interactions, and what effect management has on them. This will be achieved by studying what effect microhabitat, flood zones, hydrology and primary production has on the arthropod community; and also what beneficial effects wetland arthropods can have on the surrounding agricultural landscape. Arthropod collection will be performed by malaise-, and emergence trapping, aspiration collection and hand collecting; and gut-content analyses will be done using metabarcoding techniques and subsequent sequence comparisons to the Barcode of Life database. By looking at the effect of management on these variables, regimes for how an agricultural wetland should be managed in order to maximize arthropod diversity can be created. At the same time an understanding on how management can affect the interactions in the community is gained, which is also important when considering how management should be performed.

The power of next-generation sequencing to resolve the population structure of an invasive insect pest, Anoplophora glabripennis

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Abstract: Asian longhorned beetle (Anoplophora glabripennis – ALB), is a native forest pest in mainland China and the Korean peninsula. This species has successfully invaded and spread to hardwood forests in North America and particularly in Europe. ALB mines the heartwood of a range of tree species and poses a significant threat to all newly invaded forest ecosystems. The key to reducing this risk is via early detection and intervention. We are working on developing biosurveillance tools that allow the end-users in plant protection agencies and at the border control with a single test to identify simultaneously species, source of the intercepted specimen and adaptive traits that suggest risk for establishment. In this study, we generated genome-wide molecular markers using high-throughput sequencing technology (Genotyping-by-Sequencing) to characterize genetic variation within and among native ALB populations. Our results show clear population differences between ALB populations in China and South Korea, as well as pronounced population structure within China. These genomics-based results provide much greater clarity on ALBs native population structure than earlier work on mitochondrial DNA and microsatellites was able to. The new results also provide important insights from a genomics perspective into the history of human-mediated dispersal of ALB and the substantial potential for local adaptation within its native range. These data lay the foundation for the development of target-enriched biosurveillance tools that will help us increase preparedness and facilitate early action against ALB.

Bacterial Communities Associated with Two Parthenogenetic Aphid Species Cocolonizing Pomegranate across Morocco

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Abstract: Like many insects, aphids (Hemiptera: Aphididae) can harbor a wide diversity of inherited symbiotic bacteria that can be important drivers of their evolutionary ecology. In addition to the obligate nutritional symbiont Buchnera aphidicola, these phloem-sap feeding insects can host various facultative symbionts whose functional diversity depends on complex interactions between the genotype of the host and that of the bacterial partners, and on the other hand, between the genotype of the partners and environmental factors. In this study, we examined the distribution of two parthenogenetic aphid species (the melon aphid, Aphis gossypii, and the pomegranate aphid, A. punicae) cocolonizing pomegranate trees (Punica granatum) across Morocco. We also determined the diversity of symbionts associated with these two aphid species to compare the bacterial communities sheltered by aphid species feeding on the same host plant species, but displaying different lifecycles and a very different feeding ecology, and to test the hypothesis that environmental factors contribute to shaping the bacterial communities associated with insects. We found that A. punicae was mainly distributed in coastal areas, while A. gossypii was more widely distributed in inland areas. Deep 16S rRNA sequencing and species-specific diagnostic screening enable us to establish that the overall symbiotic diversity sheltered by these two aphid species is low compared to that found in the pea aphid Acyrthosiphon pisum. We found that the symbiont communities differed significantly between the two species: the highly polyphagous species A. gossypii harbored a more diverse bacterial community than the oligophagous species A. punicae. Prevalence of Arsenophonus infections was particularly high in A. gossypii populations. The symbiont communities also differ across aphid populations sampled from the different bioclimatic zones, suggesting that environmental factors contribute to shaping the bacterial communities associated with aphids.

Phenotypic plasticity explains violation of Dollo’s law of irreversibility

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Abstract: Dollo’s law states that traits once lost during the course of evolution will not re-appear, but recently several violations of this law have been described. Using both an experimental and theoretical approach, we show that an archetypal violation of Dollo’s law, the loss and regain of fat synthesis in parasitic wasps, actually concerns the evolution of plasticity. First, using replicated experiments, we showed that fat synthesis can be switched on or off depending on the developmental environment (fat content of the host). Second, a comparative protein domain analysis revealed that key enzymes involved in fat synthesis have remained functional over extended evolutionary times (~350 my). Third, computer simulations showed that a regulatory switch can remain functional within the genome for millions of generations, even when only sporadically used. The evolution of plasticity could explain other presumable violations of Dollo’s law. Our results can further explain how adaptations to rare and extreme environmental events can be maintained over long evolutionary times.

Cerambycid beetle pheromones: a cornucopia of new compounds and monitoring tools for invasive, endemic, and endangered species

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Abstract: The chemical ecology of the large beetle family Cerambycidae remained almost unexplored until early this century, despite the growing importance of cerambycids as invasive species as a result of ever-increasing global commerce. It had even been suggested that cerambycids made very limited use of pheromones. In fact, the reverse appears to be true; over the past 15 years, there has been a veritable explosion in the number of sex and aggregation pheromones identified from this family, with attractant pheromones now identified from several hundred species in the 5 major subfamilies, and many more in progress. Initial screening studies with known pheromones and analogs suggested that the structures might be highly conserved within related taxa. However, more recent studies targeting pheromone identifications from individual species have shown that the bioactive compounds vary from being apparently unique, species-specific compounds, through to compounds which are shared by species on all six habitable continents. Thus, the latter types of chemical signals must have persisted unchanged for millions of years as speciation occurred and the continents separated. An increasing variety of chemical structures also are being identified, including compounds containing nitrogen and sulfur. In parallel with the identification of novel pheromones, optimization of traps and lures has greatly improved the efficiency of pheromone-based trapping. In sum, this has resulted in increasing recognition of the value of this technology, and increasing uptake into monitoring and surveillance protocols, particularly for invasive species. Pheromone-based monitoring is also proving to be a valuable tool for sampling the ranges and population sizes of endangered cerambycid species. This presentation will summarize the rapid progress in elucidating the chemical ecology of cerambycids since the turn of the century. It will also emphasize some of the more basic and still unanswered ecological questions with regard to patterns of pheromone use within this large and diverse insect family.

The importance of regulatory small RNAs in small symbiont genomes

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Abstract: Organelles and host-restricted bacterial symbionts are characterized by having highly reduced genomes that lack many key regulatory genes and elements. Thus, it has been hypothesized that the eukaryotic nuclear genome is primarily responsible for regulating these symbioses. However, with the discovery of organelle and symbiont expressed small RNAs (sRNAs) there is emerging evidence that these sRNAs may play a role in gene regulation. Here, we reveal that a conserved antisense sRNA in the model mutualistic aphid endosymbiont genome, Buchnera, is important in post-transcriptional expression of an important protein involved in Arginine biosynthesis; an important symbiont product of the ~200 million-year obligate symbiosis with its insect host. We further demonstrate that conserved Buchnera sRNAs are differentially expressed under different developmental and nutritional environments and are present in other Hemipteran-symbiont systems as well. These conserved sRNAs are potentially important in regulating essential amino acid biosynthesis with its insect host.

Pheromones and neural circuitry underlying sexual isolation in Drosophila

Authors: Hansson Bill[1] Knaden Markus[1], Khallaf Mohammed[1], [1]Max Planck Institute for Chemical Ecology, Germany

Abstract: Insects use distinct sex pheromones as a reproductive isolating mechanism to attract only conspecific mating partners. Genetic and neural variations that contribute to the evolution of pheromone signaling systems remain unclear. Here, we identify various male-specific compounds in the four subspecies of Drosophila mojavensis, an established model for incipient speciation. One of these compounds, is detected by olfaction in all subspecies, is exclusively present in two of them and induces their female receptivity. This female receptivity is governed by OR65a ortholog whose neural circuit innervation and underlying behavior differ from the Or65a circuit of D. melanogaster. Mutational analysis and behavioral experiments indicate that the novel compound and the novel Or65a circuitry are major drivers of the sexual isolation among the closely-related subspecies. Together, these results advance our understanding of nervous system alterations underlying sex pheromone evolution and provides novel evidences for an ongoing speciation process in D. mojavensis subspecies.

Evolution of sex pheromones across the genus Drosophila

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Abstract: Most insects use sex pheromones as a reproductive isolating mechanism to attract only conspecific mating partners. Despite the profound knowledge of Drosophila melanogaster sex pheromones, little is known how other drosophilids regulate their social and sexual behaviors. Here we analyze the chemical profiles of 101 species within the genus Drosophila to elucidate how species-specific signals can contribute to form premating isolation barriers. Chemical and genetic analyses indicate a correlation of the chemometric profiles and the phylogenetic relation of drosophilid flies. Through a series of chemical synthesis, we identify 46 novel male-specific compounds, many of them are transferred to females during copulation. Electrophysiological recordings of pheromone sensory neurons in all species to all male-transferred compounds revealed the specificity of the pheromone detection system in Drosophila. Finally, we test all these compounds in courtship assays for their behavioral role in female receptivity and male courtship inhibition. Our results increase the understanding of the evolution of Drosophila pheromones and show how sexual isolation barriers between species can be created by species-specific olfactory signals.

Drosophila attractiveness boosted by alcohol -

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Abstract: Drosophila has in earlier studies been shown to be attracted to ethanol. Different, sometimes quite anthropomorphic explanations have been discussed. In the present study we revisit vinegar fly alcohol attraction in the context of sexual attraction. We show that access to alcohol, especially methanol, has a boosting effect on male attractiveness to females. We proceed to investigate the olfactory pathways underlying attraction to alcohol and present a possible scenario for how attraction to certain types of fruit allows access to alcohols and thereby interacts with the fly's pheromone production. We propose that this interaction is the true background to alcohol "addiction" in vinegar flies.

Neuroethology of feeding and oviposition behavior in the hawkmoth Manduca sexta

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Abstract: Female hawkmoths, Manduca sexta, use olfactory cues to locate nectar sources and oviposition sites. We investigated how a large set of ecologically important and chemically diverse odors is coded in the antennal lobe (in vivo calcium imaging), which behavioral relevance the same odors have (wind tunnel experiments), and if there is a correlation between the activity level of single olfactory glomeruli and the observed feeding and oviposition behavior. Next, we aimed at identifying odorant receptors that target these behaviorally relevant glomeruli, and therefore expressed individual odorant receptors of the moth heterologously in the antennae of the vinegar fly Drosophila melanogaster. Using the same odors as before, we were able to correlate the response profiles of odorant receptors and olfactory glomeruli. Our results are a step forward towards unraveling the neuronal circuits underlying odor-guided behaviors in the hawkmoth.

Subpopulation of lateral horn output neurons is required for odor avoidance and aggression behavior

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Abstract: Animals exhibit innate attraction or aversion behaviors in response to olfactory cues. In Drosophila, a higher-order olfactory center called the lateral horn (LH) is believed to be involved in coding olfactory-induced innate behaviors. Unlike the early olfactory processing centers, our knowledge of odor processing in the LH is still scant. Here, we identify a subset of LH output neurons that encodes and mediates odor aversion. Using 2-photon calcium imaging, we show that 3-4 neurons of this cluster respond strongly to aversive odors with no or weak responses to attractive odors. Moreover, this cluster contains, at least, one neuron that is activated exclusively by the sex pheromone cVA. Interestingly, our results show that odor representations are different between the input and the output site of these third-order neurons, which implies that odor responses are modulated along their processing pathway. Finally, silencing this cluster of third order neurons abolishes avoidance behavior while attraction is not affected. In summary, our data shows that the olfactory information from distinct input channels converges in these higher order neurons to mediate the same behavioral output.

Developmental and sexual divergence in the olfactory system of the marine insect Clunio marinus

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Abstract: An animal's fitness strongly depends on successful feeding, avoidance of predators and reproduction. All of these behaviours commonly involve chemosensation. As a consequence, when species' ecological niches and life histories differ, their chemosensory abilities need to be adapted accordingly.

The intertidal insect Clunio marinus (Diptera: Chironomidae) has tuned its olfactory system to two highly divergent niches. The long-lived larvae forage in a marine environment. During the few hours of terrestrial adult life, males have to find the female pupae floating on the water surface, free the cryptic females from their pupal skin, copulate and carry the females to the oviposition sites. In order to explore the possibility for divergent olfactory adaptations within the same species, we investigated the chemosensory system of C. marinus larvae, adult males and adult females at the morphological and molecular level.

The larvae have a well-developed olfactory system, but olfactory gene expression only partially overlaps with that of adults, likely reflecting their marine vs. terrestrial life styles. The olfactory system of the short-lived adults is simple, displaying no glomeruli in the antennal lobes. There is strong sexual dimorphism, the female olfactory system being particularly reduced in terms of number of antennal annuli and sensilla, olfactory brain centre size and gene expression. We found hints for a pheromone detection system in males, including large trichoid sensilla and expression of specific olfactory receptors and odorant binding proteins.

Taken together, this makes C. marinus an excellent model to study within-species evolution and adaptation of chemosensory systems.

Chemical and reverse chemical ecology of a moth: what can we learn from the deorphanization of Spodoptera littoralis odorant receptors?

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Abstract: In the recent years, the development of high-throughput sequencing technologies has highlighted the diversity of insect odorant receptors (ORs). These ORs are transmembrane proteins expressed in olfactory sensory neurons, and they are at the core of odorant detection. Each species has evolved a unique repertoire of ORs whose functional properties are expected to meet its ecological needs, though little is known about the molecular basis of olfaction outside Diptera. Using transcriptomics and genomics, we have identified the whole set of larval and adult ORs in the cotton leafworm Spodoptera littoralis, a herbivorous Lepidoptera model in chemical ecology. A large part of the OR repertoire has been functionally characterized using heterologous expression in Drosophila antennae coupled to electrophysiology, a premiere in a Lepidoptera. Noteworthy, we found basic conservation of function within the receptor repertoire of Lepidoptera, across the different major OR clades. Focusing on caterpillar-expressed ORs, we used these data to conduct an OR-guided approach and identified new caterpillar attractants, whereas caterpillar-enriched and caterpillar-specific ORs appeared to be tuned to repellent ligands. This reverse chemical ecology approach led us to acquire knowledge on ORs that not only helps to identify key stage-specific behavioural cues, but also open new perspectives in pest control, since such ORs may be used as targets for the design of new behavioural disruptors.

The role of farm floral diversity in Tasmania

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Abstract: Just like humans, many pollinators benefit from a diverse nutritional diet. Recent studies in Europe and North America show that the biodiversity of flower-feeding insects in modified agroecosystems can remain high provided there are varied floral resources. We are assessing whether this effect is also observed in an Australian context, by investigating the insect pollinator communities of Tasmanian orchards (apple and blueberry) and mixed fruit and vegetable market-gardens. The pollinator communities in Tasmania includes two common introduced bees (Apis mellifera, Bombus terrestris) along with solitary native bees, and other floral visiting insects. Floral-visitation networks are used to assess the role of both crop and non-crop floral resources in the diet of each insect species. To do this the diversity of plants found within and adjacent to production areas are monitored and bees are tracked using florescent dust. When looking at floristic diversity at sites the overall pollinator-plant interactions were inter-webbed, with a range overlapping food-sources, yet also preference towards particular plants. Native and introduced pollinators visited both native and introduced plants, yet there was a strong differentiation of preferences for crop and non-crop flowers. Here it was found that the two introduced bees were the dominate visitors to flowering fruit trees (with Bombus mainly on blueberry not apple) and also diverse crops in market-gardens. In some orchards solitary reed bees (Exoneura) were frequently observed visiting flowering fruit trees, yet in general native insects contributed very little to visitation of particular crops grown. Importantly, a diverse range of non-crop plants, both native plants and introduced plants (i.e. weeds, herbs) were found to play a substantial role the diet of native and introduced flower-feeding insects, consistent with a key role for floral variety in sustaining insect biodiversity in Tasmanian agroecosystems.

Selective effect of fish farming on freshwater communities

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Abstract: Fish ponds provide vital ecological services and serve as irreplaceable breading sites and key habitats for many rare and endangered species of plants, invertebrates and vertebrates, and can be considered by many as biodiversity hotspots. Nevertheless, the ecological value of ponds is decreasing due to human activities including intensive fish farming involving predation pressure of fish, reduction of macrophyte vegetation, high nutrient loads and turbidity. Although many studies indicate a strong correlation between the abundances macrophyte vegetation, predation pressure of fish and the diversity of aquatic communities, information about the functioning of the individual mechanisms is still missing. Our goal is to focus on the mechanisms behind the formation of aquatic communities. We assume that fishpond management acts as a filter of regional species pool. In other words, that the fishpond management selecting species with certain characteristics. Understanding of these mechanisms may be the key to maintaining a high ß diversity of fishpond areas.

Our research was funded by the Grant Agency of the Czech Republic - GACR no. 18-24425S

Parasitism, lack of parasitism and disruption: native and imported egg parasitoids and their potential to control pomegranate pest butterflies

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Abstract: Here we consider the relative performance of, and interactions between, imported and indigenous species of natural enemies in biological pest control. Attempts to control the pomegranate butterfly, Deudorix livia, in Oman using two imported and mass-reared species of egg parasitoids, Trichogramma brassicae and Trichogramma evanescens, have not met with great success. From field surveys and laboratory rearings, we show that almost no pest eggs become parasitized by these imported species. However, a naturally occurring parasitoid, Telenomus nizwaensis, attacks around 40% of pest eggs in the field. At present, this native pest cannot be cultured and thus mass-reared for release. Laboratory experiments based on enforced competition indicate that the Trichogramma species can disrupt reproduction by Telenomus nizwaensis. Further, Telenomus nizwaensis typically achieves parasitism too late in the fruiting season to prevent economic damage. A recent field study identified biotic and abiotic factors that affect the seasonal dynamics of butterfly attack on pomegranates and the parasitism of pest eggs by T. nizwaensis, with the ultimate goal of developing methods for improving the native parasitoid’s contribution to conservation biological control.

Quasi-social parasitoid sex ratios under multi-foundress local mate competition with reproductive dominance

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Abstract: Social Sclerodermus parasitoids in the aculeate family Bethylidae form female multi-foundress groups on large, paralysed hosts and then cooperatively care for large broods of offspring throughout their development. The sex ratios of offspring produced by multi-foundress groups are more female biased than predicted by standard Local Mate Competition (LMC) theory. Using microsatellite markers to identify maternity shows that nearly every foundress produces offspring and overall reproductive skew is mild. However, males are more often the progeny of the largest or earliest-ovipositing foundress, and many foundresses do not produce any male offspring at all. Skew in male production suggests that larger females are able to dominate the production, or the survival, of males. We incorporate reproductive dominance and/or the infanticide of developing males into LMC theory, predicting both the sex ratios of individual foundresses and those of foundress groups. The predicited group sex ratios broadly match empirical observations and thus provide feasible explanation for the extremely female-biased sex ratios produced by multi-foundress groups and more generally expand the scope of LMC theory to consider reproductive dominance.

Dampen or Amplify? The role of soils in modulating threats experienced by bees

Authors: Harmon-Threatt Alexandra, Assistant Professor Entomology, The University of Illinois at Urbana-Champaign, United States

Abstract: Disturbances like climate change, parasites, pathogens, and habitat change are among the greatest threats to bees. Despite bees spending the majority of their life cycle in the nest or in contact with nesting materials, little work has examined how nesting traits of bees (i.e. where they nest) or the environmental characteristics of nest sites may dampen or amplify the threats experienced by bees. Ground-nesting bees are particularly understudied due to the difficulty locating and accessing nest. This lack of work on bee nesting has resulted in a poor understanding of the full effects of disturbances on bees. Combining a review of the literature and recent empirical work, I will discuss how these common disturbances may affect bees and where research is needed to better predict responses of bees to environmental threats.

Evidence of long-distance hoverfly (Diptera: Syrphidae) migration through the Midwestern United States: a stable isotope study (d2H)

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Abstract: Understanding the winter biology of beneficial insects such as hoverflies (Diptera: Syrphidae) is an understudied, yet vastly important area of research. The adult stages of most hoverfly species are important pollinators of a variety of crops, while the larvae occupy a wide array of niches from detritivores to aphidophagous predators. Several European species exhibit a unique winter survival behavior in which certain individuals migrate hundreds of miles in response to seasonal changes. Few studies to date, however, have directly investigated these behaviors in North American species. The overall purpose of this project is to investigate the migratory strategies of hoverflies through the Midwestern United States using stable deuterium isotopes (d2H) from wing and leg tissues in Urbana, Illinois. Through multiple years of study, we uncover evidence of partial migration in three aphidophagous species: Eupeodes americanus, Syrphus ribesii, and Syrphus rectus. Implications of this behaviour in pollination, biological control, and other ecological phenomena will be discussed.

Pesticide drift into pollinator habitat and its implications for ground-nesting bees

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Abstract: Pesticide drift into natural and semi-natural areas from neighbouring cropland may represent a significant ecotoxicological risk to wild bees including ground-nesting species. The extent of this risk, however, is largely unknown. We quantified the concentration and identity of pesticide contaminants drifting into pollinator conservation areas in prairies bordering cropland in Illinois, United States. Within each prairie, we also quantified the diversity and abundance of wild bees using a combination of active and passive trapping methods and related differences in these variables to pesticide drift concentration and identity, floral resource availability and surrounding land cover type. Our results highlight the need to consider pesticide drift when choosing conservation areas.

New insights into best practices for management of tick vectors

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Abstract: Tick-borne diseases constitute 77% of all vector-borne disease reported to US CDC. While Lyme disease (B. burgdorferi ss) is the most prevalent vector-borne zoonotic disease, the increasing suite of human pathogens transmitted by the blacklegged tick, lone star tick and the recent introduction/establishment of the Asian longhorned tick in the Western Hemisphere, increases occupational health risk for soldiers training in the field, for military. Here, we present our work in progress, on testing efficacy and integrated approaches to tick control that will reduce tick density. We will focus on three important tick vectors: Ixodes scapularis, Amblyomma americanum and the invasive Haemaphysalis longicornis.

Social and anti-social cockroaches

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Abstract: Blattodea is an enormously diverse clade, including over 4000 cockroach species that occupy a broad range of habitats across the globe. Several major innovations have occurred within this order, including vivipary (e.g. Diploptera punctata), wood feeding (several taxa) and different levels of sociality, including the eusocial termites. Cockroach genomes belong to the largest known among insects, ranging from 2 - 5 Gb (termites: 0.5 - 2 Gb), including a high level of transposable elements. With comparative genomic and transcriptomic analyses, we aim to better understand the molecular basis of the large diversity and success of this group. We have so far found massive expansions in several gene families but no contractions in the large genome of the omnivorous pest species, B. germanica. Many of these expansions help explain their success in harsh, unsanitary conditions, allowing them, for instance, to develop multiple insecticide and pathogen resistance. Many of these gene families are contracted again within the termites, related to their much more specialist and less septic lifestyles. We have also found evidence for transposable element assisted gene family expansions along with the evolution of termites. A rewiring of important developmental pathways, strong changes in expression patterns and adaptive evolution of genes involved in chemical communication assisted this major transition to eusociality.

The Janzen-Connell Hypothesis; Do insects or microbes drive overcompensating negative density dependent mortality in a Papua New Guinean forest?

Authors: Harrison Stefan[2] and Vojtech Novotny[1], [2]Lab of Tropical Ecology, Institute of Entomology, Czech Academy of Science, Czech Republic, [1]Lab of Tropical Ecology Institute of Entomology Czech Academy of Science, Czech Republic

Abstract: We designed a series of manipulative in-situ experiments to be carried out in the 50Ha CTFS plot in a lowland tropical forest at Wanang Conservation Area in Papua New Guinea. Using an integrative approach, we combined experimental findings with plant trait measurements, and data from a long-term forest dynamics plot. 4000 seedlings of two canopy tree species were transplanted into 96 X 1m2 experimental plots that were treated with either insecticides, fungicides or water (as a control). Plots were placed close to, or far from conspecific mature “parent” trees. Individual tagging of 3840 seedlings within experimental plots allowed seedling survival and RGR to be followed over the course of a year.

In a parallel experiment, the densities of seedlings of one of these tree species were mapped at the 1m2 scale in 21 forest areas where they occurred in naturally high densities. Seedlings were removed in a controlled manner to artificially manipulate densities. Again, replicated plots, where treated with either insecticides, fungicides or water, allowing the fate of 2520 individually tagged seedlings to be tracked over the course of 18 months.

A series of complementary shade-house experiments were also established on the edge of a nearby forest clearing. Seedlings of the same tree species, as well as others, were planted into shade-houses so that within each shade-house there existed an area of seedlings at high and low densities. Insect herbivores that were known to be generalists (from pilot feeding tests) were introduced into shade houses at artificially high densities to test if they were attracted to higher seedling densities. Leaf damage, RGR and survival were recorded over the course of 6 months. Here we present the results after having tracked the survival of 2400 seedlings of two species contained within shade-houses.

These three related experiments show how the expected survival patterns produced by overcompensating negative density dependent mortality - driven by insect and microbial mortality agents - are not clearly observed in these species. Instead, seedling survival seems independent from the effect of insect herbivores and appears to be most clearly linked to mid-densities - where microorganisms are not excluded. From these results, we can hypothesise that, in the case of these tree species, mutualistic fungi are more important to their survival, allowing seedlings to escape the confines of JCH.

We now seek to explore this hypothesis by comparing how the communities of pathogenic and mutualistic soil microorganisms change using from samples taken from the experimental plots prior to the beginning - and following the harvest - of these experiments.

These findings highlight the difficulty in making simple predictions of density-dependent survival when plant-microbe-insect interactions are so complex, interactive, and species dependent.

Investigation of the aggregation pheromone of the Guam haplotype of coconut rhinoceros beetle, Oryctes rhinoceros, CRB-G

Authors: Harte Steven[2], Dewhurst Charles[1], Hall David[4] and Ero Mark[3], [2]NRI, University of Greenwich, United Kingdom, [1]Natural Resources Institute, University of Greenwich, United Kingdom, [4]University of Greenwich - Natural Resources Institute, United Kingdom, [3]Papa New Guinea Oil Palm Research Association (PNGOPRA), Papua New Guinea

Abstract: The coconut rhinoceros beetle, Oryctes rhinoceros (CRB), is a major pest of coconut and oil palm that has been effectively controlled by the Oryctes rhinoceros nudivirus for over 30 years. A new haplotype, CRB-G, that is not controlled by the virus appeared in Guam in 2007 and has since spread to other countries in the Region. There has been much research on alternative methods to control CRB-G, and there have been reports that it does not respond to the well-established aggregation pheromone of CRB.

We found that the male CRB-G beetles produce ethyl 4-methyloctanoate and 4-methyloctanoic acid in 4:1 ratio, essentially as reported for CRB previously by Hallett et al. (1995). The enantiomers of these compounds were synthesised by enzymatic resolution and both the male-produced compounds were shown to be (R)-enantiomers. Hallet et al. (1995) reported that CRB produced the (S)-enantiomers on the basis of field studies, but re-examination of the pheromone produced by CRB beetles confirmed that they also produced the (R)-enantiomers.

Electroantennogram (EAG) responses to natural volatile collections from Oryctes and to the synthetic compounds indicated that both male and female beetles respond to the ester but not to the acid. EAG responses were recorded to both enantiomers, but responses to the ethyl (R)-4-methyloctanoate were consistently greater than those to the (S)-enantiomer.

In field testing in Papua New Guinea, ethyl (R)-4-methyloctanoate was attractive to both male and female CRB-G beetles and significantly more attractive than the (S)-enantiomer. The racemic ester was as attractive as the (R)-enantiomer, and addition of (R)-4-methyloctanoic acid gave a marginal increase in attractiveness of the lure.

Thus CRB-G beetles produce the same pheromone as CRB, although the enantiomeric composition of this was previously wrongly assigned. Both male and female CRB-G are attracted by racemic ethyl 4-methyloctanoate in the field, so that the same lures can be used for monitoring and control of CRB-G as for CRB.

Hallett RH, Perez AL, Gries G, Gries R, Pierce HD, Yue J (1995). Aggregation pheromone of coconut rhinoceros beetle, Oryctes rhinoceros (L.) (Coleoptera: Scarabaeidae). J Chem Ecol 21:1549-1570

Identification of the sex pheromone of the newly described canola flower midge Contarinia brassicola

Authors: Harte Steven[5], Mori Boyd[3], Bray Daniel[2], Hall David[6], Farman Dudley[4] and Vankosky Meghan[1], [5]NRI, University of Greenwich, United Kingdom, [3]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, Canada, [2]Chemical Ecology and Plant Biochemistry Group, Natural Resources Institute, University of Greenwich, United Kingdom, [6]University of Greenwich - Natural Resources Institute, United Kingdom, [4]NRI, University of Greenwich, United Kingdom, [1]Agriculture and Agri-Food Canada, Saskatoon, Canada

Abstract: The canola flower midge Contarinia brassicola Sinclair (Diptera: Cecidomyiidae) is a newly-described species that induces galls on canola, Brassica napus Linnaeus and Brassica rapa Linnaeus (Brassicaceae). Identification of the sex pheromone of C. brassicola is essential to develop monitoring tools to elucidate the geographic range and hosts of this new pest, and the extent to which it threatens the $26.7 billion Canadian canola industry. The aim of this study was to identify and synthesise the female-produced sex pheromone of C. brassicola and demonstrate its effectiveness in attracting males to traps in the field. Two peaks were identified through GC-EADanalysis of female-produced volatiles which elicited electrophysiological responses in male antennae. These peaks were initially characterised through GC-MS and synthesis as 2,7-diacetoxynonane (major component) and 2-acetoxynonane (minor component), with the racemic compounds also eliciting EAG responses in male antennae. All four stereoisomers of 2,7-diacetoxynonane were synthesised and the naturally-produced compound was shown to be primarily the R,S-isomer by analysis on an enantioselective GC column. The configuration of the minor component could not be determined because of the small amount present, but was assumed to be R. In field trapping trials conducted in Canada during 2018, the individual stereoisomers of 2,7-diacetoxynonane were unattractive to C. brassicola males. Re-examination of the analytical data suggested that a small amount of (R,R)-2,7-diacetoxynonane was also present in volatiles from female midges. During field trials in 2019, lures loaded with a 10µg:1 µg blend of (R,S)- and (R,R)-2,7-diacetoxynonane caught large numbers of male C. brassicola and significantly more than other blends tested. Addition of 0.5 µg of (R)-2-acetoxynonane to this blend further increased the number of males caught. Planned future work will seek to identify the optimum trapping protocol for use with the pheromone lure, prior to its application in agricultural monitoring and surveillance.

How automation, machine learning, and DNA barcoding can accelerate species discovery in "dark taxa": Integration with Morphology

Authors: Hartop Emily[1], Srivathsan Amrita[1], Ronquist Fredrik[3] and Meier Rudolf[2], [1]Leibniz Institute for Evolution and Biodiversity Science Berlin, [3]Swedish Museum of Natural History, Sweden, [2]Leibniz Institute for Evolution and Biodiversity Science, Germany

Abstract: Tackling poorly known, species rich groups requires innovations in all steps of the discovery process. In this talk, we focus on species delimitation with LIT: Largescale Integrative Taxonomy. The goal of LIT is to achieve the conflicting goals of (1) basing species concepts on multiple data sources while (2) increasing the speed at which we can delimit species in complex, species rich taxa. To achieve this we first determine putative species based on data that are obtained for large numbers of specimens efficiently and at low cost. We then evaluate these preliminary species concepts using a more expensive type of data that we collect for a targeted subset of specimens based on objective criteria. We developed and tested LIT using a dataset of 18 000 phorid flies. We obtained NGS barcodes (our inexpensive primary data source) for all specimens and used them to group specimens into 315 putative species. We then validated these with morphology (secondary data source) using just 5.8% of the total specimens. To do this systematically and objectively, we tested for quantitative indicators that can predict when barcode clusters are likely to be incorrectly aligned with species boundaries. This revealed that maximum p-distance within clusters and stability across different clustering thresholds are both strong indicators of whether an initial delimitation will hold once examined using a secondary data source. We identified these indicators by thoroughly evaluating the first 100 putative species and then tested them with the remaining 215 clusters. This revealed that they correctly identify all problematic clusters, allowing us to target these clusters with greater scrutiny (more specimens examined). Formal LIT protocol requires examination of approximately 5% of the total specimens with a second data source, and further reveals that a third data source is rarely necessary because "incongruent" morphospecies were, in all cases, subsets of initial delimitations, allowing us to rectify species concepts through alteration of clustering thresholds. We evaluate our results across different barcode clustering techniques to show that levels of incongruence are similar across methods, conclusively demonstrating that "barcode only" species delimitations are problematic. In this talk, we include examples from our dataset of practical cluster evaluation to demonstrate how LIT can aide taxonomists in making objective delimitations based on multiple data sources. LIT is part of a larger workflow: an overview talk is being presented separately, and another talk focuses on robotics sorting and photography in preparation for barcoding.

Effects of prescribed fire during drought on bark beetle damage

Authors: Hartshorn Jessica[2] and Palmer Forest[1], [2]Clemson University, United States, [1]Clemson University, United States

Abstract: Prescribed fire has been used to prevent or mitigate southern pine beetle infestations and outbreaks, however, anecdotal evidence suggests that this method during drought conditions may allow for damage by other bark beetles, namely Ips. Little empirical evidence exists to show how extended drought as a result of climate change affects the use of prescribed fire in managed pine in terms of susceptibility or resistance to bark beetle and spb attack. We seek to answer these questions with field observations in burned and unburned stands through the use of prescribed fire across various levels of drought in the southeastern United States. We will trap bark beetles and measure damage, mortality, and brood production across these different treatments to elucidate the effects of drought on host susceptibility to bark beetles. Our overarching goal is to predict the effects of climate change on host resistance and susceptibility and use this information to better manage for native and invasive forest pests.

Quantitative analysis of citizen science data on Heteroptera: example of the invasive heteropteran Halyomorpha halys distribution

Authors: Hartung Viktor[1] and Schneider Alexander[2], [1]Senckenberg Gesellschaft für Naturforschung, Germany, [2]Senckenberg Research Institute and Museum Frankfurt, Germany

Abstract: Citizen science platforms such as iNaturalist.org are getting more and more popular, with tens of thousands of nature aficionados worldwide contributing new photos day by day. Although the users of such platforms often lack taxonomic expertise, the sheer number of their contributions provide a valuable resource for research, since thousands of "amateurs" can access so many regions and habitats with such a regularity that few hundreds taxonomists cannot match. Many professionals already employ citizen science data in their research – however, this research is still mostly qualitative, pertaining to new records of species and distribution shift ranges. Here, we demonstrate that the immense amount of data collected by citizen scientists also has much potential for quantitative approaches. Citizen science data on Halyomorpha halys distribution allows us e. g. to test the hypothesis of this subtropical species' spread in Germany via cities – the so-called "warmth island hopping". We compare its distribution with that of the local pentatomids Palomena prasina and Rhaphigaster nebulosa, the results supporting the city-mediated distribution of H. halys. We hope that this and some additional examples will inspire entomologists to approach more sophisticated questions using citizen-science data.

30 years of arthropod monitoring in German beech forests: outcome and outlook

Authors: Hartung Viktor[1], Schneider Alexander[2], Pauls Steffen[2], Dorow Wolfgang[2], Blick Theo, Köhler Frank, Römbke Jörg and Zub Petra[2], [1]Senckenberg Gesellschaft für Naturforschung, Germany, [2]Senckenberg Research Institute and Museum Frankfurt, Germany

Abstract: Arthropod monitoring program in Hessian forest reserves started at Senckenberg Museum in 1990 and was among the earliest initiatives of that kind in Germany. Its unique feature is concentrating not on few indicator groups, but on species-level data of many diverse taxa, i. a. Coleoptera, Aculeata, Heteroptera (ATBI-approach). 30 years of study uncovered the immense species richness in middle-European beech forest: estimated at several thousand species, 3-4 times more than the numbers accepted before. With taxa pooled and analysed together, their diversity patterns correlated i. a. with forest type, deadwood amount or forestry tradition. Diversity patterns of individual taxa mostly did not show clear environmental correlations, but high variation depending on the reserve and the group, demonstrating the analytical strength of ATBI-approach. The results of the monitoring helped to establish a list of forest affinities for taxa, enabling deeper ecological research in the future. The new monitoring concept that is being developed now will have enhanced statistical power and temporal resolution; a modular structure would make the monitoring expandable on less common forest types or habitats. It is also to integrate modern approaches such as DNA-metabarcoding with the classical morphology-based methods.

Habitat management to enhance insect adaptation to climate change and climatic extremes

Authors: Harvey Jeffrey, Netherlands Institute of Ecology, Netherlands

Abstract: Climate change is one of the greatest threats to biodiversity at all levels of organization. The biosphere has not only been warming over the past several decades, but short-term climatic extremes – in particular heatwaves – are increasing in frequency, intensity and duration. Warming over variable temporal scales poses different kinds of threats to ectotherms like insects. Over longer timescales, insects need to adjust their life-cycles over the course of a growing season, or else alter their distributions pole-wards or to higher elevations to track increasing temperatures to which they are best adapted. This poses a challenge of ensuring that they are also able to find and exploit resources (i.e. food plants, prey, hosts) that are essential for their survival. Heatwaves pose a more immediate threat to their survival, because they can push insects above thermal limits for survival and reproduction. Here, I discuss habitat management strategies to enhance insect resilience to both incipient, longer-term warming and climatic extremes.

The hidden inhabitants: unraveling the seed microbial endophytes of wild cabbage

Authors: Harvey Jeffrey[1], Garbeva Paolina[3], Tyc Olaf[2] and Putra R.[2], [1]Netherlands Institute of Ecology, Netherlands, [3]The Netherlands Institute of Ecology (NIOO-KNAW), Netherlands, [2]NIOO-KNAW, Netherlands

Abstract: Endophytic bacteria are known for their ability in promoting plant growth and defense against biotic and abiotic stress. However, very little is known about the microbial endophytes living in the spermosphere.
We isolated bacteria from the seeds of five different populations of wild cabbage (Brassica oleracea L) that grow within 15 km of each other along the Dorset coast in the UK. The seeds of each plant population contained a unique microbiome. Sequencing of the 16S rRNA genes revealed that these bacteria belong to three different phyla (Actinobacteria, Firmicutes, and Proteobacteria). Isolated endophytic bacteria were grown in monocultures or mixtures and the effects of bacterial volatile organic compounds (VOCs) on the growth and development on B. oleracea and on resistance against an insect herbivore was evaluated.
Our results reveal that the VOCs emitted by the endophytic bacteria had a profound effect on plant development but only a minor effect on resistance against an herbivore of B. oleracea. Plants exposed to bacterial VOCs showed faster seed germination and seedling development. Furthermore, seed endophytic bacteria exhibited activity via volatiles against the plant pathogen F. culmorum.
Hence, our results illustrate the ecological importance of the bacterial seed microbiome for host plant health and development.

Molecular tools reveal temporal prey selection by coccinellids in apple and peach orchards

Authors: Harwood James[2], Xu Qingxuan[1], Su Wang[1] and Da Xiao[1], [2]Beijing Academy of Agricultural and Forestry Sciences, China, [1]Beijing Academy of Agricultural and Forestry Sciences, China

Abstract: Molecular tools have revolutionized our understanding of predator-prey food webs. This research examines the structure of coccinellid food webs in apple and peach agroecosystems, documenting how prey selection occurs as prey abundance fluctuates throughout the year.

Abstract to be updated pending season 2019 results.

Low temperature induced diapause in Trichogramma evanescens and T. chilonis reared on Plodia interpunctella: Implications to biological control

Authors: Hasan Md. Mahbub[2], G. Athanassiou Christos[3] and Parveen Nishat[1], [2]Department of Zoology Rajshahi University Rajshahi 6205, Bangladesh, Bangladesh, [3]Laboratory of Entomology and Agricultural Zoology, Department of Agriculture, Crop Production and Rural Environment, University of Thessaly, Phytokou str, 3844, [1]Department of Zoology Rajshahi University Rajshahi 6205, Bangladesh

Abstract: The egg parasitoids, Trichogramma evanescens Westwood and T. chilonis Ishii (Hymenoptera: Trichogrammatidae) are important biological control agents for lepidopterous pests including the Indian meal moth Plodia interpunctella (Hübner) (Lepidoptera: Pyralidae). The role of low temperatures in inducing diapause of the parasitoids, reared on P. interpunctella, was studied in laboratory tests involving long term storage. Both species of Trichgramma could successfully undergo diapause. The temperature of 10°C was considered as a pre-storage requirement for pre-pupal stage for 7 days, while maintenance of temperature to 4°C caused diapause induction. Diapause was terminated after two months of storage with 37.67 and 53.33% of adult emergence in T. evanescens and T. chilonis, respectively. However, there was a significant reduction in longevity and parasitism rate for both species. At 37 days of storage (including pre-storage duration), adult emergence of T. evanescens and T. chilonis was 64.67 and 53.33%, respectively. Successful long term storage of both the species through diapause induction can facilitate commercial insectaries for large scale field releases.

Monitoring and Management of Drosophila suzukii (Diptera: Drosophilidae) in Berry Plantings in Florida

Authors: Haseeb Muhammad[2], Liburd Oscar[4], Parkins Albertha[1], Harmon Dasia[3], Legaspi Jesusa[5] and Kanga Lambert[1], [2]Center for Biological Control, Florida Agricultural and Mechanical University, Tallahassee, FL 32307, United States, [4]University of Florida, United States, [1]Center for Biological Control, Florida Agricultural and Mechanical University, Tallahassee, FL 32307, United States, [3]FoodCorps, Inc, Atlanta, GA 30303, United States, [5]USDA-ARS-IBBRU-CMAVE, Tallahassee, FL 32308, United States

Abstract: Drosophila suzukii (Diptera: Drosophilidae) is an invasive insect pest that was detected in Florida in August 2009 in Hillsborough County. Very limited information is available for berry growers to properly detect and monitor this serious pest in southern highbush blueberry (hybrids of Vaccinium corymbosum L. × V. darrowi Camp), rabbiteye blueberry (Vaccinium virgatum L.), and blackberry (Rubus fruticosus L.) production systems. We compared several D. suzukii traps and lures/baits at two sites in Florida. The traps evaluated included Trécé, Scentry, and a standard homemade cup trap. These traps were compared with various baits and lures, including Trécé lure, Scentry lure, yeast bait, and Suzukii trap, under Florida production systems. Early detection is important to develop an effective monitoring system so management action can be taken before economic damage occurs. Data were recorded as overall trends, as well as in 4–5 trapping periods from early to late season. Overall, the Scentry trap baited with Scentry lure, the Trécé trap baited with Trécé lure + yeast, and the Trécé trap baited with Scentry lure were the best performing traps. Yeast-based traps were also attractive to D. suzukii early in the season, but they did not provide consistent captures as the season progressed. The Scentry trap with yeast bait, the Scentry trap with Scentry lure, the Trécé trap with Trécé lure + yeast bait, and a cup trap with yeast bait caught most of the flies during the first trapping period in 2015 and 2016 in the rabbiteye blueberry. In the southern highbush blueberry, the population of D. suzukii was much lower than in the rabbiteye blueberry planting, and the Scentry trap with Scentry lure captured the highest number of flies during the first trapping period in 2016. In the blackberry, the Scentry trap with Scentry lure numerically had the highest captures during the first trapping period, but this was not significantly different from the cup trap with yeast bait, the Trécé trap baited with Suzukii trap, and the Trécé trap with Trécé lure. Overall, the Scentry trap with Scentry lure was the most consistent trap that captured D. suzukii flies throughout the season in the three production systems—rabbiteye blueberry, southern highbush blueberry, and blackberry. Growers in low pressure systems that are similar to Florida can use the Scentry trap with Scentry lure to monitor D. suzukii populations. In addition, results of the mulching practices on the density of D. suzuki in open field conditions will be discussed.

Transcriptome analysis of genes and metabolic pathways associated with nicotine metabolism and excretion in the midgut and Malpighian tubules of Trichoplusia ni. (Lepidoptera: Noctuidae)

Authors: Hassanpour Nazli[3], Kolosov Dennis[1] and Rheault Mark[2], [3]The University of British Columbia, Canada, [1]McMaster University, Canada, [2]The University of British Columbia, Canada

Abstract: The cabbage looper, Trichoplusia ni (T. ni) is a generalist insect (Lepidoptera: Noctuidae) that is an agricultural pest of crucifers and other crops of economic importance. The most common insecticides currently in use around the world are neonicotinoids, which are chemical derivatives of nicotine. Enriched metabolic detoxification of xenobiotics like nicotine have been linked to the increased expression of cytochrome P450s (CYPs) in insects. Recent studies in our lab have shown that the midgut and the Malpighian (renal) tubules of T. ni actively excrete and detoxify nicotine into the three major metabolites; cotinine, continine-N-oxide, and nicotine-N-oxide. In this study we have used High-throughput transcriptome sequencing methods to analyze the expression profile of transcripts in the midgut and Malpighian tubules of both control and nicotine exposed T. ni. Of the 24,653 putative transcripts in the T. ni transcriptome, our RNAseq analysis detected 22,331 transcripts in the midgut and 21,737 transcripts in the Malpighian tubules. In nicotine exposed insects, 21% and 14% of detected transcripts showed increased expression in the midgut and Malpighian tubules, respectively. Conversely, 16% and 10% of detected transcripts showed decreased expression in the midgut and Malpighian tubules, respectively. Of the transcripts that displayed up-regulation, 49 transcripts in the Malpighian tubules and 28 transcripts in the midgut were identified as cytochrome P450s (CYPs), which are known to play a primary role in insecticide and nicotine metabolism and detoxification. We have identified a number of additional xenobiotic metabolizing enzymes including 4 carboxylesterases (CEs), 11 glutathione-s-transferases (GSTs), and 9 uridine diphosphate-glucuronyltransferase (UGTs) that were up-regulated in the midgut tissue. In the Malpighian tubules, 11 CEs, 12 GSTs, and 16 UGTs were also shown to be up-regulated. In addition to the increased expression of metabolic transcripts, we have identified a number of transcripts associated with the excretion and transport of xenobiotics including nicotine. Dietary nicotine exposure increased expression of 2 transcripts in the midgut and 5 transcripts in the Malpighian tubules identified as ABC transporters, which have previously been shown to play a role in the excretion of nicotine by insects. 4 transcripts in the midgut and 14 transcripts in the Malpighian tubules identified as organic cation transporters (OCTs) also had increased expression. The combined use of transcriptomics, novel analytical methods and physiological studies will increase opportunities for development of new biochemical and physiological targets for the control of insect agricultural pests and disease vectors which are economically, environmentally, and medically valuable.

Tackling above and below ground pests in Potato Production in Kenya

Authors: Haukeland Solveig[2], Akutse Komivi[1], Nyongesa Moses[3], [1]ICIPE, Nairobi, Kenya, [2]International Centre of Insect Physiology and Ecology, Nairobi, Kenya, [3]KALRO Kenya Agriculture and Livestock Research Organization, Kenya

Abstract: Potato is a valuable food and cash crop in the East African region, and in Kenya it is ranked second in importance after maize. Production and yields have declined by about 50%, from about 20t/ha to less than 9t/ha in the last 15 years, despite an increase in the area grown. Pest infestations are likely to be one of the reasons for these declining yields. In Kenya, 90% of potatoes produced are grown by about 800,000 smallholder farmers often on less than an acre of land. This becomes a challenge regarding crop rotation (not enough land). Thus, year in year out growing potatoes on the same piece of land results in build up of pests and diseases. Unlike temperate climatic regions such as Europe, where potatoes are grown for one season in the summer, in Kenya the climate allows for potatoes to be grown for at least two seasons a year, three if irrigation is available, further allowing build up of pests and diseases. Reports have shown that the main production constraints are at the production level and a lack of GAP (good agricultural practices). In this presentation an overview of potato production in Kenya and the region will be presented, with emphasis on the key known pests that cause production losses. The presentation will also share current studies and results from field surveys and trials with respect to above and below ground pests recently detected in the region. Finally, points and suggestions for further studies and collaborative opportunities will be addressed.

Monitoring of insects at migratory hotspots: origins, diversity and their ecological impact on us all

Authors: Hawkes Will, University of Exeter, United Kingdom

Abstract: Insect migrants often number in the trillions and carry out vital ecological roles, connect distant ecosystems and transfer vast amounts of biomass and nutrients. Despite this, insect migration is still a comparatively understudied phenomenon with research thus far focusing primarily on Lepidoptera (moths and butterflies), Odonata (dragonflies) and the Syrphidae (hoverflies), many of which are known to co-migrate through Europe. Quantifying how the numbers and relative composition of different species vary across Europe is a formidable task but necessary if we are to understand the contribution these organisms make when moving between often-distant ecosystems. My research takes a comparative approach, identifying migratory assemblages of insects and quantifying numbers, across multiple migration hotspots during spring (northwards) and autumn (southwards) migrations in Europe across multiple years. My research combines traditional techniques of trapping, counts and transects together with high-resolution imaging to identify and quantify migrants from funnel points in European mountains and islands. We have recently quantified transit rates as high as 11 million flies per day, found evidence for multiple novel insect migrants, identified putative geographic sites of origin and began to identify drivers of annual variations in the makeup of migrant assemblages and numbers. Current research is focusing on understanding migratory routes, assessing the effect of migrants on the ecosystem as a whole and establishing long-term monitoring of migratory populations. In the current declining state of insect populations worldwide, finding out what insects are migrating (and in what numbers), as well as their effects on the global ecosystem, has never been more vital.

Updated Genome of the infamous Amikafer, Colorado potato beetle, L. decemlineata Say

Authors: Hawthorne David[1] and Schoville Sean[2], [1]Department of Entomology University of Maryland College Park, United States, [2]Dept. of Entomology University of Wisconsin, United States

Abstract: The Colorado potato beetle is a noxious insect pest on Solanum crops such as: potato, tomato and eggplant. Despite its native range of the South Western United States and Mexico it has expanded where potato is grown and become economically impactful in Europe and Asia. Its ability to develop resistance to insecticides and rapidly adapt to novel ecosystems makes it an ideal model to study genome evolution and population genetics. Using a trio-binning approach, (Koren et al., 2018) we significantly enhanced the original genome assembly from the first version, (Schoville et al., 2018), that had approximately 24K scaffolds with an N50 414Kb, to a new version with fewer than 1000 scaffolds and an N50 of approximately 8Mb. Trio binning assembly is carried out by crossing highly unrelated parents, sequencing their genomes using short, paired-end read data, sequencing their highly heterozygous offspring with long-read data at high depth of coverage, resolving the F1 haplotypes using parental short read data and ultimately generating two assemblies from one individual. These haplotype assemblies could elucidate recombination and mutation rates of this pestiferous insect, and may provide insight into novel genomic features that contribute to its success in agroecosystems.

Updated Genome of the infamous Amikafer, Colorado potato beetle, Leptinotarsa decemlineata Say

Authors: Hawthorne David[1] and Schoville Sean[2], [1]Department of Entomology University of Maryland College Park, United States, [2]Dept. of Entomology University of Wisconsin, United States

Abstract: The Colorado potato beetle is a noxious insect pest on Solanum crops such as: potato, tomato and eggplant. Despite its native range of the South Western United States and Mexico it has expanded where potato is grown and become economically impactful in Europe and Asia. Its ability to develop resistance to insecticides and rapidly adapt to novel ecosystems makes it an ideal model to study genome evolution and population genetics. Using a trio-binning approach, (Koren et al., 2018) we significantly enhanced the original genome assembly from the first version, (Schoville et al., 2018), that had approximately 24K scaffolds with an N50 414Kb, to a new version with fewer than 1000 scaffolds and an N50 of approximately 8Mb. Trio binning assembly is carried out by crossing highly unrelated parents, sequencing their genomes using short, paired-end read data, sequencing their highly heterozygous offspring with long-read data at high depth of coverage, resolving the F1 haplotypes using parental short read data and ultimately generating two assemblies from one individual. These haplotype assemblies could elucidate recombination and mutation rates of this pestiferous insect, and may provide insight into novel genomic features that contribute to its success in agroecosystems.

Modifying populations of wild Drosophila suzukii through gene drive

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Abstract: Drosophila suzukii is an invasive species and major pest of soft fruits. Thus an important goal is to develop ways of suppressing these populations. We recently developed a new method of gene drive known as Cleave and Rescue (ClvR). ClvR elements consist of two components. The first is Cas9 and gRNAs (the toxin). These target an essential gene for destruction through cleavage at multiple sites followed by inaccurate repair. The second component (the antidote) is a recoded version of the essential gene that is insensitive to clveavage and loss-of-function allele creation. Together these components create a novel selfish genetic element. Progeny of ClvR-bearing parents that fail to inherit ClvR die because they lack any functional copies of the essential gene. In contrast those who inherit ClvR always survive because they carry with them the recoded version of the essential gene. ClvR spreads under a variety of conditions, and when it spreads it proceeds to genotype or allele fixation.

We have created three different ClvR elements in Drosophila melanogaster and shown that they spread to genotype fixation in genetically diverse populations PNAS 2019). We have also shown that multiple cycles of ClvR-dependent population modification can be carried out, with second generation elements spreading into populations previously fixed for an earlier element, while at the same time driving the earlier generation element out of the population (PNAS 2020).

Here we describe our progress in developing ClvR-based strategies for population suppression for Drosophila suzukii. In brief, we are pursuing two approaches.

In the first we create ClvR elements in which the antidote is temperature sensitive, allowing susukii to survive at lower temperature, but causing death at higher temperatures. This may be useful as a control strategy in which the wildtype population of suzukii is initially replaced with ClvR-bearing versions during a low temperature season. As temperatures rise during the year the ts version of the essential gene becomes non-functional, resulting in a population crash.

In the second approach we use ClvR to drive a fitness load into the population such that 50% of individuals die in each generation. If several independently acting elements of this type were introduced into a population strong population suppression would be predicted to occur.

Potential impact of Trissolcus japonicus on populations of Halyomorpha halys and non-target species in Europe and North America

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Abstract: The brown marmorated stink bug, Halyomorpha halys, native to East Asia, is an invasive alien pest that arrived in Europe and North America in the 1990s and early 2000s, respectively. The Asian egg parasitoid Trissolcus japonicus was identified as the most promising agent for classical biological control of H. halys. Host specificity testing of T. japonicus has been carried out under containment conditions in North America and Europe and overall, these studies came to the very similar conclusions that T. japonicus' fundamental host range is restricted to the Pentatomoidea, but the parasitoid is capable of successfully parasitizing the eggs of several pentatomids and a few species of scutellerids other than H. halys. Before any laboratory risk assessment studies for T. japonicus had been completed, adventive populations of T. japonicus were detected North America and Europe. These unintentional introduction of T. japonicus provided a unique opportunity to validate retrospectively estimates of fundamental host range with realized (ecological) `post arrival´ host range as it manifested over time.

Review on the biology of Trissolcus japonicus in China and implications for its use for biological control

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Abstract: The brown marmorated stink bug, Halyomorpha halys, native to subtropical and temperate areas of East Asia, has emerged as a harmful invasive pest of a variety of crops in America and Europe. In its native range eggs of H. halys are attacked by more than ten species of parasitoids, among which Trissolcus japonicus was identified as the most promising biocontrol candidate. It parasitizes H. halys eggs over the course of the entire season in China, from May to September, and is consistently the dominant parasitoid species on H. halys eggs, with reported parasitism levels ranging from 47% to 78%. However, its host range comprises at least seven additional pentatomid hosts. Trissolcus japonicus searches for host eggs in a variety of habitats and on several host plant species, including shrubs and trees within suburban peach orchards, and forested parks as well as maize fields and vegetable crops such as green beans, eggplant, tomato, and pepper. In areas of China where H. halys undergoes two generations per year, T. japonicus may complete up to ten overlapping generations over the course of a season. Its distribution ranges from the northern, temperate province Heilongjiang to the southern, subtopical province Guangdong. Single females can produce more than 100 offspring. The development time from egg to adult was10.5 days at 25°C and the minimum threshold temperature for development was estimated to be 12.2°C, with a thermal constant of 132.5 degree-days. Frozen and unfertilized egg of H. halys can be used for mass rearing T. japonicus and in addition, adult females can be stored up to 19 weeks at 11°C with 90% survival. The optimal timing and frequency of mass releases of T. japonicus in fruit orchards is still under development.

Is the symbiotic yeast Kodamaea ohmeri playing a role in the aggregative behaviour of the honeybee pest Aethina tumida?

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Abstract: The small hive beetle Aethina tumida (Coleoptera: Nitidulidae) displays aggregative behaviour and previous research has identified an aggregation pheromone. We used laboratory assays to investigate the conditions under which of this aggregation occurs and its purpose, beyond its reported role in assisting reproduction, and to understand the role of the symbiotic yeast Kodamaea ohmeri (Ascomycotina: Saccharomycotina) in the aggregation. We investigated clustering of mated and unmated male and female conspecifics, as well as clustering with dead conspecifics. We also examined the beetle's ability to form clusters after bilateral anntenectomy; and without the associated yeast. Aggregation under laboratory conditions appears to be sex neutral, only occurs in response to other live A. tumida, and is facilitated by intact antennae (chemoreceptive organs) and the presence of K. ohmeri. We determined that antennectomised beetles and beetles reared without K. ohmeri each took longer to form clusters (=aggregation of five or more beetles) and the clusters formed were smaller. We determined that horizontal transmission of K. ohmeri is possible and appears to be facilitated by the beetle's aggregation behaviour. Following the differences in behaviour of K. ohmeri-free beetles, hexane extraction analysis showed differences in the cuticular compounds of K. ohmeri-free beetles and untreated beetles. This work extends our current understanding of A. tumida aggregative behaviour and conspecific communication, which may have potential in control and management strategies for this pest.

Harnessing EPN bacteria metabolites for new drugs and biocontrol agents

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Abstract: Xenorhabdus and Photorhabdus species are insect pathogenic bacteria that are symbiotically associated with entomopathogenic nematodes. These bacteria produce various secondary metabolites to protect insect cadavers against competitors allowing them to survive in nature with their nematode host. Antibacterial, antifungal, antiprotozoal, insecticidal, ovicidal, larvicidal, anticancer, scavenger and mosquito deterrent activities of metabolites produced by Xenorhabdus and Photorhabdus spp. have been discovered. Recently, the antibacterial activity of bacterial supernatants was tested against the multi-drug resistant pathogen Enterococcus faecalis; as a result, a compound was identified having better activity than chlorhexidine and calcium hydroxide. The novel compound eliminated 99.9% of the bacteria in dental root canals. Xenorhabdus and Photorhabdus supernatants were screened on human parasitic protozoa, Acanthamoeba castellanii, Leishmania tropica and Trichomonas vaginalis and potential new antiparasitic drugs were identified. Researchers also evaluated the antifungal activity of secondary metabolites on various plant and human pathogenic fungi and obtained promising results by identifying new antifungal compounds. To control vector-borne diseases, bacterial metabolites have been assessed against developmental stages of mosquitoes and a novel larvicidal compound showing 100% mortality in 24h was explored.

Biosynthesis of Gold and Silver Nanoparticles from the Symbiotic Bacterium, Photorhabdus luminescens of Entomopathogenic Nematode: Larvicidal Properties against Mosquito and Galleria mellonella larvae

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Abstract: The present investigation focuses on the larvicidal property of gold and silver nanoparticles (AuNPs and AgNPs) that were synthesized using the supernatant of Photorhabdus luminescens strain KPR-8B from nematode. The synthesized AuNPs and AgNPs were characterized through UV–visible spectrophotometer, X-ray diffraction analysis, Fourier transform infrared spectroscopy, dynamic light scattering and high-resolution transmission electron microscopic analyses. The characterization studies confirmed the spherical shape and size (14–46 nm) of AuNPs and AgNPs. The synthesized AuNPs and AgNPs were evaluated against 4th instar larvae of three mosquitoes, Aedes aegypti, Anopheles stephensi and Culex quinquefasciatus. The highest larval mortality was observed after 24 h from the KPR-8B derived AuNPs against A. aegypti with the LC50 and LC90 values of 5.04 and 12.65 lg/ml, respectively.

Response of the Asian corn borer to high temperature extreme

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Abstract: Global worming demonstrates not only a significant rise of average temperature, but also results in the frequent appearance of extraordinarily daily high temperature. A transient high temperature, particularly early in embryonic stage, could profoundly affect insect performance across all subsequent life stages. To understand the effects of the transient exposure to extremely high temperatures on egg, neonate and adult of Ostrinia furnacalis, the half lethal temperature (LT50) and the survival rate with 6 h high-temperature exposure,and the half lethal time (Lt50) under different high temperatures were examined. The LT50 values of egg, neonate and moth were 40.2-40.4, 38.6 and 42.8- 44.5?, respectively. The Lt50 values of egg,neonate and moth were 0.38-6.31, 0.22-8.35 and 3.80-24.15 h,respectively. In addition, we assessed the impact of a transient exposure to extremely high temperature on egg of O. furnacalis for biological parameters across subsequent life stages. Eggs were heat-shocked to 5 temperatures from 37 to 45 ? for 90 min, and then transferred to control of 25 ?. Effects of heat shock on egg hatching rate were significantly different among treatments. No larvae hatched out at treatment of 45 ?. The development times had no difference at egg stage, but a significant prolong at treatments of 41 and 43 ? at larval and pupal stages. Pupal masses were significantly increasing at treatment of 39 ? for male. There were no significant differences for fecundity and sex ratio among treatments. The phenomenon of protandry appeared at treatments of 39 and 41 ?, but faded away at treatment of 43 ?. Our findings indicate that extremely high temperatures significantly influenced the survival rate of O. furnacalis. A critical point of temperature may exist between 39 and 41 ?.

Effects of spruce budworm outbreaks and suppression on carbon dynamics in forest soils

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Abstract: Multi-year outbreaks of spruce budworm (Choristoneura fumiferana), a lepidopteran defoliator of fir and spruce, extend over millions of hectares and are the most important natural forest disturbance in the mixed and conifer forests of eastern Canada. Canopy loss and tree mortality reduce photosynthesis and presumably change microclimate and microbiota of forest soils. In the short term, defoliation also may increase carbon inputs to soil, in the form of insect frass and litterfall. However, the effects of these disruptions on carbon cycling are poorly understood. The regional management of spruce budworm through aerial application of biological insecticides offers an opportunity to understand impacts of budworm on carbon cycling. It also raises the possibility managing those effects in future – in one of the Earth's most extensive, and most C-rich, forest biomes.

We have begun a multi-year experiment in eastern Quebec, Canada to quantify carbon-cycle processes in 12 forest watersheds at the onset of a spruce budworm outbreak. We are experimentally manipulating defoliation in half of the watersheds through spraying with Btk. We are sampling soils for litter, carbon, nitrogen, and mycorrhizal colonization, measuring soil temperature, in-situ soil metabolism, and cotton-strip decomposition rates, and measuring frass and litter inputs to soils. Together, these data will reveal how defoliation influences soil biota and their roles in carbon cycling. Data from the first field season reveal patterns in frass- and litterfall among sites differing in baseline defoliation, but only subtle differences in soil parameters. These results are consistent with our pilot work in nearby sites with longer defoliation histories and suggest that carbon cycling effects are likely to accumulate over many years during the typically persistent outbreaks of spruce budworm.

Genome size evolution in the diverse insect order Trichoptera

Authors: Heckenhauer Jacqueline[1], Pauls Steffen, [1]LOEWE Centre for Translational Biodiversity Genomics, Germany

Abstract: Aquatic insects are underrepresented in genomic studies. To expand the availability of aquatic insect genomes, we generated de novo genome assemblies of 17 caddisflies covering major lineages of the order. We used these genomes to understand genome size evolution and detected a ~14-fold variation in genome size across the order. We find strong evidence that repetitive element expansions, particularly those of transposable elements (TEs), are important drivers of large caddisfly genome sizes. Using an innovative method to examine TEs associated with universal single copy orthologs (BUSCO genes), we find that TE expansions have a major impact on protein-coding gene regions, with TE-gene associations showing a linear relationship with increasing genome size. Expanded genomes preferentially evolved in caddisfly clades with a higher ecological diversity (i.e., various feeding modes, diversification in variable, less stable environments). Our findings provide a platform to test hypotheses about the potential evolutionary roles of TE activity and TE-gene associations, particularly in groups with high species, ecological, and functional diversities.

The application of environmental DNA technology to assess climate change extinction in arid-land invertebrate communities

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Abstract: The granite rock-holes present across much of arid and semi-arid southern Australia are a unique ephemeral freshwater habitat. A complex but understudied community of invertebrates (primarily insects and crustaceans) is associated with these sites. Due to a projected drying climate over the next 100 years, the security of these ephemeral freshwater ecosystems is uncertain. Increased use by invasive vertebrates (namely goats and sheep) and over-abundant native species (primarily macropods), is also impacting water quality throughout the region. We employed environmental DNA (eDNA) techniques to assess the degree to which these invertebrate communities vary both spatially and temporally. Filtered water samples were taken from a series of rock-holes in the arid-lands of South Australia that varied in distribution, shape, water chemistry and habitat structure. Next generation sequencing reads from broad and targeted Cytochrome c oxidase I and 18S eDNA metabarcoding assays recovered Operational Taxonomic Units from a range of insect and crustacean taxa known from arid-lands freshwater ecosystems. Preliminary analyses show that communities vary between rock-holes and that resampled rock-holes vary in composition between sampling events. It is likely that invertebrate species richness is affected by characteristics of rock-hole shape and vegetation structure. The use of eDNA techniques in this study show promise as a tool for assessing community composition and as an indicator of overall ecosystem health. Preliminary conservation recommendations to safeguard the invertebrate communities of these unique Australian granite rock-holes include targeted pest management and prioritisation of high diversity sites. Future research and monitoring of rock-hole communities is needed to better understand the potential impacts of climate change on invertebrate gene flow in disconnected habitats.

A major overhaul of the lepidopteran fossil record in light of recent advances in the systematics of the order

Authors: Heikkilä Maria, Finnish Museum of Natural History, LUOMUS, University of Helsinki, Finland

Abstract: In recent years, advances in research on the morphology and systematics of many groups of Lepidoptera have been made. Now, this new knowledge is applied in the re-examination of the identifications of all known fossil Lepidoptera. Previous identifications have been considered doubtful as many of them were made in the late 1800s or early 1900s when the classification of Lepidoptera was very different. For a few years now, an international network of experts has been re-examining the fossils and reviewing previous identifications. This work has proven worthwhile as unfortunately many, if not most, of these identifications have turned out to be unsubstantiated and based on overall similarity to extant species, not apomorphies. In their work, the teams have encountered fossils that cannot securely be placed in any subgroup of Lepidoptera, are not lepidopterans at all, and fossils that have been misdated. The work has helped make identifications more accurate and provided reliably identified fossils to be used e.g. in studies exploring the evolutionary history of moths and butterflies. The project is ongoing — several publications have already come out and others will in the near future. I will present new results by the teams of experts examining these fossils.

The domed functional response: a review of its potential importance to biological control and a case study

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Abstract: In the type four, or domed, functional response, per-capita attack rates by predators decline at high prey densities. This is in contrast to the more familiar functional response types 1-3, in which attack rates remain constant at high prey densities. Domed functional responses have not been routinely considered in biological control interactions but may have important implications for the ability of natural enemies to control populations of pests. We found that the aphid parasitoid Binodoxys communis exhibited a domed functional response to the soybean aphid, Aphis glycines, in a laboratory mesocosm experiment and discuss potential mechanisms that could lead to such a response. We also consider the possibility that domed functional responses may be underappreciated in biological interactions.

Ground-dwelling arthropods as vectors for phytopathogenic fungi- introducing the mobile link concept to vector biology

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Abstract: The movement pattern of a vector has a crucial impact on its ability to spread pathogens. The mobile link concept focuses on how movement patterns effect processes, resources, genetic exchange and also the spread pathogenic microorganisms. This concept can provide a different approach on how to deal with and to identify possible vector species. With first results from empirical field work, we ´d like to point out the relevance of arthropods for the spread of agricultural diseases.

We focused on the transport of phytopathogenic fungi by the ground-dwelling carabid beetles that move regularly between small isolated natural wetlands (kettle holes) and adjacent crop fields. Ground beetles could be important vectors since kettle holes also provide ideal conditions for many fungi. Therefore an indirect spatial-temporal interaction is inevitable.

Our first analyses aimed to verify our basic assumption that phytopathogenic fungi can be found on the external body surface of ground beetles. 41 carabid beetles were collected in crop fields near kettle holes and treated with a washing method that removed superficial fungal propagules from the exoskeleton. We isolated 648 fungal colony forming units (CFU). 51 CFU belonged to 8 different Fusarium species, 24 identified as F. culmorum, a fungi able to infect plants also via the root system. Furthermore 9 CFU were identified as Alternaria fungi belonging to 4 different species-groups. Both fungal genera infect different weeds and crop plants, produce mycotoxins and cause yield loss.

Ground-dwelling arthropods carry a variety of fungal propagules including phytopathogenic species. It`s very likely that this transport mechanism favors more fungal propagules that are close to the ground than the wind dispersal. The effect of insect dispersal on the fungal community could therefore be different and relevant for agricultural management.

Genetically engineered crops: Challenges and opportunities for promoting biodiversity in the agroecosystem

Authors: Hellmich Richard, USDA and Iowa State University, United States

Abstract: Growers from a generation ago would find many differences if they walked through fields with genetically engineered (GE) crops today. Now there are fewer weeds due to herbicide-tolerance traits and much less insect damage due to insect-resistance traits. On closer inspection, compared with non-GM crops, they might even note improved grain quality and more insects that are beneficial. A grower today, however, walking through the same field with a grandchild might ask, “What lays ahead, will the agroecosystem a generation from now be better and how”? This talk will explore challenges and opportunities of GE crops related to biodiversity. The talk will emphasize the whole ecosystem including non-cropped lands near GE crops. Cool-season sod-forming grasses, particularly smooth brome (Bromus inermis), dominate many of the non-crop lands in the United States. These grasses historically have been used for erosion control but do not promote biodiversity. Studies in the state of Iowa in the U.S. have focused on replacing these grasses with native habitat that includes forbs for pollinators and other insects. In addition, there may be opportunities to improve the rhizosphere and accompanying biota within fields, especially if GE crops promote the use of cover crops. Finally, if future GE crops allow growers to further decrease chemical inputs and increase reduced tillage that too would promote sustainability and biodiversity.

Challenges and opportunities for promoting biodiversity in agroecosystem

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Abstract: Biodiversity in monoculture agroecosystems is limited. This presentation will discuss challenges and opportunities for improving biodiversity through the lens of monarch butterfly conservation in the north-central United States.

Phylogenetic relationships within Eutrichophora and Pyrrhocoroidea (Hemiptera: Heteroptera) inferred from the morphology of metathoracic scent efferent system, abdominal ventrites and trichobothria

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Abstract: Eutrichophora forms a diverse, well-supported clade within pentatomomorphan true bugs, consisting of the superfamilies Coreoidea, Lygaeoidea and Pyrrhocoroidea. However, the precise phylogenetic relationships among these taxa are unclear. Previous studies proposed four mutually conflicting hypotheses, each supported by several molecular and/or morphological datasets. In our study, we focused on the comparative morphology of the external structures of the scent efferent system of metathoracic glands, including the microstructure of the metathoracic spiracle opening, and abdominal ventrites including their sensory organs (trichobothria). A cladistic analysis of 23 characters supported Pyrrhocoroidea as a sister-group to Coreoidea + Lygaeoidea. Hyocephalidae were supported as the most basal group within the Coreoidea. Within the previously poorly studied Pyrrhocoroidea (of which we examined 64 genera, i.e. 90%), Larginae, Physopeltinae and Pyrrhocoridae were each well-supported as monophyletic but their relationships to each other and their internal phylogenies remained largely unresolved. We have identified several new synapomorphies for individual superfamilies, families or subfamilies but have found no synapomorphies that support monophyly of Largidae or any of its currently recognised tribes. Future studies of additional morphological (e.g., male and female terminalia, mouthparts, and wing venation) and molecular characters are therefore necessary to better understand the evolution of the Pyrrhocoroidea.

A floral colour changing tree benefits from pollinator learning

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Abstract: We report a hitherto unknown strategy that exploits pollinator learning while uncoupling pigment synthesis, reward production and fertility. Catuneregam spinosa flowers, whether pollinated or not. transform from white to yellow, extending stigma/pollen viability, nectar secretion and bee-visitation to yellow flowers. We hypothesised that bees utilise both colour cues for long-distance location and short-distance discrimination. In Y-maze experiments with differentially rewarding artificial flower arrays, bees preferred yellow-dominated over white-dominated arrays from longer distances both spontaneously and after training to equal-proportion white and yellow array. On reaching the array, they visited white which they had previously learnt as higher-rewarding. We demonstrate that post-change flowers generate an effective long-distance colour signal and can contribute to direct fitness. Differential rewards combined with extended fertility constitute an alternative mechanism to maximise visitation in colour-changing plants.

Larval feeding behaviour and host food plant preference of endangered Poweshiek skipperling (Oarisma poweshiek) in Canada

Authors: Henault Justis[2] and Westwood Richard[1], [2]Department of Biology, University of Winnipeg, Canada, [1]Department of Biology, University of Winnipeg, Canada

Abstract: We investigated biological and structural factors within larval microhabitats of the endangered Poweshiek skipperling (Oarisma poweshiek) in Canada. This once common butterfly is endemic to remnant tall grass prairie ecosystems in North America with only two remaining population centres found in Manitoba, Canada and Michigan, United States. The Poweshiek skipperling is now in imminent danger of extirpation and increased knowledge of adult and larvae habitat requirements are urgently needed to keep the remaining populations extant. For the first time in natural habitats we determined the specific larval host plants and documented larval development and behaviour. We found larvae remain in close proximity to host plants where the initial egg was laid but that they feed on several different grass species at different times during the summer season. Larval microhabitats are occupied for over 11 months and contain very specific physical characteristics and plant diversity which is essential to successful development to adulthood. This information will be essential to help conservation experts to increase the quality of remaining habitat, prioritize suitable tall grass prairie to support reintroduction and successfully protect this species from extinction.

Overcoming Barriers for Lesbian, Gay, Bisexual & Transgender Entomologists (LGBT) to Create a More Inclusive Discipline

Authors: Hendrix William[2], Jordan Kyle[1], [1]BASF, United States, [2]Valent USA LLC, United States

Abstract: As the population in many Western cultures rapidly changes to reflect a much more diverse population and the cis white male paradigm shifts, there has been increasing interest in looking at diversity in academia. Although laudable, these efforts often focus on the more visible signs of diversity such as race and gender. Over the last 20 years, lesbian, gay, bisexual, and transgender (LGBT) individuals have seen increased parity in society, the community and the workplace both in the US and abroad. However, with rapid social change also comes concern and visible opposition. Currently, numerous countries offer no protection from discrimination if you are perceived to be gay or lesbian or transgender. Stepping into the void, many universities, government agencies, and multi-national companies prohibit discrimination against LGBT individuals, creating a situation where a potential student or employee has more rights while on campus or at the workplace than they would have in their local communities. Understanding LGBT individuals' needs within entomology and the broader sciences is also difficult due to remaining societal stigma attached to being LGBT.

For many there is still a need to develop the business case for encouraging and supporting LGBT within the research community and workforce. This presentation will provide an overview of the current status of legal recognition for LGBT and provide evidence on the financial and emotional cost for lack of LGBT protections. Additionally, information will be provided on how a professor or hiring manager can attract and retain LGBT students and employees and create an inclusive culture. Coaching on inclusive language will also be provided. In addition, transgender students and employees face different challenges as there are far fewer protections in place for transgender students or employees and policies are less established. Ultimately, the goal of this presentation is to create a better understanding regarding LGBT parity within the University or workplace.

Aedes aegypti in California – resistant mosquitoes and novel control methods

Authors: Henke Jennifer, Coachella Valley Mosquito and Vector Control District

Abstract: Detections of Aedes aegypti have occurred in California recurrently since the 1930s. This cyclical nature of detections followed by the apparent disappearance of the species led many to think that California was not a conducive habitat to the mosquito species. The most recent detections began in 2013 in Madera County, California. In 2022, Ae. aegypti has been detected across the state.

This presentation will review the work being conducted across California to control Aedes aegypti. The introduction of Ae. aegypti, along with recent introductions of Ae. albopictus and Ae. notoscriptus has fundamentally changed the surveillance, control, and outreach programs of mosquito and vector control districts across the state. As mosquito sources have changes from larger, more visible bodies of water to cryptic hidden sources in backyards, agencies have evaluated potions of their integrated vector management plan as it relates to these mosquitoes. Highlights of control strategies targeting Ae. aegypti will be presented.

Dissecting the good and bad of morphology, molecules and phylogenetic hypotheses in the Hymenoptera

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Abstract: Arguments over the results of phylogenetic hypotheses based on morphological or molecular still persist despite the increasing amount of data and plethora of analytical tools. This talk will focus on agreements and disagreements in hypotheses developed in large genomic data sets across Hymenoptera, but with a focus on Chalcidoidea and the families Eucharitidae and Perilampidae.

Comparative Anatomy of the Insect Tracheal System (Apterygotes, Paleoptera, Polyneoptera) using micro-CT

Authors: Herhold Hollister[1], Davis Steven[1] and Grimaldi David[1], [1]American Museum of Natural History, United States

Abstract: The respiratory system of insects is defined by tracheae, tube-like invaginations of the epidermis that wind throughout the body, providing tissues with direct access for gas exchange. Although some basic structure of the tracheal system has been known for several centuries, broad comparative studies of tracheal systems across multiple orders of insects are lacking. Micro-CT scanning enables non-destructive visualizations of micron-sized, intricate structures and is especially well suited for visualizing tracheae, where air spaces are easily distinguished from tissues. Here we present a broad comparative study of insect tracheal architecture visualized via micro-CT scanning with representatives from apterygotes, Paleoptera, and Polyneoptera, totaling 29 species across 13 insect orders. A unified system of tracheal nomenclature is presented using 3D visualizations of example species. Patterns in respiratory architecture, both phylogenetic and functional, are presented along with a discussion of future studies into evolutionary processes to be investigated.

Population genetic structure of the invasive insect Corythucha marmorata in North America and it´s invaded range in Japan

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Abstract: The introduction of a species to a new environment can modify the ecological interactions that exist between the organisms at that place. The determination of the native geographical distribution or origin of invasive alien species is crucial for the development of management strategies and biological control, as well as offering a window to evolutionary processes at short time scales. The recent invasion of the North American lacebug Corythucha marmorata to Japan, is an important case study for recent introduction and spread of both host plant and herbivorous insects. For this reason we use the cytochrome oxidase I gene to perform an analysis of genetic diversity between the invaded range (Japan) and the native one (North America) to find the phylogenetic relationships. We sequenced only the inverse complement and the length of the sequences once edited was 233 base pairs. The results indicated a greater diversity in the native populations, just as the haplotype distribution was greater in the southern regions, both of the invaded range and of the native population. On the other hand, the phylogenetic tree shows a good support and a clear division of the populations of Japan, mixing in a clado populations of the south of Japan with the populations of the south of North America. These data suggest at least two introductions, with the South American region being one of the invasion routes. We compare and contrast these findings with the analyses of nuclear SNPs data, and discuss our results in the context of geography and potential adaptive variation in the invaded range.

Barcode and genomic inference of genetic structure of introduced lacebug (Corythucha marmorata) populations in Japan and in its native range in North America.

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Abstract: Debate continues over the extent to which diversification of insect herbivores is coupled to the diversification of their host plants, with the bulk of information derived from macro-evolutionary studies. Only recently has attention been shifted to the population and landscape levels of insect-plant herbivory, which represent the arena of the evolutionary arms race and diversification, as insects feed on plants that vary geographically in genetic structure, defence strategies, nutritional value or chemical composition, leading to local adaptation and variation in their resistance to herbivory. The interaction between the tall goldenrod Solidago altissima (Asteraceae), and the lace bug Corythucha marmorata (Hemiptera: Tingidae), provides an ideal system for understanding the potential role of genetic variation in local adaptation for an invasive plant - invasive herbivorous insect. S. altissima was introduced to Japan ca. 100 yr ago and it has extensively invaded abandoned fields and disturbed areas across the country. C. marmorata is one of the major herbivorous insects on S. altissima in North American native populations, and it was introduced to Japan around 15 yrs ago, much later than its host plant. It has quickly expanded its range from south to north, being absent only on Hokkaido Island in northern Japan. In all neocolonized regions in Japan where the lace bug is present, it maintains permanent outbreak densities, accounting for 61% of all herbivorous insects observed on S. altissima. Taking advantage of the good ecological and physiological characterisation of the interaction in both the native and invaded ranges, we analysed mithochondrial DNA (mtDNA) and nuclear (SNP) diversity and structure of multiple populations of C. marmorata at its native and invaded ranges. Our aims are to (1) determine the levels of variation and infer populations genetic structure; (2) identify the source populations of lineages invasive in Japan; and (3) to infer how it spread in Japan and whether the invasion pattern and routes track those of its host plant.

Microbiota protection against lepidopteran pathogens

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Abstract: Many moth species are serious agricultural pests, against which pathogenic bacteria, fungi, and viruses are widely used as biological control agents. But treatment efficacy may vary, in particular on different crops. Advances in sequencing technology have shown that the microbial community associated with insects varies on different food plants, while some of these natural gut microbes could evolve to facilitate pathogen infection. We have observed similar interactions with baculoviruses. Therefore, we aim to uncover how elements of the microbiota may confer additional pathogenic activities to microbial control agents or conversely protect insects against pathogens. Altogether, these investigations will integrate interactions between Lepidoptera, food, microbiota, and pathogens to understand how they affect insect health. The knowledge obtained will be fundamental to tailor new biological control applications and to optimize insect mass rearing methods.

DNA and eDNA metabarcoding approaches to characterize insect communities and their response to the ecological impact of conifer-dominated forest decline in the Pyrenees

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Abstract: Forests suffer from an increase in frequency and severity of summer droughts and infestations of pathogens and insects. Those factors cause high mortality of some keystone tree species (forest die-offs). How tree mortality and associated changes in forest composition will affect local diversity and ecosystem functions remains unknown. Here, we aim to quantify the impact of climate-induced forest decline on biodiversity by measuring changes in the taxonomic structure of insect communities along silver fir (Abies alba) dieback and salvage logging gradients in the French Pyrenees.

From May to September 2017, a total of 224 samples of Malaise traps (filled with a solution of monopropylene glycol plus ethanol) and 448 Flight interception traps (filled with a solution of monopropylene glycol plus water) were collected over 56 different silver fir dominated plots in the Central and Eastern Pyrenees. We developed both DNA metabarcoding on milled insects as well as eDNA metabarcoding on preservative solutions used in the traps to characterize insect communities. We found more than 3000 OTUs and revealed the poor taxonomic coverage of DNA reference libraries for the Pyrenean biodiversity. We highlight their response to forest disturbance by their similar species richness but altered species compositions. Finally, we consider the usefulness of genomic techniques when implementing wide scale bio-monitoring programs, and we discuss the utility and limitations of eDNA metabarcoding of trap preservative solutions for bio-monitoring programs, in comparison to conventional metabarcoding approaches.

Could DNA metabarcoding of preservative media be used as a non-destructive method for insect biomonitoring?

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Abstract: Large-scale biodiversity and biomonitoring programs are being developed worldwide to evaluate changes in species richness and composition across biomes. One method being used is DNA-metabarcoding of samples that are dried and homogenized. While this has made possible the harmonization and robustness of sampling, the destructive nature of this approach impedes voucher storage and thus morphological comparison with sequencing results, confirmation of descriptions and integrative taxonomical post-studies for long-term monitoring.

We filtered and extracted environmental DNA from preservative media (ethanol or monopropylene glycol) that was used in 26 Malaise traps and 27 window-flight traps (WFT) to collect insects for 30 days in the Central Pyrenees. We compared species diversity obtained from DNA metabarcoding of preservative media with that of destructive metabarcoding of bulk samples (Malaise) or morphological analysis (WFT) of the same traps. We also analyzed whether signals of community changes due to environmental conditions could be detected and if they were similar to signals found with destructive metabarcoding or morphological data. Finally, we discuss the cost, efficiency and reproducibility of this non-destructive method in large-scale monitoring programs.

Validating a metabarcoding pipeline for the assessment of local wild bee biodiversity in Luxembourg

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Abstract: Over the past few decades several investigations have reported large declines in insect diversity, abundance, and biomass, a trend from which wild bees are not excluded. The potentially catastrophic implications of this situation call for effective conservation efforts targeting wild bees. However, considerable documentation gaps complicate the implementation of efficient management strategies in Central Europe. Conservation projects aiming to protect local wild bee populations must first retrieve accurate taxonomic information, applying the pertinent tools. While facing the current shortage of taxonomic experts, the development of new DNA-based approaches rises as a promising approach for large data gathering. Among them, DNA metabarcoding is one of the leading techniques for biodiversity assessment, having the potential to become a cost-effective tool to identify large amounts of specimens.

Here we present the advances made in the development and validation of a metabarcoding pipeline targeting local wild bee biodiversity in Luxembourg. A sample processing designed for specimen-saving DNA extraction and customized metabarcoding protocols are at the core of a survey strategy that aims to supply valuable insights regarding the biodiversity of European wild bees in the country, providing genetic and ecological data to be considered in national conservation strategies.

Chemical aphid mimicry as a driver of host specialisation in parasitoid Lysiphlebus wasps

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Abstract: Parasitoids in the genus Lysiphlebus mimic the cuticular hydrocarbon (CHC) profiles of their aphid hosts to avoid detection by aphid-tending ants. This mimicry raises questions about how these wasps adapt to novel hosts. There is evidence of genetic differentiation among Lysiphlebus wasps collected from different hosts; however, no previous work has explored variation in the CHC profiles of wasps parasitizing different aphid species. We collected Lysiphlebus wasps from different aphids in the field and identified key features of their CHC profiles, including many methyl-branched alkanes, that were consistently more similar to the profile of the host aphid than to that of other aphid species. To explore how genetic and host-derived factors influence wasp CHC profiles, we reared asexual wasp lines on different aphid species and discovered that the wasps' short-chained methyl alkanes were host dependent, while linear and long-chain methyl alkanes were determined by wasp genetics. In behavioural experiments, aphid-tending ants attacked wasps based on their genetically determined CHCs, which indicates that these compounds are key mimicry compounds. Our research shows that Lysiphlebus wasps are chemically adapted to their host species and that the key mimicry compounds are heritable, which strongly suggests that this chemical mimicry drives host specialisation.

Variation in the diapause phenotype expression in Neotropical Euschistus (Hemiptera: Pentatomidae) species

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Abstract: Diapause is a mechanism of developmental suppression employed by arthropods to survive unfavorable periods. Stink bugs may express a facultative adult diapause triggered by short-day photoperiod. The sibling Neotropical Euschistus species, E. taurulus, E. crenator and E. heros [this last represented by two strains (South Strain:SS; North Strain:NS)] are found in distinct latitudes in South America. Our aims were: 1) to verify the diapause phenotype expression of the three species/strains under different light and temperature regimes and, 2)to evaluate the adult reproductive resumption of the three species/strains after diapause induction. We submitted the insects to two photoperiods [long-day:14h light and 10h dark;short-day:10h light and 14h dark] and two temperatures [21ºC; 25ºC]. At 25ºC and long-day conditions, all species/strains did not express diapause. Under short-day and both temperatures, E. taurulus expressed an intense diapause and spent more time to resume reproduction than the other species. SS expressed the diapause with more intensity and spent more days to resume reproduction than NS under short-day and low temperature. Euschistus crenator did not express diapause and resumed reproduction immediately. Our results suggest that diapause is very plastic in Euschistus, and the expression of diapause is higher in Euschistus species/strains from regions with higher latitude.

Enhance Cytoplasmic Incompatibility in Wolbachia using Quorum Sensing Inducers to support Incompatible Insect Technique in Liriomyza trifolii

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Abstract: Liriomyza trifolii is a major insect pest around the world. The symbiosis between L. trifolii and Wolbachia is recognized as an important thing, because Wolbachia can manipulate host reproduction and offspring sex through cytoplasmic incompatibility (CI). Wolbachia induced CI is a promising tools for Incompatible Insect Technique (IIT). Previous studies have reported an association between CI and Wolbachia density, which may involve a quorum sensing (QS) mechanism. We study about the effect of manipulating QS in Wolbachia using several QS inducers including 3O-C12-HSL; C2HSL; and spermidine. The results showed that inducing QS with 3O-C12-HSL decreased the proportion of hatched eggs and increased Wolbachia density. We show for the first time that Wolbachia density and the proportion of hatched eggs of L. trifolii can be controlled by inducing QS in Wolbachia, which is potent to apply as an IIT.

The effect of pollinators on the microbiome of willow catkins

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Abstract: Flowers are known to inhabit diverse and unique microbial communities. However, much of knowledge about the flower-associated microbiota comes from nectar, agricultural plants and managed growing conditions. Fundamental knowledge of flower-associated microbiota on natural plants remains largely unknown. Moreover, microbes associated with pollen are poorly investigated despite ecological relevance in plant-pollinator interactions. Even less well understood are the changes that flower-associated microbial communities experience through flower visitation. We investigated the effect of pollinator visitation on microbial community in willow (Salix phylicifolia) catkins. Salix phylicifolia is the first plant to offer pollen and nectar in large quantities in early spring as the first wild pollinators become active in Finland. It is of great importance especially to the survival of the bumblebee (Bombus spp.) queens during a period when few other productive sources are available. Queen bumblebees require pollen to feed their larvae and to establish the colony. In addition to bumblebees, the willow catkins are visited by cultivated honeybees (Apis mellifera) in some localities. These two insect groups are likely to mainly affect willow catkin microbiome and also receive microbes from each other through the shared resource. In our study, we specifically investigated the effect of i) native pollinators, mainly bumblebees and (ii) the additive effect of cultivated honeybees (Apis mellifera) on the composition of bacterial and fungal communities in willow male inflorescences under natural conditions in early spring. The microbiomes in the willow inflorescences were surveyed using amplicon sequencing of the bacterial 16S ribosomal RNA gene and fungal ITS (intergenic transcribed spacer) region. We hypothesized that the composition of flower microbiota differs between visited and non-visited inflorescences and visited inflorescences have higher diversity. The amount of pollen removed from catkins by insect visitors ranged between 0-90% and was on average 40%. Honeybees had no statistical effect on the amount of pollen removed from catkins in this study. We used pollen loss in visited flowers as a proxy for visitation frequency and related that to microbial diversity in visited flowers. We expected honeybees to increase microbial richness in willow catkins. Further determination of flower microbiome of different plant species is an important step to understand the plant-pollinator-microbe interaction.

Psyllid vectors of Candidatus Liberibacter solancearum in the Scottish landscape – is there a risk to agriculture when crops are not the preferred hosts?

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Abstract: Insect-vectored plant pathogens are generally well studied within agricultural systems, however their interactions with wild hosts are often overlooked. Pathogen spillover from natural reservoirs may significantly impact on the success of disease control within neighbouring crops. Additionally, as wild spaces become increasingly fragmented by agriculture, host-shifts of either the pathogen or its insect vector are increasingly likely, leading to the emergence of new crop diseases. ‘Candidatus Liberibacter solanacearum’ (Lso), a psyllid transmitted bacterium which was first reported as causing disease to Solanaceous crops in 1994 (Mexico) and Apiaceous crops in 2008 (Finland), has recently been found to be present in several species of psyllid in Scotland. Whilst disease symptoms associated with Lso have has not been reported in Scottish crops, Trioza anthrisci (whose preferred hosts are Apiaceous plants) was identified as a newly recorded species for the country and was also found to be carrying Lso. In order to better understand the potential risk posed to Scottish agriculture we carried out transmission studies from wild Apiaceous hosts to carrot (Daucus carota) using T. anthrisci and conducted further investigations into the diversity of psyllids and their associated Lso haplotypes in the Scottish landscape. By developing an understanding of the natural distribution and diversity of these plant-bacterium-insect interactions within our landscapes we aim to better inform policymakers of the risk posed by changes in land use, agricultural practice or the introduction of new potential vector species and/or bacterial haplotypes.

Investigating the feeding behaviour of UK psyllids and the potential for Candidatus Liberibacter solanacearum (Lso) transmission to commercial crops

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Abstract: ‘Candidatus Liberibacter solanacearum’ (Lso) is a phloem-limited bacterium transmitted by psyllids that causes disease in both Solanaceous and Apiaceous plants. Lso is responsible for significant losses to the potato industry in the Americas and New Zealand. In Europe, Lso predominantly affects Apiaceae such as carrot. Several new species of psyllid have been found to carry Lso in the UK, including Trioza anthrisci and Trioza urticae. However, very little is known about their ability to transmit Lso in their wild reproductive hosts and economically important crop species. As Lso is transmitted to plants through saliva when the psyllids feed, its success greatly depends on the feeding behaviour of these psyllids. One of the most powerful and widely accepted tools for studying insect feeding behaviour is the electrical penetration graph (EPG) technique. This allows for observation of psyllid feeding behaviours and how they may vary on a range of plants, along with the potential for Lso transmission. We are currently using EPG methods to investigate the feeding behaviours of T. anthrisci and T. urticae on their host plants (cow parsley (Anthriscus sylvestris) and nettle (Urtica dioica) respectively) and crop species, including carrot and potato. Initial experiments are being carried out to correlate waveforms to feeding behaviours.

Transmission experiments indicate that Trioza anthrisci can feed and reproduce carrot and Lso is detectable after 12 weeks of feeding. Survival rates on carrot and potato are lower than on cow parsley, while potato and carrot are unsuitable for Trioza urticae survival. The impact of T. anthrisci and T. urticae on carrot and potato seems minimal. Further transmission and EPG work will confirm this.

This work will also contribute to wider research into the risk of Lso to UK crops and provide advice for plant health policy and stakeholders.

Early herbivore alert: Plant chemical and molecular defense responses to insect eggs

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Abstract: Plants respond to egg depositions of herbivorous insects on their leaves by various defenses. The egg-induced plant responses may target the eggs themselves and the hatching larvae. When targeting the eggs, plant responses can directly harm the eggs by various means, or they result in indirect defense and attract egg parasitoids or predators by egg-induced leaf volatiles. In case of egg survival, the plant’s response to insect eggs can result in earlier and amplified feeding-induced defenses against the hatching larvae. This egg-mediated priming effect of feeding-induced plant defense is associated with fine-tuned changes in the kinetics of transcriptomic and phytohormonal plant responses. Based on the findings that plants can take eggs as warning of impending larval feeding damage and prime their defenses against the larvae, we asked whether plants can also respond to cues warning of impending egg deposition by priming their defenses against the eggs. We hypothesized that insect sex pheromones serve as such warning (priming) cues. Indeed, our studies showed that pine exposed to sex pheromones of the pine sawfly Diprion pini amplifies its defenses against sawfly eggs. Mortality of sawfly eggs laid on pine pre-exposed to sawfly sex pheromones is significantly higher than on non-exposed pine. The pheromone-mediated priming effect is linked with increased accumulation of hydrogen peroxide and differential expression of several defense-related genes in pheromone-exposed, egg-laden pine needles. Hence, plant defense against insect infestation follows a multi-step strategy starting with responses to the insect’s sex pheromones, thus priming defense against the eggs followed by well-prepared defense against the eggs, and, in case of egg survival, the plant responses to the eggs prepare defenses against hatching larvae.

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Priming by timing: How plants use insect eggs to prepare their defense against impending larval herbivores in time?

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Abstract: When herbivorous insects lay eggs on plants, it is likely that they will be attacked by voracious larvae hatching from these eggs. To avoid the larval attack, plants can fend-off the eggs directly. Additionally, some plants use the eggs as warning cues to prepare their defense against the hatching larvae. Thus, larvae that start to feed on previously egg-deposited plants perform worse compared to larvae on egg-free plants.

We elucidate the molecular and chemical mechanisms that are involved in egg-mediated priming of plant defense and the ecological dependencies of these mechanisms. In particular, we ask i) why the larvae perform worse on previously egg-deposited plants, ii) how this egg-enhanced plant defense response is regulated, and iii) how the dynamics of these regulations change over time when a plant carries eggs, or when the larvae subsequently start feeding on the plant. For our studies we used the cabbage butterfly (Pieris brassicae), a Brassicaceae specialist, and the model plant Arabidopsis thaliana.

We found that A. thaliana maximizes its egg-priming response shortly before the P. brassicae larvae hatch. The subsequently enhanced defense response against the feeding larvae seems to result from an accelerated induction of the plant's anti-herbivore defenses. The egg-enhanced anti-herbivore defense response depends, amongst others, on salicylic acid-mediated signaling, enhanced expression of several defense-related genes, including PR5 (PATHOGENESIS-RELATED GENE 5), and it is linked to the induction of flavonoids.

Hence, the feeding-inducible plant defenses and their regulation can be optimized, when plants perceive insect eggs as an herbivore-related cue reliably indicating future stress by feeding larvae.

Can simple envelope ensembles improve transferability of invasive insect distributions?

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Abstract: Invasive insect species comprise some of the most recognised vectors of human disease, and cause billions of dollars in direct agricultural losses through reduced yields and transmission of plant pathogens, and indirect losses including increased application of pesticides and trade. Predicting the distribution, spread and impacts of invasive insects is thus an important challenge and is required to inform geographically-targeted policies in order to prevent new invasions and manage existing invasive species.

Species distribution models (SDMs) have become increasingly popular to predict the potential geographic range of invasive species, by correlating the known distribution of a species with environmental variables, and transferring these relationships into novel environments and geographic space. There are a range of challenges when using SDMs to predict distributions outside of native ranges, and to date the SDM literature has largely focused on improving the statistical fit of models when projecting into novel geographic space. An area that remains challenging and under-discussed is methods to choose predictive variables that will result in models that transfer between regions. This is challenging as non-causal variables may still show significant associations with distributions. Here we propose methods to finesse this problem by using multiple simple models to search for the most appropriate variables from a given set, and then apply them as two variable envelopes in an ensemble approach. We also explore the use of a presence-only method, range bagging, which examines how often a given environment occurs inside niche boundaries across all environmental dimensions, providing an alternative way to determine 'good' predictive variables.

We apply these methods to both virtual species and a dataset of 22 globally invasive insect species, and find that methods that focus on predictor uncertainty generally perform well against conventional approaches for statistically fitting numerous variables in a single model. While our methods only consider simple ecological relationships of species to environmental predictors, they allow for increased model transferability as they largely avoid over-fitting, background selection and collinearity issues. We transform a model selection problem, for which there is no true correct answer amongst the typically distal covariates on offer, to one of model uncertainty, which appears more tractable. We argue that increased model transferability at the expense of model interpretability is perhaps more important for effective rapid predictions and management of non-native insects and biological invasions.

Age matters: regulation of antennal transcription throughout a mosquito's first gonotrophic cycle

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Abstract: The behaviours of mosquitoes that are associated with maturation, feeding and reproduction, directly influence disease transmission capacity. Odours mediate each phase of the gonotrophic cycle from pre-blood meal host seeking through post-blood meal refuge seeking, oviposition site seeking and oviposition to post-oviposition reassertion of host seeking while sugar seeking throughout. The blood meal-induced regulation of chemosensory, neuromodulatory and other signal transduction genes was investigated in the antenna of female mosquitoes during maturation on 1 and 3 days post-eclosion, and subsequently every 24±1 h from 5 to 10 days post-eclosion from two cohorts: 1) blood fed and 2) non-blood fed. Using a transcriptomic approach, genes-of-interest implicated in the behavioural changes associated with age and with a blood meal were identified from multiple chemosensory-related gene families investigated. The observed concerted regulation of multiple genes within the sensory pathways of the antenna likely play a key role in modulating the behavioural changes observed with age and post-blood meal. Functional characterization of the proteins generated by the genes-of-interest identified in this study may provide a better understanding of the regulation of gonotrophic feeding and a pool of potential targets for vector control strategies.

Management and the role of Ips typographus in diverse environment – the case of Bialowieza primeval forest

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Abstract: Spruce bark beetle Ips typographus is considered a species which activity brings a number of beneficial phenomena in relation to the functioning of the ecosystem and broadly understood biodiversity, which is particularly important in the case of protected areas. Many studies indicate the ecological significance of spruce bark beetle as a key species or so-called "An ecosystem engineer". Nowadays, strong fragmentation and isolation of forest areas largely changes the positive meaning of the bark beetle, which is associated with limited possibilities of migration of living organisms. In specific cases, outbreak in large areas, also in species-diverse forests stands, pose a threat to sensitive stenotopic species, especially those with low dispersal capabilities. In the presentation, an attempt was made to assess the role of spruce bark beetle and its management in multi-species stands of the Bialowieza Primeval Forest.

Leveraging plant volatiles for enhanced biocontrol with entomopathogenic nematodes

Authors: Hiltpold Ivan, Agroscope, Switzerland

Abstract: There is an increasing number of evidences suggesting that entomopathogenic nematodes are able to use volatile cues to perceive and assess their environment. Either to recognize their potential insect host, to evaluate host health status, or to locate insect damaged root systems, entomopathogenic nematodes have evolved the ability to respond to diverse volatile organic compounds to locate, recognize, and efficiently infect hosts. Our recent understanding of these interactions and the identification of several of these environmental cues allows us to manipulate agroecosystems to enhance biological control potential of entomopathogenic nematodes. Focusing on plant emitted cues, we will discuss how to exploit these finely tuned signals to manage major insect pests threatening crop yield and food security in various systems. We will also explore some ideas on how to use this knowledge in the (close) future of digital farming.

Plant response to the third trophic level: An underestimated interplay shaping multitrophic interactions

Authors: Himmighofen Paul, University of Bern

Abstract: Volatile-mediated defense priming occurs in maize leaves, but not roots

Plant leaves that are exposed to herbivore induced plant volatiles (HIPVs) respond by increasing their defenses. Whether this phenomenon also occurs in the roots is unknown. Using maize (Zea mays), whose leaves respond strongly to leaf HIPVs, we measured the impact of HIPVs from maize roots that are infested by the banded cucumber beetle (Diabrotica balteata) on constitutive and herbivore-induced levels of root soluble sugars, starch, total soluble proteins, free amino acids, volatile and non-volatile secondary metabolites and defense gene expression of neighboring plants. HIPV exposure did not alter constitutive or induced levels of any of the measured root traits. Furthermore, HIPV exposure did not reduce the performance and survival of banded cucumber beetle larvae on maize or teosinte. Cross-exposure experiments revealed that maize roots neither emit nor respond strongly to defense-regulating HIPVs. Together, these results demonstrate that volatile-mediated defense regulation is restricted to maize leaves, which is in line with the lower diffusibility of volatiles in the soil and the availability of other, more efficient information conduits below ground

Males of West Indian sweetpotato weevil Euscepes postfasciatus (Coleoptera: Curculionidae) use accessory gland substances to inhibit remating by females

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Abstract: The West Indian sweetpotato weevil, Euscepes postfasciatus (Fairmaire) (Coleoptera: Curculionidae), is a major pest of sweetpotato, Ipomoea batatas (L.) Lam. (Convolvulaceae), in the South Pacific, the Caribbean Basin, and parts of Central and South America. It is now distributed throughout the Ryukyu Islands (Okinawa Prefecture) and Amami Islands (Kagoshima Prefecture) in Japan. In Okinawa Prefecture, a sterile insect technique (SIT) program for eradicating this weevil is underway. Mated females of E. postfasciatus temporarily become unreceptive to subsequent mating, however the physiological mechanism underlying this has not been clarified, despite its practical importance. To elucidate this mechanism, we investigated the effects of male-derived substances on the inhibition of mating receptivity of virgin females by injecting the substances into their abdomens. The length of time from injection to mating in virgin females was significantly longer in females injected with an accessory gland solution than in those injected with control solution. For those injected with the contents of seminal vesicles, or other two accessory glands, there were no significant differences compared to the control. In this study, we showed that mated females have a long refractory period (about 14 d) because males of E. postfasciatus inhibit female remating by using seminal fluid substances. We discuss the optimal timing of the release of sterilized insects in SIT eradication programs, to exploit the mating system of E. postfasciatus.

New integrated strategy for controlling whiteflies in tomato greenhouses by a combined use of zoophytophagous mirid bugs, banker plants, violet LED lights, red insect-proof nets, and a novel repellent

Authors: Hinomoto Norihide[1] and Nagasaka Koukichi[2], [1]Kyoto University, Japan, [2]National Agriculture and Food Research Organization, Japan

Abstract: Whiteflies are one of the most important pests in global tomato production because they transmit plant viruses, causing serious damage to tomatoes. Whiteflies have developed resistance to the chemical insecticides frequently applied as a control. Therefore, a new strategy to reduce chemical pesticides use is now required. The zoophytophagous mirid bug, Nesidiocoris tenuis, is the most promising biological control agent (BCA); it feeds actively on whiteflies and other insect pests, whereas other commercially available predatory BCAs perform poorly on tomatoes due to glandular trichomes restricting their movement on the tomato surface. However, use of N. tenuis has some limitations: a relatively long developmental time, a strong preference for certain insectary plants, and tomato plant damage when numbers increase beyond requirements. In this study, we conducted experiments to develop a new strategy that overcomes these problems in the successful control of whiteflies.

The sides of greenhouses in which the experiments were conducted were covered with newly developed red insect-proof nets (mesh size, 0.8 mm). The nets did not prevent whitefly intrusion, but had advantages in preventing very high temperatures that would reduce tomato quality and quantity in mid-summer. The red-colored nets were able to reduce intrusion into the greenhouses in comparison with standard white-colored nets of the same mesh size. In order to enhance N. tenuis numbers prior to pest invasion into the greenhouses, we employed a banker plant system using insectary plants: garden verbena, spider flower, and sesame. At the time of transplanting, N. tenuis were released onto the insectary plants, on which their numbers increased without pest species. In the early stages of tomato cultivation before N. tenuis numbers had sufficiently increased, instead of spraying conventional chemical pesticides on the tomato plants we used a novel repellent, acetylated glyceride, reducing the risks of viral infection. Violet LED lights, for which N. tenuis shows a strong preference, were turned on when whiteflies were frequently observed in the greenhouses; and N. tenuis individuals were removed from the banker plants on which they had been reared and placed onto the tomatoes. The combination of these newly developed tools resulted in successful whitefly control while avoiding extreme tomato damage, through appropriate maintenance of N. tenuis.

Development of microsatellite markers for the Japanese orange fly, Bactrocera tsuneonis (Diptera: Tephritidae)

Authors: Hinomoto Norihide[1], Opadith Pattara[2] and Ono Hajime[1], [1]Kyoto University, [2]Kyoto University, Japan

Abstract: To monitor and control Japanese orange fly Bactrocera tsuneonis is subject to strict quarantine controls worldwide that is restricted to Japan, southern China, and Taiwan. There is a risk of expanding its distribution, several countries require quarantine and permit imports only from unaffected areas. Therefore it is important to determine their dispersal ability. If geographically isolated strains exist, the control are affected. Since information about genetic structure and geographical variability could contribute to the prediction of mobility of pest species, the development of molecular markers is crucial for the pest management. To determine the genetic structure of this species, we developed microsatellite markers at 17 loci from transcriptome data. A total of 80 adult females and males, which were randomly collected from abandoned orchards in the two prefectures isolated by sea, were used for polymorphism analysis. The average number of loci was relatively low at the value of 2.65, and observed heterozygosity was relatively low at 0.00 to 0.11. Although significant genetic differentiation between females and males of the same population was not observed, populations between both prefectures were diverse. These results suggest a high degree of inbreeding in this species and the adults only disperse short distance.

What makes a good classical weed biological control agent?

Authors: Hinz Hariet[1], Schwarzländer Mark[4], Panta Sujan[3] and Winston Rachel[2], [1]CABI, Switzerland, [4]University of Idaho, United States, [3]University of Idaho, [2]MIA Consulting

Abstract: Since the 1970s, biocontrol practitioners are trying to improve success rates of weed biological control programs. Initially, agent characteristics thought to be associated with greater success were based on experiences gleaned from previous programs, best guesses or simply intuition. From the 1980s, several retrospective analyses of existing data were conducted to identify specific agent life history traits and other characteristics associated with a greater probability of controlling a target weed. Similarly, analyses were conducted to identify traits of target weeds associated with greater biocontrol success. More recently, agent and target weed traits were combined in analyses to reach more refined conclusions. Alternatively, ecological theory has been to used to extrapolate and identify factors related to the agent the target weed or the receiving environments, which may influence control success. This talk will give an overview of existing approaches, their strengths and shortcomings, and recommend potential steps forward.

The residues required for nuclear localization and masculinization of Ostrinia furnacalis Masculinizer protein (Masc) are different from those of Bombyx mori Masc

Authors: Hirota Kanako[2], Matsuda-Imai Noriko[1], Kiuchi Takashi[1] and Katsuma Susumu[1], [2]The University of Tokyo, Japan, [1]The University of Tokyo

Abstract: The Masculinizer (Masc) gene was discovered in Bombyx mori as a regulator of both masculinization and dosage compensation. To date, Masc homologues have been identified from several lepidopteran insects. We previously reported B. mori Masc (BmMasc) has a bipartite nuclear localization signal (NLS) and two residues, lysine at 274 (K274) and arginine at 275 (R275), are essential for its function. We also identified two cysteines at residues 301 (C301) and 304 (C304) in BmMasc, both of which are required for its masculinizing activity. Although the sequences of NLS and masculinizing domain are conserved among lepidopteran insects, their functions are unknown in Masc proteins other than BmMasc. In this study, we characterized these domains in the Ostrinia furnacalis Masc (OfMasc) using B. mori ovary-derived cell line. Deletion and alanine scanning mutagenesis revealed the putative NLS is required for nuclear localization of OfMasc, but mutations at both K227 and R228, correspond to K274 and R275 of BmMasc, respectively, do not greatly abolish the NLS activity. Additional mutagenesis revealed triple mutations at K227, R228, and K240 almost completely inhibit OfMasc nuclear localization. Furthermore, mutations at C253 or C256, correspond to C301 and C304 of BmMasc, respectively, had little impact on its masculinizing activity.

Different parasitic strategies of chrysidid egg parasitoids of phasmids (Hymenoptera: Chrysididae)

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Abstract: Amiseginae and Loboscelidiinae are chrysidid wasps that are parasitoids of stick insects. It has been suggested that the two subfamilies are closely related (Kimsey & Bohart 1991). However, while Amiseginae retains the general morphological characteristics of the Chrysididae, Loboscelidiinae has an elongated vertex, ribbon-like setae that grow on it, and flat legs with flanges. It is so specialized that it deviates from the normal characteristics of the family. As the two subfamilies differ in morphology, it is surmised that their environments and parasitic behavior may also be different (Kimsey 2012), but the life histories are mostly unknown. No host relationship has been revealed in Loboscelidiinae other than its emergence from stick insect eggs, and there is only fragmentary evidence of parasitic behavior in Amiseginae (Tormos et al. 1998; Kimsey et al. 2012). Existing observations indicate that the wasps climb onto stick insect eggs, lay eggs on them (Redshaw 1965), and then transport the (stick insect) eggs (Windsor et al. 1996).

In this study, we observed two species, Nipponosega yamanei (Amiseginae) and Loboscelidia sp. (Loboscelidiinae), and recorded the stages and duration of their parasitic behavior. When N. yamanei found the egg, she climbed on it, touched it with her antennae, and carried the egg backward with her forelegs. She transported the egg to concealed environments, such as crevices, where she pierced the eggshell with her mandibles and laid an egg. This parasitic behavior, searching for hiding places and oviposition, was time-consuming. On the other hand, when Loboscelidia sp. found an egg, she made a hole in the eggshell using mandibles and laid her egg. Then, like N. yamanei, she carried the egg with her forelegs, but in this case, transported it to a hole in the ground, where she gathered soil with her forelegs and buried it. In Loboscelidia sp., much time was spent laying eggs and filling host eggs. In addition, a concentration of insects gathering on the stick insect eggs showed that the eggs concealed by fallen leaves showed a significantly lower detection rate than eggs exposed on the ground.

It was observed that the transport and hiding of host eggs found in other Chrysidoidea and primitive Aculeata also occur in N. yamanei, and Loboscelidia sp. Besides, experiments with stick insect eggs suggest that these actions help in avoiding detection by other parasitoids and predators. On the other hand, the burying of host eggs in soil, found only in Loboscelidia sp., implies a greater degree of concealment than that practiced by N. yamanei, which only placed the eggs out of sight. Egg burials in the soil pose the problem of the adult having to emerge to the ground, but the Loboscelidiinae have unique morphological characteristics (also found in Diapriidae and Tiphiidae) such as setae growing on the head and pronotum, large tegula, and legs with spines. For Loboscelidiinae, they may be useful for escape.

Urban heat island effects disrupt insect-plant interactions on street trees at multiple scales

Authors: Hochuli Dieter[2] and Chen Tony[1], [2]The University of Sydney, [1]School of Life and Environmental Sciences The University of Sydney, Australia

Abstract: Cities are typically perceived as hostile environments for biodiversity, with a combination of stressors disrupting interactions in these novel ecosystems. Street trees are seen as vital for enhancing human wellbeing, playing a role in combating urban heat islands and pollution. However, urban stressors may also affect their health and capacity to thrive. We examined the ecology of Sycamore Lace Bugs (Corythucha ciliata) on London Plane Trees (Plantanus x acerifolia), a common street tree in Sydney, Australia. We compare the insect assemblages, C. ciliata development and levels of damage at fourteen hot and cool sites. These sites were identified through satellite thermal imaging, and detailed 21 day thermal profiles of over 50 trees were described using data loggers to confirm thermal traits. Sites were sampled in spring, and summer.

While hot sites were significantly warmer than cool sites during both spring and summer, the ecological effects of urban heat on insect-plant interactions were only detected during summer. We found that trees at hot sites supported significantly higher densities of C. ciliata and suffered almost four times the leaf damage than trees at cool sites. Examination of individual tree thermal profiles revealed that variation within sites in these patterns was primarily driven by the extent of impervious surfaces within a 50m buffer of trees. Understanding how landscape traits drive the effects of urbanization at multiple scales, from individual trees to stands of trees, is central to identifying the most effective ways to maintain healthy green infrastructure in cities.

Phenological adjustment of the Pine Processionary Moth to contrasting climatic environments along an elevation gradient: how to cope with abiotic factors and biotic interactions

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Abstract: Survival of an ectothermal organism requires that development and reproduction be synchronized with the appropriate periods of the annual cycle, and those inadequate with the phases of inactivity, but the sum of the times required for all phases of the life cycle cannot exceed one year in univoltine species. It is known that the pupation time (prolonged diapause apart) of the pine processionary moth (Thaumetopoea pityocampa) is variable and adjusts to the climate of the site in which inhabits, but little is known on 1) what factors (genetic, ambient, or both) determine the time spent as pupae, and 2) how pupation time and larval development interact with the biotic pressures (predation, parasitoidism) operating at each site. Taking advantage of the altitudinal gradient of Sierra Nevada mountains (SE Spain), in which PPM inhabits from sea level to the altitudinal treeline (2200 m a.s.l.) showing a wide variation in pupation time, we want to understand if variation in the phenological strategy along the gradient responds to an optimization of the pupation length, dragging as a consequence the rest of the cycle, or if on the contrary, it aims to diversify the possibility of avoiding predators and parasites, tracking a less optimal but broader period and playing with the climatic variety between years. Answering this question implies to understand what factors regulate the pupation length of the processionary and how non-climatic selective pressures (mainly predators and parasitoids) vary in each environment of the gradient. We performed a translocation experiment, moving a total of 8100 larvae in three altitudinal levels (180, 1000 and 1900 m a.s.l.) evidencing that the locality of origin determines the duration of pupation and the rate of prolonged diapause, but that abiotic conditions modulate the phenology of moth emergence. Furthermore, egg batch predation and parasitoidism increases at lower altitudes, probably being the main factor setting the optimal window for emergence, while at higher altitudes climate is the determinant.

Leaning In: The case of proactive biological control of invasive insect pests

Authors: Hoddle Mark, Department of Entomology, University of California, Riverside, United States

Abstract: New macroarthropod species establish in California at rate of around nine per year, of which about three or so will become pests causing economic or ecological damage and subsequently requiring some form of control. A significant number of these new pests likely enter California from invasion bridgeheads established elsewhere in the USA. Typically, responses, such as the development of biocontrol programs, to these incursions are reactive and are initiated after the pest has established, spread, and caused damage. An alternative approach would be to take a proactive stance, identify potential invaders, like spotted lantern fly, brown marmorated stink bug, or Asian citrus psyllid, in advance of their anticipated arrival, and have natural enemies pre-screened and pre-approved for release. This presentation will cover the concepts underlying proactive biological control.

Are the Benefits of Classical Biological Control Under Appreciated?

Authors: Hoddle Mark, Department of Entomology, University of California, Riverside, United States

Abstract: Classical biological control of invasive arthropod pests is a powerful tool for suppressing damaging populations injurious to agricultural, wilderness, and urban areas. Despite numerous successes this powerful tool for population regulation is often not well understood or nor are successes widely appreciated. These are major obstacles for promoting the use of safe efficacious natural enemies for suppressing pest populations and for reducing pesticide use. This presentation will provide examples of successful classical biological control programs targeting an invasive pest that was killing native plants in the Galapagos Islands, a world heritage site, the complete halt of the invasion South Pacific Islands by the glassy-winged sharpshooter, and successful suppression of the Asian citrus psyllid in urban citrus in southern California.

Flight Mills as Tools for Assessing the Invasion Potential of Pest Insects

Authors: Hoddle Mark[1], Kresslein Robert[2], [1]Department of Entomology, University of California, Riverside, United States, [2]University of California Riverside, United States

Abstract: The natural dispersal capabilities of an invasive pest can play an important role in population growth and phenology which in turn influences understanding of factors affecting aspects of pest invasion biology (e.g., rates of spread) and development of management plans (e.g., establishment of quarantine boundaries and deployment distances between traps). Natural flight dispersal of insects is difficult to observe and quantify in the field. Laboratory-based systems, such as computerized flight mills, which measure the flight activity of tethered insects, can provide useful insight into dispersal potential and assessment of experimental co-factors influencing flight capacity. Factors of interest affecting flight propensity may include effects of sex, size, and time of year and age and diet. The spread of invasive insect pests may be characterized by long range movement which can occur with considerable frequency and result in faster than expected rates of range expansion as long distance dispersants may establish incipient infestation foci from which new populations develop and coalesce. Measuring these natural types of dispersal events in the field are almost impossible to do. Flight mills are ideally suited for identifying and assessing invasion risk posed by insect pests by elucidating whether or not they are capable of long distance dispersal. This presentation will cover aspects of 24 hr flight mill studies for three species of invasive palm weevil, Rhynchophorus ferrugineus, R. vulneratus, and R. palmarum. Of interest here is whether or not flight distance data exhibit a leptokurtic distribution which is considered characteristic of pests capable of rapid natural spread at the leading edge of the invasion front.

Quantifying Potential Lifetime Flight Capacity of South American Palm Weevil: Management Implications

Authors: Hoddle Mark[1], Kresslein Robert[2], [1]Department of Entomology, University of California, Riverside, United States, [2]University of California Riverside, United States

Abstract: Palm weevils, Rhynchophorus spp. (Coleoptera: Curculionidae), are a perennial invasion threat to areas with large ornamental and edible date palm industries. Once established in new areas weevils may spread naturally via flight or through movement of infested palms. The lifetime flight capacity of R. palmarum, the South American palm weevil, an invasive pest in the USA, is unknown. In order to assess risk of natural spread via flight, we first need to understand the lifetime flight potential for these insects. Computerized flight mills were used to quantify life time flight capacity. While not all palm weevil species will have the same life time flight capabilities, they may be similar enough that these data for R. palmarum could help with the development of quarantine and containment regulations that manage natural spread via flight. Here, I will discuss the results of lifetime flight capacity generated from mill data for 80 R. palmarum that were field collected from San Diego County in southern California (USA). Results will be used to assess invasion risk via natural flight and potential management applications for palm weevils.

Repellent semiochemicals for effective areawide management of agriculture, forest and urban pests

Authors: Hoddle Mark[2], Mafra-Neto Agenor[5], Coats Joel[3], Bernardi Carmem[4], Fettig Christopher[7], Barai James[4], Saroli Jesse[5], Bortoli Ligia[6], Wright Mark[9], Borges Rafael[6], Silva Rodrigo[1], Machota Ruben[6], and Dekker Teun[8], [1]Bedoukian Research, United States, [2]Department of Entomology, University of California, Riverside, United States, [3]Iowa State University, United States, [4]ISCA Inc., CA, United States,[5]ISCA Technologies, Inc., CA, United States, [6]ISCA Tecnologias Ltda, Brazil, [7]Research Entomologist and Team Leader Forest Service Pacific Southwest Research Station, United States, [8]SLU Swedish University of Agricultural Sciences, Alnarp, Sweden, [9]University of Hawaii at Manoa Honolulu, Hawaii, United States

Abstract: An insect repellent is a chemical compound or a blend of compounds that deters insect activity on or near otherwise attractive substrates. Although contact repellents have played a key role in the control of hematophagous insect bites (e.g., DEET), and a number of repellent semiochemicals, including some pheromones, have already been characterized for insect pests, repellents have not been widely commercialized in agriculture or forestry. The vast majority of repellents are labile semiochemicals that quickly vanish once applied in the field, as conventional slow-release formulation technologies are often difficult to apply and/or inefficient in controlling the emission rate of the active ingredient. Though the use of repellents, alone or in combination with attractants as part of a push-pull strategy, has been shown to be effective in a few circumstances, the effective application of such compounds requires the user to have a more comprehensive knowledge of insect behavior than the use of conventional insecticides, which are not only simpler to use, but typically less costly.

The specificity of semiochemical repellents, which are often best adapted for a limited number of insect species in a restricted number of crop or forest systems, presents another challenge to their successful implementation on a large scale, as do the intricacies of the regulatory agencies ruling the registration process for new biopesticides, which can be very costly and time-consuming. This specific market, currently seen as small-size, combined with the high cost of AIs, product development, and registration, hamper the commercialization of repellent technologies for pest control in agriculture and vector control. Despite the many impediments to the commercialization of insect repellents, there are some situations where their use in agriculture and forestry is desirable and warranted. ISCA Inc., together with collaborators from academia, government and private sectors, has actively been developing and commercializing novel repellent formulations against several important pest and vector species around the globe. Here we will describe a few case studies on the use and commercialization of repellants against phytophagous and hematophagous arthropods of importance.

Can selection of biological control agents be improved to decrease the risk of releasing ineffective agents?

Authors: Hoelmer Kim A., U.S. Dept. of Agriculture, Agricultural Research Service, Beneficial Insect Introduction Research, Newark, Delaware, United States

Abstract: My presentation addresses advances that help to improve the success in identifying effective natural enemies. Although classical and augmentation biological control differ in scope, agents used for both approaches share many of the requisite characteristics needed to be effective natural enemies. Accurate identification of species is a cornerstone of biological control, and close collaboration with taxonomists ensures that important biological and identifying characteristics are properly associated with the correct taxa and biotypes. Advances in molecular biology have enhanced this collaboration. Native range studies are important to identify natural enemies that cause significant mortality of the target pest, as well as contributing information on anticipated non-targets. While tried-and-true physiological no-choice and choice tests conducted in the laboratory are still used to estimate host specificity for regulatory applications, they are recognized as often being overly conservative, which risks rendering an effective agent off-limits. Modern genomics research now has the potential to identify the genetic bases of host specificity, along with advances in electrophysiology and chemical ecology that help to identify the environmental and behavioral cues important in host habitat recognition and host finding. Increased awareness of endosymbionts and their influence on natural enemy biology has become another consideration in agent evaluation.

Risk and impact assessment for exotic natural enemies

Authors: Hoelmer Kim A.[2] and Haye Tim[1], [1]CABI, Delémont, Switzerland, [2]U.S. Dept. of Agriculture, Agricultural Research Service, Beneficial Insect Introduction Research, Newark, Delaware, United States,

Abstract: Our presentation addresses various risks to consider when utilizing exotic natural enemies for biological control of invasive species. These include not only accurately assessing the risk of reproducing in non-target species, but also non-reproductive mortality due to unsuccessful attacks, competitive interactions with native biocontrol agents and potential secondary effects on non-target hosts that are not directly attacked by the exotic agents. Risk also includes considering the consequences of not including biological control as a management option. Accurate identification of biocontrol agents is a cornerstone of biological control, thus close collaboration with taxonomists ensures that important biological and identifying characteristics are correctly associated with taxa and biotypes. Advances in molecular biology have enhanced this collaboration. Native range studies contribute information on anticipated non-targets. Traditional laboratory physiological no-choice and choice tests remain valuable for estimating host specificity for regulatory applications, although they are likely to be excessively conservative, which risks rendering an effective agent off-limits. Advances in electrophysiology and chemical ecology now make it possible to identify the environmental and behavioral cues important in host habitat recognition and host finding and which may moderate physiological host ranges.

Status of adventive Trissolcus japonicus in the United States

Authors: Hoelmer Kim A.[1] and Tatman Kathleen[1], [1]U.S. Department of Agriculture Agricultural Research Service Beneficial Insects Introduction Research Unit Newark, DE, United States

Abstract: The egg parasitoid Trissolcus japonicus (Hymenoptera: Scelionidae) is thought to be the most important natural enemy suppressing the agricultural pest Halyomorpha halys (Hemiptera: Pentatomidae) in its native range in China. Since the invasion of H. halys into the United States (first record from 1996), adventive populations of T. japonicus have been documented in several states where H. halys is present. The first report of adventive T. japonicus was in Maryland in 2014, and it is now present in at least 13 other U.S. states and Washington D.C. Within many states where adventive populations have been documented, mass rearing and redistribution efforts are underway. Additionally, because quarantine requirements have been lifted in these areas, an increase in research capability has improved our understanding of T. japonicus biology and its impact on H. halys. We will discuss some highlights of this research, including studies on longevity, maximum fecundity, and attempts to understand colonization processes as T. japonicus moves into new habitats and regions.

Using acoustic signals to manage bark beetles and other wood-infesting pests

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Abstract: Wood-infesting insects (such as termites, bark beetles, wood borers and ambrosia beetles) are one of the most significant biotic disturbance agents in forest ecosystems, and when introduced into new habitats typically lead to extensive economic losses, transitions of forest communities, and negative impacts on local recreation and food production. These insects have well developed chemical communication systems that allow for aggregations on host trees, which is often exploited in control strategies and management. However, these insects also use acoustic signals to communicate at the tree surface and within tree tissues. These acoustic signals can be complex and provide a context for species recognition, premating interactions, pair formation, mate selection, intra-species aggression, territoriality and predator deterrence. Acoustic communication provides an avenue for species detection in wood materials and also strategy for beetle management and tree protection. We will discuss technical and applied applications of acoustic tools for management of wood-infesting insects and fungi.

Prospects for biological control of bagrada bug in California using egg parasitoids

Authors: Hogg Brian[2], Pickett Charlie[1] and Grettenberger Ian[3], [2]United States Department of Agriculture, United States, [1]California Department of Food and Agriculture, United States, [3]University of California, Davis, United States

Abstract: Bagrada bug, Bagrada hilaris, a native of southern Asia, quickly became a damaging pest of cole crops (i.e., cabbage, broccoli, cauliflower, kale) in California after its discovery near Los Angeles in 2008. Conventional pesticides are currently the most effective means for controlling bagrada bug, but are unavailable to organic growers. Two potential biological control agents for bagrada bug, the egg parasitoids Gryon gonikopalense and Trissolcus hyalinipennis, were collected from Pakistan in 2016. Host specificity testing indicates that G. gonikopalense is more specific to bagrada bug than T. hyalinipennis. Further tests showed that G. gonikopalense could locate and attack bagrada bug eggs in the soil, where most bagrada bug eggs are laid, and appears to search preferentially at ground level. In contrast, T. hyalinipennis could only attack eggs on the soil surface. In 2016-2019 we also conducted surveys throughout northern and central California to evaluate attack rates by resident egg parasitoids on bagrada bug eggs. To survey parasitoids, we used sentinel bagrada bug eggs glued to waterproof index cards, and placed the cards in plant foliage and on the ground in cole crop fields and adjacent patches of weedy bagrada bug hosts. Few parasitoids emerged from the 1000s of eggs we deployed, and parasitism occurred almost exclusively in plant foliage and not on the ground. Several adventive egg parasitoid species attacked bagrada bug eggs in laboratory tests, but only at low levels of efficiency. Thus, results indicate that an exotic egg parasitoid is needed to help control bagrada bug in California, and that G. gonikopalense is a particularly promising candidate.

More stable flies, Stomoxys calcitrans, will be captured with proper placement of traps

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Abstract: Stable flies are an important livestock pest in many parts of the world. Both sexes are blood feeders and they can adversely affect production and animal comfort. Traps have been used for many years, mainly to sample stable fly populations, but with some efforts to affect a population reduction. Claims have been made that traps will protect host animals by catching the stable flies before they can bite the animals. Some claims also include the size of the area protected by individual traps. We could not substantiate these claims by surrounding tethered horses with traps placed only 3.7 m from the animals. Traps must be placed out of the reach of host animals because animals tend to destroy traps. This limits the placement sites for traps. Stable flies on animals are usually there to feed and afterwards they tend to rest on nearby objects while digesting their meal. If traps must be placed outside of fenced paddocks and fields, the traps are outnumbered as resting sites for blood-fed flies by the many other choices in the environment. Traps placed outside of fences do not necessarily reflect fly activity, population size and fluctuation. Traps surrounds by small squares of electric fence can be placed inside of pastures and paddocks where they are quite close to the host animals. Numbers of trapped flies increases compared with traps placed outside of the fences as does the sensitivity of population fluctuations. Flies can be so numerous in locations near host animals that more than one trap is required inside the protective electric fence if traps are to be serviced on a weekly basis. Converting the traps into attract and kill devices increases the life of the traps in the field and reduces the time required for servicing.

Lycaenid caterpillar secretions manipulate attendant ant behavior

Authors: Hojo Masaru, Kwansei Gakuin University, Japan

Abstract: Ants engage in mutualistic interactions with various organisms, such as plants, aphids and butterflies, by exchanging defense and nutritious rewards. In such mutualism, partner recognition and behavioral flexibility based on the inter-specific communication are important mechanisms underlying the regulation of mutualism. In a mutualistic interaction between a Pristomyrmex punctatus ant and a lycaenid Narathura japonica butterfly, the ant workers learn to recognize mutualistic lycaenid caterpillars as partners by feeding on the nectars provided from the caterpillars. Caterpillar’s cuticular hydrocarbons are used as a key recognition olfactory signature in this context. Furthermore, naïve workers who have interacted with learned workers also increased attending behavior to caterpillars, so the ants can transmit the partner information through social interactions. However, after feeding on the nectar secretions of the caterpillars, the workers modified aggressiveness, locomotor activity and brain biogenic amine levels. This suggests that the chemical signals contained in nectar secretions manipulate worker behavior to enforce the cooperation. I will discuss the possible function and mechanisms of behavioral manipulation in a lycaenid-ant mutualism.

Entomopathogenic nematodes as a component of IPM and Ecosystem Services

Authors: Hokkanen Heikki[2], Menzler-Hokkanen Ingeborg[1], [2]Organizer, Finland, [1]Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio, Finland

Abstract: Several ways of incorporating entomopathogenic nematodes (EPN) in IPM systems are possible, and indeed they are a highly potent but underexploited component of ecosystem services. EPN can in many cases, and increasingly so, be used as directly substituting chemical pesticides as means of curative treatment. They can for example substitute for neonicotinoid seed dressing for the control of the corn rootworm in maize, or for flea beetle control in oilseed rape. EPN can also be utilised inundatively in sensitive ecosystems to control outbreaking pest species, to allow other natural enemies (parasitoids, predators, pathogens) to gain back control. We have shown this possibility at a large scale in successfully stopping an outbreak of the great web spinning sawfly Acantholyda posticalis in Finland. When EPN occur in the soil at densities typical of many natural habitats, they can be very effective parts of the insect pathogen complex constituting “insect pest suppressive soils”. Unfortunately, this role of EPN in supporting pest control ecosystem services has largely been lost, because agricultural soils usually harbour EPN at very low densities. We have shown that with very basic IPM measures it is possible rapidly to increase the incidence of EPN in agricultural soils, and with targeted management EPN densities can reach levels where they can permanently suppress some key pests. One such management measure is to increase the botanical diversity in the field, and we have shown that particularly the inclusion of leguminous plants results in higher densities of EPN in the soil over time. We propose to develop crop and field management practices that support the natural occurrence of EPN in the soil at densities that provide good control of many key crop pests. This transition can be accelerated by augmentation of field soils with EPN at the beginning of this process.

Landscape influences on an invasion front

Authors: Holland Jeffrey, Department of Entomology Purdue University, United States

Abstract: Landscape spatial characteristics can influence the velocity of insect invasion fronts. Small-scale movements and mating success of individuals coalesce to determine the speed and direction of the population. Insect invasions provide an opportunity to explore influences on range boundaries. We used 30 years of trapping data on the gypsy moth Lymantria dispar invasion of north-eastern United States to examine the influence that the arrangement of host tree density in the landscape had upon the spread of this species. Various techniques for modeling the spread were compared. This landscape ecology work is being combined with concurrent studies of gene flow and population dynamics to build a complete cross-scale model of invasion processes.

Long-term changes in invertebrate abundance on two areas of arable farmland in England.

Authors: Holland John[2], Ewald Julie[1], Aebischer Nicholas[1] and Moreby Steve[1], [1]Game & Wildlife Conservation Trust, United Kingdom

Abstract: The Game and Wildlife Conservation Trust has monitored “in crop” invertebrate abundance in two areas of arable farmland in the southern half of England, with invertebrate collection beginning in 1970 at one of the study areas in the county of West Sussex, and in 1992 at the other in the county of Leicestershire. Overall invertebrate numbers on the Sussex area have declined by a third since 1970, but individual taxa showed a variety of patterns of change. For example, most families of Coleopterans have declined by over 80%, while Dipterans as whole have declined by a third and Lepidopterans have increased by 80%. The effect of cropping, pesticide use, weather and field size on these changes will be considered as drivers of the trends identified. Results from the Leicestershire site, where monitoring began later and management has been directed towards best practice for wildlife, have shown fewer significant changes. The ability of agri-environment options directed towards conserving farmland wildlife (conservation headlands, beetle banks) and agricultural practices aimed at conserving soil (reduced tillage) to mitigate some of these changes in invertebrate abundance will be discussed.

The BEESPOKE project

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Abstract: Insect pollination is worth €15 Billion in the EU, however, wild pollinators are declining because of loss in flower-rich habitats. The North Sea Region (NSR) of Europe is one of the most productive agricultural areas but has been identified as having low pollination potential. A new project called BEESPOKE (Benefitting Ecosystems through Evaluation of food Supplies for Pollination to Open up Knowledge for End users) aims to increase levels of pollinators and crop pollination at local and landscape scales by providing land managers and policy makers with new expertise, tools and financial knowledge to create more sustainable and resilient agroecosystems. BEESPOKE brings together a wide range of partners from policy makers, research institutes, advisory and end users from 6 NSR countries to develop new products and approaches to increase the diversity of insect pollinators and crop yields. We will develop bespoke seed mixes and habitat management guidelines to support the suite of pollinators required for 14 crop types across 72 demonstration sites. Sites for each crop will showcase best management practices and training materials will be developed for biodiversity monitoring and measuring pollination. The same agroecosystems occur across the NSR and transnational cooperation will also give economies of scale for development of these novel tools. The approach will empower land managers to adopt pollinator management as a routine practice, fostering a bottom-up, land manager approach, creating a legacy to ensure continuing improvements for insect pollination of food crops. The project will run from July 2019 until January 2023.

BEESPOKE is carried out in the framework of the Interreg North Sea Region Programme (www.northsearegion.eu) under the Programme Priority 3 “Sustainable North Sea Region” and the Specific Objective 3.2 “Develop new methods for the long-term sustainable management of North Sea ecosystems”. The programme is funded by the European Regional Development Fund (ERDF) of the European Union.

Comparative ecology of geometrid moths: in search of contrasts between a temperate and a tropical forest

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Abstract: Understanding the variation in life-history strategies lies at the core of modern evolutionary ecology. Comparative studies on insect life histories are facilitated by the increasing availability of reliable phylogenies but are hampered by the scarcity of comparable data. Data are especially scant for the highly vulnerable tropical regions, where the species themselves and interactions between them are still largely unknown.

Worldwide there are approximately 24 000 described geometrid species, but we know very little about the life histories of tropical species. We present the results of a phylogenetically informed analysis comparing the values of life-history traits for a sample of tropical geometrid moth species to a selection of species representing a temperate habitat. For about 250 temperate and tropical region geometrid species, data on host-plant specificity, longevity and breeding strategy were collected. A phylogeny was derived for these species and the collected data compared in phylogenetically informed analyses.

Larval diet breadth of tropical and temperate species was compared in host-plant acceptance trials. There were broadly polyphagous species in both regions. Oviposition latency (i.e. pre-oviposition waiting time of a female; an indirect measure of host specificity) was also found to be similar in both regions. Adult lifespans of wild-caught individuals were found to be similar for both regions. Larger species showed a tendency to have longer lifespans. Although, it was predicted that income breeding (i.e. usage of adult-derived nutrients for reproduction) may be more prevalent in the tropics than in temperate habitats, the patterns found were inconclusive and do not provide clear evidence in support of major differences

The results of this study suggest that host-plant specificity, longevity and breeding strategy are rather similar for the studied temperate and tropical moths. This allows us to conclude that the world the moths experience and the factors that shape their life histories may not be so different for the tropical and temperate regions after all.

Assembly of food webs during Afrotropical forest restoration

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Abstract: The rapid decline of natural tropical forest ecosystems has caused severe changes and the loss of insect communities. Restoration of these forests has now emerged as a global priority. Yet, it is still poorly understood how efficiently forest restoration can bring back the complexity of functioning ecosystems, such as the crucial networks of species interactions.

We study the assembly of food webs in different-aged natural and actively restored Afrotropical rainforests at Kibale National Park, Uganda. We are focusing on food webs consisting of trees, lepidopteran larvae feeding on them, and the parasitoids of the lepidopteran larvae. In this presentation, we will report the first results of the fieldwork season carried out in 2019. We will make a preliminary overview on lepidopteran communities from the different-aged restored forest and show how these communities change during the restoration process. We will also briefly introduce our fieldwork results from 2021.

Long-term population census of the mulberry tiger moth, Lemyra imparilis (Butler) in Japan

Authors: HONDO MASARU, Osaka City, Japan

Abstract: The population density of some insects occasionally reaches outbreak level. As such extraordinary density changes often cause serious damage on forests and farm products, to monitor the density of insect pests and analyze the pattern of population fluctuations is an important task economically. The mulberry tiger moth, Lemyra imparilis (Butler) (Lepidoptera: Erebidae), is a univoltine species that is distributed from south to east Asia. It is widely distributed across Japan. The larvae hatched from the egg mass are gregarious and form communal nests covered with silk webs on the host tree during autumn. By contrast, the larvae in spring are solitary and feed on various plant species. The mature larvae pupate in underground litter from May to June. In the southwestern Japan, outbreaks of the moth have widely occurred from the eastern area, Shizuoka Prefecture to western area, Kyushu Island during 1968 and 1973. In these periods, various crops, for example, citrus, pears and tea plants were severely damaged by the sprig larvae. Thereafter, outbreaks have been sometimes observed at local areas in the southwestern Japan. Historical records of population peak years of the moth observed in the southwestern Japan exhibited that the peaks appeared periodically with periods of 7 or 9 years. In the northeastern Japan, on the other hand, it is well known as an insect pest of the mulberry tree. However, no wide-ranged outbreaks like those in the southwestern Japan have been recorded. On Hachijo Island where is oceanic island far from about 300Km south from Tokyo, moreover, the outbreak of the moth was suddenly observed in late 1970s and the moth has been recognized as a major pest of ornamental plants that is specialty of the island since then. In this work, the population changes have been surveyed by counting larval nests of the moth every year at several sites in Japan since 1989. It was found that the population fluctuations of the mulberry tiger moth in Japan exhibited four patterns of geographic variation: (A) cyclic population fluctuations with relatively high amplitude and sharp peak shape in the southwestern Japan, (B) non-cyclic population fluctuations with high density and flat peaks at the southern coastal Kinki in the southwestern Japan, (C) non-cyclic population fluctuations with low density and stable density change in the northeastern Japan, and (D) non-cyclic population fluctuations with very high density and stable density change on Hachijo Island. Comparing to some moth populations which exhibited cyclic fluctuations in harsh environments, for example, in the north rather than in the south and in mountainous rather than in lowland regions, the mulberry tiger moth showed cycles in mild environments in the southwestern Japan. To clarify mechanisms making these different geographic patterns of population fluctuations of the mulberry tiger moth is a next challenge.

A new Mymaromma sp. (Mymarommatoidea: Mymarommatidae) in Hawaii and first host record for the superfamily

Authors: Honsberger David[1], Huber John and WRIGHT MARK[1], [1]University of Hawaii at Manoa Honolulu, Hawaii, United States

Abstract: A new species of Mymaromma (Mymarommatoidea: Mymarommatidae) was found emerging from eggs of a Lepidopsocus sp. (Psocodea: Lepidopsocidae) in Hawaii. This provides the first host record for the superfamily Mymarommatoidea, the last superfamily of parasitoid Hymenoptera for which no hosts were known, and comes approximately 100 years after the first extant species was described.

Tiny Targets – from a research project to large scale tsetse control operations for the elimination of gambiense Human African Trypanosomiasis in Uganda

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Abstract: Historically, the control of gambiense Human African Trypanosomiasis (gHAT) has relied on the large-scale screening and treatment of populations. Great progress has been made reducing case numbers, but it is recognised that additional interventions are required if elimination goals are to be met. Vector control did not play a major role in gHAT control initiatives because methods that were developed for the control of “savannah” tsetse flies were too expensive and logistically challenging for use against the “riverine” species that transmit gHAT. Research into the responses of “riverine” tsetse to visual and olfactory cues led to the development of a new tool, the Tiny Target.

In 2011, Tiny Targets were trialled on islands in Lake Victoria, 20 Tiny Targets were deployed per round of deployment and this led to a greater than 99% reduction in tsetse densities. Further trials followed in Uganda using 50km2 blocks, then increasing to 500km2 before launching into a large-scale control operation covering 2,500km2 in five Districts in 2014, representing the largest gHAT vector control programme in the world. The intervention area doubled in size in 2016 and include two further Districts. Further expansion was initiated when northern Uganda experienced a huge influx of refugee populations from gHAT endemic South Sudan. Currently, over 40,000 Tiny Targets are deployed annually in Uganda. Regular monitoring of tsetse densities across the intervention areas demonstrates that Tiny Targets are achieving reductions of more than 80% in tsetse densities. Uganda has had a great decline in gHAT case numbers over the last decade, only one case was recorded in 2018, and in the next phase of our programme we will start to scale back vector control.

Tiny Targets provide a cost-effective, easy to use technology which can be readily implemented by national control programmes. Tsetse control is now recognised as an essential part of the fight to eliminate gHAT and is a named part of the WHO elimination strategy. The Tiny Target story provides an example of how a new technology can be developed and rolled out at scale in a relatively short time period.

Genetics of host specificity, climatic tolerance, and other traits affecting biological control by introduced parasitoids

Authors: Hopper Keith, United States Department of Agriculture, Agricultural Research Service, Beneficial Insect Introductions Research Unit, Newark, DE, United States

Abstract: One way to increase the efficiency of species used in biological control would be to breed or transform organisms to improve their performance. To do this, we would need to determine which traits are likely to improve performance, how much variation already exists in these traits, how this variation is distributed within and among populations, and the genetic architectures underlying this variation. Multiple approaches are used to measure genetic variation in traits, and these include resemblance in traits among family members, crosses between lines that differ in traits, response to selection on traits, association between traits and genetic differences within populations and between populations, differences in gene expression underlying trait differences, analysis of tissue-specific expression of candidate genes, effects of manipulation of expression of candidate genes on traits, and effects of genetic transformation on traits. All these approaches can be used separately but are most powerful when used in combination. I discuss how some of the older approaches, in particular, family resemblance, line crosses, response to selection, can be used in any laboratory were insects are reared to gather information about genetic variation with small changes in book-keeping or protocol. This being said, there have been huge advances over the last decade in DNA/RNA sequencing that have provided much higher throughput at much lower costs for genotyping-by-sequencing and analysis of gene expression. Furthermore, there has been a revolution in our capacities to manipulate gene expression using RNAi, to study tissue-specific expression of genes using fluorescent in-situ hybridization and modern imaging, and to silence, modify, or insert gene sequences using CRISPR/Cas9. These advances in technology have opened up the possibility of using these approaches in a wide variety of non-model organisms, and I discuss examples of each, where possible in biological control introductions. I review the evidence concerning genetic variation in traits that are considered likely to affect performance of species introduced for biological control and discuss the implications for breeding or transformation to improve performance. In particular, I discuss what is known about the genetics of host specificity and climatic adaption. The latter is particularly important given the likely impact of climate changes on interactions between pests and natural enemies. Although the pace of progress is accelerating, we still have much to learn, and given imminent changes in climate, we need to learn rapidly.

Genetics of insect rearing

Authors: Hopper Keith, United States Department of Agriculture, Agricultural Research Service, Beneficial Insect Introductions Research Unit, Newark, DE, United States

Abstract: Rearing insects is critical to much of entomological research and pest management, and genetic changes, i.e., evolution, during rearing can have profound implications for the results of research and management. Whether evolution in traits of importance occurs depends on how much variation exists in the traits and the genetic architecture underlying this variation. Several processes can cause genetic changes: mutation, migration, drift, non-random mating, and selection. Mutation and migration are the original sources of genetic variation in natural populations. However, mutation is unlikely to be important in reared insects because the populations are small and mutation is rare. Furthermore, migration can be controlled with reared insects so it is more easily managed than the other processes. Genetic drift is random loss of genetic variation in small populations, either from founder effects or population bottlenecks. Drift can lead to loss of adaptability and poor performance in field. Non-random mating can cause inbreeding depression when mating of close relatives exposes deleterious alleles or to outbreeding depression when crosses between populations create deleterious genotypes. Both inbreeding and outbreeding depression lower fitness and cause colony decline. Selection is systematic change in gene frequencies, and it can be intentional in a breeding program or unintentional when there is inadvertent adaptation to the rearing environment, which can lead to poor performance in field. I review methods managing drift, non-random mating, and selection during insect rearing. Drift and inbreeding depression can be reduced by starting and maintaining large colonies. Inbreeding depression can also be reduced by controlling matings. Outbreeding depression can be avoided by not mixing different source populations. Inadvertent selection can be reduced by making the laboratory environment resemble the field environment and by maintaining sub-populations or even isolines. I review methods for measuring genetic variation: family resemblance, line crosses, selection responses, associations between genetic markers and traits, gene expression especially tissue-specific expression, manipulation of expression of candidate genes, and genetic transformation. These approaches can be used separately but are most powerful when used in combination. I discuss how some of these approaches can be used in any rearing program with small changes in book-keeping or protocol. There have been huge advances over the last decade in DNA/RNA sequencing and a revolution in our capacities to manipulate gene expression, study tissue-specific expression, and modify sequences. These advances in technology have opened up the possibility of using all these approaches in model and non-model organisms.

Role of tarsal gustation in chrysomelid beetles

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Abstract: It is known that Diptera and Lepidoptera have tarsal gustatory sensilla that allow them to recognize tastes and select suitable hosts by using their legs. However, in Coleoptera, the largest insect order, the existence of tarsal gustatory sensilla and their role in taste recognition have not been fully investigated. In a previous study, through morphological observations by using a scanning and transmission electron microscope, we found that all subfamilies of Chrysomelidae have gustatory sensilla on the tarsus. Additionally, we revealed that Galerucella grisescens (Coleoptera: Chrysomelidae) could positively respond to the leaf surface wax of host plants with their legs but not to the waxes of the non-host plants. These results indicate that tarsal gustatory sensilla are used for host selection in Chrysomelidae. However, the mechanism for reception of the diverse tastants by the tarsal gustatory sensilla of chrysomelid beetles is still unclear. In this study, we investigated the electrophysiological response of the tarsal gustatory sensilla of G. grisescens to a range of substances with different tastes by using a tip-recording method. Various tastants, including NaCl, KCl, brucine, sucrose, and the leaf surface wax of Rumex obtusifolius (the host plant of G. grisescens), were perceived by the tarsal gustatory sensilla of the beetles in a dose-dependent manner. The previous and present studies indicate that tarsal taste recognition is important in host selection. On the other hand, in some insect species, including members of Chrysomelidae, it is known that gustation is important in mate recognition as well as host selection. We have previously reported that chrysomelid beetles use cuticular wax as a contact sex pheromone. However, the role of tarsal gustation in mating behavior has not yet been clarified. Therefore, we investigated the ability of G. grisescens to recognize contact sex pheromone through their tarsi by using a behavioral test. The male beetles could mate with female beetles even if their antennae and maxillary and labial palps were ablated. This suggested that male beetles can recognize female contact sex pheromone with their tarsi alone. Next, we compared the chemical composition of the leaf surface wax of R. obtusifolius and the cuticular wax of G. grisescens by GC-MS analysis. The chemical compositions of both waxes were very different, although a small number of common components (e.g., n-alkanes) were detected. Therefore, the beetles may also be able to perceive contact-sex-pheromone components that are not contained in the leaf surface wax by their tarsal gustatory sensilla. Further studies are necessary to clarify the relationships between the mechanisms of taste recognition in host selection and those used in mating behavior.

Blue light irradiation: a novel method for mosquito control.

Authors: Hori Masatoshi[1], Taniyama Katsuya[1] and Saito Yoshino[1], [1]Tohoku University, Japan

Abstract: We previously reported that visible blue light (400-500 nm) has lethal effects on several insect species (i.e. Drosophila melanogaster, Galerucella grisescens). However, the details of these effects on mosquitoes are not yet clear. In this study, we examined the toxicity of blue light in two species of mosquitoes, Culex pipiens molestus and Aedes albopictus., which are important pests and vectors of various diseases. C. pipiens molestus occurs mostly in urban underground structures and transmits the West Nile virus to humans, while A. albopictus occurs mostly in natural areas and transmits Zika and dengue viruses. We first investigated the effects of various wavelengths of blue light (375, 406, 417, 427, 438, 452, 467, and 493 nm) at different photon flux densities (5, 10, and 15 × 10^18 photons·m^-2·s^-1) on the eggs, larvae, pupae, and adults of C. pipiens molestus using light emitting diodes. The mortality of larvae that hatched from eggs irradiated with 417 and 427 nm lights at 10 × 10^18 photons·m^-2·s^-1 was 70% or more, whereas that in the dark condition (control treatment) was less than 10%. Seventy percent or more of larvae irradiated with 417, 427, and 438 nm lights at 10 × 10^18 photons·m^-2·s^-1 died before eclosion, whereas only 10% of death was observed in the dark condition. The mortality of pupae irradiated with 417 nm light at 10 × 10^18 photons·m^-2·s^-1 was approximately 60%, whereas that in the dark condition was less than 5%. The longevity of the adult males and females irradiated with any of the tested wavelengths of light at 10 × 10^18 photons·m^-2·s^-1 were approximately half of that for individuals in the dark condition. Blue light also had lethal effects on A. albopictus larvae. All larvae irradiated with 417 nm light at 10 × 10^18 photons·m^-2·s^-1 died before eclosion, whereas the mortality of larvae in the dark condition was less than 10%. Our results show that blue light around 420 nm was the most effective wavelength to kill C. pipiens molestus and A. albopictus species. Our findings may lead to the development of non-chemical killing techniques for mosquitoes with the use of blue light.

Lethal effects of blue light on insects and mechanisms of action

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Abstract: We previously reported that blue light (400–500 nm) has lethal effects on various insects. The effective wavelength of blue light is species-specific and is not always associated with the amount of photon energy delivered. However, the mechanism responsible for the lethal effects is not known. Blue light injures organisms by inducing the production of reactive oxygen species (ROS). We, therefore, investigated the generation of H2O2, which is one of the main ROS, by irradiating Drosophila melanogaster pupae with blue light. The generation of H2O2 increased with an increase in the number of photons at all the tested wavelengths of blue light. Furthermore, the H2O2 generation was wavelength-specific. This specificity was similar to the wavelength-specific lethal effect on fly pupae. We surmised that blue light transmitted through the integument and/or compound eyes is absorbed in certain inner tissues and induces the production of ROS. Next, we compared the lethal effects of blue light between the adults of nine fly strains, namely two wild-type (Canton-S and Sumika) and seven mutant (white: white eyes, sepia: sepia eyes, Bar: bar eyes, eye missing: absence of eyes, Cryb: loss of cryptochrome function, norpA: defection of phototransduction, ebony: melanic integument) strains of D. melanogaster. The mortality of Cryb was similar to that of wild type strains. Therefore, we believe that cryptochrome does not contribute to the toxicity of blue light. The tolerance of Bar and eye missing to blue-light irradiation was lower than that of the wild type strains. Hence, it is believed that the penetration of blue light through the compound eyes is not very important for toxicity. In contrast, the mortality of ebony was notably lower than that of the other strains. The blue-light transmittance through the integument was measured using a hyperspectral camera and it was observed that the fly strains with lower transmittance tended to be more tolerant to blue light.
Blue light also exerted injurious effects on Drosophila Schneider 2 (S2) cells. Irradiation with blue light (405–470 nm) suppressed the growth of S2 cells whereas irradiation with blue-green, green, yellow, and red light (490–660 nm) did not do so. Interestingly, fluorescence microscopy revealed that the mechanisms underlying the injurious effects on S2 cells differed between blue light of short (405 nm) and long wavelengths (470 nm). Furthermore, we analyzed the cell-cycle distribution of non-irradiated S2 cells and those irradiated with 405 or 470 nm light using flow cytometry. It was inferred that the growth of S2 cells irradiated with short-wavelength blue light was suppressed because of S-phase arrest, whereas in cells irradiated with long-wavelength blue light, the growth was suppressed because of G2/M arrest. Our findings suggest that the toxicity of blue light to insects results from cell injury caused by the ROS produced upon irradiation with blue light transmitted thorough the integument.

How mating disruption controlled an orchard pest when insecticides could not.

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Abstract: Synanthedon pictipes (Lepidoptera: Sesiidae) is a serious pest of peach in the eastern US. Larvae feed on the cambium of trunks and limbs where their tunneling behavior protects them from applied insecticides. Historically, in-season cover sprays of the organophosphate insecticide methyl-parathion, having a long residual on limbs, prevented populations of S. pictipes from building in orchards. After this insecticide was removed from peach production, populations of S. pictipes increased in the southeastern US and their management with other insecticides was negligible. Part of this poor control is due to the tunneling behavior of larvae but also due to the seasonal activity of this pest being active from mid-March through late November thus preventing an economical solution with insecticide application. Mating disruption was tested as a management technique for this pest. Trap shutdown in plots treated with the mating disruption pheromone was easily achieved regardless of plot size. Over years of testing with increasing plot sizes, even up to 8 ha, plots were not large enough to prevent larval feeding injury. Even at 8 ha, plots were not large enough to exceed the flight capacity of females mated outside the treated plot from invading mating disruption plots. Results from these replicated failures supported the need to address the problem at an areawide scale. Using an areawide approach to mating disruption, all peaches in a 50 sq km area (about 400 ha) were treated with a mating disruption product. As with past studies, male capture in traps was negligible. In stark contrast to past studies, S. pictipes reproduction in these orchards declined significantly. After a two-year demonstration, the success of this areawide mating disruption trial has led to the adoption of mating disruption of S. pictipes as a grower management strategy in the southeastern USA.

Characterization of the piercing behaviors of white-backed planthopper in transmission of a plant virus

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Abstract: Using an electrical penetration graph, we characterized the piercing behaviors of the white-backed planthopper (WBPH) in relation to infection status of the southern rice black-streaked dwarf virus (SRBSDV), transmission success, and host plant species.

When feeding on uninfected rice plants, viruliferous WBPH spent more time in salivation and phloem sap ingestion than non-viruliferous insects. In contrast, infected rice plants showed an arresting effect on non-viruliferous WBPH for phloem sap ingestion.

The WBPH that inoculated SRBSDV exhibited more probing bouts, salivation events and phloem sap ingestion events and longer salivation than those that failed to. The WBPH that acquired SRBSDV were quicker to reach phloem and spent more time in phloem sap ingestion than those that failed to.

When provided with different species of infected plants, the insects showed impaired phloem sap ingestion on corn plants in comparison with on rice plants, which accounted for the high mortality of and low virus acquisition by WBPH on corn plants and resulted in asymmetric spread of SRBSDV between rice and corn.

The vector’s behaviors in relation with viral infections status may have adaptive advantages for virus transmission because greater salivation by viruliferous vectors will promote virus inoculation, whereas more sap ingestion by non-viruliferous vectors will promote virus acquisition. The asymmetric spread of SRBSDV between rice and corn is of significance for assessing SRBSDV transmission risks and field epidemiology.

Consumer acceptance of insects as food and feed in Europe

Authors: House Jonas, Wageningen University, Netherlands

Abstract: The potential of insects as an environmentally-friendly and resource-efficient protein source is now clearly established, and considerable advances have been made across the insect value chain in Europe. Nevertheless, consumer acceptance remains a key challenge for the broader success of the sector. This presentation draws on research with European consumers, outlining a number of key findings and considerations regarding consumer acceptance of insects as food and feed. The presentation highlights a ‘demand-side’ tendency in current research, in which public attitudes are identified as the main barrier to consumer acceptance. Some drawbacks of this perspective are discussed, and an alternative ‘supply-side’ approach is proposed. In this view, attainment of consumer acceptance is the responsibility of actors in the insect value chain, who must work together to create insect-based products which are tasty, affordable, easily available, and which integrate into existing diets in a coherent manner. Key recommendations include a focus on potential ‘early adopter’ consumers rather than whole populations, and consideration of appropriate dishes and cuisines for the introduction of insect-based products.

Towards global standards for automated insect monitoring

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Abstract: Advances in computer vision and deep learning provide new solutions to the challenge of understanding the potentially global insect decline. Cameras and other sensors can effectively, continuously, and non-invasively perform entomological observations throughout diurnal and seasonal cycles. The physical appearance of specimens can also be captured by automated imaging in the lab. When trained on these data, deep learning models can provide estimates of insect abundance, biomass, and diversity. Further, deep learning models can quantify variation in phenotypic traits, behaviour, and interactions. Emerging prototypes of new digital sensors hold the potential to generate automated and globally standardised insect monitoring data. However, to reach this transformative goal, international collaboration and coordination on a range of outstanding challenges is critical. Such challenges include defining minimal requirements and standards for hardware design, recording software, metadata collection, machine learning models, analyses pipelines, and the integration with existing monitoring programs. I will present examples of how these technologies are being applied to longstanding questions in insect monitoring. I will also present current steps towards global collaboration on these challenges and highlight future research avenues to facilitate the transition of these technologies from the current level of demonstration to broad scale application in global insect monitoring.

Use of Biological Control for Fall Armyworm by Smallholder Farmers

Authors: Hruska Allan, Michigan State University

Abstract: Fall Armyworm (FAW) (Spodoptera frugidperda) has been an important invasive pest of maize and other crops in Africa, Asia, and Oceania since 2016. Native to the Americas, FAW is an important pest of maize and other crops throughout its range. While commercial maize farmers who produce for stable markets use a wide range of integrated management tactics, the vast majority of maize farmers in Africa, Asia, and Oceania are smallholder farmers who produce maize under very different economic conditions. These conditions severely constrain the farmers' access to and viability of certain tactics, including among biological control options. The economic and risk management context of commercial farmers permit the development and use of commercial biological control approaches, including the use of VPN, Bt, egg parasitoids, and botanical insecticides. Smallholder farmers may have access to the some of the same organisms, but their use of them is constrained to local, non-commercial uses, largely based on farmer recognition of the organisms and how to attract or use the organisms. This work reviews the subset of biological control options that are accessible and economically viable for smallholder maize farmers to manage FAW.

Wolbachia titer affects the fitness of biological control hosts and its proliferation after Wolbachia transmission

Authors: Hsiao Yi-Ting, Lai Ching-Ting and Wu Li-Hsin

Abstract: Wolbachia is arguably among the most abundant endosymbiont in arthropods, and two major reasons accounted for such success are effective maternal transmission and various phenotypic traits induced. However, Wolbachia transfer to a new host through interaction, but it may not always proliferate and transfer successfully. In this study, we found Wolbachia strain wCcep infected Trichogramma chilonis in Taiwan, which came from the alternative host Corcyra cephalonica that raring mass in our laboratory. To realize the association between horizontal transmission of wCcep and wCcep titer on the host, we found that the host egg hatch rate declined gradually (49%) as Wolbachia titer decreased. After we established the uninfected wCcep C. cephalonica population (wCcep-) and re-established the uninfected wCcep T. chilonis population, T. chilonis (wCcep-) parasitized the host egg separately. The result shows that the titer of wCcep rises rapidly on the second generation of the T. chilonis population, presenting no significant difference with the infected population. In summary, the decreasing concentration of wCcep on C. cephalonica affected its fitness negatively. The higher titer of wCcep when parasitism occurs, the titer of wCcep on T. chilonis increased more efficiently, and the chance of successful horizontal transmission of wCcep is improved.

Integrated Trichogramma wasp control for Asian corn borer can help decrease insecticide use on maize in Taiwan

Authors: Hsieh Chia-Hung[1], Lin Chung-Pin[6], Chang Kuang-Hua[3], Lin Li[2], Chen Sheng-Kuan[5] and Chuang Yu-Hsiang[4], [1]Department of Forestry and Nature Conservation, Chinese Culture University, Taiwan, [6]Taiwan Sugar Research Institute, Taiwan Sugar Corporation, Taiwan, [3]Hualien District Agricultural Research and Extension Station, Taiwan, [2]Hualien District Agricultural Research and Extension Statiom, Taiwan, [5]Tainan District Agricultural Research and Extension Station, Taiwan, [4]Huatung Operation Branch, Taiwan Sugar Corporation, Taiwan

Abstract: The Asian corn borer (Ostrinia furnacalis) is the main pest of maize in Taiwan. The larvae damage all parts of the maize plant and causes corn yield loss. Chemical control is commonly used by farmers to manage this pest. However, insecticides residues raises problematic issues of food safety, insecticide resistance, and environmental pollution. Reducing insecticide use has become a current global issue. Biological control of nature enemies can help manage pest and reduce insecticide use. In this study, integrated parasitoid wasps and insecticide controls were designed to evaluate the pest management efficiency. Parasitoid wasps of Trichogramma have been proposed to control the Asian corn borer. Three pest control programs (commercial insecticide control, parasitoid wasp control, and integrated parasitoid wasp and insecticide controls) were designed to compare the pest management efficiency for Asian corn borer. The results showed that integrated parasitoid wasp and insecticide controls program could efficiency reduce corn damage, insecticide use and cost. The integrated control program combined the advantage of commercial insecticide control and parasitoid wasp control to reach the goal of reducing insecticide use.

Ant rafts are both liquid and solid

Authors: Hu David, Georgia Institute of Technology, United States

Abstract: Fire ants can link their bodies together to build waterproof rafts to survive floods. In this talk, I will discuss the structures that fire ants build, and how these structures are limited by the strength of the connections between the ants. We use time-lapse photography and x-ray scanning to characterize the construction of rafts and towers. We relate the shapes observed to the rheology of the ants, their viscosity and their elasticity, which are measured using a rheometer, a device which usually characterizes the properties of chocolate and yogurt.

Self-introduced egg-parasitoid established and successfully suppressed an invasive pest: a 10-y case study

Authors: Hu Xing Ping[1] and Liu Yang[2], [1]Auburn University, United States, [2]Cortiva

Abstract: The kudzu bug, Megacopta cribraria (F.), a native to the Old World, was first observed in Georgia of the United States in 2009. The following couple of years, the bug moved rapidly into all the southeastern states. The exponential increase in numbers and populations of the kudzu bug enhanced its pest status from an urban nuisance problem to be a top yield-limiting pest of soybean crops and a great concern of international trade and commerce. The failure in discovering native egg parasitoids or effective predators of Kudzu bug in the US motivated initiation of introduction-acclimatization of an exotic host-specific egg-parasitoid wasp that has been successfully used in kudzu bug's native regions. Paratelenomus saccharalis (Dodd) was identified as the candidate, evaluated, and propagated in quarantine at the USDA-ARS Biological Control Research Laboratory in 2011 and 2012. In May 2013, a month before the scheduled initial field release, this egg-parasitoid wasp was surprisingly observed in soybean fields across several states. Here we report a 10-year systematic survey of population dynamics of kudzu bugs and the parasitism rates of kudzu bug eggs and in 4 soybean fields across the state of Alabama.

Understanding the impact of temperature change on niche dynamics among Drosophila parasitoids?

Authors: Hua Lue Chia, Biology Centre of the Czech Academy of Sciences, Czech Republic

Abstract: Climate change can impact ecological communities in many ways, including altering the niche breadth of component species. But precisely how abiotic change such as warming interacts with biotic factors to determine niche breadth remains unclear. Host-parasitoid systems offer a unique opportunity to investigate this important question. Many studies have documented how climate affects host-parasitoid interactions, and there are also the possibilities with this system to perform experimental works. Drosophila species and their parasitoids are one such group. In this study, we examine how warming impacts host-parasitoid interactions, specifically focusing on the shift of their niche breadth. We set out to address three questions 1) Does elevated temperature reduce the change in the degree of specialization for parasitoids? 2) Does the presence of multiple parasitoids narrow alter the diet breadth of parasitoids? 3) Is temperature and parasitoid niche-breadth correlated? What are the impacts on their life-history traits? We conducted laboratory experiments using a naturally co-occurring Australian Drosophila-parasitoid system at three temperatures. Here, 24°C is ambient temperature, 28°C is experimental warming, and 20°C is the coldest temperature they experience in the field. Seven host species and three larval parasitoid species were tested and reared for a total of 58,500 individuals. Results from question one showed that experimental warming caused a decrease in niche breadth across the three parasitoid species, and that successful hatching rate was significantly lower at 28°C. Among the three species Leptopilina sp. is a specialist, specialization follow by Asobara sp., and Ganaspis sp. is a generalist. The results from multiple parasitoid species showed that niche breadth decreased when multiple parasitoid species were present, but the niche breadth of the specialist occasionally increased when in the presence of other parasitoid species. In this experiment, we also found that temperature impacted the diet breadth of the generalist species more strongly than the specialist species. Finally, as temperature increased, mean interaction strength increased as a consequence of the narrowing of parasitoid diet breadth. Changes in temperature affect life-history traits, and significantly shifted trait values (mean and variance) in developmental time, body size and sex ratio of parasitoids. This has the potential to alter host-parasitoid community structures. Our study provides a better understanding of how climate change could impact the complex pattern of interactions in host-parasitoid communities, with implications for predicting the consequences for biological control and ecosystem functioning.

Dengue Vector Monitoring and Management in Southern Taiwan

Authors: Huang Chin-Gi[2], Liao Chin-Len[2], Hsiao Hsiang-Yu[2], Ho Hsin-Yi[2], Cheng Hui-Ching[2], Tseng Jing-Chun[2], Wu Kuo-Chih[2], Chen Pei-Qi[2], Chen Szu-En[2], Shih Ting-Chun[2], Tsai Tsung-Ju[2], Tu Wu-Chun[1], Chen Yi[3] and Wu Yi-Jun[2], [1]Department of Entomology, National Chung Hsing University, Taiwan, [2]National Mosquito-Borne Diseases Control Research Center, National Health Research Institutes, Taiwan, [3]Public Health Bureau, Tainan City Government, Taiwan

Abstract: Among factors associated with the 2015 dengue fever outbreak in southern Taiwan, the existence of vector mosquitoes in communities is probably the most prominent factor in the spread of the disease. Thus, the existing mosquito vector surveillance systems which focused on adult mosquito survey and the Breteau index may need to be improved. In the autumn of 2016, we started the pilot program: deploying ovitraps widely to monitor dengue vectors in hot zones – recording the numbers of mosquito eggs and the percentage of positive ovitraps weekly. Based on this, the standard operating procedure is established. In 2017, a partnership between local governments and ourselves set up 4,109 ovitrap monitoring sites in 359 villages in Tainan, Kaohsiung and Pingtung. Relevant data were presented weekly for immediate reference and appropriate environmental management measures for all levels of governments. Also, the effectiveness of the management can be evaluated by comparing the data before and after the measures were taken. Furthermore, the current data revealed that mosquito vectors increase significantly in the second week after rain, and the distribution of mosquito species are affected by human population densities. This information will be valuable for governments to prioritize areas and timing of management measures' execution in the future. In addition to this surveillance system, we also developed indoor control method for dengue vector. Our survey revealed that mosquitos of Aedes tend to lay eggs primarily in the bathroom and toilet, followed by kitchen, living room, and lastly the bedroom. So for indoor control, we propose the deployment of two small-scale indoor gravitraps on those egg-laying sites described above at each household in communities. We anticipate a significant decline of indoor vector in number while the installed rate of gravitrap reaches 50 percent in the tested community. With the implements of surveillance system and the indoor gravitrap strategies into current precise chemical control and other control strategies such as biology control, we can construct a more Integrated vector management for Taiwanese dengue fever to more efficiently decrease the vector number and prevent it from spreading

Rethinking the functional dominance levels and fitness costs of insect resistance to Bacillus thuringiensis crops

Authors: Huang Fangneng, Department of Entomology, Louisiana State University Agricultural Center, United States

Abstract: Transgenic crops expressing Bacillus thuringiensis (Bt) proteins have become an important tool for managing some major insect pests of corn, cotton and soybean. Evolution of resistance to Bt crops in target pest populations is a great threat to the sustainability of the Bt crop technology. Incidents of field resistance that led to control problems of Bt crops have increased rapidly, especially during the recent years. Based on the knowledge generated from earlier studies on resistance to Bt insecticides, high level of resistance to Bt plants was typically thought to be functional recessive with fitness costs. The objective of this study was to use the recently published data to test if this early inference is valid. Very surprisingly, functionally non-recessive resistance and lack of fitness costs in resistance to Bt crops are found to be not uncommon. Analysis of globally published data showed that 61.5% and 60.0% of the cases of resistance with major alleles that allowed homozygous resistant genotypes to survival on Bt crops were functionally non-recessive and did not involve fitness costs, respectively. Dominance levels (DFLs) measured on Bt plants ranged from –0.02 to 1.56 with a mean (± sem) of 0.35 ± 0.13 for the 13 cases of single-gene resistance to Bt plants that have been evaluated. Among these, all six cases with field control problems were functionally non-recessive with a mean DFL of 0.63 ± 0.24, which was significantly greater than the DFL (0.11 ± 0.07) of the seven cases without field resistance. In addition, index of fitness costs (IFC) of major resistance was calculated for each case based on the fitness of resistant (RR) and heterozygous (RS) genotypes on non-Bt plants divided by the fitness of their susceptible (SS) counterparts. The estimated IFCs for 15 cases of single-gene resistance were similar for RR and RS, and for the cases with and without field resistance; and the values averaged 1.10 ± 0.12 for R'R' and 1.20 ± 0.18 for R'S'. Limited published data suggest that resistance of insects to dual/multiple-gene Bt crops is likely to be more recessive than the related single-gene resistance, but their IFCs are similar. The quantitative analysis of the global data documents that the prevalence of non-recessive resistance has played an essential role in the widespread evolution of resistance to Bt crops, while the lack of fitness costs is apparently not as critical as the non-recessive resistance. The results suggest that planting of 'high dose' traits is an effective method for Bt crop IRM and more comprehensive management strategies that are also effective for functionally non-recessive resistance should be deployed.

Salivary DNase II from Laodelphax[4] striatellus acts as an effector that suppresses plant defence

Authors: Huang Hai-Jian, Institute of Plant Virology, Ningbo University, Ningbo, China

Abstract: • Extracellular DNA, released by damaged plant cells, acts as a damage-associated molecular pattern (DAMP). We demonstrated previously that the small brown planthopper (Laodelphax striatellus, SBPH) secreted DNase II when feeding on rice plants. However, the function of DNase II in plant-insect interactions remained elusive.

- The influences of DNase II on SBPHs and rice plants were investigated by suppressing expression of DNase II or application of heterogeneously expressed DNase II.
- We demonstrated that salivary DNase II is mainly expressed in the salivary gland and is responsible for DNA degrading activity of saliva. Knocking down the expression of DNase II resulted in decreased performance of SBPH reared on rice plants. The dsDNase II-treated SBPH not influenced JA, SA, ET-pathways, but elicited a higher level of H2O2 and callose accumulation. Application of heterogeneously expressed DNase II in DNase II-deficient saliva reduced the wound-induced defense response.
- We propose a DNase II-based invading model for SBPH feeding on host plants, and provide a potential target for pest management.

Nicotinic acetylcholine receptor modulator insecticides act on diverse receptor subtypes with distinct subunit compositions

Authors: Huang Jia, Institute of Insect Science, Zhejiang University, China

Abstract: Insect nicotinic acetylcholine receptors (nAChRs) are pentameric ligand-gated ion channels mainly expressed in the central nervous system of insects. They are the directed targets of many insecticides, including neonicotinoids, which are the most widely used insecticides in the world. However, the development of resistance in pests and the negative impacts on bee pollinators affect the application of insecticides and have created a demand for alternatives. Thus, it is very important to understand the mode of action of these insecticides, which is not fully understood at the molecular level. In this study, we systematically examined the susceptibility of ten Drosophila melanogaster nAChR subunit mutants to eleven insecticides acting on nAChRs. Our results showed that there are several subtypes of nAChRs with distinct subunit compositions that are responsible for the toxicity of different insecticides. At least three of them are the major molecular targets of seven structurally similar neonicotinoids in vivo. Moreover, spinosyns may act exclusively on the alpha6 homomeric pentamers but not any other nAChRs. Behavioral assays using thermogenetic tools further confirmed the bioassay results and supported the idea that receptor activation rather than inhibition leads to the insecticidal effects of neonicotinoids. The present findings reveal native nAChR subunit interactions with various insecticides and have important implications for the management of resistance and the development of novel insecticides targeting these important ion channels.

Identification of potential mechanosensitive ion channels involved in egg-laying behavior of the fruit pest Drosophila suzukii

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Abstract: Drosophila suzukii (spotted wing drosophila) has become a major invasive insect pest of soft fruits in the America and Europe, causing severe yield losses every year. The female D. suzukii shows the oviposition preference for ripening or ripe fruit by cutting the hard skin with its serrated ovipositor. A recent study reported that mechanosensation is involved in the texture discrimination during egg-laying behavior in D. suzukii. However, the underlying mechanism and molecular entity that control this behavior are not known. We first identified candidate ion channels with known mechanosensory roles from the D. suzukii genome by bioinformatic analysis, including Transient Receptor Potential (TRP) channels, Degenerin/Epithelial Sodium Channels (DEG/ENaC), Piezo and TMC. The reverse transcription PCR results showed that some of them are expressed in the ovipositor. Besides, transcriptome sequencing of ovipositors from D. melanogaster and D. suzukii have identified additional TRP and DEG/ENaC channels expressed in both species. Exposure to drugs targeting TRP and DEG/ENaC channels abolished the oviposition preference for harder texture in female D. suzukii. Therefore, mechanosensitive ion channels may play significant roles in the texture assessment of egg-laying behavior in D. suzukii, which has promising implications to further research on the development of novel control measures.

Multiple immune-regulation roles of serine protease inhibitors in Cotesia vestalis teratocytes

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Abstract: Endoparasitoid wasps have developed strategies to regulate host's inner-physiological environment to guarantee the survival and growth of their progenies. The parasitic factors including venom, polydnavirus, and teratocytes were found to have the immune-suppression, nutrient metabolism alteration and developmental regulation abilities when wasps parasitized their hosts. In some literatures, teratocytes, an embryonic factor formed by parasitoid progeny self were shown to has multiple functions during the parasitism. Serine proteases inhibitors (SPIs) play an important physiological role in regulating immunity and nutrient metabolism in insects by specifically acting on serine proteases (SPs). The transcriptome analysis of Cotesia vestalis teratocytes indicated 27 SPIs in total were produced and delivered into the hemocoel of Plutella xylostella host. In this study, we summarized the immune-suppression functions of the SPIs derived from C. vestalis teratocytes: (1) strongly suppress the prophenoloxidase (proPO) activation of host hemolymph by interacting with phenoloxidase activating proteases (PAPs) of PO cascade; (2) reduce the mortality of P. xylostella larvae by inhibiting the growth of bacterial pathogens. Our results will not only provide evidences for the roles of teratocyte SPIs in inhibitions of host immunity, but also expand our knowledge about the regulating mechanisms of parasitoid on host physiology.

Inhibition of encapsulation and bacterial agglutination activity in Bracoviruse-like lectin

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Abstract: C-type lectin acts as a pattern-recognition receptor which participates in diverse cellular activities such as cell-cell adhesion, apoptosis and immune response to pathogens. Polydnaviruses (PDVs), mutualism of parasitoid wasps, can express several genes to regulate physiology of the host for their development. However, the function of lectins in PDVs remain largely unknown. In association with PDVs from Cotesia vestalis (CvBV), an endoparasitoid of diamondback moth, Plutella xylostella, we found a lectin gene CvBV-BLL28-1 can specifically induce Gram+ bacterial agglutination, but not for Gram–. We further showed that CvBV-BLL28-1 could inhibit the differentiation of plasmatocyte and lamellocyte lineages, subsequently reduce the encapsulation reaction in host larvae after wasp infection. Therefore, the bracovirus-like lectin provides compensatory anti-microbial function and help to suppress the host cellular immune responses for the successful parasitism.

Effects of salts on eggshell structure and gene expression of Aedes aegypti, Culex quinquefasciatus and Forcipomyia taiwana

Authors: Huang Rong Nan[1], Weng Ling-Wei[2], Chen Mu-En[2] and Jiuun Chen Shiang[3], [1]Department of Entomology and Research Center for Plant Medicine, College of Bioresources and Agriculture, National Taiwan University, Taipei, Taiwan, [2]Department of Entomology, College of Bioresources and Agriculture, National Taiwan University, Taipei, Taiwan, [3]Department of Life Science, College of Life Science, National Taiwan University, Taipei, Taiwan

Abstract: Allergy to blood-sucking pests, such as Aedes aegypti (Linnaeus), Culex quinquefasciatus Say, and Forcipomyia taiwana (Shiraki) is common and impairs the quality of life for many people around the world. Traditional control strategies for these annoying pests mostly ignored the egg stage, since it is the least known life stage. We investigated the effect of salts on the structure and gene expression of eggs. The results showed that melanization of eggs was significantly reduced when laid on milieu containing NaCl, but not MgSO4. The NaCl-infiltrated eggs became shorter in length and possessed enlarged central tubercles occupying the whole area of the outer chorionic cell, indicating shrinking due to the failure of melanization. Moreover, eggs laid on salted milieu had no serosal cuticle, as evidenced by the absence of chitin-staining. Transmission electron microscopy analysis showed that intact exochorion and endochorion layers existed in NaCl-infiltrated eggshells, however the endochorion layer was significantly widened compared to that of melanized eggs. Three down-regulated (yellow, chorion peroxidase (CpO) and cytochrome P450) and four up-regulated (glutathione s-transferase (GST), superoxide dismutase (SOD), aromatic-L-amino acid decarboxylase (DDC) and tyrosine 3-monooxygenase(TH)) genes in NaCl-infiltrated eggs were first identified by next generation sequence (NGS) and further confirmed using quantitative reverse transcription-polymerase chain reaction. This information might aid in understanding the mechanisms involved in the process of chorion hardening, and will be the basis for further studies on molecular mechanisms of NaCl-induced failure of egg melanization.

Drought and vector-borne disease: thresholds, cycles, and potential futures

Authors: Hudson Amy, USDA-ARS, United States

Abstract: The typical narrative of climate effects on vector-borne diseases and futures is dominated by the role of warmer temperatures in increasing vector abundance and expanding the transmission season. However, especially in the case of aquatic insect vectors, particular attention needs to be paid to drought thresholds and spatio-temporal characteristics. Leveraging multiple drought indices, streamflow gages, and a satellite-derived surface water product, we explore the role of drought on the spread of multiple livestock diseases in the United States. Vesicular Stomatitis (VS) disease, with symptoms similar to foot and mouth disease, experiences a full stop in spread when drought corresponds to low streamflow. Black flies are the primary vector of VS and require flowing water for their abundance and lifecycle, likely driving this response. West Nile has a more nuanced response to drought in different regions, linked to thresholds and lagged effects of mosquito and avian reservoir hosts on spread. We then explore the frequency of these respective drought events. Finally, we weave in how other vector-borne diseases and data collection efforts can supplement our conceptual understanding of temperature-drought interaction likelihoods and impact on transmission cycles and spread.

Japanese Beetle Incursion on the West Coast of Canada: Now What?

Authors: Hueppelsheuser Tracy, British Columbia Ministry of Agriculture, Canada

Abstract: Japanese Beetle Popillia japonica was detected in annual survey by the Canadian Food Inspection Agency for the first time in July 2017 in Vancouver, British Columbia, Canada. The climate is ideal for establishment of most temperate insects, with moderate summers and lots of moisture and minimal freezing during the winter. The Vancouver area is highly urbanized and surrounded by a highly valued and diverse agriculture sector, as well as unique and diverse natural environment. In response to the beetle detection, we established a steering committee and operations committees made up of staff from various agencies. Partner organizations include federal, provincial, and local governments, the landscape, nursery, and turf industry, and non-government organizations such as invasive species councils. A Regulated Area and Treatment Area have been determined based on beetle trap catches.

Movement control of green waste (grass clippings, tree prunings) and soil has been implemented. Ground treatment of turf and landscape beds with insecticide has been done for two seasons, 2018 and 2019. In 2019, the number of beetles caught decreased over 85% compared to 2018. We are very encouraged by this significant decrease in beetles and believe it represents a drop in the pest population. There is a coordinated communications effort to inform the public and partners, and to date, response to the program has been generally positive. Our efforts will continue until we reach our goal of pest eradication, which we expect will take at least 2 more years. The partners unanimously agree that no individual group would have been successful on their own and successes to date are a result of the collaborative efforts of all the partners.

Transcriptomic analysis of the photoperiodic response of pea aphid lineages genetically able or not to switch of reproductive mode

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Abstract: As phloem sap feeding hemipteran, aphids can strongly affect the physiology of the plants but also transmit phytoviruses, making them important crop pests worldwide. They are also particularly well adapted to the fluctuations in their environment due to their remarkable ability to display phenotypic plasticity. The most striking example is the reproductive polyphenism they can display during their life cycle. In response to the autumnal photoperiod shortening signal, they are indeed able to switch from parthenogenetic reproduction (viviparous females) that causes most of the damages during spring and summer to sexual reproduction ended up with the production of sexual morphs (oviparous females and males) that mate to lay overwintering diapausing eggs. Lineages that are able to perform this switch are termed as CP (Cyclical Parthenogenesis). In nature, some lineages lost this ability and are referred as to OP (Obligate Parthenogenesis). Population genomic studies revealed that a region under divergent selection located on the X chromosome discriminates CP and OP lineages. The genes present in this genomic region show homologies with Drosophila genes known to be involved in functions such as embryogenesis, oogenesis and the development of the visual and nervous systems. Mutations on the sequence of genes located in the region are likely to explain the inability of the OP lineages to form oviparous females. We can hypothesize that these causal mutations might affect either the perception and neuroendocrine transduction of the photoperiodic signal (that occur in the head) or the ability of embryos germlines to switch their reproductive fate. To characterize the consequences of these mutations on the transcriptomic response of OP and CP lineages when submitted to short photoperiod we used RNA-seq approaches to compare the expression of the genes in the heads and embryos of a CP and an OP lineage at different stages of development. We thus collected, in 3 replicates, heads of aphids at the larval stages L2, L3, L4 and L4 + 24h and embryos at developmental stages 17 and 18 for each of the two lines. The 36 RNAs samples were sequenced (Illumina, PE100, 4 lanes) and analyzed using the latest version of the pea aphid genome. Statistical analyzes revealed that approximately 500, 700, 400 and 1700 genes were differentially expressed between the heads of the CP and OP lineages at the L2, L3, L4 and L4 + 24h stages respectively. In addition, more than 2000 genes were found as differentially expressed between CP and OP embryos both at stages 17 and 18. Functional annotation of the sets of differentially expressed genes will help reveal the tissue where the photoperiodic response is affected in OP lineages but also the biological functions that are no more operative in those lineages as a downstream consequence of the causal mutations.

Communication is power: let’s use it

Authors: Hulcr Jiri, School of Forest, Fisheries, and Geomatics Sciences, University of Florida, United States

Abstract: Entomologists can offer solutions to many major problems of humanity, but complex entomology messages compete poorly in the current information avalanche. One reason for it is the widespread belief among academics in the “information deficit model”, which assumes that the public will change attitudes and behaviors if given greater amount of information. This model has been discredited in contemporary communication research. Instead, I suggest that entomologists, and the academia as a whole, take several powerful lessons from the contemporary world of strategic communication.

First, the most important part of communication is strategy. I will discuss designing communication campaigns from the end goal backwards. First we define the goal, which then defines the ideal audience and the desired change. Only afterwards we choose the medium, and content comes last.

Second, I will argue that in today’s media landscape oversaturated with professional content, only attractive content has a chance to have impact. Rather than imploring scientists to focus on both research and communication and being less effective in each, I will present examples of collaboration with professional communicators where the investment paid off.

Lastly, even though the research community and the well-being of nations both depend on public science literacy, science communication is under-rewarded in contemporary academia. I will discuss strategies to advocate for science communication support to university and agency administrators.

Invasive ambrosia symbioses: paradigm changes and questionable assumptions

Authors: Hulcr Jiri, School of Forest, Fisheries, and Geomatics Sciences, University of Florida, United States

Abstract: Ambrosia beetle research is experiencing a boom of interest, partly because of several destructive invasions. The goal of this presentation is to discuss important new paradigm shifts in our understanding of the symbiosis in light of recent new data, and challenge assumptions that lack evidence and seem to hinder conceptual progress.

1) There is not one, but many ambrosia symbioses. The 14 origins in beetles and at least 8 in fungi offer a unique array of symbiotic phenotypes, degree of specificity, and symbiont swaps on evolutionary as well as ecological timescales. This replication of independent cases not only offers statistical convenience, but it actually requires comparative phylogenetic approach.

2) Do ambrosia beetles change their behavior in newly invaded regions? I will argue that this is an anthropocentric observation of an emergent ecological effect, while there are no data documenting a change in individual beetles’ behavior or symbiotic associations during or after the invasion.

3) Symbiosis, metasymbiosis or holobiont – which ecological concept fits the ambrosia symbiosis? In the wood, ambrosia fungi interact with each other and with free-living fungi, and the interactions mediate interactions between the beetles. This is important for understanding the ecology of invasive beetle-fungus symbioses.

The effect of apple orchard management and landscape on pollinator communities, pollination and production in reference to a semi-natural benchmark

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Abstract: Agricultural land use change and intensification are among the main drivers of global insect pollinator declines, yet many crops depend on these pollinating insects to enhance production. Alternative farming systems, such as organic farming, aim to mitigate the negative impact of intensive farming on biodiversity and have indeed been indicated to sustain a higher diversity of pollinators. However, evaluations of the effectiveness of agricultural management for biodiversity conservation mostly lack an appropriate natural benchmark. Here, we assess the direct and indirect effects of management and the surrounding landscape on bee and hoverfly communities in 24 Belgian apple orchards. We used structural equation modelling to quantify management and landscape effects on pollinator abundance and diversity, functional diversity, pollination services and fruit production. We also included 12 semi-natural grasslands as a benchmark in general(ized) linear mixed models and redundancy analyses to adequately evaluate the effectiveness of management for wild pollinator conservation. Though we found positive effects of organic management on biodiversity indices and pollination - but not on functional diversity - direct negative effects of organic management on production counteracted higher net productivity. Including a semi-natural benchmark reduced the significance of biodiversity gains in organic farming.

Distribution of Gonipterus species and their egg parasitoids in Australia: Implications for biological control

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Abstract: An appropriate taxonomic understanding of the native distribution and species diversity of pests and their natural enemies is a fundamentally important requirement in classical biological control. The egg parasitoid Anaphes nitens has been introduced into many countries on five continents as a biological control agent to manage populations of the Eucalyptus snout beetle (ESB), an insect native to Australia. Recent taxonomic advances have revealed that the ESB, previously considered the single species, Gonipterus scutellatus, represents a cryptic species complex, including three species that have become invasive. These taxonomic changes have important implications for the biological control of ESB. Consequently the native species composition and distribution of the ESB and its parasitoids were investigated to better understand opportunities for improved biological control. ESB adults and egg capsules were collected in south-eastern Australia and Tasmania. Adult Gonipterus were identified using morphology and DNA barcoding techniques. Parasitoids were reared and identified from Gonipterus egg capsules. Twelve Gonipterus species were identified in this study: seven described and five undescribed species. Eight of the twelve species were grouped based on phylogeny as part of the G. scutellatus complex. Five egg parasitoid species that infest Gonipterus were identified. Eleven Gonipterus species were found on the Australian mainland and one species in Tasmania. Three parasitoid species were found on the Australian mainland and two species in Tasmania. The distribution records for both Gonipterus and their parasitoid species will play an important role in improving ESB biological control.

Invasive forest insect pests of plantation trees in Africa

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Abstract: Plantation forestry is growing in sub-Saharan Africa and provides an important socio-economic role in many countries, providing fuel and fibre and supporting a diverse range of stakeholders. These plantations mainly comprise non-native trees such as Pinus and Eucalyptus. However, the sustainability of these plantations is challenged by the introduction of invasive forest insect species. We provide a summary of current and ongoing studies to investigate the distribution and diversity of these insect pests, to determine pathways of invasion and to develop management responses and regional networks. Survey data has revealed a much broader distribution of these invasive insects then previously realized, with high diversity in some of the species indicating possible multiple introductions. Fortunately, in some cases the natural enemies of the insect pests have also been unintentionally introduced. South Africa is indicated as a donor of insect pests to other regions, although this is likely influenced by differences in reporting efficiency. Issues in terms of governance and limited capacity are likely contributors to the increased introduction and regional spread of invasive species.

Understanding the gall community associated with Leptocybe invasa (Hymenoptera: Eulophidae) using the South African community as a case study

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Abstract: The gall wasp, Leptocybe invasa, is native to Australia and induces bump-like galls on various species of Eucalyptus. Since 2000, it has been detected outside its native range, with two genetically distinct lineages. Lineage A has been reported worldwide, whereas Lineage B has a more limited distribution in Asia and Africa. Gall wasps have intricate and unique communities consisting of the gall former, parasitoids and inquilines. The communities will differ in each country. It is difficult to study the gall communities as most of the interactions between species occurs within the confines of the gall. We investigated the interactions between the hymenopteran species associated with L. invasa in South Africa. The species investigated included the parasitoid wasp, Selitrichodes neseri, a biological control agent released in 2012 and three other hymenopteran species found to emerge from L. invasa galls, namely Quadrastichus mendeli, a known parasitoid of L. invasa, Megastigmus zebrinus and M. pretorianensis. Galls were dissected and the interactions within a single gall were observed. For each interaction, DNA was extracted from both larvae and species-specific primers and restriction enzymes were used to confirm larval identity. The results showed that Selitrichodes neseri, Q. mendeli and M. zebrinus parasitize Lineage A, and S. neseri was also confirmed to parasitize Lineage B. The results also showed direct interactions between these parasitoids. The role of M. pretorianensis was not confirmed from this study. Furthermore, the distribution and prevalence of these species was examined. Galled Eucalyptus material was collected at infested sites across South Africa, and emerging adults collected and identified. Morphology and restriction enzymes were used to differentiate between the various species and lineages. The results indicated that L. invasa lineage A has spread throughout South Africa while lineage B has a more limited distribution. The Leptocybe lineages were found to co-occur on individual trees increasing the chances of admixture. Selitrichodes neseri, M. zebrinus and M. pretorianensis were present throughout South Africa and all emerged from trees that contained both Leptocybe lineages.

Sentinel plant research reveals two cryptic non-native cypress-feeding aphid species in South Africa

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Abstract: Aphids residing in the sub-genus Cinara (Cupressobium) are important pests of trees in the Cupressaceae. Two of these species, C (C). cupressi and C (C). tujafilina, native to North America and Asia, respectively, have become invasive in various parts of the world. Cinara (C) cupressi has been reported as an invasive in Africa, Europe, the Middle East and South America. In Africa, it has established in several Eastern and Southern African countries, causing severe damage to Cupressus, Juniperus and Widdringtonia trees. Cinara (C) tujafilina has been reported as an invasive in many countries of Europe and South America. It feeds on a broader host range, infesting species of Callitris, Chamaecyparis, Cupressus, Juniperus, Libocedrus, Thuja, Thujopsis and Widdringtonia. Distinguishing between these aphid species based on morphological features is difficult because the two species share many morphometric characters. In South Africa, a project monitoring plant health in botanic gardens and arboreta was initiated under the framework of the International Plant Sentinel Network (IPSN) with the aim of using botanic gardens and arboreta as sentinel sites to improve surveillance and identification of new and emerging pest and pathogen risks. As part of this project, aphid samples were collected from Widdringtonia wallichi and W. nodiflora trees exhibiting branch dieback in Kirstenbosch National Botanical Garden, Cape Town. The barcoding region of the cytochrome oxidase I (COI) gene of the aphid specimens was sequenced. Analysis of sequence data revealed the presence of C (C). cupressi and C (C). tujafilina, the former on W. nodiflora and the later on W. wallichi. Cinara (C) cupressi was previously reported from South Africa, but with little information regarding its distribution and host range. This is the first report of C. tujafilina in South Africa as well as on the African continent.

The greenhead horse fly as bioindicator of marsh health – population decline and recovery after the Gulf of Mexico oil spill

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Abstract: Population census and genetics studies in the aftermath of the 2010 Gulf of Mexico oil spill established the greenhead horse fly (Tabanus nigrovittatus Macquart) as an invertebrate bioindicator of saltmarsh health. This species is bound to coastal marshes, since its larval stages develop as top invertebrate predators in the marsh soil and are thus dependent on a diverse food web in the Spartina saltmarsh. Immediately after the oil spill (2010-2011) populations of this horse fly crashed in oiled areas of Louisiana marshes with significant impacts on genetic structure detected via microsatellite genotyping. However, five years after the catastrophic event (2015-2016) we observed signs of recovery of populations in oiled areas. Fly numbers were rising. Genetic bottlenecks detected in formerly oiled populations were disappearing. Migration into oiled areas replenished formerly depleted horse fly populations in impacted regions. Parameters of family structure that had been impacted by the oil spill (number of breeding parents, effective population size, number of family clusters) rebounded to levels similar or exceeding those in non-oiled control areas. Saltmarsh horse flies are useful bioindicators for the assessment of changes in Spartina marsh caused, for example, by pollution and saltwater intrusion with sea level rise.

Popillia japonica in the Midwestern U.S.: Overwintering larval survival, adult monitoring, and foliar feeding impact on wine grapes and raspberry

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Abstract: Although Popillia japonica Newman was first detected in the U.S. in 1916, the pest did not reach Minnesota (MN, Midwest region) until 1968. As P. japonica continues to spread, it's important to better understand the larval overwintering capacity in a cold-climate as well as efficiently monitor adult populations. For 3 years we confirmed high levels of larval overwintering survival, 35-70% (October-April). This level of survival is much higher than other insect species studied in the Midwest. High survival is attributed to the overwintering depth of 15-20cm. To assist growers with monitoring, we evaluated the use of commercially available semiochemical-based traps. Due to high beetle densities, a volumetric calibration ($R2=0.98$) was developed. For wine grapes, foliar feeding studies found negative effects on titratable acid, soluble solid content, and phenolic compounds ($P<0.05$). Yield was not affected. An action threshold of 25 beetles/m-row, or ~30% defoliation would warrant management action. For primocane raspberry, cumulative insect days (CID) were used to quantify beetle pressure on marketable yield. We found a non-linear relationship between proportional yield loss as a function of CIDs; yield began to decline quickly at ~400 CIDs. This information is being used to develop an economic threshold.

The role of GPCRs in metabolism and physiology of the pea aphid, Acyrthosiphon pisum

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Abstract: G-protein coupled receptors (GPCRs) mediate many important physiological and behavioral processes. In insects, neuropeptides regulate development, growth, reproduction, metabolism and behavior. Neuropeptides signal through GPCRs and stimulate multiple intracellular downstream signaling cascades. Many insect neuropeptides and GPCRs were found to regulate gut motility and feeding behavior.

The order of Hemiptera is ranked in the top three of important insect orders with the largest number of high-risk pest species. To date, little is known about the role of GPCRs in regulating feeding and metabolism of Hemiptera. A well-known family of Hemiptera are the aphids which feed exclusively on carbohydrate-rich plant phloem sap. To cope with the lack of essential amino acids in their diet, aphids rely on the obligatory endosymbiotic bacteria Buchnera aphidicola, located in the bacteriocytes.

In this study five pea aphid GPCRs were selected based on their expression in two metabolism-associated essential tissues, gut and bacteriocytes. The ligand specificity for these GPCRs has been determined in an in vitro cell system. The spatiotemporal distribution of the ligands and the receptors was mapped and dynamic changes following nutrition-related changes determined. We are currently working on characterizing the role of the GPCRs in physiology and metabolism in vivo.

Novel Pest Control Method of Spodoptera litura using Plant Extracts

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Abstract: Since juvenile hormone (JH) controls development and reproduction in insects, we constructed insect species-specific assay systems to identify phytochemicals that function as juvenile hormone disrupt (JHD), which disrupt JH-mediated insect development by interfering with the binding of JH receptors to methoprene-tolerant (Met) and its partner protein, steroid receptor coactivator (SRC). Using a yeast two-hybrid system transformed with Met and SRC from the Spodopter litura, we tested the interfering activity of 3704 plant extracts against JH III mediated Met-SRC binding. Plant extracts from iridaceae, especially members of the gladiolus exhibited strong interfering activity. As a result of the bioassy, the larvae fed the gladiolus did not develop into pupae. These results suggest that the JHD of Gladiolas prevents the development of pupae by interfering with JH-mediated binding of Spodoptera litura Met and SRC.

Symbionts and microbiome diversity in sucking lice

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Abstract: Sucking lice (Anoplura) host phylogenetically diverse spectrum of symbiotic bacteria. This indicates that the lice experienced a complex history of symbiont acquisition, loss, and replacement during their evolution. The symbionts which have so far been phylogenetically characterized show relationships to very different ecological types of bacteria. Some of them originated within the groups known as frequent insect symbionts (e.g. Arsenophonus or Sodalis) others within groups only rarely associated with insects. Recently, we described two louse symbionts with phylogenetic affiliations to vertebrate pathogens, namely Legionella polyplacis in Polyplax spp. and Neisseria-related symbiont in Hoplopleura spp. Combination of genomic and amplicon data shows that these two bacteria differ considerably in many genomic characteristics, and are probably symbionts in different stages of evolution. L. polyplacis possesses features typical for obligate mutualist. It has small genome (approx. 0.5 Mb, coding for less than 500 genes) with severe AT bias. It also displays striking genomic similarity with Riesia and Puchtella, possibly due to convergent adaptation to similar hosts. On the other hand, some metabolic differences are likely to reflect different phylogenetic origins of these three genera, and hence availability of particular metabolic function in the ancestor. This can be demonstrated, for example, by different arrangements of thiamine metabolism in L. polyplacis and Riesia. An interesting adaptive feature, associated with the role of L. polyplacis in the host's metabolism, is horizontally acquired operon coding for synthesis of biotin. In contrast to the strongly reduced L. polyplacis, the Neisseria-related symbiont in Hoplopleura lice has three times larger genome with many features similar to free living relatives: it possesses much more complete metabolic pathways, many mobile elements, and signatures of a frequent horizontal gene transfer. On the other hand, its regular presence in amplicon data, and intracellular localization within bacteriocytes, suggests that the bacterium is already an obligate symbiont, probably in its early stage of symbiogenesis. Interestingly, another Neisseria-related bacterium, closely related to the Hoplopleura symbiont, is occasionally found in microbiomes of Polyplax lice, accompanying the dominant L. polyplacis. Finally, microbiomes of both louse genera display phylogeny dependent pattern of their composition. In some lineages of the lice, they contain various additional bacteria related to the known insect symbionts, such as Arsenophonus or Buchnera. The distribution and characteristics of L. polyplacis and Neisseria-related symbionts, and phylogenetic background of the louse microbiomes, thus illustrate high ecological dynamics of the symbiogenesis in Anoplura.

A new symbiotic lineage related to Neisseria and Snodgrassella arises from the dynamic and diverse microbiomes in sucking lice

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Abstract: Most of the examined lice (Anoplura) harbour intracellular, highly modified bacterial symbionts. The best known examples are Riesia pediculicola from human lice and Legionella polyplacis, described in our previous work from the genus Polyplax. For many lice, only 16S rRNA genes or morphological observations are available, indicating that this insect group has been undergoing particularly dynamic acquisition, loss, and replacement of symbionts. In this this study, we analyze the background of these processes by combining several approaches (genomics, phylogenetics, amplicons, FISH) across several populations of the two louse genera Polyplax and Hoplopleura. We reveal a novel louse symbiont lineage related to Neisseria (common human pathogen) and Snodgrassella (symbiont of bees), and show its evolutionary origin as an independent event in these two unrelated louse genera.

Characterization of this Neisseria-related symbionts includes comparison of their genomes, distribution across several populations, phylogenetic origin and intra-bacteriocyte localization demonstrated by FISH. While the genomes of these symbionts are highly similar in both lice genera, their respective distributions and status within lice microbiomes indicate that they have different functions and history. In Hoplopleura acanthopus, the Neisseria-related bacterium is a dominant obligate symbiont universally present across several host's populations, and seems to be replacing a presumably older and more degenerated obligate symbiont. In contrast, the Polyplax microbiomes are dominated by the obligate symbiont Legionella polyplacis with the Neisseria-related bacterium co-occurring only in some samples and with much lower abundance. In addition the extensive amplicon screening of Hoplopleura and Polyplax microbiomes revealed presence of other possible symbiotic lineages from the Enterobacteriaceae family distributed in some louse populations.
Using broad spectrum of approaches, we demonstrate that sucking lice possess taxonomically diverse microbiomes which harbour both the bacteria related to vertebrate pathogens (Neisseria-related bacteria) and the typical insect-associated taxa (Enterobacteriaceae symbionts). We show an independent origin of Neisseria-related symbionts in two unrelated louse genera, Hoplopleura and Polyplax, and present their taxonomically diverse microbiomes as background/source for acquisition of obligate mutualistic symbionts.

How dark of a taxon is Microgastrinae (Braconidae) really?

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Abstract: Entire families or subfamilies Hymenoptera are referred to as so-called “Dark Taxa”: They are hyperdiverse, taxonomically neglected and with numerous overseen and undescribed species – even in Germany. In order to make these enormously species-rich groups more tangible to science, we use an integrative approach within the project GBOL III: Dark Taxa for the Microgastrinae, a subfamily of parasitoid wasps within the Braconidae (Hymenoptera) specialized in attacking Lepidoptera larvae. Specimens are selected from a large number of malaise trap samples from various habitats in Germany. Samples are sorted and individuals selected for DNA-Barcoding by parataxonomists. Using DNA-Barcoding as a way of pre-sorting samples, we are able to identify distinct clusters and lineages that putatively represent species. Finally, representative specimens of these clusters (which correlate with BINs = Barcode Index Numbers) are morphologically verified by experts. Using this workflow allows to accelerate taxonomic work and glance at results, even with morphological identifications still in the future. We were able to identify 245 BINs within one single bulk submission of 1,898 specimens. This almost equals the number of Microgastrinae species recorded for Germany (248), and indicates that the actual species diversity must be much higher than currently known.

Phenotypic plasticity in a myrmecophile that exploits multiple ant hosts (Orthoptera: Myrmecophilidae)

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Abstract: Ant colonies act as islands for numerous arthropod parasites and guests that invade them. Like islands, ant colonies differ in size and quality. The desert ant-cricket, Myrmecophilus manni, is a generalist parasite (myrmecophile) found with at least 24 ant host species. Ant hosts vary tremendously in body size, colony size and diet. Although it is one of the world’s smallest Orthopterans (< 5 mm), M. manni exhibits surprising phenotypic plasticity across its many hosts. We found that cricket body size, shape, color, abundance, development, dispersal ability, egg number, sex ratio, and cuticular hydrocarbon profile corresponded to host species traits.

Cricket identity was confirmed using mitochondrial DNA barcoding for major and minor morphs from 15 sites across Mexico and the Western United States. Individual sites included up to 8 unique hosts, and a full range of cricket phenotypes. In the laboratory, we bred crickets and cross-fostered offspring to parse out the heritable and environmental aspects of cricket phenotype.

Our results suggest that certain host-colony characteristics increase clutch size and mating opportunity for parasitic crickets. We ask why M. manni maintains its generalist lifestyle, and consider how the use of spermatophores, and risk of desiccation during dispersal might favor plasticity over host specialization in this unusual myrmecophile.

Monitoring of Tuta absoluta (Meyrick, 1917) (Lepidoptera: Gelechiidae) on tomato under greenhouse conditions and various environmental zones in Romania

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Abstract: Careful monitoring and regular inspection of solanaceous plants in greenhouses and adjacent areas for Tuta absoluta presence represent crucial activity in developing the integrated control program for this invasive species. The study was done in two successive years, in a sampling network that included 20 greenhouses cultivated with tomatoes from south and central Romania in which pest monitoring was performed by placing pheromone traps, Delta type with pheromone lure Atra-TUT-S. Dynamics of the traps captures were correlated with associated local pedo-climatic conditions in order to establish the influences of abiotic parameters on moth activity and pest population build-up across various environmental zones in Romania. The paper further discusses the influence of local factors on the potential for the establishment of the pest on the area of central Romania and also the variability of factors influencing the numbers of adults caught in pheromone traps and the relationship between trap catches and tomato damages.

Literature-based food webs and agro-ecological community characteristics

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Abstract: Understanding the inter-organism interactions in ecological communities allows assessment, and even prediction, of how communities respond to natural and anthropomorphic impacts. The trophic interrelationships of invertebrates within a community often form an extensive feeding web composed of several trophic levels. Food webs, or trophic webs, can be constructed directly from empirical field studies or, alternatively, by using literature records to map all the trophic interrelationships in natural and agro-ecosystems. For terrestrial communities, this includes the plants, herbivores and the complex of natural enemies associated with these herbivores. We will focus on the literature-based trophic webs that were recently constructed for coconut and date palm agro-ecosystems to infer large-scale community ecology consequences of shared and non-shared natural enemies, such as the relative importance of direct and apparent competition. We will discuss the utility of the less labour-intensive, though likely less local-scale and accurate literature-based approach as an alternative or supplement to field-based studies.

Factors from Tachinid fly can attract host fat body cells.

Authors: Ichiki Ryoko[2], Nakamura Satoshi[2] and Furukawa Seiichi[1], [1]Graduate School of Life and Environmental Sciences, University of Tsukuba, Japan, [2]National Agriculture and Food Research Organization, Japan

Abstract: The tachinidae are one of the largest families of Diptera with more than 10,000 species worldwide. Tachinid flies are also considered to be useful natural enemies against agricultural pests, especially Lepidopteran larvae. Drino inconspicuoides (Diptera: Tachinidae) is an ovolarviparous endoparasitoid that develops in a host body during the larval period. The host responds by using hemocyte encapsulation defense mechanisms. In order to survive, a mechanism for tachinid fly larvae to avoid this defense mechanism is necessary. How D. inconspicuoides can survive in the host is still unknown. Therefore, in this study we focused on clarifying the parasitic strategies of this tachinid fly. In a previous study, Yamashita et al. (2019) showed that D. inconspicuoides larvae form a structure, called the cloak, by surrounding themselves with hemocyte cells and fat body cells derived from the host Mythimna separata (Lepidoptera: Noctuidae). On the contrary, only hemocytes were found in the encapsulated transplanted dead fly larvae. From these results, we hypothesized that the fat body cells contained in the cloak were attracted to the fly larvae by secretions. Therefore, to analysis whether secretions can attract host fat body cells, we collected first instar flies from the hosts (final stage) 2 hours after parasitism and tested the secretions of fly larvae by incubating larvae in physiological saline for 24 hours. Six hundred µm polystyrene beads were soaked in this solution for 12 hours to coat the beads with the fly secretions. Then, the beads were transplanted into M. separata larvae (final stage) and the attractant activity of host fat body examined. Although only hemocytes were attached to uncoated beads, both hemoctyes and fat body cells were attached to the coated beads. Therefore, we concluded that fly larvae secrete substances that attract host fat body to create the cloak after parasitism. To identify the secretory organ of the host fat body attractant, candidate secretory organs of the tachinid larvae such as the salivary glands, midgut, malpighian tubules and epidermis were collected 24 hours after parasitism. Extracts from the tissues were then mixed with 600 µm beads in saline to prepare coated beads. The beads were then transplanted into M. separata larvae and adhesion of fat body on the bead surface examined 24 hours later. As a result, host fat body attractant activity was observed in the homogenate from the salivary glands. These results indicate that D. inconspicuoides larvae secret factors from the salivary gland to attract host fat body cells.

Historical review of Japanese rose gall wasps (Hymenoptera: Cynipidae: Diplolepidini) and their communities

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Abstract: Two species of rose gall wasp occur in Japan: Diplolepis japonica (Walker) and Liebelia fukudae (Shinji). The former induces spherical galls, scattered with short spikes on the surface, with diameters of 7–9 mm on leaves and young twigs of Rosa multiflora. This species was described from Japan as Rhodites japonica in 1874 and then transferred to Diplolepis in 1967. At the same time of this transfer, Rhodites hakonensis Ashmead, which was described from Japan in 1904, was synonymized with D. japonica based on examinations of both type specimens. The latter induces irregularly globular galls, covered with thorns, with diameters of 30–60 mm on buds of Rosa rugosa and R. nipponensis in Japan. This species was described from Japan as Rhodite [sic] fukudae Shinji in 1941 and then transferred to Liebelia in 1963. In addition to the two species, Rhodites eglanteriae Hartig was recorded from Japan in 1919 as a gall inducer of R. multiflora. However, this record has been regarded as D. japonica and ignored in recent studies. Moreover, some other Japanese cynipid species were also treated as Diplolepis but they can be regarded as being not true rose gall wasps. Inquilines and parasitoids of Japanese rose gall wasps were also reported. In D. japonica, Peliclistus natalis Taketani & Yasumatsu and P. quinlani Taketani & Yasumatsu were described as inquilines in 1973, and Eurytoma sp. (Eurytomidae) and Tetrastichus sp. (Eulophidae) were reported as parasitoids. Orthopelma japonicum Kusigemati (Ichneumonidae) was also described as a parasitoid of D. japonica in 1974, but this D. japonica is thought to be an unidentified rose gall wasp species because its gall was collected from R. rugosa. In L. fukudae, no inquilines have been recorded including our observations, and Glyphomerus stigma (Fabricius) (Torymidae), Eurytoma sp., and Orthopelma sp. were reported as parasitoids. In addition to L. fukudae, two unidentified cynipid galls are known from R. rugosa in Japan. Our field surveys focusing on R. rugosa reveals presence of additional cynipid galls induced on this plant in Japan. Galls of Japanese rose gall wasps have been found only from three common Rosa species. Since there are 12 native Rosa spp. in Japan, more field surveys concerned with various Rosa species will clarify Japanese rose gall wasp fauna and its communities in the future.

Genetic diversity of Citellophilus tesquorum (Siphonaptera: Ceratophyllidae)

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Abstract: Citellophilus tesquorum is a flea with the trans-Palearctic range that parasites on different species of ground squirrels. In most regions, this species is considered an active plague vector. Nine subspecies are described, namely C. t. tesquorum and C. t. transvolgensis in the Southern of the East Europe; C. t. transcaucasicus (Ioff et Argyropulo, 1934), C. t. elbrusensis Goncharov, 2011, C. t. ciscaucasicus in the Caucasus, C. t. altaicus in the South Siberia and west of Mongolia, C. t. dzetysuensis and C. t. mongolicus in Mongolia and the Northern China, and C. t. sungaris in the Transbaikal and the Northeast China. Delimitation of these subspecies is based on morphology traits such as the shape of the movable process of the sex clasper, and also 8th and 9th abdominal sternites in males and the shape of the apical margin of 7th abdominal sternum in females. Variation of these traits often overlaps between subspecies. Here we report the results of comparative analyses of morphology and genetic data on C. tesquorum diversity.

Transcriptome analysis of cotton aphid, Aphis gossypii in response to the entomopathogenic fungi Beauveria bassiana JEF-544

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Abstract: In agricultural pest management, cotton aphid, Aphis gossypii is a widespread crop pest and acts as a vector of serious plant viruses. Cotton aphid shows high resistance to chemical insecticides due to its rapidly growing genetic diversity which is resulted from a short life cycle and geographical migration. As an alternative, entomopathogenic fungi can be used to control cotton aphids in an environmentally sound way. Herein, the early stage of the response of aphid to Beauveria bassiana JEF-544 was analyzed at transcriptome level to figure out how the cotton aphid responds to the fungal infection. First, B. bassiana JEF-544 with high virulence against cotton aphids was selected through bioassays. Infected aphids were collected two days after treatment, which was LT_{25}, and total RNA of uninfected and infected aphids were sequenced. When JEF-544-infected aphids, a large proportion of aphid genes were up-regulated from an enrichment analysis, energy production-related, and immune response genes were significantly up-regulated. Particularly, insect hormone biosynthesis pathway that included ecdysone and juvenile hormone was actively working when infected. In conclusion, when infected by the B. bassiana JEF-544 at an early stage, cotton aphids seemed to protect themselves by immune response or molting hormones biosynthesis to remove infected cuticles.

Moss resemblance par excellence: a synthesis of crypsis, herbivory, and ecomorphology of long-bodied crane flies (Diptera: Cylindrotomidae: Cylindrotominae)

Authors: Imada Yume, Graduate School of Science and Engineering, Ehime University, Japan

Abstract: Many animals camouflage themselves in the surrounding environment, making use of various components including body coloration, patterning, morphological structures, and behavior. Ecological and evolutionary significance of such structures (i.e. devices for mimicry) are, in general, much less investigated than the coloration and patterning. Larvae of long-bodied crane flies, Cylindrotominae (Diptera: Cylindrotomidae), resemble plants due to a combined set of morphological and behavioral traits. They are all free-living, obligate plant-feeders and consist of three ecologically distinct groups: terrestrial moss-feeders, aquatic moss-feeders, and terrestrial herbaceous plant-feeders. Notably, numerous elongated cuticular projections, the most conspicuous morphological feature of the cylindrotomines, is various in size and shape among these groups. Although this structure apparently constitutes a device for mimicry, it may also be the accessory device for respiration and locomotion. A question therefore arises as to how a device for mimicry can simultaneously be physiological, structural, and behavioral adaptations to habitat. In this talk, I lay out a synthetic overview on biology and morphology of this group as the first step to explore the evolution of cryptic mimicry in Cylindrotominae. This will contribute to our understanding of the complex adaptive traits that constitute cryptic mimicry from the ecomorphological perspectives.

STING-dependent antiviral immunity in drosophila

Authors: Imler Jean-Luc, University of Strasbourg, CNRS, France

Abstract: Insects evolved powerful systems to fight against viruses, among which the best known is the RNA interference pathway. However, it is now clear that insects also developed other strategies to resist viral infections, including inducible responses. Working on the model organism Drosophila melanogaster, we recently discovered a new antiviral pathway involving the ortholog of the well-known mammalian antiviral protein STING (Stimulator of interferon genes). We showed that two cGAS-like receptors, cGLR1 and cGLR2 sense viral RNA and produce cyclic dinucleotides (CDN) that act as second messengers and activate drosophila STING (dSTING). STING in turn triggers activation of two components of the IMD pathway, the kinase IKKβ and the NF-kB-like transcription factor Relish, resulting in expression of antiviral genes. Strikingly, co-injection of the CDN 2′-3′-cGAMP or 3′-2′-cGAMP together with several viruses belonging to different families results in significantly reduced viral replication. The protective effect of the CDN is abolished in Relish mutant flies, but not in AGO2 and Atg7 null mutant flies, indicating that it does not require RNAi or classical autophagy. Altogether, our results reveal that, besides RNAi, an inducible transcriptional response controlled by STING and NF-kB participates in immunity against a broad range of viruses in flies.

Climate change is a great challenge for the conservation of an endangered stingless bees species in Brazil

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Abstract: Melipona scutellaris is an endemic stingless bee species considered endangered on the Brazilian red list and locally (Bahia state) vulnerable. Therefore, understanding whether its natural habitat will lose area due to climate change may assist in their future conservation. The main goal was to assess such a potential habitat loss on climate change for two periods (2021-2040; 2041-2060), under the CMIP6 scenarios being SSP5-8.5 the selected scenario. Occurrence data of the target species were collected from GBIF, SpeciesLink Network, and Brazilian scientific collections. Suitability area was modeled with five algorithms (GLM, GBM, GAM, RF, MAXENT) and five rounds (75% training, 25% tests) using 12 layers of environmental variables selected after variance inflation factor. We generated 375 models according to 207 exclusive occurrence points for M. scutellaris. Our findings suggest that, currently, this species has a suitable area of 230,000 km2. Nevertheless, for the next 20 years, it is expected a loss of 100,000 km2 (or 41%) of suitable area. Similarly, within 40 years the loss will be 130,000 km2 (or 55.8%). The main area loss will be in the Bahia state.

The complexity of insecticide resistance in malaria mosquitoes

Authors: Ingham Victoria, Liverpool School of Tropical Medicine, United Kingdom

Abstract: Vector control tools are the most important contributor to malaria eradication programs; foremost amongst these are long lasting insecticide treated bednets, which accounted for around 70% of the reduction in malaria cases between 2000 and 2015. All distributed bednets are impregnated with pyrethroid insecticide; resistance to which is now widespread. Worryingly, the WHO World Malaria Report details a plateauing of averted malaria cases for the past three years, which closely mirrors the spread of insecticide resistance.

Insecticide resistance in Anopheles mosquitoes has, until recently, been attributed to four characterised resistance mechanisms: changes in the target site; differential regulation of detoxification enzymes; behavioural changes; and thickening of the cuticle. Recently, through data mining multiple transcriptomic datasets of resistant mosquitoes we have shown that resistance is multi-faceted and involves a number of gene families and transcriptional pathways. These data were combined into a publicly accessible, easy to use ShinyR web-based application (IR-TEx). Critically, from searching these data we found that a chemosensory protein (CSP), SAP2, is upregulated in multiple resistant populations across West Africa. Further characterisation of SAP2 demonstrated it is crucial for pyrethroid resistance through direct binding of pyrethroid insecticides and the point of bednet contact. The involvement of CSPs in resistance has been hinted at in agricultural pests and so these findings likely apply to resistance in a wider context. In this talk, I will highlight potential new insecticide resistance mechanisms in Anopheles mosquitoes with a particular focus on chemosensory proteins.

Dual-species transcriptomics to investigate parasitism resistance in a classical biological control system

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Abstract: The Argentine stem weevil (Listronotus bonariensis, ASW) is an economically significant pasture pest in New Zealand (NZ) primarily controlled by Microctonus hyperodae, an endoparasitoid wasp biological control agent. Initial parasitism rates were as high as 80% but they are now declining significantly, resulting in severe pasture damage costing an estimated NZ$160M per annum. This is the first reported example of developed resistance in a previously successful biological control system worldwide, and a genetic basis for this parasitism resistance is suspected. Resistance to parasitism is most likely to be either a host-mediated immune response towards the oviposited parasitoid egg, or a barrier preventing the parasitism event itself such as a behavioural change in ASW.

A large RNA-seq experiment was carried out comparing ASW from susceptible and resistant populations. Parasitized and unparasitized ASW were collected from both locations, allowing for transcriptomic comparisons between locations, and between ASW that were or were not attacked by M. hyperodae. While this did not detect a clear explanation for parasitism resistance, it has significantly improved our understanding of this biocontrol system. Dual-species transcriptomics was also used to simultaneously examine gene expression of the parasitised ASW and the internally developing parasitoid eggs. This detected changes in ASW gene expression that could be linked to M. hyperodae venom components, as well as a novel viral infection transmitted from M. hyperodae to ASW during parasitism, related to a virus that manipulates parasitoid behaviour.

Resistance to imidacloprid and baseline susceptibility (LD50S,LD90S) to Thiacloprid and Chlorantraniliprole and Field efficacy of them in Colorado potato beetle (Coleoptera: Chrysomelidae)

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Abstract: The Colorado potato beetle (CPB) Leptinotarsa decemlineata (Say) has developed resistance to many groups of insecticides worldwide and in many regions (three generations) in Greece. It is the most serious pest of the Solanaceae (potato, tomato, eggplant).

Our objectives were to determine the distribution and severity of any insecticide resistance and to define the mortality doses LD50s andLD90s for Imidacloprid (technical), Thiacloprid (Calypso 48%) and Chlorantraniliprole (Coragen 20%) in CPB. We tested thirty nine (39) geographically discrete field populations, collected from potato fields from different areas of Northern Greece mainly from Nevrokopi and Kozani regions and six (6) populations collected from the controls of the field experiments and lab strains, through the hole season. The adults were collected from the fields before the application of the corresponding sprays.

Collected adults were bioassayed using topical application, applying 2μl/adult on the ventral area of the abdomen using an Arnold hand micro applicator. In the bioassays at least four concentrations in acetone solutions (imidacloprid) or in distilled water solutions for the other were used. Mortality was assessed 3 days after treatment. For analysis of the data the method of probit analysis by Finey was used. Based on a pooled group of susceptible populations the LD50s and LD90s (from the lab bioassays) for imidacloprid, Thiacloprid and Chlorantraniliprole were 0.7, 0.23 and 2.35 μg active ingredient/adult and for LD90s 11.87, 4.76 and 35.78 respectively.

Among the collected field populations resistance was found only for imidacloprid with a wide range of determined LD50s. In Neurokopi region for a field collected population was found resistance ratio 86.77 fold, 3,905 μg/adult / lab sensitive 0,045 μg/adult. With regard to Thiacloprid and Chlorantraniliprole it was not found any resistance and did not observe any statistical differences among the tested field collected and lab keeping populations. Also the effectiveness of the Thiacloprid and Chlorantraniliprole insecticides in the field experiments and in the commercial fields was excellent almost 95-98%,compared to Imidacloprid with 60-70% effectiveness. These results are in accordance with the bioassay results.

The log dose-probit mortality regressions were used to analyze the data and calculate the doses LD50s and the discriminating doses LD90s. The determined doses can be used in the lab tests for quick monitoring of possible development of resistance. Based on the found doses of LD50s and LD90s and also on the established base-line data for the Colorado potato beetle for the Greek conditions of potato production. It will be possible to design a IPM (Integrated Pest Management) program for CPB and for other insects.

Halyomorpha halys a new threat to horticulture in northern Greece

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Abstract: The brown marmorated stink bug, Halyomorpha halys Stål (Hemiptera: Pentatomidae), was accidentally introduced from Asia into the United States and Europe, and due to climate change, as a xenobiotic species away from its natural environment and enemies, it caused severe damage to many annual and perennial crops, although at the beginning it was mainly considered as an urban and household pest. In Greece, since 2017 it was found to affect significantly kiwi fruits, render them unsuitable for the market. However, H. halys is an extremely polyphagous species that easily flies from plant to plant and affects more than 180 different host plants with preference for those belonging to the Rosaceae and Fabaceae families. In this study infestations on cherries as well as on peaches and nectarines in the regions of Pieria and Imathia (northern Greece), respectively, are presented. Cherry infestations are caused by adults that have just emerged from hibernation and occur when the fruits are green and small, causing deformations in the shape that render them completely unsuitable for both marketing and consumption. Concerning peaches and nectarines, infestations are caused by both nymphs and adults, where we observed characteristic dark, sunken areas on the skin of the fruits that make them unsuitable for marketing. Moreover, we observed that in the kiwi H. halys completes two full generations, whereas in 2019 apples were added to the list of its hosts in northern Greece by attacking the flesh and causing characteristic spots. In addition, the population dynamics in the different cultivations are presented. This new enemy is constantly increasing the number of its hosts year by year and has become a serious problem for farmers in Greece.

Co-evolution and biological control: multitrophic interactions between the tree of heaven, brown marmorated stink bug and their natural enemies.

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Abstract: Ailanthus altissima, commonly known as tree of heaven, is an invasive plant species of eastern Asian origin and it has been introduced in Europe, Africa, South America and North America at the end of 18th century. It is able to germinate and grow in a wide variety of soil and site conditions proving that it has been and still is troublesome from urban landscapes to woodlands. Moreover, in addition to its non-native invasive status, the tree of heaven may also play an important role in the biology of two invasive alien insect pests, both of the same geographic origin: brown marmorated stink bug (BMSB, Halyomorpha halys) and spotted lanternfly (Lycorma delicatula). The tri-trophic interaction between the target weed, the associated insect pests and one of its potential biocontrol candidate agents, the eriophyid mite Aculus mosoniensis, is presented and evaluated in the framework of invasion ecology assessment. We evaluated if the impact of the eriophyid mite on the fitness of the invasive plant species, in particular the induced changes in its physiological patterns, can influence the evolutionary responses and population dynamics of the associated insect pest species.

Unravelling the reproductive biology traits of Drosophila suzukii as a basis for specific and long-term control of this species

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Abstract: The rapid and extensive establishment of D. suzukii outside of its indigenous regions has been facilitated by tolerance to a broad range of climatic conditions, and by its high reproductive potential.

Overwintering of adult males and females and early season reproductive behaviour play important roles in the seasonal buildup of the populations. The females are reproductively active from early spring until late autumn, and the most stringent bottleneck for D. suzukii populations is from January to March in temperate climates. Overwintered D. suzukii females are thought to store sperm from autumn matings to counteract the winter bottleneck that may result in a scarcity of mature males in early spring. This strategy would allow them to resume oviposition when they exit reproductive diapause in the early spring, without needing to mate again. Given this background, an important unexplored aspect of D. suzukii reproductive behaviour is the assessment of the number of times that a female mates in the wild across the seasons. This influences the effective population size and may constitute a critical factor in determining the success of control methods. Using molecular markers, we investigated the presence and the extent of polyandry in different seasons. Moreover, we evaluated sperm utilization by females. These aspects of D. suzukii mating behaviour may locally be a constraint to the application of the environmental friendly control methods such as the Sterile Insect Technique (SIT).

Predatory Potential of Various Predators on Citrus Leafminer, Phyllocnistis citrella (Gracillariidae; Lepidoptera) under laboratory conditions

Authors: Irfan Ullah Muhammad Irfan, Abdullah Asad, Afzal Muhammad, Arshad Muhammad, Altaf Nimra, Ali Shaukat and Muhammad Ali Zahid Syed

Abstract: Citrus leafminer (CLM), Phyllocnistis citrella Stainton (Gracillariidae: Lepidoptera) is a pest native to Southeast Asia which has threatened the citrus industry worldwide. To control this menace, different insects were screened to determine their predatory potential in the laboratory at 26 ± 2? temperature and 65 ± 5% R.H. Six different potential predators used against citrus leafminer included ants (Solenopsis invicta and Lasius niger), green lacewing (Chrysoperla carnea), ladybird beetle (Coccinella septempunctata) and spiders (Zygiella x-notata and Myrmarachne sp,). Results revealed that S. invicta (red fire ant) showed the highest predation (5.8 CLM larvae) followed by C. carnea (green lacewings) (2.6 CLM larvae) against citrus leafminer. Ladybird beetles and both spider species did not feed on CLM but caused slight mortality by scratching or damaging the mines and larvae. L. niger showed no harm to CLM larvae during the study. Observations for the time of feeding activity confirmed that S. invicta and C. carnea are both active diurnally because both showed maximum activity into the photophase. During CLM predation, the searching period was found highest in S. invicta followed by C. carnea (132 and 111.5 minutes respectively) while handling period was maximum in C. carnea (37.5 minutes) followed by S. invicta (26.5 minutes). The retreat period (no locomotion, no body movement) was found maximum in the case of both spider species as the spiders mostly remained inside their webs. Least retreat period was observed in S. invicta and C. carnea (21.5 and 31 minutes respectively).

Molecular characterisation of the enzymes that activate and inactivate steroid hormones in Anopheles funestus, a new target for malaria vector control

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Abstract: Malaria remains a leading killer worldwide. The ability of mosquitoes to transmit malaria parasites to humans is greatly influenced by the hormonal regulation of ecdysone (20E) and their blood-feeding habits. Despite this, very little is known about the 20E inactivation pathway in the Anopheline mosquito, which is vital for metamorphosis, vectorial competence, and reproduction. We investigated the role of cytochrome P450 enzymes, CYP314A1 and CYP18A1, in regulating 20E titre in Anopheles funestus and the downstream effects of manipulating these pathways. Transcriptomic analysis revealed life-stage and tissue-specific expression of Afcyp314a1 and Afcyp18a1 genes. Furthermore, we demonstrated that the Af-CYP314A1 enzyme catalyzes the conversion of ecdysone prohormone to 20E by using recombinant protein expression and LC-MS/MS. The cyp18a1 gene is absent in Anopheles gambiae, so we created An. gambiae mosquito lines carrying the Afcyp18a1 gene, which encode a 20E deactivation enzyme. In pupae and embryos of An. gambiae, overexpression of Afcyp18a1 leads to phenotypic lethal defects that are not reversible after exposure to 20E. RNA interference knockdown of Afcyp18a1 significantly reduced female An. funestus appetite for blood feeding and fecundity, confirming this P450 to be a good target for the genetic and chemical control of malaria vectors.

Recent horizontal transmission of P transposable element in the fruit fly species

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Abstract: P element, one of the DNA transposable elements (TEs), was first found as the causative factor of the P-M hybrid dysgenesis including gonadal dysgenesis (GD sterility) in the fruit fly, Drosophila melanogaster. P elements can increase their copy number by means of repairing the DNA gaps after transposition. Two of size variants are predominant among P elements in D. melanogaster. One is full-size P (FP) element (complete element; 2,907 bp), which can produce transposase and repressor. The other is one of the incomplete elements, KP element (1,154 bp), which is characterized by a deletion of the internal region (nt 808-2,560) and can transpose if the transposase is provided. The "FP and KP predominance" can be explained by KP element's effect of restraining harmful effects of P-M hybrid dysgenesis. P elements are known to be horizontally transmitted (HT) twice recently; first, from D. willistoni to D. melanogaster in the 1950s, and secondly, from D. melanogaster to D. simulans probably in Europe around 2006. To understand the evolutionary dynamics of TEs, especially in the early stages of invasion, we addressed (1) their spreading patterns, (2) effects of hybrid dysgenesis, and (3) behavior of KP element in D. simulans.

We examined more than hundred lines of D. simulans established from natural populations in Japan in 2002-2018. Based on PCR, P homologous sequences, many of which were FP element, were detected in the lines established after 2008. There was a variety in structure of the elements, but neither KP nor other elements increasing specifically in number was found. All elements examined shared "A" at the nucleotide position 2040, which is representative of the direct descendants of the original P element that invaded in D. simulans, implying that P elements arrived at the east end of Asia very quickly after the initial invasion in Europe.

In D. simulans undeveloped gonad was induced by the cross of females of M strain (P element free) and males carrying many FP elements in their genomes at 29°C, but not by the reciprocal cross. This female sterility is quite similar to the GD sterility of P-M hybrid dysgenesis in D. melanogaster.

Furthermore, to study the transposing nature of KP element, we artificially introduced an intact KP element into D. simulans. The KP elements jumped and their genomic copy numbers increased if the transposase is provided.

These results suggest that the basic mechanism of P transposition and the phenotype of GD sterility are not largely different between D. melanogaster and D. simulans. However, the process of structural decay of P elements may be different from species to species.

Willingness to share biological control agents: how accessible is Africa?

Authors: Ivey Philip, The Centre for Biological Control Rhodes University Makhanda, South Africa

Abstract: Of the approximately 15,000 weed or introduced plant species with their origin recorded in the Global Compendium of weeds, 36% (5,476) are recorded to have originated in Africa. Africa is thus the second highest "donor" of introduced species to the rest of the world with East Asia, the origin of 13 more introduced species than Africa. While many of these 5,476 species are not necessarily invasive species, a fair percentage of them are or will become invasive over time. A closer look suggests that approximately 1,900 of these originated in Southern Africa.

Yet, Africa is the "provider" of biological control agents that target only 10 different plant species that originate from here. Thus there is vast scope for exploration and development of biological control agents from Africa to target invasive plants from the continent.

43 African states have either ratified, acceded or accepted the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity. Africa has historically "shared" plant species that may pose risk of invasion in new host territories, how willing is Africa to share its genetic resources for the development of biological control agents? This paper investigates the willingness to share.

Optimizing metabarcoding as a tool to accurately describe insect communities

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Abstract: Little is known about the composition or spatial and temporal dynamics of insect communities. Recent reports indicate that we are facing rapid declines in insect abundance and dramatic changes in community structure, highlighting the urgency to close this knowledge gap. Metabarcoding (high-throughput sequencing of marker genes) has emerged as a promising and cost-effective method of describing insect communities, however it is still unclear how accurately metabarcoding can describe species diversity (presence/absence) and community composition (abundances of species). Here we use individual insect barcoding of full Malaise traps and mock communities to evaluate and optimize metabarcoding protocols. Specifically, we investigate how consistent are the recovered composition profiles across replicate mock communities? How are community estimates affected by non-destructive mild lysis and destructive homogenisation? And whether it is possible to acquire adequate species abundances estimates through the use of spike-ins? By addressing these questions, we arrive at a non-destructive, cost-effective and rapid protocol, which provides reliable information about species diversity. The non-destructive nature of the protocol allows for future morphological or molecular work on the material. Additionally, our modelling results suggest that it is possible to accurately quantify species in a community sample by combining homogenization with biological and artificial spike-ins.

Potential strategies and future demands for insect pest management in major legumes under the climate change scenario

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Abstract: The 68th session of the UN General Assembly declared 2016, as the International Year of Pulses (IYP 2016), emphasizing the nutritional significance of legumes and their potential role for achieving global food security. Even though the IYP ended with enhanced public awareness about the nutritional aspects, other health benefits, and importance in mitigating climate change, and its role in promoting biodiversity, further studies are required to increase the global production and trade of pulses. Biotic stresses including insect pests and diseases significantly limits the legume productivity and yield by hampering the quality and quantity of the produce. Major food legumes include chickpea, pigeonpea, cowpea, field pea, lentil, faba bean, black gram, green gram, and beans, which play a vital role in food and nutritional security along with sustainable crop production. Several insect pests damage grain legumes, of which Helicoverpa armigera; Maruca vitrata; Etiella zinckenella; Spodoptera litura and S. exigua; Melanagromyza obtusa; Ophiomyia phaseoli; Aphis craccivora and Bemisia tabaci; Empoasca spp., Chilo partellus; Spodoptera frugiperda Megaleurothrips dorsalis, and Caliothrips indicus; Mylabris spp.; and Collasobruchus chinensis causes extensive losses. Appreciable progress has been made in formulating techniques to evaluate germplasm, mapping populations and genetically modified crops for resistance to insect pests. However, these techniques cannot be used for stem and pod flies, leaf hoppers, thrips, and aphids which requires formulation and standardization of methods for mass multiplication of such insects. Also, identifying the lines with diverse mechanisms/components of resistance is of utmost importance, facilitating gene pyramiding to explicate cultivars with a stable source of resistance to insect pests. Prominent levels of resistance to the pod borers have been found in the wild accessions of chickpea, pigeon pea and cowpea, which can be exploited to introgress genes to enhance the levels and diversify the basis of insect resistance in the cultivars. Moreover, declining sequencing cost has provided opportunities to deploy modern genomics approaches in understanding the genetics of insects, host plants and their interactions. Therefore, legumes and millets can be benefitted from the combinations of efficient insect screening methodologies and advancing genomic technologies to achieve the goal of developing insect-resistant varieties for sustainable crop production.

Biology of fall armyworm, Spodoptera frugiperda (J.E. Smith) (Lepidoptera: Noctuidae) on three different crop based artificial diets under lab conditions

Authors: Jaba Jagdish[1], Kumar Badbadwal Rajendra[2], Kota Sathish[2] and Prashad Mishra Suraj[2], [1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India, [2]The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India

Abstract: With the aim to develop a suitable crop-based artificial diet for rearing feasibility of fall armyworm(FAW) Spodoptera frugiperda (J. E. Smith) (Lepidoptera: Noctuidae), to study the biology of fall armyworm under laboratory conditions. The FAW is one of the important recent invasive polyphagous pest causing economic losses to Maize, Sorghum and other millets crops. The study revealed that the lowest life cycle period (egg to adult) was recorded on chickpea crop-based diet 31-39 days as compared to sorghum and maize diets 37-44 and 40-48 days respectively. Fully developed larvae recorded the highest length, width and weight on chickpea diet were 34.03mm, 4.92mm and 560mg respectively whereas, maize and sorghum diets 31.28mm, 3.69mm, 440mg and 33.69mm, 4.74mm, 530mg correspondingly, the fecundity was recorded highest on chickpea diet 983. A developing a novel and cheap method to rear S.frugiperda on different crop based artificial diets were developed for a regular supply of eggs, larvae, pupae and adult moths for research

Can green roofs compensate for the loss of (Hymenopteran) biodiversity in cities?

Authors: Jacobs Jeffrey, University Hasselt, Belgium

Abstract: In an urbanizing world, the roles and benefits of urban green space cannot be denied. The aim of our study is to check if green roofs can compensate, for this loss of biodiversity in cities. However, research on Hymenoptera and more specifically on pollinator communities and what is driving their species richness and community composition on green roofs is limited.

We have sampled invertebrate communities on eighteen extensive green roofs over a half year period from march until September, in the city of Antwerp, Belgium. Our assumption was that the more isolated the roof was the less biodiversity we would find there, as it becomes more and more difficult for species to colonize these isolated habitats.

Our results show that we found significant more Hymenoptera per trap on the ground level sites then on the green roofs. However, we were unable to support our hypothesis that we would find significantly less biodiversity in more isolated roofs compared to roofs closer to green spaces.

We will try to understand which species traits are best for surviving on these green roofs and which green roof traits are needed to support a wide variety of invertebrates.

Decline of bumble bees in northeastern North America

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Abstract: Concerns about the rapid and severe declines of many bumble bee (Bombus spp.) species in Europe, and more recently North America, have spurred research into the extent and possible causes for these losses. Drawing conclusions has been difficult due to a lack of long-term data, especially in underrepresented regions or those that may have different factors at play than the global trend. 150 years of museum collection data from the University of New Hampshire were examined to track shifts in distribution and relative abundance over time of bumble bees in New Hampshire, USA. In addition, floral records provided insight into the diet breadth of species of concern, which may affect their vulnerability. New Hampshire has experienced major re-foresting as a result of farm abandonment, thus the expansion of agriculture witnessed elsewhere may not be the major factor at play driving changes in bumble bee assemblages. Evidence of drastic decline or extirpation from the state was confirmed in three species of concern, including the federally endangered Bombus affinis (rusty-patched bumble bee), mirroring national trends. Severe range contraction to high elevations was found in Bombus terricola, also in line with observations in the national range of this species. Lastly, unexpected declines were seen in the generalist Bombus vagans, displaying an inverse correlation in range shifts and abundance with the presence of Bombus impatiens (common eastern bumble bee), which has increased dramatically in the last century and come to dominate bumble bee assemblages. Further research should be conducted to investigate the potential interaction of these two species and differing responses to anthropogenic change, and the ecological consequences of the biotic homogenization observed in bumble bee assemblages in the northeastern U.S.

Response of Wild Bee Assemblages to Management of Restored Wetlands

Authors: Jacobson Molly[1], Leopold Donald[1], Fierke Melissa[1] and Schummer Michael[1], [1]SUNY-ESF, State University of New York College of Environmental Science and Forestry, United States

Abstract: To effectively protect wild bee pollinators and the services they provide, it is critical to understand their interactions with plants among a diversity of land uses. Wetlands are underrepresented in bee surveys worldwide, and although restoration of degraded and fragmented wetlands from agriculture produces quality habitat for breeding and migratory waterbirds, it is still poorly known how hydrological management influences bee assemblages and the availability of floral resources. In this study, restored wetlands that were actively or passively managed were surveyed to determine wetland structure and plant and bee assemblages in central New York, USA, June – September 2019 and 2020; over 9,000 bees were collected, representing ≥ 113 species in 25 genera. 340 unique plant-pollinator associations were recorded, with pickerelweed (Pontederia cordata), goldenrod (Solidago spp.), beggarticks (Bidens spp.), and perennial smartweeds (Persicaria spp.) being particularly important for richness and abundance of bees. Bee and entomophilous plant assemblages were similar between treatments, and their diversity and frequency were negatively influenced by increasing percentage of open water, invasive graminoids, and monotypic cattail. Flowers of wetland plant species were 6x more diverse in the later portion of the growing season than the early portion, suggesting wetlands are most important for bees, particularly social species and specialists, in late summer and autumn. Passively and actively managed wetlands were each used by a rich assortment of generalist and specialist bees; maintaining a complex of wetlands with differing hydrological regimes, and controlling densities of invasive plants like Phragmites australis, can diversify the resources available for pollinators while also meeting management goals for waterfowl and other target vertebrate taxa.

Top-down control of non-native herbivores by natural enemies in mixed forests: a meta-analysis

Authors: Jactel Herve[2], Stemmelen Alex[3] and Castagneyrol Bastien[1], [2]INRA, France, [3]UMR BIOGECO, French National Institute for Agricultural Research, France, [1]Inra, France

Abstract: The escape from native enemies contribute to explain the ecological success of many non-native herbivorous insects outside of their native range. However, generalist enemies can successfully exploit non-native prey. The 'enemies hypothesis' predicts that the abundance and diversity of herbivores' enemies increases with the diversity of plants, which could increase their top-down control on herbivores. One of the main reasons is that more diversified forests would provide more suitable habitats and greater resource availability to many natural enemies, making them more effective at controlling herbivorous insect. This would be particularly relevant to non-native pests that are often introduced without their own natural enemies. However, although this hypothesis has received considerable support in agricultural systems, fewer studies have been conducted on forest ecosystems and a synthesis of previous work is still lacking.

In this study, we conducted a meta-analysis on ca. 100 publications comparing richness, abundance or activity of various groups of natural enemies (including birds, bats, spiders and insect parasitoids) in pure vs. mixed stands. To interpret further the outcomes of our quantitative review, we tested the effects of forest biome, mixed forest composition and host specialization of natural enemies.

Overall, our study builds toward a better understanding of the "enemies hypothesis" in forest systems and provide useful information on the mechanisms involved. It outlines interesting avenues for strengthening forest resistance to the growing threat of biological invasions.

Carabid diversity in the context of climate change: can forest diversity mitigate the effects of drought?

Authors: Jactel Herve[2], Jouveau Séverin[1], Castagneyrol Bastien[2], Poeydebat Charlotte[1], Vétillard Fabrice[1] and Van Halder Inge[1], [1]Biogeco, INRAE, Univ. Bordeaux, France, [2]INRA, France,

Abstract: Microclimate is suggested as a local driver of soil macrofauna biodiversity, while it is increasingly recognized that forest diversity can alter microclimate conditions, buffering temperature variations and increasing soil and air moisture. We therefore asked whether mixed-species forests could mitigate the effects of drought on the species diversity of ground beetles, an important group of predatory insects.

We used the ORPHEE tree diversity experiment to test the effect of forest biodiversity on carabid communities. In this manipulative experiment, eight blocks have been established with 32 plots corresponding to all possible combinations of one to five tree species (Betula pendula, Quercus robur, Q. pyrenaica, Q. ilex, and Pinus pinaster). In addition, half of the blocks are irrigate, the other half being subject to summer drought. We installed pitfall traps in selected plots to collect carabid beetles in spring and summer and assessed the response of carabid species richness and activity-density to the tree diversity gradient. In addition, we retrieved carabids species traits from the literature to test the effect of forest diversity on carabid functional diversity. We found that i) drought had a significant effect on carabids communities; (ii) understorey plant and tree diversity benefited carabid communities by improving the quality of their habitat (abiotic conditions) and the provision of food resources (especially prey); (iii) plant diversity mitigated the negative effects of drought on carabid communities. These results shed new lights on the role of forest biodiversity in mitigating the negative effects of climate change on insect biodiversity.

Genetic diversity and biotypes of rice gall midge (GM), Orseolia oryzae (Wood-Mason) and identification of a new resistance gene GM12 for resistance to GM in Thailand

Authors: Jairin Jirapong[3], Suthanthangjai Arissara[3], Uparang Chanita[3], Darwell Kulchana[1], Vejchasarn Phanchita[3], Leelagud Phikul[3], Kawichai Rungnapa[3], Kongsila Sakda[3], Chamarerk Varapong[2] and Phansenee Yotwarit[3], [1]Phrae Rice Research Center, Thailand, [2]Rice Department, Thailand, [3]Ubon Ratchathani Rice Research Center, Thailand,

Abstract: Rice gall midge (GM), Orseolia oryzae (Wood-Mason) is one of the most destructive insect pests of rice, causing significant yield losses annually in Asian countries. A mitochondrial gene, cytochrome C oxidase I (COI) was used to analyze the genetic diversity among GM populations. The phylogenetic tree indicated that Thai GM populations were homogeneously distributed throughout the country, except for some populations in the central and northeast, which most likely became isolated from the main population. According to the reaction of resistant varieties carrying different R genes revealed different biotypes found in Thailand. Exploiting host plant resistance to the GM is an economical and environmentally friendly approach to manage this pest. In this study, we identified a novel genetic locus for resistance to the GM, designated as GM12 on the short arm of rice chromosome 2. The locus was initially identified by significant SNP that separated resistance and susceptible groups. The locus was then confirmed and mapped using SNP and SSR markers with an F2:3 population derived from a cross between susceptible cultivar KDML105 and GM-resistant cultivar MN62M. Based on the linkage analysis in 150 F2 plants, we were able to map the locus near the SNP and SSR markers S2_430576 and RM3340, respectively. The new resistance gene provides important information for MAS to develop cultivars with broad-spectrum resistance against GM in Thailand.

The Side effects of 10 Insecticides used to control Tuta absoluta in tomato field on egg parasitoid Trichogramma cacoeciae in Hofuf, Alhasa, Saudi Aribia.

Authors: Jamal Hajjar M., King Faisal University, Saudi Arabia

Abstract: The tomato borer, Tuta absoluta, was detected in the north of Saudi Arabia (Tabuk, Al-Jouf and Hail) in summer 2010, while recorded in Alhasa April 2011.
The parasitoid Trichogramma cacoeciae Marchal is one of the most important components of Tuta absoluta bio-control. The side-effect of 10 commonly used insecticides in agricultural field in Alhasa, were estimated on the adults of the egg parasitoid Trichogramma cacoeciae Marchal, using standard protocol (of IOBC/WPRS-group), under in vitro conditions. Our results showed that the insecticides; Cypermethrin, Deltamethrin, Malathion, Phenthoate, Methomyl, Carbosulfan, were moderately harmful (class 3) to the adults of T. cacoeciae. Moreover, the botanical insecticides, Azadirachtin was moderately harmful (class 3) to the adults, while, Matrine was slightly harmful (class 2). The insect growth regulator (IGR) insecticide, Pyriproxyfen was slightly harmful, but the Bistrifluron was harmless (class 1) with mortality not exceeded 7.3%. The parasitism ratio of the alive adult are reduced as compared to control, Pyriproxyfen, and Azadirachtin reduced the parasitism ratio to 48.98, 57.95%, respectively and were in class 2, while Bistrifluron and Matrine were in class 1 (harmless) with reduction of 9.21 and 27.64%, respectively. However, the age longevity decreased significantly as compared to control of 4.67 days, while the average longevity of for adults exposed to (Bistrifluron) and (Matrine) was 3.6 and 3.27 days, but with (Pyriproxyfen), and (Azadirachtin) were lowered to, 1.67 and 1.33 days respectively. In semi-field tests, most insecticides considered as moderately to harmful to T. cacoeciae after 24 hours, post treatment on treated tomato leaves, the toxicity declined with time and became slightly harmful after 7 and 14 day post treatments.

Oh BEE-have: Assessing sublethal effects of chronic pesticide exposure on bumble bee learning and memory.

Authors: James Laura[3], Reynolds Andy[2], Davies Emyr[2], Mellor Ian[4], Lim Jason[2], Field Linda[1] and Williamson Martin[2], [1]Department of Biointeractions and Crop Protection, Rothamsted Research, Harpenden, UK., United Kingdom, [2]Rothamsted Research, United Kingdom, [3]Rothamsted Research, United Kingdom, [4]University of Nottingham, United Kingdom

Abstract: This project aims to assess the sub-lethal effects of pesticides on bumble bee (Bombus terrestris) mobility, navigation, learning and memory through the development of novel behavioural assays. Non-Apis bees are important crop pollinators, in some cases even providing pollination services over and above honey bees. B. terrestris is readily available for commercial pollination in Europe and is increasingly used as a model for testing pesticide impacts on non-Apis social bees. The development of species specific behavioural assays adds core tools to our ability to assess sub-lethal effects across a broad behavioural range and to provide a sound basis to compare pesticide impacts across a range of assays. These assays can be utilised to investigate a link between behavioural observations and underlying molecular mechanisms.

One such assay is the thermal-visual arena. The assay considers the ecologically relevant behaviour of relocating due to temperature preference and utilizes an aversive conditioning paradigm to train bees to find a cool reward zone, in an otherwise unappealingly hot arena utilizing spatial patterns around the arena's walls.

Most recently, the project has examined the unique trajectories which bees produce when walking in the thermal-visual arena. These 'signature' trajectories may appear simplistic, but each adheres to a mathematical law that describes hidden regularities. The occurrence of this law appears ubiquitous across nature, having been demonstrated across a range of movements and organisms, from human handwriting to Rhesus monkey eye movements and Drosophila larval crawling. The existence of such a regularity is remarkable given that animal behaviours are often shaped by individual psyches and by complex social and environmental interactions. We show that the same law describes the meandering patterns of walking bumblebees. The paths traced by bees could easily be mistaken for human signatures. These individual identifiers provide baseline movement templates which can be used as a tool to examine chronically pesticide exposed individuals, whose movements may vary from this baseline.

Spatial genetic consequences of cyclic irruptive population dynamics

Authors: James Patrick, University of Toronto, Canada

Abstract: Spatially synchronous outbreaks of native and invasive forest insect pests cause significant damage to forest resources. These outbreaks pose unique challenges to land and resource managers who seek to mitigate the negative consequences associated with outbreaks and to maintain ecosystem functioning. Population genetics and genomics present exceptional opportunities to learn more about demographic history and contemporary patterns of spatial and temporal connectivity in outbreak systems which could then be used to inform management. For example, population and landscape genetics can help us to better understand what drives patterns of spatial connectivity, outbreak spread risk, dispersal capacity, and spatial population dynamics. Population and landscape genomics can help us to identify potentially adaptive loci that are assisting outbreak expansion. Although rich in potential, the value of these analyses may be limited we currently know very little about the expected spatial population genetic and genomic patterns in outbreaking systems. Most theoretical population genetic expectations do not consider the potential effects of large-scale spatially synchronous changes in population density over several orders of magnitude. As a result, there is a significant risk of making incorrect inference using traditional approaches. Using examples from the spruce budworm (Choristoneura fumiferana) system, this talk reviews some of the challenges and assumptions of applying population genetic and landscape genetic approaches to outbreaking insect populations and highlight immediate research opportunities to resolve these them.

Behavioural studies on a newly identified Phoretic Egg Parasitoid Paratelenomus anu On Megacopta Cribaria (Hemiptera : Plataspidae)

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Abstract: Dolichos bean, Lablab purpureus (L.) is an important pulse cum vegetable crop and Megacopta cribaria (F.) (Hemiptera : Plataspidae) is one of the pests of L. purpureus (L.). Y tube Olfactometer and Electroantennogram studies on a newly found phoretic egg parasitoid Paratelenomus anu sp.nov on different sex and stages of Megacopta cribaria revealed the parasitoid’s ability to discriminate between the sex and different adult stages of the female insect . It was also detected that not all the bugs were chosen for phoresy but only very few female bugs were selected. Behavioral studies were conducted using olfactometer and EAG to find out the discrimination between male and female and different stages of adult female bug given an insight that the parasitoid had an ability to discriminate between male, female, pre-reproductive, reproductive and post reproductive stages of the adult female bugs. Results of olfactometer studies using parasitoids showed that percentage of attraction was more for reproductive females with an 80% of attraction when compared with pre-reproductive females (70 %) and post reproductive females (60%). EAG studies also substantiated the above results. From EAG studies it was evidently proved that each of these stages of female bug had got different chemical stimuli and based on these chemical stimuli parasitoid identifies and choose the females host insect for Phoresy.

Symbiont-mediated defense in molting life stages

Authors: Janke Rebekka, University of Mainz, Germany

Abstract: Almost all organisms are challenged by different opponents during their life span and need to find ways to get along with attacks or infections. Among insects, various strategies to cope with natural antagonists have evolved like mechanical, structural and chemical defenses, behavioral avoidance or camouflage. To overcome environmental threats like pathogens or parasites the use of defensive mechanisms provided by microbial symbionts can be another effective strategy. In general, symbionts can be protective to their hosts by outcompeting detrimental pathogens or by producing bioactive compounds or their precursors. Microbial symbionts can be housed within specialized insect cells, inside the gut, in the reproductive tract or colonizing the exoskeleton, which might be also associated to their functional roles. Some Lagria species of the family Tenebrionidae house the bacterium Burkholderia gladioli in specialized structures connected with the female reproductive system. These structures in the reproductive tract of females are morphologically described in multiple Lagriinae species, but the symbiotic association with Burkholderia is only described for few. Female beetles of the European L. hirta and the African and South American L. villosa harbor several strains of B. gladioli, which are transmitted to the egg surface during oviposition in the soil. By producing a range of antimicrobial compounds, the symbionts are able to protect eggs against pathogenic fungi from the environment. Since larvae and pupae of L. villosa are also living in the soil, they are likely under frequent exposure to pathogens and could benefit from a symbiotic association, especially during molting and pupation, while the cuticle is not melanized and more susceptible. Therefore, we tested for the symbionts and compounds in the developing life stages and could confirm the presence of the main compound and symbiont strain throughout larval and pupal development in both sexes, whereas male adults lack them. In the developing embryo three dorsally located invaginations are formed, which are then colonized by the symbionts during hatching. The symbiont structures retain a narrow opening to the outside, which is a possible starting point for symbiont and compound release. This kind of symbiotic structure in larvae and pupae is unique among insects and their presence has been so far confirmed only in L. hirta and L. villosa, albeit other Lagria species might also have similar structures. We could show that first instar larvae and pupae that have a unmelanzied cuticle are in addition to the dorsal structures partially covered with the symbionts. Additionaly, young symbiotic larvae show a higher survival, when exposed to an pathogenic fungus, than aposymbiotic individuals. Together this indicates an important defensive role of the symbionts and their produced compounds in the developing life stages of Lagria beetles, facilitated by peculiar symbiotic structures in larvae and pupae.

Evidence of functionally graded cuticle in Polyneopteran head capsules

Authors: Jansen Michael[1], Luktuke Amey[3], Chawla Nikhilesh[3], Labonte David[2] and Blanke Alexander[1], [1]Bonn University, Germany, [2]Imperial College London, [3]Purdue University

Abstract: The insect head capsule is a geometrically complex structure that is responsible for providing mechanical support during the generation of bite forces. The shape of the head is crucial for distributing stresses incurred during bites to prevent undue structural deformation and minimize loss of force while biting. Although the contribution of head capsule shape to biting mechanics has been considered in a handful of taxa, the role of cuticle composite structure in this context remains largely uncharacterized. Here we present evidence of composite-structure differentiation between regions of the head in the cuticle of four Polyneopteran species, as determined using a suite of electron and light microscopy techniques. Additionally, we present a preliminary analysis of nanoindentation data obtained from (1) isolated cuticle samples from individual regions of the head, and (2) from entire head-capsules embedded in epoxy. Based on differences in composite-structure and stiffness of the cuticle across the head capsule, we advance the hypothesis that profound functional gradients in the cuticle are essential for the transmittance of bite forces to tough substrates. Finally, we consider the implications of our results for future work involving finite element modeling of cuticular structures in biomechanical studies of insects.

Are selective pesticides compatible with biological pest control?

Authors: Janssen Arne[1], van Rijn Paul[1], [1]University of Amsterdam, Netherlands

Abstract: The impact of pesticide applications on pest populations in the presence of their natural enemies will be discussed using a range of predator-prey models - from general and unstructured to more specific and stage-structured. Pesticide applications will be varied in frequency, as will the mortality they induce in the pest and in its natural enemy. The compatibility of pesticide applications with natural and augmentative pest control will be discussed.

Ecological consequences of phytophagy by the omnivorous predator Macrolophus pygmaeus

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Abstract: Omnivorous predators can induce plant defences when feeding on plants, affecting the performance of herbivores. We showed previously that the omnivorous predator Macrolophus pygmaeus induces direct defences in sweet pepper plants, which negatively affects the performance and host plant choice of several herbivores. Furthermore, the omnivore can also affect plant phenology and reproduction. Herbivores were found to be less attracted by plants previously exposed to omnivorous predators than to clean plants, which suggests that plant volatiles were involved in the host plant choice of the herbivores. Besides affecting the host plant choice of herbivores, these volatiles may also affect the searching behaviour of other predators. Here we studied the effects of plant responses induced by the omnivorous predator Macrolophus pygmaeus on other natural enemies that share the same prey. We show that the predatory mite Phytoseiulus persimilis prefers plants previously exposed to the omnivore M. pygmaeus over clean plants even when its prey was absent, showing that the plant response to omnivore feeding may interfere with the searching behaviour of this important natural enemy. The predatory mites were equally attracted by plants previously exposed to the omnivore and subsequently infested by spider mites (Tetranychus urticae, the prey of the predatory mite and the omnivore) and plants infested with spider mites alone. In contrast, the predators were more attracted to plants infested with prey and subsequently exposed to the omnivore than plants infested with prey but not exposed to the omnivore. The predatory mites were also significantly more attracted to plants on which the omnivores were still present. Experience of the predatory mites with volatiles from plants previously exposed to the omnivore and without prey resulted in a loss of the preference for volatiles emitted by plants exposed to the omnivore. Furthermore, different ratios and quantities of plant volatiles were produced by plants exposed to the omnivore than by clean plants. Together, these results suggest that omnivorous predators induce the production of plant volatiles that attract other predators. Thus, the presence of omnivorous predators not only alter performance of plants, herbivores, but also other natural enemies that share the same prey, making these interactions more complex.

Manipulation of plant defenses by mites

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Abstract: Plants are under constant pressure from herbivores and have therefore acquired countless traits to defend themselves against their attackers. In response, herbivores have acquired their own traits to cope with the resistances of plants. Decades of research have meticulously mapped the resistance mechanisms of plants. Especially the way and extent in which plants can align their defenses to the type of attacker is well documented. However, as we have come to understand more of these mechanisms, we have come to realize that plants not always succeed in successfully establishing the necessary defenses. It turned out that there are quite a few herbivores who manipulate their host plant by gaining control of its metabolism via tempering with hubs in molecular signal networks. We have discovered that some herbivorous mites are able to suppress plant defenses. They do this by injecting saliva into their host that contains substances (proteins) that alter or down regulate the defense mechanisms of the plant. This has obvious advantages when these mites are alone on their host plant, but it can also have adverse effects in communities when facilitating competitors. In this talk I will explain what we currently know about how mites manipulate their host plant and how we can use this knowledge to make our crops more resilient.

Radiations or Oscillations? Insights into the diversification of butterflies

Authors: Janz Niklas, Department of Zoology, Stockholm University, Sweden

Abstract: Ever since the publication of Ehrlich and Raven's classical paper on coevolution between butterflies and plants, the potential codiversification of herbivorous insects and the plants they feed on have been at the heart of the coevolution discussion. This is not surprising, considering that both these groups have seen remarkable levels of diversification over the last 100M years, so that they now together make up about half of all species on Earth. Ehrlich and Raven's theory of "escape-and radiation" remains the most well-known hypothesis to account for this diversification, but it has more recently been challenged by an alternative scenario that relies more on retaining variability in host interactions than on key innovations leading to radiations. Here I will explore the differences between the two scenarios and relate some recent efforts to evaluate their relative importance for the diversification of nymphalid butterflies.

Molecular systematics and evolution of host plant associations in Lymantriinae:Support for the oscillation hypothesis from extreme polyphagous feeders

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Abstract: Plant-feeding insects represent about one-quarter of all described species on earth, but the mechanisms that have driven the diversification of these insects are poorly understood. An oscillation hypothesis on insect-plant associations suggests that the diversification of plant-feeding insects has been promoted by expansion of their host plant range, but the evidence for this hypothesis comes mainly from butterflies that are mostly specialized feeders. The moth subfamily Lymantriinae, belonging to Erebidae in Lepidoptera, represents a species-rich group of plant-feeding insects in terrestrial ecosystem, and comprises over 2500 described species. The subfamily is well known for extreme levels of polyphagy in host plant use, and thus can be used to further test the generality of the oscillation hypothesis as a suitable polyphagous insect group. In our studies, we firstly presented a broad-scale molecular phylogenetic framework for Lymantriinae by employing multi-locus sequence data and sampling 154 exemplars from 55 genera representing all recognized tribes drawn from all major biogeographic regions, proposed that the subfamily was composed of seven well-supported tribes: Arctornithini, Leucomini, Lymantriini, Orgyiini, Nygmiini, Daplasini and Locharnini, and revealed that Heracula discivitta, a mysterious taxon placed previously in Lymantriinae, represented a new subfamily of Pseudobistonidae. Based on the phylogenetic framework, we investigated the evolutionary patterns of host use at the order levels of plants in Lymantriinae using the method of comparative phylogenetic analysis between sister clades. Our results showed that Lymantriinae clades with higher diversity of host use contained more species than their sister clades, and these clades also consistently contained the most extremely polyphagous species, which meant the increased species diversity of Lymantriinae could be promoted by expansion of their host plant range. These results provided a further support for the oscillation hypothesis.

Results of faunistic studies in Lagodekhi Protected Areas

Authors: Japoshvili George, Professor, Director, Institute of Entomology, Agricultural University of Georgia, Tbilisi Head of the Board, Invertebrate Research Center, Telavi, Georgia

Abstract: The survey was completed during 2014 vegetation season in Lagodekhi Protected area. Seven Malaise traps were located in single transect from 500 to 3500 m asl and replaced every 10 days. From Arthropoda only Class Aracnida, orders Neuroptera and Mecoptera, and families Encyrtidae, Ichneumonidae (Hymenoptera) and Chrysomelidae (Coleoptera) has been identified completely to species level. Others such as families Eulophidae, Aphelinidae (Hymenoptera) are identified only partially. Total 699 species has been identified up to now. Fourteen are species new to science, 5 new genera records for Caucasus, 284 new species records for Caucasus and 146 new for Georgia. Thus Arthropod fauna of Georgia Increased by 5 genera and 444 species in total.

Halyomorpha halys (Hemiptera: Pentatomidae) in Georgia and potential for its biological control

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Abstract: Since brown marmorated stink bug (Halyomorpha halys Stal) first appeared in Georgia in 2015, intensive chemical control measures have been applied for its management. During our study in the 2019 growing season, we found 15 species of Pentatomidae in Georgia, including at least four polyphagous pests: Graphosoma lineatum (L.), Halyomorpha halys Stal, Palomena prasina (L.) and Pentatoma rufipes (L.). Georgian literature records 71 species of Pentatomidae, including Nezara viridula (L.), which has quite wide host plant range as well. Except for H. halys, no any other pentatomid has been recorded as an important pest for Georgian agriculture, even though some other species have been found damaging different agricultural crops in neighboring countries. Biocontrol agents may be controlling some of these bugs. Literature surveys list ten species of Trissolcus (Platygastridae), which have been recorded from the Caucasus region and one more from Georgia in particular. Ooencyrtus telenomicida (Encyrtidae), which is considered as a potential effective natural enemy for H. halys, has also previously been recorded from Georgia. Therefore, these parasitoids may be important biocontrol agents of these pest stink bugs in Georgia, holding them below their economic thresholds. Our studies identified that damage by insects (including H. halys) on hazelnut was varied between 11-25% (loss of nuts), while damage by fungus was between 10-41%.

Omnivorous zoophytophagous and non-zoophytophagous phytoseiids can induce plant defense responses of interest for crop protection

Authors: Jaques Josep A.[1], Cruz-Miralles Joaquín[1] and Flors Víctor[1], [1]Universitat Jaume I, SpainI

Abstract: Citrus aurantium L. (sour orange) displays higher constitutive and earlier inducible direct defenses against the two-spotted spider mite, Tetranychus urticae Koch (Acari: Tetranychidae), than Citrus reshni hort. ex Tanaka (Cleopatra mandarin). We have characterized the response of these citrus species to three predatory mites (Acari: Phytoseiidae) co-occurring with T. urticae in citrus. These predators display different levels of specialization on this herbivore: Phytoseiulus persimilis (Athias-Henriot) is a strict entomophagous whereas Neoseiulus californicus (McGregor) and Euseius stipulatus (Athias-Henriot) are omnivores. The latter is suspected to engage in cell-sap feeding in citrus. We have characterized (1) the volatile blends associated to these mites and to plants harbouring them through gas-chromatography, (2) plant gene expression induced by these predators through qRT-PCR, (3) the behavior of these mites when exposed to the volatile blends produced by infested and uninfested plants in Y-tube two-choice tests, and (4) non consumptive-effects of these predators on the herbivore. As expected, zoophytophagous E. stipulatus was able to trigger genotype-dependent defensive responses in citrus similar to T. urticae. Likewise, the strict entomophagous P. persimilis was not. However, unexpectedly, omnivorous N. californicus could also activate citrus species-specific defensive responses. These responses included the production of different volatile blends triggering different behavioral responses in these mites. Furthermore, the presence of either N. californicus or E. stipulatus on the plant reduced T. urticae densities in distal leaves. Therefore, these mites can affect their potential prey beyond predation through plant-mediated non consumptive effects. Our results may pave the way to develop new more sustainable tools to manipulate these agriculturally relevant species.

Phytoseiids can induce plant defense responses of interest in crop protection

Authors: Jaques Josep A.[1], Cruz-Miralles Joaquín[1], Guzzo Michela[1], Flors Víctor[1] and Ibáñez-Gual M. Victoria[1], [1]Universitat Jaume I, Spain

Abstract: Recent studies have revealed that the generalist predator Euseius stipulatus (Athias-Henriot) (Acari: Mesostigmata: Phytoseiidae) can feed on citrus cell-sap while triggering plant defense responses similar to those elicited by one of its potential preys, Tetranychus urticae Koch (Acari: Prostigmata: Tetranychidae). Changes in the jasmonic acid, the salycilic acid, and the flavonoids defensive pathways occurred. Changes were also observed in the plant volatile blends induced by E. stipulatus, which did not prevent T. urticae, from choosing E. stipulatus-infested plants. Interestingly, another phytoseiid, Neoseiulus californicus McGregor (Acari: Mesostigmata: Phytoseiidae), which co-occurs in citrus with E. stipulatus but cannot feed on plant cell-sap, can induce similar defense responses. Changes in the volatile blends produced by plants infested with N. californicus were also observed and were repellent for the shared prey, T. urticae. The results obtained so far demonstrate that plant defense responses triggered by phytoseiids are species-specific, depend on plant genotype, and may be also triggered by activities different from plant-feeding. Studies aimed at understanding the mechanisms behind these responses could pave the way for the development of new sustainable and efficient tools to protect our crops.

Illuminating the unknown insect diversity – the GBOL III: Dark Taxa project

Authors: Jaume Santiago, Zoologischen Forschungsmuseums Alexander Koenig, Germany

Abstract: For the overall goal of species discovery, shedding light on „Dark Taxa“ is pivotal. Taxonomy delimits species and is a crucial component in this context. Modern integrative taxonomy needs morphology, DNA barcodes, genomes, life histories, and new researchers that continue tackling the overall goal with a deep understanding of organisms, methods, evolution, and species concepts.

GBOL III: Dark Taxa is a taxonomy and a DNA barcoding initiative funded by the German Federal Ministry of Education and Science (BMBF), the first of its kind, focusing solely on the understudied part of biodiversity.

After 10 years of study by professional and citizen scientists in previous project phases, about half of the animal species occurring in Germany are covered within the DNA Barcode libraries of the German Barcode of Life (GBOL). Even diverse groups like Coleoptera or Lepidoptera are well represented. Yet, considering the estimated number of species in Germany, only about 25% of Hymenoptera and about 33% of Diptera are covered in the GBOL barcode library, i.e., these abundant and megadiverse insect orders pose the largest Dark Taxa problems and are studied in GBOL III: Dark Taxa. This includes characterizing species, creating reference DNA barcodes, and training a new generation of taxonomists.

Fungal diseases in insect rearing for food and feed

Authors: Jensen Annette Bruun[1] and Lecocq Antoine[1], [1]University of Copenhagen

Abstract: Food security is one of the great challenge of the future. Insect production has been recognized as a sustainable solution and many new mass rearing facilities have been established worldwide in recent years. Insects, like all biological production systems, are challenged by pathogens and when thousands of insects are reared in high densities epidemics can develop. Therefore, management and prevention of existing and emerging insect diseases is urgently needed. The insect pathogenic fungi Metharizhium and Beauveria have for decades been used as biological control agents towards pest insects. These fungi have a broad host range and can infect insects produced for food and feed. We will show examples of our research with fungal infection in Acheta domesticus, Hermetia illucens and Tenebrio molitor. Acheta domesticus are relative resistant to infection by Metharizhium and Beauveria, but could be a trigger of the potent AdDV virus. Hermetia illucens larvae are highly resistant to fungal infection, whereas adults are susceptible to Beauveria resulting high mortality and decreased egg production. Tenebrio molitor are susceptible to fungal infection and certain probiotic bacteria has proven to increase survival and growth but also boost the insects immune response helping them to fight off Metharizium infections.

Effects of cold acclimation on predation and predator fitness

Authors: Jensen Kim, Aarhus University, Department of Animal Science, Denmark

Abstract: Biological control is well established and functional in greenhouses, but relatively little used in the outdoor environment. In the temperate zone, temperatures are often low especially in early spring when biological control agents should be released to prevent pest establishment. Furthermore, since the pest has not yet established, food is scarce and predators may starve. In a series of experiments using the soil predatory mite Gaeolaelaps aculeifer, we tested whether acclimation to cold would improve predator performance under cold conditions. This species is used in biological control against a range of soil-dwelling pests and occurs naturally in both southern and northern Europe. Our results showed that G. aculeifer had higher tolerance to severe cold following cold acclimation. Furthermore, starvation tolerance was improved. In contrast, the kill rate of prey and predator egg production were reduced following cold exposure. This was the case both when prey were the flour moth Ephestia kuehniella and the springtails Folsomia candida and Protaphorura fimata, the latter of which is a pest in lettuce and other crops. In the experiment on springtails, a significant interaction between prey species and test temperature showed that low temperature reduced kill rate and reproduction on fast prey (F. candida) more than on slow prey (P. fimata). Importantly, the negative impact of cold pre-exposure on kill rate and reproduction was also significantly higher when preying on the slow springtail than on the faster springtail. This indicates that the fast springtail was increasingly harder to catch relative to the slow springtail at lower temperature, but also following lower pre-exposure temperature of the predator. In contrast, prey thermal pre-exposure did not significantly affect predator kill rate nor reproduction, indicating that the ability of prey to escape was not reduced after exposure to low temperature. Our results show that cold acclimation positively affects predator robustness by increasing severe cold- and starvation tolerance and thus survival under challenging conditions such as expected in early spring. However, predator impact via individual kill rate and population growth were reduced following cold acclimation. Followup experiments further showed that a winter of constant mild cold (10°C) reduced predation and reproduction less than a temperate winter including down to 0.8°C exposure, and that the higher starvation tolerance following cold exposure was caused by larger lipid accumulation during cold but not by reduced metabolism following cold exposure. Based on our experiments, we recommend cold acclimating G. aculeifer for prevention of pest establishment in early spring where robust predators are advantageous to improve survival until the pest appears. However, if the pest is already established in the crop we recommend using standard, non-acclimated predators that are more voracious and have higher potential population growth.

Entomopathogenic fungi-mediated biological control of Spodoptera frugiperda

Authors: Jeon Insoo[2], Kim Jae Su[2], Im Yeram[2], Park Yulim[2], Jeong Yujin[1], Song Gahyeon[2], Kim Jong Cheol[1], KIm Kijung[1], Park Soeun[1], [1]1Department of Agricultural Biology, Jeonbuk National University, Korea, [2]Jeonbuk University, South Korea

Abstract: Fall armyworm, Spodoptera frugiperda is an invasive polyphagous pest derived from America. It has been annually invading Korea during summer since it was firstly reported in 2019. Biological control is one of the strategies to eradicate this serious lepidopteran insect. This study aims to assess the potential of entomopathogenic fungi as biological control agents against S. frugiperda. Ninety-three isolates of entomopathogenic fungi were selected to investigate their insecticidal activities against second instar larvae of S. frugiperda. Of the isolates, thirty-four isolates showed 100% mortality at 8 days after treatments in laboratory conditions. The productivity and thermotolerance of conidia cultured on 1/4 SDA were evaluated to figure out the potential for field application. About ten isolates were determined to have high virulence against S. frugiperda and reasonable fungal production. Of the ten isolates, two-isolate showed the virulence of 83.3% mortality to pupae at soil treatment test. Another two-isolate caused 93.3% and 86.7% of larval mortality. Herein, we evaluated the virulence of entomopathogenic fungi against different stages of S. frugiperda including larva and pupae. The results indicated that entomopathogenic fungi would be practical biological control agents for the management of S. frugiperda.

Production of Beauveria bassiana JEF-350 blastospores with high thermotolerance through liquid culture

Authors: Jeong Yujin

Abstract: Compared to fungal solid culture, liquid culture reduces production time and is easy to prevent contamination. However, it has been reported blastospores are generally unstable to external environments such as heat. In this study, the characteristics of Beauveria bassiana JEF-350 from different culture media were investigated to produce heat-resistant propagules. After liquid cultures of JEF-350 at SDB, SSYP, and YPG media for seven days, the productivity and thermotolerance of JEF-350 blastospores were investigated. Solid cultures at the same media served as controls. The blastospore productivity was the highest in SSYP-liquid medium (6.4×10^7 blastospore/㎠), conidia productivity was the highest in SSYP-agar medium (27.1×10^7 conidia/㎠). As a result of heat exposure of JEF-350 cultured in each medium to 45°C for 60 minutes, blastospores produced in SSYP-liquid medium showed the highest germination rate (22.6%) after being incubated on 1/4SDA for 18 hours. From a virulence test against T. palmi in laboratory conditions, the mortality of T. palmi on all treatments showed more than 95% in day 7 after fungal treatment. In conclusion, JEF-350 blastospores produced in SSYP-liquid medium were excellent in productivity, thermotolerance, and insecticidal activity against T. palmi. SSYP liquid medium was considered an excellent substrate to produce B. bassiana JEF-350.

Development of Push-Pull strategies for biting insect control

Authors: Jerry Zhu Junwei, USDA-ARS, AMRU Lincoln, Nebraska, United States

Abstract: Stable flies are one of the most important arthropod pests of livestock. With changing climate and agronomic practices, they expand their roles as pests and disease vectors as well. Their infestation reduces livestock productivity, annoy companion animals, and interfere with recreational activities.

Volatiles associated with cattle including dimethyl trisulfide, butanoic acid, p-cresol, skatole and especially 1-octen-3-ol have been reported previously to be attractive to stable fly adults. Recently, new compounds, such as phenol, p-cresol and m-cresol, from cattle manure slurry, have been identified and demonstrated with enhanced attraction in the field. Furthermore, stable fly outbreaks in crop residues including pineapple, cabbage, and sugarcane have also been reported. Volatiles released from those stable fly favorable larval development habitats are identified with different chemical profiles compared with livestock associated substrates, which indicates that stable fly use additional attractants associated with their development environments for host and habitat location.

Plant-based repellent compounds have been widely used against blood sucking insects in veterinary and public health fields. However, one of the biggest shortcomings of plant-based repellents are short-lived in their effectiveness. Therefore, it is necessary to discover and explore more resources of plant origins with extended longevity in repellency. In the last 10 years, we have discovered several long-lasting repellent compounds from coconut oil that can provide repellency lasting up to 2 weeks against several types of blood-sucking insects. Over 90% of repellency/feeding deterrence have been demonstrated against biting flies including stable flies and horn flies, ticks, mosquitoes, cockroaches and bed bugs. Some of these compounds' derivatives also act as strong bio pesticide that inhibit stable fly larval growth and deters female oviposition. In some cases, the strength of repellency from these natural repellent products is even stronger than the golden standard, universal insect repellent, DEET (N,N-Diethyl-3-methyl-benzamide).

In this presentation, I will report the results from several studies related to our primary project on "How to use the attractant- or repellent-based semiochemicals to develop an economically- and environmentally sound strategy for biting insect control, particularly against stable flies. I will also introduce several of our recent technology transfers with industry partners in developing novel technologies for stable fly infestation reduction and animal well-being via Push-Pull strategies.

Bioactivity of Smoke Waters towards Bactrocera oleae (Rossi) (Diptera: Tephritidae) adults.

Authors: Jesu Giovanni[2], Vinale Francesco[3], Salvatore Germinara Giacinto[1], Bonanomi Giuliano[2], Pistillo Marco[1] and Laudonia Stefania[2], [1]University of Foggia, Italy - Department: Sciences of Agriculture, Food and Environment, Italy, [2]University of Naples "Federico II", Italy - Department of Agriculture, Italy, [3]University of Naples "Federico II", Italy - Department of Veterinary Medicine and Animal Productions, Italy

Abstract: Biochar is a recent deeply studied material due to the opportunity to reuse raw materials. Smoke-Waters (SWs) obtained during the Biochar production process are currently sold since they have been shown to promote seed germination. In this study, effects of SWs obtained from 5 different materials: alfalfa, cellulose, maize, wood (Quercus ilex L.), and olive mill waste, each obtained at both 300° and 500°C were investigated. The SWs have been tested in two separate mixtures for their toxic and olfactory effects on the adult of the olive fruit fly (OFF), Bactrocera oleae (Rossi) (Diptera, Tephritidae). The first mixture (OLI) was made of olive mill waste 300° and 500°C SWs in equal parts, for the second one (MIX) we used equal parts of all the other remaining SWs.Bioassays to assess the toxicity of OLI and MIX on B.oleae were performed according to testing for oral and contact exposure. Ingestion assays were evaluated by adding a standard amount (200 µl) of MIX or OLI to a 0.6 g sucrose (10%) diet used to feed OFF adults. After 14 days, different degrees of toxicity by ingestion were recorded among the mixtures tested. In particular, MIX occurred the most toxic with a mean mortality of 35,42% (ds 26,68) on females. With subsequent oviposition tests on olives, there was recorded also a reduced number of punctures and an increase in those that were sterile for females treated with the MIX. No toxic effects were detected by contact, assessed by topical application of 0.5 µl on the thorax of adult insects (n = 30) and by checking mortality 24 and 48 hours later. EAG tests showed that the antennal olfactory systems of male and female OFF are able to perceive, in a dose-dependent manner, volatile compounds present in the different SWs. However, the more toxic (MIX) elicited the strongest EAG responses in both sexes. Interestingly, the same SW mixture exhibited a significant repellent effect towards OFF males and females. On the contrary, OLI was attractive almost as fresh olive. In 2019 preliminary field tests were carried out in two different italian regions with different pedoclimatic conditions during the period of activity of the pest until the harvest of the drupes. Adult catches of B. oleae, by yellow sticky traps activated with pheromones and ammonium salt, were significantly reduced by 85,63% and 82,89% compared to control by the simultaneous application of 3 MIX distributors per plant.

CZ-SK SOUTH LIFE: Optimalization of Natura 2000 sites management delivery in the South Bohemia Region and the territory of South Slovakia (LIFE16 NAT/CZ/000001)

Authors: Ježková Eva, South Bohemia Region, Czech Republic

Abstract: The ongoing threats to habitats and insect species in the 55 Natura 2000 networks sites targeted by this project include the abandonment of traditionally-managed pastures and meadows and their overgrowth with dense vegetation; the spread of invasive species; changes to water regimes in wetland and peat bog habitats caused by drainage; and intensive forest management and the removal of old trees. This transboundary LIFE project (CZ-SK) is improving the conservation status of EU priority woodland and grassland habitats to benefit priority species Osmoderma eremita and raised bog and bog woodland priority habitat for Carabus menetriesi pacholei through actions to improve the hydrological function of bog habitats, restore mowing and grazing regimes on grasslands, and tree-planting and invasive species removal in forests. The project intends to purchase 40 ha of land and enter into long term leases for a further 30 ha of land to increase long term security of some of the conservation actions.

In silico identification of neuropeptides and functional study of Adipokinetic hormones in termites

Authors: Jiang Shixiong[1], Marco Heather G, Scheich Nina, He Shulin, Gäde Gerd and McMahon Dino Peter, [1]Bundesanstalt für Materialforschung und –prüfung (BAM), Germany

Abstract: Termites are a diverse group of social insects. As with other insect groups, they possess different neuropeptide classes for regulating various physiological processes. To date, only two neuropeptidomes have been characterized in termites. Here, we aimed to carry out a comparative analysis of neuropeptides across the major termite lineages, including solitary cockroaches and subsocial wood roaches. We characterized the major classes of neuropeptides across these lineages, focusing particularly on a comparative molecular analysis of adipokinetic hormones (AKH) and their receptors (AKHR). Molecular evolutionary analyses and evidence of post-translational modifications (PTMs) of AKHRs are also discussed. We then examine the functional role of termite AKHs by measuring the mobilization of carbohydrates and lipids in the hemolymph of Reticulitermes flavipes following experimental injection with synthesized peptides. Finally, we explore interactions between AKH activity and host immunity by testing the effects of AKHR downregulation (dsRNA injection) on resistance to pathogen challenge.

Our study provides important information concerning the diversity of termite neuropeptides as well as the metabolic role of AKH and its intersection with host immune function. In addition to providing a fresh perspective on the feasibility of using AKHs as potential candidates for biorational pest control agents against invasive termites and cockroaches.

Production of recombinant human angiogenin using hyper-enhanced baculovirus expression system

Authors: Ji Ho Young[1], Woo Soo Dong[1], Im Jin Woong[1] and Kim Hyun Soo[1], [1]Chungbuk National University, Republic of Korea

Abstract: Human angiogenin is a single-chain basic protein consisting of 123 amino acids, belonging to the superfamily of RNase A, and has angiogenesis-inducing activity. Due to these characteristics, it can be applied to the treatment of diseases requiring new blood vessels, and the social necessity is expected to be high in the development of therapeutic substances and various fields. However, there are few reports on the production of recombinant human angiogenin in eukaryotes. In this study, recombinant human angiogenin was produced in insect cells and its activity was evaluated using a newly constructed hyper-enhanced baculovirus expression system and various expression-enhancing fusion partners. As a result, the production potential of human angiogenin in insect cells was confirmed, and the expression level increased by the fusion partner was observed. The activity of recombinant angiogenin, including RNase activity, was also evaluated.

Selection of entomopathogenic fungi against the green peach aphid, Myzus persicae, through simultaneous evaluation of virulence and environmental stability

Authors: Ji Ho Young[1], Lee Jin Yong[1], Woo Ra Mi[1], Kim Hyun Soo[1] and Woo Soo Dong[1], [1]Chungbuk National University, Republic of Korea

Abstract: The green peach aphid, Myzus persicae, is an economically important pest for agricultural and horticultural crops because this aphid causes direct damage by feeding on plant nutrients and indirect damage by transmitting many virus vectors. Control of this pest relies almost exclusively on the application of chemical insecticides. Unfortunately, the green peach aphid has developed multiple resistance to many chemical insecticides. Therefore, this study was conducted to select an entomopathogenic fungus effective against the green peach aphid as a new biological control agent. In order to select entomopathogenic fungi effective in controlling the green peach aphid, the virulence and environmental stability of conidia were evaluated for various fungal strains. For the first selected 20 fungal isolates, the most efficient isolates were selected through additional evaluation of thermal stability and UV stability of conidia. High environmental stability is expected to further increase the possibility of commercialization of the selected entomopathogenic fungi.

Juvenile hormone antagonistic activity of actinobacteria and their insecticidal activity against Plutella xylostella

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Abstract: agricultural pests causes serious damage to crops and economical losses. chemical insecticides were widely used to control pests. However, due to their toxicity to the environment and the development of insect resistance. Insect growth regulators are friendly alternatives to traditional chemical insecticides because of their specification to target insects and low toxicity to non target organisms. However, juvenile hormone agonists causes increased economic damage to crops because of their status quo effect. Recently, novel IGR compounds with juvenile hormone antagonist activity which can effectively control agricultural pests was discovered.

In this study, to identify novel IGR compounds from actinobacteria, culture media of 1,904 actinobacteria isolated from Korean soil samples were discovered for their juvenile hormone (JH)-based IGR activities. Among them, 4 isolates showed insecticidal activity with Juvenile hormone antagonist activity. Identification and characterization of these actinobacteria was performed.

Natural selection has driven the recurrent loss of an immunity gene that protects Drosophila against a common natural parasite

Authors: Jiggins Francis[1], Arunkumar Ramesh[1], Leitao Alexandre[1] and Day Jon[1], [1]University of Cambridge, United Kingdom

Abstract: Parasitoid wasps are common natural enemies of Drosophila melanogaster, and yet most genotypes in nature are susceptible to infection. We have identified a gene that encodes a lectin that is expressed in the fat body and localises to the surface of the parasitoid egg before the attachment of hemocytes. When we mutated this gene, the flies became susceptible to infection. In natural populations multiple alleles of this gene contain deletions to cis-regulatory elements that reduce expression or premature stop codons, and in southern Africa natural selection has driven these loss of function mutations to high frequency. We conclude that in some populations there is a selective advantage to losing an important component of the anti-parasitoid immune system.

The evolution of parasitoid resistance in Drosophila

Authors: Jiggins Frank[1], Leitao Alex[1], Ramesh Arunkumar[2] and Day Jon[1], [1]University of Cambridge, United Kingdom

Abstract: Parasitoids are likely the most important natural enemy of Drosophila melanogaster, and there is considerable genetic variation within and between populations in susceptibility to infection. Using the parasitoid Leptopilina boulardi we have investigated how changes to the activation of the cellular immune response can underlie the evolution of parasitoid resistance. Using single cell RNA sequencing of immune cells called hemocytes, we found that genetically resistant populations have constitutively activated cellular immune systems. By partially bypassing the steps of recognition, signalling and cell differentiation, this may allow the parasitoid to be killed more rapidly. A second mechanism of resistance is associated with a cis-regulatory polymorphism upstream of a gene encoding a putative pattern recognition receptor. In resistant genotypes this gene is massively upregulated after infection, and this is associated with a more rapid immune response. We conclude that changes to the recognition of infection and activation of cellular immunity both play key roles during the evolution of resistance.

Unique peptidic agonists of a juvenile hormone receptor with species-specific effects on insect development and reproduction

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Abstract: Juvenile hormones (JHs) act through a receptor complex consisting of methoprene-tolerant (Met) and taiman (Tai) proteins to induce transcription of genes including Kr-h1. Among diverse synthetic JH mimics (juvenoids), peptidic juvenoids stand out as highly potent yet uniquely selective to a specific family of true bugs. Their mode of action is unknown. Here we demonstrate that, like established JH receptor agonists, peptidic juvenoids induce expression of Kr-h1 and act upon Met to halt metamorphosis in the linden bug, Pyrrhocoris apterus. Peptidic juvenoids induce dimerization between Met and Tai proteins from P. apterus but, consistent with their selectivity, not from other insects such as the beetle, Tribolium castaneum. Our models for the ligand-binding pockets of Met orthologs from P. apterus and T. castaneum suggest a structural basis for the selective action of peptidic juvenoids. We synthesized >100 new derivatives, many of which acted at sub-nanomolar range and outperformed existing juvenoids including fenoxycarb. Importantly, their potency in inducing Met-Tai interaction correlated with the biological activities in live bugs. Our data establish peptidic juvenoids as highly effective and species-selective JH receptor agonists.

Supported by grant 20-05151X (Czech Science Foundation) and project LM2018130 (MEYS) to the National Infrastructure for Chemical Biology CZ-OPENSCREEN.

Development of novel pest controlling strategies targeting dietary sterol absorption

Authors: Jing Xiangfeng[2] and Zheng Jin-Cheng[1], [1]Guizhou University of Traditional Chinese Medicine, China, [2]Northwest A&F University, China

Abstract: Cholesterol exists as the major sterol in animals including insects. It is essential because it is not only one of the structural components in the cellular membrane but also serves as signaling molecules in eukaryotic cells. Moreover, it is the precursor to the molting hormones. However, unlike mammals, insects cannot synthesize cholesterol because of the loss of the biosynthesis genes. Therefore, dietary sterol uptake is critical for insect survival and growth. Insects and mammals seem to share the conserved dietary sterol uptake mechanism. We identified insect orthologs to the key factors of the NPC1L1-flotillin complex involved in sterol uptake in mammals by comparative genomic analyses. We investigated the function of these orthologs, i.e., NPC1b and flotillin, in a lepidopteran pest, Helicoverpa armigera. First, we confirmed that the insect cannot grow and did not eat much if dietary cholesterol supply was reduced. We then used CRISPR/Cas9 technology to investigate the functions of these genes. Compared to the wild-type insects, the CRISPR/Cas9-edited mutant larvae seemed to have problems in acquiring dietary cholesterol and NPC1b mutants died in the early stage. NPC1b was mainly expressed in the midgut verified by gene expression analyses and in-situ hybridization analyses, indicating that the midgut was the major region for dietary sterol absorption. NPC1b expression was especially upregulated during early larval instars but dropped in the following instars. This variation may be associated with the sterol nutritional status. Interestingly, the substrate binding regions of NPC1b proteins, NPC1b_NTD, are relatively conserved among lepidopteran insects but highly divergent from bees-derived sequences. Therefore, NPC1b and other factors involved in dietary sterol uptake can be promising targets for the development of novel pest-management approaches to control economically significant lepidopteran pests with little off-target effect on bees and sterol-autotrophic mammals.

Review of the subfamily Hypenodinae (Lepidoptera: Erebidae) in Korea

Authors: Ji-Young Lee[1] and Bong-Kyu Byun[1], [1]Hannam University, South Korea

Abstract: The aim of this study was to review of the subfamily Hypenodinae in Korea. This group has small sized moth with wingspan 5.5-12mm, belonging to the family Erebidae. They are known as distributed only in the Holartic region, including temperate zone of eastern Asia (Fibiger, 2011). However, the subfamily Hypenodinae of Korea has been poorly studied to date, including the larval information, host plants and so forth. In this study, totally 13 species of 7 genera under 2 tribes were recognized from Korea. Among them, 2 subspecies are described as new to sciences from Korea. All the known species are redescribed with their available information, including images of adults and genitalia of all species and key to the species.

UCE phylogenomics to elucidate the evolution of wing coloration patterns in the geometrid tribe Palyadini (Ennominae)

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Abstract: The evolution and development of butterfly wing color patterns have been extensively studied across multiple fields in Biology. In contrast, the evolution of wing color patterns in “moths'' has been traditionally less explored. In this ongoing study, we are investigating the evolution of wing color patterns in the geometrid tribe Palyadini, a group that is characterized by having various wing color patterns formed by metallic scales. For this, we generated a phylogenetic hypothesis based on ultraconserved elements (UCEs) and using a wide taxon sampling that includes the six genera belonging to the tribe and multiple outgroups. We use this cladogram to identify patterns of character change of multiple color elements such the presence and absence of eyespots on the dorsal surface of the hindwing. The preliminary results of this study represent a window to the sparse knowledge about wing color evolution outside Papilionoidea.

Temporal variation in spatial genetic structure during population outbreaks: distinguishing among different potential drivers of spatial synchrony

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Abstract: Spatial synchrony is a common characteristic of spatio-temporal population dynamics across many taxa. While it is known that both dispersal and spatially autocorrelated environmental variation (i.e., the Moran effect) can synchronize populations, the relative contributions of each, and how they interact, is generally unknown. Distinguishing these mechanisms and their effects on synchrony can help us to better understand spatial population dynamics, design conservation and management strategies, and predict climate change impacts. Population genetic data can be used to tease apart these two processes as the spatio-temporal genetic patterns they create are expected to be different. A challenge, however, is that genetic data are often collected at a single point in time, which may introduce context-specific bias. Spatio-temporal sampling strategies can be used to reduce bias and to improve our characterization of the drivers of spatial synchrony. Using spatio-temporal analyses of genotypic data, our objective was to identify the relative support for these two mechanisms to the spatial synchrony in population dynamics of the irruptive forest insect pest, the spruce budworm (Choristoneura fumiferana), in Quebec (Canada). AMOVA, cluster analysis, isolation by distance and sPCA were used to characterize spatio-temporal genomic variation using 1370 SBW larvae sampled over four years (2012-2015) and genotyped at 3,562 SNP loci. We found evidence of overall weak spatial genetic structure that decreased from 2012 to 2015 and a genetic diversity homogenization among the sites. We also found genetic evidence of a long-distance dispersal event over > 140 km. These results indicate that dispersal is the key mechanism involved in driving population synchrony of the outbreak. Early intervention management strategies that aim to control source populations have the potential to be effective through limiting dispersal. However, the timing of such interventions relative to outbreak progression is likely to influence their probability of success.

Proviral and antiviral microRNAs impact the outcome of infection with diverse RNA viruses

Authors: Johnson Karyn, School of Biological Sciences The University of Queensland, Australia

Abstract: Insects host a variety of viral infections and can act as vectors of virus disease. The small RNA pathways can be important regulators of the outcome of infection in insect hosts. miRNAs are recognised as widespread regulators of gene expression across many biological functions including antiviral defence and immunity. miRNAs are 22 nucleotide non-coding RNAs that are transcribed from the genome and bind in a sequence-specific manner to the target messenger RNAs. miRNAs act as guides for effector complexes, enabling modulation of gene expression primarily via mRNA decay or translational inhibition. Using the Drosophila model, we have demonstrated that two miRNAs (miR-956-3p and miR-8-5p) can have considerable impact on virus infection, one being proviral and the other antiviral. However, the influence of the vast majority of miRNAs on virus infection remains untested and it is not yet known whether there is generality in the influence miRNAs across diverse viruses. The recent development of genetic tools in Drosophila made the possibility of functional analysis of a large number of miRNAs in whole flies achievable. We conducted an unbiased screen of Drosophila miRNA loss-of-function lines. We challenged the flies with three different virus families: Drosophila C virus (family Dicistroviridae), Flock House virus (family Nodaviridae) or the arbovirus Sindbis virus (family Togaviridae). This study provides answers to questions about the proportion of miRNAs that impact virus infection, and to what extent the impact of the miRNAs is conserved across diverse virus families.

Phylogenomics of the Hemipteroid Insects

Authors: Johnson Kevin, Illinois Natural History Survey, University of Illinois, United States

Abstract: The hemipteroid insect orders (Psocodea, Thysanoptera, and Hemiptera) comprise a diverse assemblage of over 120,000 species with a diversity of feeding habits. New phylogenomic datasets are revealing insights into the evolutionary history of this group at a variety of timescales. At the deepest level, a transcriptome dataset of over 2300 genes for around 200 species provides support for backbone relationships within and among these orders. A sister relationship between Thysanoptera and Hemiptera is strongly supported, while the position of Psocodea remains uncertain. Within Hemiptera, Sternorrhyncha is sister to all remaining suborders, and Coleorrhyncha is sister to Auchenorrhyncha. For small-bodied insects for which transcriptome sequencing is not feasible, whole genome shotgun sequencing approaches can yield gene assemblies to produce similar datasets. Additional uses of these genomic datasets include read-mapping to identify polymorphic sites for population genomic analyses and assembly of bacterial symbiont genomes to uncover repeated replacement of these symbionts and consequences for molecular evolution.

Increased toxicity to honey bees of insecticides, fungicides and adjuvants applied to almonds during bloom

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Abstract: Beekeepers providing honey bees to pollinate almonds continue to experience unacceptable losses of adult and developing bees, sometimes resulting in colony failure. Many beekeepers attribute these losses to exposure to insecticides, fungicides, spray adjuvants and combinations of all three, that are applied during bloom. Results indicate that particular combinations of fungicides and insecticides, particularly Altacor and Tilt, have the potential to kill adult bees when sprayed directly and larvae when fed contaminated diet. Addition of the adjuvant Dyne-Amic makes this combination more toxic, causing adult mortality at levels below the maximum label rate. The effects observed may explain some of the problems beekeepers are experiencing during and after almond bloom and provide support for recommendations to avoid using insecticides and adjuvants during bloom.

Identification of a potentially novel subclass of insect cys-loop ligand-gated ion channels

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Abstract: Introduction: Members of the cys-loop ligand-gated ion channel superfamily, such as nicotinic acetylcholine receptors (nAChRs), are targets of highly effective insecticides. Heterologous expression of these receptors provides useful insights into their functional and pharmacological properties.

Methods: Phylogenetic analysis of insect nAChR gene families has identified the alpha5 subunit in non-Dipteran species (cockroaches, beetles, moths and bees) as being potentially part of a novel sub-group of ion channels. In order to determine their functional and pharmacological properties, the alpha5 subunit from the honey bee, Apis mellifera, was heterologously expressed in Xenopus laevis oocytes, to which was applied two-electrode voltage-clamp electrophysiology.

Results: The A. mellifera alpha5 nAChR subunit expresses robustly in X. laevis oocytes without the need for co-expressing with chaperone proteins. The alpha5 receptor has low sensitivity to acetylcholine with an EC50 of 2.37 mM and is insensitive to the agonist actions of neonicotinoids and the modulatory actions of spinosad. However, serotonin and other biogenic amines, such as dopamine, act as agonists with a considerably lower EC50 in the micro molar range that are also more efficacious than acetylcholine in activating the receptor. Molecular modelling indicates that residues in the complementary binding site may be involved in selectivity towards serotonin.

Discussion: This is the first report of a ligand-gated ion channel activated by biogenic amines from an insect. The study, therefore, highlights a distinct subgroup of ion channel subunits present in certain non-Dipteran insects with unusual pharmacological properties, which may represent targets for the development of novel classes of insecticides.

Baculovirus manipulation of plant defenses and impacts on insect behavior and performance

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Abstract: Baculoviruses are arthropod-specific viruses that often target lepidopteran larvae and can be used as biological control for agricultural plant pests. Viral infections cause larval body tissues to liquify and the cadavers release millions of viral occlusion bodies (OBs) and bacteria onto plant surfaces. Healthy larvae ingest OBs which dissolve in the gut, releasing virions that invade midgut cells and establish systemic infections. Interactions between insects and baculoviruses can be modulated by plants. For example, plant defensive compounds including polyphenol oxidase (PPO), peroxidases, and quinones can reduce viral efficacy in the insect midgut. These tritrophic interactions may also function in the opposite direction, whereby baculoviruses manipulate plant defense traits to enhance efficacy or alter host behaviour or performance in a manner that enhances the likelihood of viral transmission.

We explored plant–insect–baculovirus interactions using cabbage looper (Trichoplusia ni) caterpillars, tomato (Solanum lycopersicum), and Autographa californica multiple nucleopolyhedrovirus (AcMNPV). We hypothesized that virus-killed T. ni cadavers (VK) suppress plant defenses and alter behavior and performance of healthy T. ni. We applied water, homogenized VK, or homogenized freeze-killed (FK) cadavers to tomato plants that were undamaged or mechanically damaged. Damaged plants that received water or FK cadavers had significantly higher levels of PPO activity compared to undamaged plants ($F = 4.67$, $P = 0.0007$). However, the induction of PPO was suppressed in the VK treatment. By suppressing the induction of PPO, we hypothesized that AcMNPV increases the attractiveness of plants for oviposition or larval feeding. We present data from neonate choice assays, no-choice performance bioassays, and moth oviposition experiments to examine these hypotheses.

Because VK cadavers contain both OBs and bacteria, we also conducted experiments to explore the roles of these microbes in mediating plant defenses. We found that VK cadavers had significantly more bacterial colony-forming units per mg tissue than FK cadavers ($t = 4.90$, $P < 0.0001$). Using Illumina MiSeq high throughput sequencing, we also compared bacteriomes between VK and FK cadavers to determine how virus infection alters the composition of bacterial communities present in dead insects. To disentangle the role of OBs and bacteria in mediating plant defenses, we will explore plant responses to the application of varying concentrations of purified OBs and bacteria separately.

Our study provides evidence that microbial natural enemies can alter plant traits directly, and highlights the complex roles that bacteria and viruses play in mediating plant–insect interactions.

Getting out of a sticky situation: Peppermint Stick Insects adjusting chemical defensive behaviour relative to predatory threat

Authors: Jones Braxton[1] and Bulbert Matthew[1], [1]Department of Biological Sciences, Macquarie University, Australia

Abstract: Flight initiation is a decision made by prey to deploy defensive tactics during a predator attack. As this predator-prey interaction effects the survival of the prey, there is strong evolution for these defensive strategies. When considering the importance of such a strategy, the timing of when this defence is used in a predator attack is also critical. Accordingly, the ‘flight initiation hypothesis’ describes the ability for prey to choose optimal times to ‘fight or flight’ based on the costs and benefits of either option. This decision-making process relies on the defence strategy being used, where the prey is in relation to its refuge, where the predator is and the speed at which a predator attacks. Whilst this concept is extensively researched among defence strategies, there is no understanding for where chemical defence fits in this hypothesis. By looking into the chemical defence of the Peppermint stick insect (Megacrania batesii), we will use this insect as a model to bring chemical defences into light with flight initiation. Experiments on wild individuals were conducted to examine the relationship between likelihood of spraying relative to distance and slope to refuge. We further considered sex differences, and variation in reproductive preferences of multiple populations (Population 1: sexual, Population 2: asexual). Our presentation will attempt to showcase phasmids as a model taxa for examining the evolution of chemical defences and the genus Megacrania as an excited taxonomic group for examining both dispersal and defensive strategies in Phasmids.

Task allocation by age in Australian native bee colonies

Authors: Jones Lachlan, University of Queensland, Australia

Abstract: In large social insect colonies, effective division of labour is a critical hurdle. Queens of most eusocial species are entirely occupied by laying eggs. The workers, which can number tens of thousands, must therefore coordinate their activities to store food, maintain and defend the colony nest. While many ants rear worker castes of different sizes and morphologies to carry out specific tasks, other insects such as honeybees and stingless bees (Melliponini) progress through each task as they age. Here I present behavioural observations with two species of Australian stingless bee, Tetragonula carbonaria and T. hockingsii. I aimed to define the age range for each distinct behaviour or task carried out by worker bees. I extracted and marked newly emerged adult bees (callows) with coloured paint before releasing them back into wooden observation hives. I then regularly observed activities of marked bees through and observation window and hive entrance tube. While there was substantial overlap in the ages of bees carrying out different behaviours, both bee species progressed similarly through tasks from brood care to food pot and hive structure construction and eventually foraging, with numerous other rarer behaviours.

Abundance decline corresponds with reduced biodiversity in hoverflies, but not in aquatic insects

Authors: Jongejans Eelke, Radboud University, Netherlands

Abstract: Whether declines in insect abundance reflect biodiversity loss is still an open question. We analyse the abundance of hoverflies, at six locations in wet or tall perennial meadows in the German Wahnbachtal in 1989 and 2014, and over multiple years since 1982 in a Dutch forest. We show isometric decline rates between total insect biomass and total hoverfly abundance and a scale-dependent decline in species richness, ranging between −23% over the season to −82% at the daily level. Observed persistence rates were disproportionately lower than expected for species of intermediate abundance, while the rarest species showed decline and appearance rates consistent with random expectation. Contrastingly, aquatic insect communities in the Netherlands showed increasing richness and diversity since 1990, even though abundance declined by -55%. Improved water quality after heavily polluted and eutrophic conditions by the 1980s, can explain much of these patterns. Abundant taxa that tolerate poor water quality declined strongly, while positive indicator taxa were found more often and increased in abundance. This suggests that insect communities can bounce back at least partially when proper management is applied. Adequate target values for pristine communities are lacking though, while water quality is still insufficient in half of the samples.

Effects of intensified agriculture on weed seedbank regulation by seed predators

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Abstract: Agricultural intensification has markedly increased the productivity of a few commodity crops but taken a heavy toll on the environment by reducing biodiversity and its associated ecosystem services, such as pollination and biological pest control. Weeds are a major constraint to intensified crop production and can cause substantial yield losses. Consequently, farmers have a vested interest in minimising weed load and thus fields are intensively managed. It has been suggested that abundant seed predator communities can reduce the size of annual weed seedbanks but it remains unclear how agricultural intensity impacts weed regulation and service provisioning by the seed predators. Using data derived from a large scale study of 60 cereal fields across Europe, and combing combining molecular gut content analysis with metabolic theory we compute a metric of seed predation strength that links the performance of seed predator communities to the provision of weed regulation. We then investigate how three aspects of agricultural intensity (field management intensity, landscape heterogeneity, and crop rotation simplification) affect weed seedbank regulation via effects on seed availability and seed predation strength. Our results provide compelling evidence that intensive agriculture reduces seed predation strength, which has a positive effect on weed seedbank regulation. Increased field management intensity, crop rotation simplification, and reduced landscape diversity all directly or indirectly reduced seed predation strength with cascading negative effects on weed seedbank regulation.

Effects of elevated CO2 on the life table parameters and population transition of Riptortus pedestris (Fabricius) (Hemiptera: Alydidae)

Authors: Joon Ahn Jeong[1], San Choi Kyoung[1] and Koh Sangwook[1], [1]Research Institute of Climate Change and Agriculture, National Institute of Horticultural and Herbal Science, RDA, South Korea

Abstract: Riptortus pedestris (Fabricius) (Hemiptera: Alydidae) is one of economically important insect pests in soybean field. We investigated the effects of elevated CO2 levels (400, 600, 1000, 1500 and 2000ppm) on the development periods, fecundity and life table parameters of R. pedestris. We collected life table data, log stage structure curves and stage growth rate for R. pedestris using viable eggs and the age-stage, two-sex life table method. R. pedestris developed successfully from the egg to the adult stage in the range of 400~2000ppm. Egg and pre-adult duration of 400ppm were longer than those of other concentrations. Overall female life span was also longest at 400ppm but overall male life span was longest at 600ppm. Although oviposition days and eggs per female were decreased with increasing CO2 concentrations, eggs per oviposition day, net reproductive rate, intrinsic rate of increase and finite rate of increase were increased at the higher CO2 concentrations. We concluded that the R. pedestris population size may be increased within elevating CO2 concentration at atmospheric environment.

The historical role of Madagascar in the diversification of Afrotropical bark and ambrosia beetles

Authors: Jordal Bjarte, University of Bergen, Norway

Abstract: Madagascar is well known for its high endemicity of plants and animals. The origin of the Malagasy fauna is nevertheless poorly known for insects and other arthropod groups. The origin of endemic lineages was likely fostered by rare overseas dispersal, primarily from the African mainland. Due to a shift in the wind and current direction after the island drifted northwards during the Oligocene, it has been argued that colonization from Africa to Madagascar should be older than Miocene age and more recent faunal interchange have occurred from Madagascar to the mainland. Here we show that bark and ambrosia beetles in Madagascar have many different colonization histories. Based on molecular phylogenetic analyses of 11 beetle lineages, we reconstructed the ancestral distribution and approximate age for traversing the Mozambique channel. While a few lineages in Madagascar may be older than 50 Ma, others arrived on this island during the last 10 Ma. The most frequent pattern was colonization of Madagascar in the Paleogene and recent dispersal back to the mainland during the Neogene – in line with biogeographical theory for the area. The recolonization of the mainland generated increased overall diversity and illustrates how the island function as a diversification agent in the Afrotropics.

Potential role of insect growth regulators on Stephanitis pyrioides (Hemiptera: Tingidae)

Authors: Joseph Shimat V., University of Georgia, United States

Abstract: The azalea lace bug, Stephanitis pyrioides (Scott) (Hemiptera: Tingidae), is an important insect pest of azaleas (Rhododendron L. spp.) in the USA. Stephanitis pyrioides feeds on azalea foliage and causes extensive chlorosis, which reduces the aesthetic value and marketability of these plants. Because the use of neonicotinoid insecticides has been dramatically reduced or discontinued, growers and landscape managers are seeking alternative tools or strategies to control this insect. Although insect growth regulators (IGRs) are known for their activity against immature insect stages, their transovarial, ovicidal or nymphicidal activity has not been addressed thoroughly, specifically against S. pyrioides. Thus, a series of experiments was conducted to understand the transovarial, ovicidal or nymphicidal activity of IGRs using novaluron, azadirachtin, pyriproxyfen and buprofezin against S. pyrioides. A low number of S. pyrioides young instars was produced when adults were exposed to topical novaluron compared with non-treated adults. When adults contacted dried residues of novaluron and buprofezin, production of young instars was reduced relative to non-treated controls. When insects exposed to 1.0× and <1.0× doses of novaluron were compared, the number of young instars produced was similar. The number of newly emerged young instars was significantly lower when leaves implanted with eggs were sprayed on both sides with novaluron, azadirachtin and buprofezin compared to nontreated and pyriproxyfen treatments. When IGRs plus adjuvant were applied to the adaxial surface of the leaves, the densities of the newly emerged nymphs were significantly lower under the novaluron treatment compared to the nontreated leaves. However, there was no significant difference in the number of nymphs that emerged in the absence of adjuvant. Furthermore, close monitoring revealed reduced levels of egg hatching in the presence of adjuvant with novaluron compared to its absence. The data show that the survival of S. pyrioides 1st instars was not affected by exposure to dried IGR residues.

Parasitism and predation of Halyomorpha halys egg masses in woodlands, and orchard, vineyard, row, and vegetable crops in the southeastern US

Authors: Joseph Shimat V.[3], Toews Michael[3], Sial Ash[3], Blaauw Brett[3], David Buntin[3], Talamas Elijah[2], Kesheimer Katelyn[1] and Balusu Rammohan[1], [1]Auburn University, United States, [2]Florida Department of Agriculture and Consumer Service, United States, [3]University of Georgia, United States,

Abstract: Reproductive populations of Halyomorpha halys (Stål), are rapidly building in the Piedmont and expanding into Coastal Plains Regions of Georgia and Alabama. Consequently, this study was conducted to evaluate parasitism and predation of H. halys sentinel egg masses by indigenous parasitoids and predators in woodland habitats and orchard, vineyard, row, and vegetable crops alongside these habitats in the southeastern US. Laboratory-reared H. halys egg masses were hung as sentinels on plants for 48-72 h. In the laboratory, retrieved egg masses were examined for predation and held for emergence of adult parasitoids. Of the ten parasitoid species, Anastatus reduvii (Howard), Anastatus mirabilis (Walsh & Riley), Trissolcus brochymenae (Ashmead), and Trissolcus euschisti (Ashmead) were the most prevalent ones in woodland and orchard habitats. Trissolcus edessae Fouts occurred primarily in orchards. Telenomus podisi Ashmead and Ooencyrtus sp. were the predominant species in row crops. Trissolcus basalis (Wollaston) and Gyron obesum Masner were mainly present in vegetables. Trissolcus solocis Johnson and Trissolcus basalis (Wollaston) are new records for H. halys eggs. Gryllidae, Acrididae, and Tettigoniidae fed on eggs in field, and complete chewing damage characteristic of these taxa was detected on retrieved eggs. Some egg masses exhibited incomplete chewing predation characteristic of Coccinellidae, Carabidae, and Dermaptera. Anthocoridae, Geocoridae, and Pentatomidae fed on eggs in the field resulting in stylet sucking predation. Some sentinel eggs exhibited typical puncture sucking predation by Salticidae. Solenopsis invicta Buren removed eggs from egg masses in cotton and soybean. At times, percent parasitism was higher for blueberry compared to other crops except for peach and apple. Percent predation was higher in soybean and cotton than in other crops. Generally, predation was higher than parasitism, and chewing predation was the most prevalent type of predation. In conclusion, native stink bug parasitoids and predators are serving as biological control agents of H. halys in the southeastern USA.

Seasonal occurrence of Drosophila suzukii and pesticide use pattern after its invasion in small fruit crops

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Abstract: Drosophila suzukii (Diptera: Drosophilidae) is a major invasive pest of caneberries (e.g., blackberries and raspberries) and other thin-skinned small fruit crops. In recent years, it has been reported as an economically important fruit pest in many countries. In caneberries, timely detection and management of invasive insect pests like D. suzukii is important to maintain profitability and to avoid fruit export restriction. Invasions by such new pest species in commercial crop production often changes pesticide use patterns and frequency as growers try to control pest populations on their farms. In this study, we examined the seasonal population of D. suzukii and pesticide use patterns before and after D. suzukii invasion in primocane-fruiting raspberry and floricane-fruiting blackberry crop production in Pennsylvania. The result of seasonal monitoring conducted over two years showed higher populations of D. suzukii fruit flies during the period of invasion. Evaluation of crop-specific pesticide programs showed increase in the pesticide use frequency com-pared to the crop season before D. suzukii invasion in the blackberry planting. Similarly, over fivefold increase in pesticide application was recorded in the raspberry planting in the year following invasion. Implications of increased pesticide use patterns in small fruits production will be discussed and presented.

Habitat enhancement strategies for conservation and management of pollinators in tree fruit orchards

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Abstract: Different species of bees, syrphids, moths and other flower visiting insects provide pollination services and play an important role in production of several types of tree fruit crops. In recent past, decline in pollinators' populations due to multiple interactive factors including lack of floral food resources, nesting habitats, landscape diversity has led researchers to develop viable strategies to conserve their populations in different ecosystems. In multiyear studies, we examined the impact of establishing native floral resource plantings on orchard bee diversity, seasonal occurrence, and community composition in tree fruit production system. We also examined strategies to enhance nesting of tunnel nesting orchard bees and their preferences for different types of artificial nest substrates and different ways to protect them from their natural enemies. Major findings from these studies will be presented and implications of different habitat enhancement strategies for conservation and management of pollinators in tree fruits will be discussed.

The feeding process of an adult dragonfly (Odonata: Anisoptera): Functional morphology and behavioral analysis

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Abstract: Insects have developed specialized mouthparts, which show various adaptations to their respective type of feeding. Dragonflies, for example, are predators showing the carnivorous type of biting-chewing mouthparts. They catch their prey during flight and process the food item while flying or perching. To gain insights into the feeding process of adult Anax imperator LEACH, 1815, we combine results from micro-computed tomography (µCT), confocal laser scanning microscopy (CLSM), morphological movement angle measurements and synchronized high-speed videography. Living specimens of A. imperator were filmed during the feeding process to analyze the movement of every single mouthpart, as well as the concerted movement of all mouthparts. We then combined the obtained results: i) µCT-data, delivering a visualization of the 3D-geometry of each mouthpart including the muscle attachment points; ii) the CLSM-data providing information about the material composition of the cuticle of different mouthparts; iii) the morphological angles of the movements allowing for a quantitative evaluation of the movement range of each mouthpart; and finally iv) the behavioral observations allowing us to evaluate the in vivo movements of the mouthparts and to identify different aspects of feeding behavior. This approach aided in further understanding of the role of individual mouthparts in the feeding process.

Are pitfall traps measuring the tip of the iceberg?

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Abstract: With increasing pressures on food systems, and concerns over associated environmental impacts, agricultural land needs to increase yields with less inputs, notably pesticides. In the arsenal of sustainable solutions, natural enemy pest control offers a potentially efficient tool and habitats such as grass margins and beetle banks are used to boost abundance and diversity of beneficial agents such as carabid beetles. Such interventions, however, need to be demonstrated to have economic benefit in order to justify outlay and upkeep.

Carabid beetles are proven predators of many notable crop pests, and have been estimated to reduce weed seed stock by up to 90%. These estimates are based largely on laboratory diet studies and plot level sampling, often using a small set of carabid species that are commonly caught in pitfall traps on farmland. The contribution of soil dwelling carabid larvae are little studied and their contribution seldom considered. This is partly owing to the reliance on pitfall traps that selectively sample surface-active invertebrates.

In our study we addressed these limitations, working towards a more holistic view of ecosystem service delivery by carabids in agricultural landscapes. We measured the response of carabid beetles to experimental margins across a 330 hectare arable farm landscape with multiple crops, in Hertfordshire, England.

We developed novel subterranean traps, based on a design seldom used on carabid beetles. This was run against standard pitfall traps. Trapping was undertaken in crop areas; margin treatments (wildflower/ grass/control); across boundary features; and in adjacent habitats.By sampling the margin, spill-over zone, crop and adjacent habitat, we aim to elucidate the relative influences of landscape and management on carabid community composition- notably incorporating the relative distributions of adults and larvae, and relate this to service provision at the farm scale.

We quantified the difference in response to trapping techniques and trap type in the context of estimates of ecosystem service delivery by carabids. We argue for the value of considering these outcomes of different trap types when designing sampling methodology based on our experience relative to the literature.

Ecologically based IPM package for rice in Cambodia: Results from experiments and adoption study

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Abstract: Cambodia has recently experienced trade setbacks due to pesticide residues in rice. Clamor for safe food is growing in the country; however, the sharp increase in pesticide use is strikingly evident. These provide impetus for reducing reliance on pesticides through Integrated Pest Management (IPM). We present an IPM package that was tested in Cambodia from 2016-2019. We examine how the components of this package performed in the field compared with the current practice of farmers. Also, we explore outcomes in terms of changes in behavior of rice farmers indicating adoption of IPM in the sites where the package was introduced.

A core component was a set of agronomic practices that form the base for a pest-resilient rice ecosystem, termed Basic IPM (BIPM). For insect pest management, BIPM augmented with Beauveria bassiana showed the lowest number of insect pests and defoliator injury, and highest abundance of natural enemies. BIPM only (no insecticide spraying) as well as BIPM augmented with orange oil had significantly better performance for insect pest management than farmer's practice (FP) of 2-3 insecticide sprays per season. For weed management, BIPM augmented with well targeted pre- and post-emergence herbicide spraying resulted in significantly lower weed count and higher crop biomass compared with FP. Furthermore, use of a blast resistant variety showed the best performance for managing leaf blast and neck blast, which are among the top disease constraints in the country. Where use of resistant variety was not possible, biological control is an option. Use of Trichoderma harzianum resulted in significantly lower incidence of neck blast and leaf blast compared with FP. For rodent pests, use of trap barrier system shows significantly lower damage of <2.2% compared with FP (3-18%). Farmers in the experiment sites adopted varied combinations of the IPM package components. Randomly sampled farmers from four province sites in 2016 and 2019 (N=199 paired data) showed significant reduction in insecticide, herbicide and rodenticide spraying.

This IPM package for rice tested in Cambodia showed that practices enabling a pest-resilient ecosystem have better outcomes than current practices of farmers. Introducing these in communities can result in reduced pesticide reliance. Further measures to address constraints in information flow, strengthen policies for production and trade of biological control, and create cost incentives for IPM products can broaden the impacts of IPM in Cambodia.

Plodia interpunctella and Corcyra cephalonica infestation of cricket-based flour

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Abstract: The continuous population growth is raising the food demand. In this context, the interest in novel food such as insect-based products is increasing. These products could be attacked by stored product pests, including pyralid moths that are among the main pests of food industry.

The present work aims to evaluate whether cricket-based flour (CF) is susceptible to infestation by Plodia interpunctella (Hübner) (Lepidoptera: Pyralidae) and Corcyra cephalonica (Stainton) (Lepidoptera: Pyralidae).

Plodia interpunctella and C. cephalonica were reared separately on CF and on a standard diet (SD) as control. Data collected included survival and performance of emerged adults and the t-test was used to determine the statistically differences.

Results showed the ability of both species to develop on CF. Nevertheless, in both cases the number of emerged adults was significantly lower on CF, compared to SD. Diets also affected the adult dimension and determined a delay in the emergence for adults derived from larvae reared on CF. Moreover, both species showed a lower offspring produced when reared on CF.

Cricket flour has shown to be susceptible to P. interpunctella and C. cephalonica infestation, thus the protection of cricket-food products must be taken into account to avoid stored product moth damage.

The complex effects of the larval environment on Aedes aegypti as vectors

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Abstract: Conditions in the aquatic environment of larvae can have profound effects on populations of terrestrial adult insects, and on the traits of individual adults that emerge from the larval environment. For mosquitoes that are important vectors, these effects on adult numbers and traits are both inherently interesting aspects of the ecology of complex life cycles, and important influences on the ability of vector populations to transmit vector-borne pathogens. Detailed studies of the effects of the larval environment of Aedes aegypti reveal major effects of population density of larvae and of mortality due to predation on survival to adulthood, and more subtle effects of density and nonlethal threat of predation on adult traits. These density- and trait- mediated effects are integrated to affect both population rate of change and vectorial capacity of A. aegypti. We present information from field and laboratory experiments on effects of density and predation on the likelihood off overcompensatory responses (=production of more adults with, vs. without, mortality) of A. aegypti in response to mortality of larvae. We also use sensitivity analysis of a demographic model of population growth to assess the relative importance of effects on number of survivors, development time, and size-dependent fecundity for population growth. Finally, we test for nonlethal effects of threat of predation on adult traits of size, longevity, body composition, and blood feeding that are relevant to vectorial capacity. Though both density- and trait-mediated effects can occur, it appears that effects that alter the number of surviving adults have the greatest impact on both population growth and vectorial capacity. Because overcompensation can occur in A. aegypti, simply imposing mortality on larvae is no guarantee of reducing adult production, and therefore no guarantee of reducing A. aegypti populations or vectorial capacity.

Different response of cerambycid and curculionid beetles (Coleoptera) to burned-Pinus densiflora forests in South Korea

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Abstract: We investigated the changes in species richness and abundance of two major saproxylic beetles, such as cerambycid and curculionid beetles, along a fire severities gradient in burned-Pinus densiflora forests. The wildfire was occurred in May 5~6, 2017 and about 86 ha of forests were burned. We classified the study area according to fire severity classes, such as unburned, light, edge of light-moderate, edge of moderate-severe, and severe. For sampling of the beetles, the Lindgren multi-funnel traps were placed in each fire severity classes from March to October in 2018. A total of 34,529 beetles were collected and identified as 87 beetle species. Xyleborinus saxeseni (19,423 individuals) and Xylosandrus germanus (7,216 individuals) were dominant in every burned-pine forests, and they accounted about 77% of all collected beetles. Species richness of curculionid beetles in all fire severity classes were high compared to unburned area, while those of cerambycid beetles in the edge of moderate-severe and severe areas were high compared to others. Among burned areas, however, species compositions of two beetle families were slightly different according to fire severity classes. Some beetle species were selected as potential indicators on burned-Pinus densiflora forests.

Sensitivity of olive fruit fly (Bactrocera oleae (Gmelin)) to insecticides

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Abstract: To control olive fly, there are studies on the effectiveness of chemical preparations as well as environmentally friendly preparations, but susceptibility tests have not yet been conducted. Infested olive fruits were delivered to the laboratory and placed in climate chambers for cultivation. After the release of the adult forms, an experiment was conducted according to the method of Kakani et al. (2010). Insecticides based on the active ingredients dimethoate and deltamethrin were prepared at dosages of 100%, 50%, and 20%, while water served as a control. Adult flies were anesthetized with CO2 and an insecticide was applied to each individual from the dorsal side using a microapplicator. In 2018, reduced sensitivity to the active ingredient dimethoate was found in only one tested population of olive flies, which originated from the Cres locality, while 71% of the tested population showed reduced sensitivity to the active ingredient deltamethrin. In 2019, as in 2018, only one population (from site Polje) was found to have reduced sensitivity to the active ingredient dimethoate, while the other tested populations were sensitive. Only one test population was sensitive to the active ingredient deltamethrin, while the other tested populations were found to have reduced sensitivity.

Every transcriptome has virus sequences in it

Authors: Jurvansuu Jaana, Ecology and Genetics Research Unit, University of Oulu, Finland

Abstract: Viruses are the most abundant and diverse life form. Insect virology is booming due to the reduced prices of the next generation sequencing. In recent years, about 2000 new insect virus species including new virus orders have been identified. Insects are particularly suitable for virome studies as they are often so small that a whole animal can be analysed at once and so abundant that many individuals can be easily collected and processed. Furthermore, the massive amounts of existing next generation sequencing data in public databases enables directly identification of many more new viruses from multitude of insect species.

However, despite the considerable advances, the basic biology of most insect viruses is still obscure. Next generation sequencing data can provide some information about the virus biology, such as, virus prevalence, virus replication activity, virus genome evolution, and of virus-virus interactions. Yet, in combination with other methods and ecological studies we can further analyse how the viruses affect host fitness, virus seasonality, host anti-virus defenses, and how do viruses transmit among caste, colonies and different species. Examples from our work with the common glow-worm (Lampyris noctiluca), Argentine ants (Linepithema humile), and varied spider species (Arachnida) are discussed.

Aspects of developments in biological control in greenhouse botanical collections

Authors: Kaas Jan Piet, Bio Pre, Netherlands

Abstract: Pest groups and their biological in collection plantings are discussed. An overview of past, present and future of small scale planting- integrated pest management is given. Different interests of governement and non- governemet agencies in the development of new ways of pest control are mentioned.

Pre-application of Metarhizium brunneum for wireworm control in seeded and transplanted crops

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Abstract: Entomopathogenic fungi, including Metarhizium brunneum, are promising active ingredients for wireworm control in field vegetables, but often do not achieve high efficacy because their slow speed-of-kill still allows the larvae to feed on the crop for weeks after application. In a two year study, pre-plant application of attract-and-kill wireworm control products aimed to achieve an increase in yield and marketability of organic lettuce and turnip in Agassiz, British Columbia, Canada. Pre-plant application of granular products formulated with M. brunneum LRC112 conidia, and containing a CO2 attractant reduced wireworm root tuber damage in turnip by 30% compared to the untreated control in a field highly infested with Agriotes obscurus and A. lineatus, signifying the value of this application strategy.

Horizontal transmission of Metarhizium brunneum conidia between click beetle, Agriotes obscurus, pairs during mating

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Abstract: Due to the subterranean nature of the damaging wireworm larvae, recent efforts have begun to focus on targeting adult click beetles with the fungal entomopathogen, Metarhizium brunneum. In the present study, we examined the transmission of M. brunneum between mating pairs of click beetles. We exposed male or female beetles to conidiated rice granules after which the beetles were paired with an opposite sex unexposed beetle, 2, 24 and 48 hours after initial M. brunneum exposure. Behavioural observations were recorded during each pairing. The time to death of beetles exposed directly to M. brunneum conidia, or indirectly via pairing with a contaminated partner, or contact with the contaminated substrate was compared. In addition, the impact of courtship and mating behaviours on the transmission of conidia between mating pairs will be discussed.

A review of the sterile insect technique against Malaria vectors in South Africa

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Abstract: Malaria control remains a key priority in South Africa and the country has set an agenda of eliminating local transmission by 2023. The backbone of malaria control is vector control, mainly achieved through indoor residual spraying (IRS) using insecticides. Although this strategy has made significant progress in regressing the number of malaria transmitted cases over the years, low-level transmission continues in the endemic regions of north-eastern Limpopo, the Mpumalanga low-veld and far northern KwaZulu-Natal. The continued residual malaria transmission necessitated investigation of additional vector control interventions to supplement existing strategies. The use of the Sterile Insect Technique (SIT) was proposed. A multi-year plan for testing the feasibility of SIT was developed by a consortium of collaborating parties in 2010. Over the last eight years optimization of key aspects of mosquito SIT applications, including entomological baseline surveys, mating competitiveness studies, population size estimation, irradiation studies, development of sex separation systems and extensive community engagement activities have been carried out culminating in the construction of a mosquito vector mass rearing factory. This development provides a unique opportunity to proceed with the first field demonstration of SIT against African malaria vector. The purpose of this study is to review the experience and knowledge gained in developing the SIT as a complementary malaria vector control tool focusing on the challenges and current status of the project. An insight on the pending pilot sterile release male programme will be given.

Circadian timing adaptations in the intertidal insect Clunio marinus

Authors: Kaiser Tobias S, Max Planck Institute for Evolutionary Biology, Germany

Abstract: The marine midge Clunio marinus (Diptera: Chironomidae) lives in the intertidal zone of the European Atlantic coast. Its life cycle is timed to the tides by circadian and circalunar clocks. As the tides differ along the coastline, C. marinus populations show many local genetic adaptations in circadian and circalunar timing. QTL mapping indicates that these timing adaptations are controlled by few major effect loci.

In order to pinpoint the adaptive timing loci, we sequenced a C. marinus reference genome, assembled it to chromosome-scale and annotated it. Then we sequenced individuals from five populations of C. marinus, which differ in circadian and circalunar timing. Genome-wide we detected timing-associated genes based on the correlation of genetic divergence with timing differences. In one circadian QTL there was a strong evolutionary signature of local adaptation, which pointed to the Ca2+/Calmodulin-dependent protein kinase II (CaMKII) gene.

Subsequent molecular analysis substantiated that adaptation in circadian timing relies on modulating the alternative splicing of CaMKII. CaMKII phosphorylates the CLOCK protein, changing its transcriptional activity. Strains with differences in CaMKII splicing also differ in their endogenous clock period and phase. These findings entail a mechanistic model of how DNA sequence changes translate into adaptive timing phenotypes. We currently test if other population of C. marinus rely on the same mechanism for local adaptation in circadian timing or if new solutions were found in every location along the coastline.

Phylogeny, evolution of termitophily and higher classification of Aphodiinae (Coleoptera: Scarabaeidae)

Authors: Kakizoe Shotaro[1] and Maruyama Munetoshi[2], [1]Kyushu University, Fukuoka, Japan, [2]The Kyushu University Museum, Japan

Abstract: [Introduction]

The subfamily Aphodiinae (sensu lato; proposed in Scholtz and Grebennikov 2005) is composed of 6 subfamilies, 9 tribes, 387 genera, 3732 species, including Aphodiinae Leach, 1815 and its related subfamilies. Some of them are known as "dung beetles," but they occupy various niches, feeding on detritus, dung, carrion, fungi, or living plants, with several groups living with termites or ants (Scholtz and Grebennikov 2005). Therefore, this subfamily is one of the ideal taxa to study the evolution of feeding habits, termitophily, and myrmecophily. However, phylogenetic relationships within the subfamily are poorly understood. Because of the lack of molecular phylogenetic information, higher-level classifications of subfamilies and tribes have been confused among researchers. Therefore, we reconstructed the phylogenetic relationships within Aphodiinae using molecular data.

[Materials and Methods]

We reconstructed the phylogenetic trees using maximum likelihood and Bayesian inference methods for a total of 4,900 bp (4,573 bp after trimming) of 138 OTUs selected from all 6 subfamilies, 9 tribes, and outgroups of Aphodiinae (sensu lato). The following molecular markers were used as sequence information: mitochondrial COI (800 bp), 16S (1040 bp), nuclear 28S Domain 2 (620 bp), 28S Domain 3–6 (560 bp), and 18S (1880 bp). For the outgroups, 3 species were used from Scarabaeinae, which is a sister group of Aphodiinae (Ahrens, Schwarzer and Vogler 2014).

[Result/Conclusion]

Molecular phylogenetic analysis revealed that Aphodiinae (sensu lato) is a monophyletic group and termitophily evolved independently at least twice. Specifically, we suggested that termitophily evolved in the Stereomerini lineage and in the lineage consisting of Termitotroginae, Corythoderini, and Termitoderini. This study clarified that Termitotroginae is monophyletic along with Corythoderini and Termitoderini, and suggested that previous classification that treated Termitotroginae as a subfamily was an exaggeration of the specialized morphology associated with termitophily. Moreover, this result was different from the phylogenetic tree based on morphology in a previous study (Vårdal & Forshage 2010).

With the revelation of these phylogenetic relationships of the higher taxonomic groups of Aphodiinae, including the result that Euparini, Odontolochini, and Aphodiini are polyphyletic, we suggest that the current classification of the subfamily should be revised along with the abovementioned termitophilous groups.

Potential of plant essential oils to control the oilseed rape pest

Authors: Kallavus Triin, Sulg Silva, Kaasik Riina, Sakkool Mariette and Veromann Eve

Abstract: Plant essential oils (EO) contain wide range of active compounds with several biological activities. Their insecticidal activities, as some of them are repellent or toxic for insects, have potential to be used as an alternative to synthetic pesticides. We examined insecticidal efficacy of six plant EOs on the cabbage seed weevil (Ceutorhynchus obstrictus Marsham), one of the main pests of oilseed rape (Brassica napus L).

To determine the effect of EOs on direct mortality of cabbage seed weevil we treated oilseed rape leaf and flower surfaces with six different EOs, with one negative control and one positive control and assessed the mortality of weevils after 3h and 24 h.

The results of the bioassay indicated higher cabbage seed weevil mortality on surfaces treated with various concentrations of Cuminum cyminum L. and Cinnamomum verum J.Presl. EOs, suggesting their potential as complementary or alternative measure to control cabbage seed weevil populations.

The effects of changing land-use on the temporal dynamics of B. tabaci on cassava in Uganda.

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Abstract: Cassava (Manihot esculenta Crantz) is an important commercial and food security crop in many countries in Africa. However, diseases of cassava (e.g. Cassava mosaic disease, CMD, and Cassava Brown streak disease, CBSD) continue to cause significant yield losses throughout eastern and central Africa. Additionally, populations of species in the cassava whitefly Bemisia tabaci (Hemiptera: Aleyrodidae) cryptic pest complex, that vector both CMD and CBSD, have been increasing in abundance over the past 20 years. We know that insect populations are influenced by a number of factors associated with both cultivated and uncultivated habitats in the landscape surrounding a target field. In smallholder farming landscapes in Uganda, land-use patterns often change due to highly flexible crop rotation plans that are dependent on several other factors such as family, village and regional demand for food and fiber. However, we don't understand how these dynamic land-use decisions impact pest and disease risk. We investigated how a change in land-use across a season around a focal cassava field affects the population dynamics of B. tabaci. Ten sites were planted with two cassava genotypes and the change in B. tabaci abundance monitored over 12 months alongside the change in surrounding land-use. We also determined the B. tabaci species identity commonly found at these sites through sequence characterization of the partial mitochondrial DNA cytochrome oxidase subunit I (mtCOI) gene. Early results identify some of the important landscape factors that lead to high population densities in cassava. The implications of these results for developing landscape manipulation practices to help manage B. tabaci pests in smallholder farming landscapes will be discussed.

A Novel Educational Method for Prevention and Control of Vector-Borne Diseases in the Villages of Bardsir, Kerman Province, Iran

Authors: Kamali Maryam, Department of Medical Entomology and Parasitology, Tarbiat Modares University, Iran

Abstract: Education regarding vector-borne diseases using social media tools can empower rural communities to better identify vectors, and understand diseases and methods of avoiding exposure. We report the results of a quasi-experimental study examining the effectiveness of a novel method of educating individuals through social networks on local insects and ticks of medical importance (mosquitoes, sandflies, ticks, lice, bed bugs, and fleas) which was carried out in 2021, in 12 villages of Bardsir county, a rural community in Kerman Province, Iran. Questionnaires were administered at baseline and following a 4-week educational program offered through a social media app (WhatsApp) on the participants' personal cellphones. Interventions included short educational videos on the insects and ticks of medical importance, that included information on general identification, diseases transmitted by them, and disease prevention methods, distributed through a moderated social media group. Results show a statistically significant increase ($p< 0.01$) in the level of awareness regarding symptoms of diseases transmitted by insects and ticks and prevention methods for these diseases after training. Participants also found the educational material on social media useful and convenient ($P< 0.01$). Social media can be effectively used to increase the level of awareness regarding diseases transmitted by insects and ticks.

Multiple evolution of termitophily in the rove beetle subfamily Aleocharinae

Authors: Kanao Taisuke, Yamagata University, Japan

Abstract: Termitophiles, insects associate with termites during at least one stage of life cycle, are known from 12 insect orders. In termitophilous insects, a remarkably high species diversity, more than 700 termitophilous species, is found in the rove beetle subfamily Aleocharinae. Many of termitophilous rove beetles exhibit specialized body forms, such as physogastry (swollen abdomen with developed membrane area between abdominal segments) and limuloid body shape (resembling a horseshoe crab). Although the host specificity and nature of interaction between termitophiles and host termites vary substantially among termitophilous species or groups, beetles with the specialized body forms generally have species-specific relationships with their host termites and live deep within the host termite nest. Termitophilous species in Aleocharinae are currently classified into 17 tribes, of which 12 tribes are exclusively composed of termitophiles. However, phylogenetic positions of each termitophilous group are not well resolved. To clarify evolutionary history of termitophily in Aleocharinae, robust phylogenetic reconstruction is necessary.

I present the result of molecular phylogenetic analysis as well as a brief summary of taxonomic study. During field surveys in Afrotropical, Neotropical, and Oriental regions, I recognized the species diversity of termitophilous Aleocharinae was quite underestimated. Some of the new species implied polyphyly of the subtribe Termitozyrina in the tribe Lomechusini. I also performed a molecular phylogenetic analysis using six loci of 229 species including termitophilous, myrmecophilous, and free-living species. The results revealed multiple origins of termitophily and convergent evolution of the two specialized body forms of termitophilous species in Aleocharinae. Some termitophilous species were found to form monophyletic groups with myrmecophilous species, which indicates that the beetles experienced dynamic host shifts between termite and ant. Termitophilous species from a single clade were typically associated with termites from a single subfamily, but host switches to different termite subfamilies were also uncovered in several clades. The molecular phylogeny further highlighted systematic problems in Aleocharinae. In addition to the polyphyly of Termitozyrina, this analysis revealed that several termitophilous groups were reconstructed in clades of other termitophilous, myrmecophilous, or free-living groups.

Precision guided Sterile Insect Technique (pgSIT): a novel environmentally friendly technology for insect population suppression

Authors: Kandul Nikolay, UC San Diego, United States

Abstract: Sterile insect technique (SIT) is an environmentally safe and proven technology to suppress wild insect populations. In a classic SIT, sterile males are generated with radiation, sex-sorted to remove females, and released in large numbers into a wild population, where they compete with wild males for female mates. Mating with sterile males results in no progeny and consequently can be used to suppress populations; however, the low fitness of sterile males and inability to adequately sex-sort most insects has limited the application and efficacy of SIT. To overcome these limitations, we developed a novel CRISPR-mediated SIT termed “precision guided SIT” (pgSIT) system. This system is comprised of two separate homozygous lines each carrying Cas9 or double guide RNA (dgRNA). When these lines are crossed in the laboratory, they produce F1 progeny with precise knock outs of two specific genes targets, in this case, one required for female survival and the other for male fertility, resulting in emergence of 100% sterile males from genetically identical F1 eggs. pgSIT mechanistically relies on a dominant genetic technology that enables simultaneous sexing and sterilization, permitting the release of eggs into the environment. To date, we have engineered multiple pgSIT systems in the model organism, Drosophila melanogaster, the crop pest, Drosophila suzukii, and the disease vector, Aedes aegypti, which consistently produce 100% sterile males. Importantly, unlike irradiated sterile males made with a classic SIT, pgSIT generated males in these species are fit and competitive compared to wild type males. Modelling has also predicted that pgSIT will induce greater population suppression over time than can be achieved by current approaches. Taken together, pgSIT may transform our ability to control insect agricultural pests and disease vectors.

Predators’ learning about aposematic prey affects the survival of prey with hidden conspicuous anti-predator defences

Authors: Kang Changku[2], Choi Sei-Woong[1], Hwang Yerin[2] and Kim Yongsu[2], [2]Mokpo National University, South Korea, [1]Mokpo National University

Abstract: Some camouflaged insects have conspicuous hindwings hidden normally. They display them to predators transiently only when their primary defence (camouflage) fails. Such secondary defences are called deimatic displays or flash displays. The conspicuous signals used for deimatic/flash displays resemble those of aposematic signals, thus if predators already learned to avoid aposematic prey, it may benefit the prey that uses deimatic/flash displays. Here, we investigated whether predators’ learning about aposematic prey affects the survival of prey with hidden conspicuous signals. We conducted two separate experiments for deimatic and flash displays using chicks and human subjects as predators respectively. We found that educated predators were more likely to avoid the prey with hidden conspicuous signals than non-educated predators in both deimatic and flash display experiments. This helps explain the pattern we found in 466 macrolepidopteran species: the species with hidden conspicuous signals occur later in seasons than both aposematic and camouflaged species.

Adaptation to cold environments - case studies from a northern malt fly species Drosophila montana

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Abstract: Drosophila montana from D. virilis species group is one the most cold-tolerant Drosophila species. It is distributed to northern hemisphere and has adapted to live on high latitudes close to, or even above the Arctic Circle in Northern Scandinavia and Alaska. In addition, it has occupied high altitudes (above 3 000 m) on the Rocky Mountains but also warmer areas on the Western coast of North America. Flies of this species can survive up to six months of subzero temperatures in the adult photoperiodic reproductive diapause. This northern fly has been investigated for several decades already, and we have learned many things from its ecology, physiology and genetics. Gene expression studies with microarrays almost a decade ago from diapausing and non-diapausing flies revealed interesting patterns and produced a list of core candidate genes. More lately, we have concentrated more on the genomic level by investigating montana’s cold adaptation across the latitudes and between the sexes. Our latest studies on chromosomal inversions and transposable elements will increase our understanding on how these crucial genomic factors are connected to adaption to variable climatic conditions.

Morphology and significance of antennal sensilla of aphids (Hemiptera, Aphididae)

Authors: Kanturski Mariusz, Faculty of Natural Sciences, University of Silesia in Katowice, Poland

Abstract: Aphids are one of the most economically important groups of bugs and insects due to their great evolutionary success, which they have achieved due to their ecological plasticity, life cycles and polymorphism. Undoubtedly, one of the equally important aspects of this success is the specific sensory organ system on their antennae – setae, rhinaria and rhinariola, which represent various types of sensilla. For several years aphids become a great number of interests in the case of molecular and genomics Research but morphological studies have been neglected. In this presentation, I present comparative scanning electron and light microscopy analyses of antennal sensilla of selected aphid species. Different types of sensilla can be found on aphids antennae, like small multiporous placoid sensilla (primary and secondary rhinaria), large multiporous placoid sensilla (primary rhinaria), sunken coleoconic sensilla (rhinariola and accessory rhinaria) and different types of trichoid sensilla (setae). Besides their morphology and ultrastructure, I will try to show their significance in taxonomy and the phylogeny of particular groups.

Phylogenetic reconstruction of Tuberolachnini and Lachninae aphids (Insecta: Hemiptera)

Authors: Kanturski Mariusz, Faculty of Natural Sciences, University of Silesia in Katowice, Poland

Abstract: Lachninae aphids (Aphididae: Lachninae) are one of the most interesting and consist of so far five tribes and Tuberolachnini seems to be especially interesting group in morphologically and biologically diverse with Pyrolachnus, considered to be rather poorly known. So far only one representative – P. imbricatus nipponicus have been known from Japan and characterized by unique features. We tested the current tribal system of Lachninae including the largest number of Pyrolachnus as well as another poorly known genus Sinolachnus based on four genes. Our phylogenetic analyses inferred that Tuberolachnini is not a monophyletic tribe by separation of Pyrolachnus imbricatus nipponicus and Sinolachnus sp. from the core Tuberolachnini (e.g. Nippolachnus, Pyrolachnus and Tuberolachnus). Detailed morphological investigations (including lignt and scanning electron microscopy) strongly supported our molecular phylogeny. We present and discuss the morphological characters of viviparous and bisexual generations of P. imbricatus nipponicus and related Tuberolachnini genera.

Dissecting overwintering mechanism of Asian tiger mosquito, Aedes albopictus

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Abstract: Aedes albopictus (Ae. albopictus) is one of Aedes mosquito species and also known as Asian tiger mosquito. Ae. albopictus is originally a native species to Southeast Asia. This mosquito species, however, is rapidly expanding its distribution throughout the world and now selected as one of species of the 100 of the World's Worst Invasive Alien Species by International Union for Conservation of Nature and Natural Resources (IUCN). The spread of Ae. albopictus is emerging problem because Ae. albopictus mosquitoes are effective vectors of severe human diseases such as Dengue, Chikungunya, and Zika fever. Therefore, the vector control of this invasive species is currently needed to develop.

The reason why Ae. albopictus could be established in temperate to subarctic zones is that eggs of Ae. albopictus are able to survive in a diapause state during winter. In tropic zone, Ae. albopictus repeats their life cycle throughout the year. On the other hand, in temperate zone, such as Japan, when adult females of this species are exposed to short daylength and low temperature in late autumn, they lay diapause eggs. In diapause eggs, development is paused in the stage of pharate first instar larva. The arrest of hatching behavior is maintained until early summer and the pharate larvae show strong resistance to coldness, drying, and starvation. Interestingly, only temperate strain can form diapause eggs but tropic strain never forms them even if females are reared under the late autumn condition.

To reveal the genetic mechanisms of preparation and maintenance of diapause in Ae. albopictus, we focused on two strains, tropic strain and temperate strain. We confirmed that Kuala Lumpur strain and Hiroshima strain shows the difference in hatching rate when adult females were reared under the short daylength and low temperature. And furthermore, we compared temporal and comprehensive gene expression between eggs from tropic strain and diapause eggs from temperate strain using RNA-seq to identify genes involved in diapause mechanism. Our results showed several candidate genes involved in environmental resistance and maintenance of diapause state. Then, we produced deletion mutants in Ae. albopictus using CRISPR/Cas9 system to estimate the function of these genes. Here, we would like to discuss about the molecular basis that enables Ae. albopictus to overwinter, along with ongoing experimental results.

Spatio-temporal distribution of Cydia pomonella L. (Lepidoptera: Tortricidae) populations in local and regional scale

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Abstract: Detailed information about pest population trends in spatial and temporal dimensions is essential for integrated management programs. In this study the spatio-temporal distribution of codling moth, Cydia pomonella L. (Lepidoptera: Tortricidae) was investigated by integrating spatial analysis by distance indices (SADIE) and geographic information system (GIS). Also, the correlation of population oscillations with elevation, weather condition, and chemical treatments was evaluated. This study was conducted during three growing seasons, 2017, 2018, and 2019 in an agricultural landscape (258 km2) located in Ahar County, East Azarbaijan Province of Iran. The activity of codling moth adult males was monitored using delta-shaped traps baited with sex pheromone of the insect (PH-227-1RR, Russell IPM, UK) in two spatial scales. So that 45 traps were placed within a 12 ha orchard, set between 50-200 m apart, and 30 traps over the entire study area set between 500-7000 m apart. Results of spatial analysis indicated that there was an aggregated spatial distribution for adult males both in local and regional scales. Also, the association index of SADIE and the maps generated confirmed the stability of this aggregation pattern during the growing season. Negative significant correlation was observed between the codling moth population and the number of frost days. The number of chemical treatments in a year was negatively correlated with codling moth population fluctuations too. But there was no significant correlation between pest populations and elevation. These findings can be used for spatial and temporal forecasting and management of codling moth in local and regional scales.

Interspecific competition among three fruit fly species infesting watermelon and zucchini (Cucurbitaceae)

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Abstract: Interspecific competition occur among arthropod pest species that share hosts, thereby, influencing their population dynamics. In sub-Saharan Africa, the native fruit fly species Dacus vertebratus (Bezzi) and Dacus ciliatus (Loew) (Diptera: Tephritidae) and the exotic Zeugodacus cucurbitae (Coquillett), are concurrent pests in the same host fruits, hence competition among them is likely to occur. We explored interspecific competition among these three fruit fly species on zucchini (Cucurbita pepo L.) and watermelon (Citrullus lanatus Thunb) (Cucurbitaceae) to improve our understanding of the interaction between the species and their capacity to coexist. We exposed the vegetable fruits to different densities of fruit fly species and studied their behavioural activities, evaluating the extrinsic competition. To assess intrinsic competition and understand the effect of co-occurrence inside the fruits, eggs of the three fruit flies were pairwise inoculated into the same fruits. Results showed that the behaviour on the fruits differed between the species, and that the interspecific competition affected their developmental time and larval survival in both watermelon and zucchini. Zeugodacus cucurbitae were more aggressive than the other species and managed to oviposit more frequent. Emergence was reduced for D. ciliatus and D. vertebratus when inoculated together with Z. cucurbitae in watermelon but not in zucchini. Physical confrontations were more common in zucchini than in watermelon and were more frequently won by Z. cucurbitae than D. vertebratus and D. ciliatus. Interspecific competition information obtained about behavioural differences and interaction effects, providing background for explaining the present fruit fly guild on certain Cucurbitaceae fruits in West Africa.

Estimation of mutation role rate of nutritional genes in Blattabacterium endosymbionts of Periplaneta americana

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Abstract: Cockroaches are associated with Blattabacterium, an intracellular endosymbiotic bacterium that has been transmitted from mother to offspring for >235 Million years. The large population and low nutrient environment has lead to constant gene acquisition with loss and recombination from free living state. This process has led organisms to transition from a short history with host to a long history, such as Blattabacterium. The genomes of Blattabacterium strains sequenced to date vary between 590kbp to 640 kbp. In this study, we sequenced 8 Blattabacterium genomes from Periplaneta americana specimens maintained in colonies in four universities over the last 20 years. Because the origin and the timing of separation among samples is known, we were able to measure the mutation rate in Blattabacterium symbiont. Altogether, we detected several mutations that occurred over an evolutionary period of 20 years. This mutation rate is lower than that estimated for Buchnera, the endosymbionts of aphids. Our results therefore suggest that Blattabacterium evolve slowly in comparison with other endosymbionts.

Species Composotion of Phlebotomines (Diptera: Psychodidae: Phlebotominae) as Vectors of Disease Agents in South Western Iran

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Abstract: Introduction and Objectives: Sandflies are the main vectors of Leishmania) a neglected tropical pathogen), Bartonella bacilliformis, and some arboviruses. Cutaneous Leishmaniasis (CL) is one of the most prevalent types of leishmaniasis in Iran. The objective of this study was to determine the faunistic, sex ratio, seasonal activity, physiological status and relative abundance of sandflies as vectors of Leishmaniasis in Iran.

Materials and Methods: This descriptive cross- sectional study was carried out in Abadan county, Khuzestan province, during 2015-2016. Totally 10 villages and 1 city were selected in order to Phlebotomine sandflies collection. Sandflies were captured by using the sticky paper traps. Traps were installed before sunset in internal and external places and were collected the next day before sunrise. Females were considered to determine abdominal condition and recorded as unfed, blood-fed, semi-gravid and gravid. Sandflies were mounted on a slide containing a drop of puri's mediumand and were identified using the diagnostic keys of sandflies.

Results: During this study, 6173 phlebotomine sandflies were caught and identified. A collection including 13 species (2 species of Phlebotomus and 11 species of Sergentomyia) was identified as the sand fly fauna in the County. Species of P. papatasi (45.64%), P.alexandri (31.31%) and S. sintoni (15.9%) were in the first to third order in terms of relative abundance. Four species, including S.tiberiadis, S. clydei, S.antennata and S. christophersi are reported for the first time in Abadan.The sex ratio of the sandflies of genus Phlebotomus and Sergentomyia were 362.4 and 92.2 males per 100 females, respectively. The sex ratio of Phlebotomine species was 249.1. The analysis of physiological status of sandflies in outdoors and indoors revealed 61.2% and 71.1% unfed, 2.9% and 4.8% blood-fed, 26.7% and 17.7% semi-gravid, 9.2% and 6.4% gravid, respectively. The population size of sandflies was diverse, as it showed two activity peaks, one in July and the other in September.

Conclusions: Phlebotomus papatasi and P. alexandri respectively play the role of primary and secondary vectors of CL in Khuzestan Province, due to their high abundance, attendance in whole the monthly activities and attendance in whole regions affected with CL. Knowledge about peak activity times and faunistic of sandflies, can be useful in developing strategies and planning programs to control the sandflies and CL.

The Present Status of Cutaneous Leishmaniasis in a Focus in South-West of Iran

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Abstract: Introduction and Objectives: Cutaneous Leishmaniasis (CL) is caused by protozoa of the genus Leishmania and can be transmitted by sand fly bites. It is an important health problem in many parts of Iran as well in Dasht-e-Azadegan County, Khuzestan Province. To identify the epidemiologic status of CL with emphasis on trend of its incidence rate in Dasht-e-Azadegan County.

Materials and Methods: This investigation was a descriptive and analytical study. A total of 1093 cases were considered for the study who were reffered to the health centre during the duration of four years (2014-2017). Giemsa staining was used for preparing the expanded smear. Epidemiologic characteristics and clinical information of CL cases were collected by the means of a checklist and analysed by means of chi-square and t-tests. The p-values <0.05 were considered as statistically significant.

Results: Most cases were in the age group of below 10 years. Highest disease frequency was observed in students (30.1%). The majority (57.8%) had one lesion. The hand was most commonly involved (38.9%). About 73.8% of patients used topical injection along with cryotherapy for treatment. In over half of the cases (92.4%), the wound size was less than or equal to one centimetre. There was a significant difference between the residential areas, age groups, genders, occupation, month of reporting, lesion sites on the body and number of ulcers with the prevalence of active lesions.

Conclusion: Cutaneous leishmaniasis is considered as an important health problem in this county. So it is necessary to take certain measures for controlling the disease and reducing its incidence.

Descriptive- Analytical Evaluation of Scorpion Sting Incidence in Masjed-Soleyman County, Southwestern Iran

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Abstract: Introduction and Objectives: Scorpions are dangerous for humans due to having deadly and toxic sting. Scorpion sting is a major public health challenge in many countries. The south and southwest of Iran with about 95% species of scorpions are the most heavily occupied regions in the country. Khuzestan Province is highlighted for its scorpions and scorpionism amongst the provinces of Iran. Khuzestan with 19 species of scorpions is one of the most important regions in terms of scorpionism problem in the southwestern Iran. Therefore, this study was conducted with the aim of survey epidemiology of scorpion sting in Masjed-Soleyman County from 2015 till 2017.

Materials and Methods: This research is a descriptive - analytical study. All the scorpionism cases who were referred to the 22-Bahman Hospital of Masjed-Soleyman during the study period were included in this research. The required information was extracted from the patients' recorded data in the hospital. Information for each case were recorded in a special checklist and imported into the computer for statistical analysis. Epidemiologic and demographic data were analyzed using the software SPSS-20. Descriptive statistics, including frequency and percentage were used for data analysis. The Chi square test (X2) and the T test were used to compare variables. P- values of 0.05 or less were considered statistically significant.

Results: Out of 11685 cases of scorpionism, 5894 cases were women (50.5 %) and 5791 cases were men (49.5%). Most cases (25% and 24.3%) were in the age groups between 10- 24 and 25-34 years old, respectively ($P<0.01$). Scorpion sting cases took place throughout the year, however the highest frequency happened in May (1637, 14%) ($P<0.05$). Moreover, results showed that the highest rate of scorpion stings cases occurred in summer (36.5%) followed by spring (35.4%) ($P<0.05$). The place of residence was rural district in 3551 (30.3%) patients and the urban in 8134 (69.7%) ($P<0.05$). Among 11685 cases of scorpion sting, 4538 (38.8%) were found on hand, and 3956 (33.8%) on leg. About 31.3% of scorpion cases did not receive any the antiscorpion venom vaccine. The rest of the stung patients received the antiscorpion venom vaccine within 6 hours after the sting. No cases were exposed to multiple stings. Nocturnal and diurnal stings accounted for 78.2% and 21.8% of stings, respectively ($P<0.05$). All scorpion sting cases have gotten better throughout the study and one death (a five- year- old girl, stinged by Androctonus cradssicauda from the leg in 2015) have been reported.

Conclusions: Scorpionism information are able to guide responsible persons to reduce the cases of scorpion sting. Considering that the highest percentage of scorpion stings have been reported in urban regions accordingly, training prevention methods of scorpion sting to urban people and also development and improving human dwellings can greatly reduce the scorpion sting.

Does the little mean a lot? Bacterial endosymbiotic microbiome of aphids of the genus Dysaphis Börner, 1931

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Abstract: Ant-aphid mutualism is a phenomenon widely researched for more than a century, being the subject of interest mostly of ecologists but also aphidologists, myrmecologists and researchers dealing with pest management. The primary symbiont of most aphids is a bacterium Buchnera aphidicola, belonging to a subdivision of the Proteobacteria. In addition to the primary symbiont some aphids also harbor other prokaryotic intercellular symbionts – secondary or facultative symbionts. It is proven that endosymbiotic bacteria may protect aphids against a fungal pathogen or make aphids resistant to parasitism. The aim of our research was to analyze the symbiotic composition in aphids of the genus Dysaphis, together with ecological analysis for aphids from primary and secondary hosts and the degree of relationship with ants (Lasius niger); colonies regularly visited by ants and without ants were examined. For this purpose we investigated a few Dysaphis species feeding on Sorbus, Malus, Crataegus, Pastinaca, Heracleum, Valeriana and Ranunculus using the NGS (Next-Generation Sequencing) method and discovered symbiotic bacterias including groups of primary (Buchnera aphidicola) and secondary symbionts (Serratia, Pelomonas, Wolbachia, Regiella and others.).

This work was supported by the PRELUDIUM grant number 2018/29/N/NZ8/00360 from the National Science Center, Poland to Natalia Kaszyca-Taszakowska.

Effectiveness of a novel window screening technology for malaria control in insecticide resistant areas of north-eastern Tanzania: Study design for a two-armed cluster randomized trial

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Abstract: In a growing scenario of insecticide resistance, the demand for a sustainable insecticide free malaria control tool is higher than ever. We have been working on a novel strategy focusing on blocking mosquito-host contact to reduce malaria by using a state of the art screened (3D screens) window double screen traps (WDST) developed in Finland. In Phase I laboratory studies, one 3D prototype captured 92% of the mosquitoes in a double screen setup. Phase II semi-field trials in Muheza, Tanzania (2017) found that 3D-WDST were quite effective in capturing (up to 80%) mosquitoes compared to the ones collected in the control setup. In the next step of evaluation (Phase III), we set up two-armed trial in Muheza that will compare houses with 3D-WDST (Treatment) combined with insecticide treated nets (ITNs) and against houses with ITNs only (control).

Phase III evaluation initiated with a baseline cross sectional (CS) study in June 2019. Twenty settlements were selected initially based on household (HH) density and accessibility and were subjected to malaria screening, mosquito density and insecticide resistance (IR) assessment. Based on the entomological, epidemiological and IR profile, 14 clusters with higher malaria prevalence and IR were selected for the study and randomized into control (7 clusters; 458 household) and treatment arms (7 clusters; 443 HH). Both arms were observed for 52 weeks (until May 2021) in which epidemiological and entomological data collection were conducted (every 10 weeks). Sociological studies for community feedback is in progress with dissemination plans in July 2022.

Gustatory polymorphism drives adaptive shifts in food and mating preferences

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Abstract: Shifts in food or host preferences in insects, accompanied by changes in the peripheral gustatory system, offer some of the best examples of adaptive behavioral evolution. A remarkable example is the German cockroach, a major indoor pest with a highly diverse omnivorous diet. Strong and persistent selection pressure with toxic baits has induced rapid evolution of behavioral resistance in multiple cockroach populations. While typical cockroaches detect and accept the sugar glucose as a feeding-stimulant via information processing by peripheral gustatory receptor neurons (GRNs) in the mouthparts, behaviorally resistant cockroaches avoid eating glucose-containing toxic baits by processing glucose as a bitter tastant via different GRNs which particularly respond to various deterrents. This glucose-averse (GA) trait is heritable, and controlled by a single major gene that follows Mendelian inheritance patterns. Neuroanatomical observations of GRN projections from the mouthparts to the central nervous system showed no differences in GRN projection between wild-type (WT) and GA cockroaches. The results indicate that qualitative changes of the ligand binding sites on bitter-GRNs contribute to glucose-aversion. Importantly, because GA cockroaches consume less glucose-containing diet, this trait is maladaptive in bait-free environments, as GA cockroaches must seek glucose-free foods. However, under human-imposed lethal environments, the trait protects individuals that bear the mutation(s).

Additionally, we found that the GA trait drives other behavioral polymorphisms in German cockroach populations, even in bait-free natural environments. During courtship, the female mounts the male and evaluates his quality by tasting a nuptial secretion that he offers on his tergum; the secretion contains glucose-related sugars, which stimulate the female's sugar sensitive-GRNs (sweet taste).This nuptial gift evolved under sexual selection to lure the female and position her for copulation. WT and GA males do not preferentially court WT or GA females. WT females accept both WT and GA males. On the other hand, GA females tend to accept GA males more than WT males after tasting the nuptial secretion. The differential mating success observed in this study suggests that WT and GA males have evolved nuptial secretion components that suit the gustatory preferences of the respective females in their population. Our model is that as WT males increase the amount of glucose-related sugars in their nuptial secretion in response to WT female preferences, nuptial feeding by GA females on the nuptial secretion of WT males is interrupted by the taste of glucose. Thus, the reversed modal specificity of glucose causes GA females to sense the nuptial gift components as deterrents, impeding the completion of the courtship sequence. Consequently, WT and GA cockroaches show assortative mating that would impact population dynamics and the frequency of the GA trait.

Evolution of morphological diversity in ant mandibles

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Abstract: Along with the radiation of species, ant mandibles diversified to perform a broad repertoire of functions carried out by even more variable forms. Some evolved to fulfill specific tasks, while all are used to forage and manipulate nest and colony. Shapes range from short and stout to long and curved with many states in between. However, it is unclear whether the array of forms is the result of random diversification patterns or whether they are tied to predictor variables. Here, I show how diet relates to shape diversity and whether more diverse ant lineages also have a broader range of mandible shapes. I quantify mandible shape with geometric morphometric methods based on 3D micro-CT segmentations of 200 genera considering different worker polymorphisms. Initial results suggest that variations of the standard "triangular mandible" are prevalent in most ant lifestyles, found in all subfamilies. However, specialized predatorial, elongated mandibles arose in most lineages. Only rarely, shapes are restricted to certain lineages and even in species-poor clades, extreme shapes occur. In the future, I aim to investigate whether evolutionary patterns in mandible shape are also reflected by the mandible musculature and how mandible performance, head and mandible shape relate to each other.

Increasing surveillance of invasive species at Hawaii's ports of entry through inter-agency collaboration

Authors: Kaufman Leyla, Hawaii Invasive Species Council (HISC) Pacific Cooperative Studies Unit (PCSU), University of Hawaii, United States

Abstract: This presentation will describe the Mamalu Poepoe program, a five-year pilot program funded by the Department of Transportation (DOT) to increase surveillance of priority target species at six main Hawaii airports. The program brings together different state agencies with related goals surrounding the protection of airport infrastructure and users and the presence of invasive species, including the Hawaii Department of Transportation (HDOT), Hawaii Department of Agriculture (HDOA), Hawaii Department of Health (HDOH), the University of Hawaii (UH) and the Department of Land and Natural Resources (DLNR). Monitoring targets under this program include mosquitoes (in the genera Aedes, Culex and Anopheles), invasive ants (including the little fire ant, Wasmannia auropunctata, and the red imported fire ant, Solenopsis invicta) the Coconut Rhinoceros Beetle (CRB, Oryctes rhinoceros), and Africanized honeybees (Apis mellifera scutellata). The program aims to foster coordination and communication among the partner agencies, improve the State's capability to prevent invasive species introductions through systematic monitoring efforts, and increase the security of Hawaii's people, natural resources, food supply and economy.

While monitoring efforts for the above species existed prior to the implementation of Mamalu Poepoe, the program enhances those monitoring efforts through research, additional capacity, and strategic guidance. The program funds multiple research groups at UH. There are several studies testing efficacy of various mosquito traps across different trapping parameters, as well as an economic analysis. This presentation will provide information about the current program progress, future efforts, and how this program fits in the overall biosecurity program.

Probabilistic risk assessment, generalist natural enemies and realized risk

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Abstract: Typically, arthropod biological control employs relatively specialized natural enemies, to avoid potential non-target impacts in release environments. There is interest in the using more generalist species in certain circumstances, and there may be ways to use them that reduce non-target risks, yet provide effective suppression of certain pests. This paper will briefly review probabilistic risk assessment (PRA) relevant to biological control agents and consider ways that the approach can be used to reduce potential negative environmental impacts of generalists. We have analyzed historic natural history and retrospective non-target impacts studies and show that probabilistic methods have the potential to provide accurate predictions of likely non-target impacts. Actual impacts, or realized prey or host ranges of natural enemies outside of quarantine environments can be very different to what may be observed under highly artificial conditions. Many generalist natural enemies used under very controlled circumstances such as greenhouses may be maladapted to persisting outside those environments. PRA provides an option for forecasting outcomes of such applications. Also, relative generalists may be specialized in a new environment, depending on regional and local species pools. Adopting PRA could increase the number of natural enemies considered for release despite being oligophagous and typically considered inappropriate options.

Urban Landscapes in Paradise: Identifying and Managing Pests in Hawaii's Urban Landscapes

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Abstract: The Hawaiian Island's are one of the world's most popular vacation destinations with approximately 7 million visitors a year. Along with the many visitors to Hawaii the state has a permanent population of around 1.2 million. One of the most significant features that make Hawaii such a popular travel destination and place to live is the aesthetic beauty of the natural and urban landscape. In addition to people, many insects find Hawaii a desirable destination to live and raise their young. Hawaii is the most isolated landmass in the world, yet is considered the invasive species capital of the world. It is estimated that to eradicate current invasive species and to understand the risks, it would cost approximately 50 million dollars a year. Currently, funding to battle invasive species is only 10-15% ($4 million dollars) of needed levels with an additional 6% being contributed by federal sources. Considering the elevated costs, particularly in the depressed economy, there needs to be a concerted effort dedicated to securing funding sources to enable proper urban landscape management. This funding is needed to combat the onslaught of new urban landscape pests, as well as concentrating on identifying, management and prevention. In order to address the overall issue of urban landscape pests, this presentation provides methodologies in understanding the barriers and opportunities for identifying and then managing the current and future establishment of invasive pets to protect Hawaii's urban landscapes.

Looking for the invisible? A meta-analysis and critical review of remote sensing approaches to timely detect bark beetle infestations

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Abstract: Despite rapid technical advances in remote sensing and the urgent demand due to increasing outbreak intensities over recent decades, an approach that can reliably detect bark beetle infestations in time for its sanitation is still missing. Do we long for the unattainable – or will promises soon to be met? We employed an in-depth review and meta-analysis on recent advances, challenges and limitations for remotely-sensed early (or so-called ´green-attack´) infestation detection regarding the European spruce bark beetle – Norway spruce system. We screened and analyzed recent research (2000-2021) on satellite-, airborne-, UAV- and terrestrial-based sensor systems. Among all studies (n=21), satellite imagery and multispectral data were most frequently investigated. Major methodological drawbacks include small sample size, low observation frequency and missing ground-truth verification of bark beetle infestation status. Accuracy metrics revealed an insufficient reliability for the timely detection of infested trees, i.e. user accuracy <80% in all studies. Most promising spectral bands for early detection were within the short wave infrared spectrum – however, the variability of ´promising´ spectral ranges or indices was also high among the studies. Cloud cover analyses we examined across Europe suggest further limitations for the operational use of satellite imagery for supporting a timely infestation detection.

Repellency as an ultimate countermeasure for Aedes mosquito control

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Abstract: N, N-Diethyl-m-toluamide (Deet) and Icaridin are representative mosquito repellents used for human protection from mosquito biting. Almost 100 % protection lasts at least several hours by direct treatment of the repellents on human skin. Pyrethroids are the predominant insecticides used for malaria and dengue vector control and have been the only class of insecticides used for LLINs. Pyrethroids have unique modes of action such as fast knockdown, excito-repellency, spatial-repellency, and disruption of blood feeding motivation. Space spray, fumigation, residual treatment on the wall, impregnation into plastic materials and fabrics, etc. are major delivering measures for pyrethroids.

Use of the repellency of mosquito repellents and pyrethroids might be biorational, since such repellency will not induce the development of any physiological resistance since they do not kill the affected insects or reduce the chance of contact to the insecticides and causes low selection pressure on insect populations. However, little is known about the modes of action, sensing organs, and the relationship between insecticide resistance and repellency.

The aim of this study is to investigate the difference in the repellency of Deet, Icaridin, Permethrin, and Metofluthrin against Aedes aegypti and Ae. albopictus by using the attractive blood feeding apparatus. Relationship between pyrethroid resistance and repellency is also discussed.

Eight simple actions that individuals can take to save insects from global declines

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Abstract: Insects constitute the majority of known animal species and are ubiquitous across terrestrial ecosystems, playing key ecological roles. As prey, they are critical to the survival of countless other species, including the majority of bats, birds, and freshwater fishes. As herbivores, predators, and parasites, they are major determinants of innumerable plants and animals. The majority of flowering plants, the dominant component of most terrestrial ecosystems, depend on insects for pollination and hence reproduction. As consumers of waste products, insects are essential to the recycling of nutrients. Humans and their agriculture rely heavily on such "ecosystem services" provided by insects. Even as insects gain recognition as essential members of ecosystems, a concern has arisen that their diversity and abundance may be in global decline. There is every reason to suspect that such forces, combined with human population growth and urbanization, are leading to declines among insects and many other organisms. To help individuals broaden participation in the conservation of insects and to promote the adoption of behaviors and habits expected to mitigate insect declines, we propose eight simple actions, most with immediate impact, that many people can undertake on their own, regardless of background, occupation, or geographic location.

Phylogenomics and the evolutionary timing and pattern of butterflies and moths

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Abstract: Lepidoptera are one of the major super-radiations of insects, comprising nearly 160,000 described extant species. They have been central to the development of coevolutionary hypotheses, such as butterflies with flowering plants and moths' evolutionary arms race with echolocating bats, but these hypotheses have not been rigorously tested. We inferred a comprehensive phylogeny of Lepidoptera, using the largest dataset assembled for the order (2,098 genes from transcriptomes of 186 species, representing nearly all superfamilies), and dated it with carefully evaluated fossils. The oldest members of the Lepidoptera crown group appeared in the Late Carboniferous (-300 Ma) and fed on nonvascular land plants. Lepidoptera evolved the tube-like proboscis in the Middle Triassic (-241 Ma), which allowed them to acquire nectar from flowering plants. This morphological innovation, along with other traits, likely promoted the extraordinary diversification of superfamily-level lepidopteran crown groups. The ancestor of butterflies was likely nocturnal, and our results indicate that butterflies became day-flying in the Late Cretaceous (-98 Ma). Moth hearing organs arose multiple times before the bat-moth evolutionary arms race, perhaps initially detecting a wide range of sound frequencies before being co-opted to specifically detect bat sonar. Our talk may also include new, unpublished data and results.

The impact of temperature stress on the octopaminergic system of honeybee flight muscles

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Abstract: Once environmental conditions change drastically, species must decide whether they relocate to new habitats or adapt. The latter requires physiological plasticity. The Western honeybee (Apis mellifera) represents a eusocial insect species that is able to adapt to changing conditions. Their thermoregulatory capabilities allow them to withstand extreme conditions and contribute to their almost worldwide distribution. In this context, the workerbee flight muscles are of special importance. These organs are primarily used during foraging flights. Flight muscles are of central importance for thermoregulation, as their activity enables both cooling and warming. The latter is realized by muscle shivering (thermogenesis) and is important for winter survival, breeding and defense.

We showed that workerbee thermogenesis relies on octopamine signaling. This monoamine activates β octopamine receptors and the subsequent intracellular cascade boosts glycolysis in the flight muscles. Now that we understand this molecular mechanism, we further investigate the flexibility of this system. Here, we will analyze certain aspects while applying short and long term temperature stress. Both phenomena occur naturally, but extreme weather events are expected to increase substantially due to global anthropogenic impact. First results indicate functionality of the flight muscles is maintained under these conditions and any breakdown could have dramatic consequences.

Trehalose metabolism during parasitoid infection in Drosophila.

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Abstract: Trehalose is a nonreducing disaccharide that is present in many organisms. In insects, it usually occurs in much higher concentration than glucose. Trehalose can be rapidly cleaved to two glucose molecules by the trehalase enzyme. In Drosophila, two versions of trehalase exist, cytoplasmic and secreted. The secreted version is used to maintain circulating glucose at a stable level and appears to be part of systemic regulation of carbohydrate metabolism. Nevertheless, the physiological role of trehalose during the immune response after parasitoid infection remains largely unclear. Gene expression analysis shows that hemocytes increase expression of both trehalose transporter and cytoplasmic trehalase. Knocking down trehalose transporter and trehalase enzyme, specifically in hemocytes, significantly decreases number of lamellocytes. We also observed that hemocytes prefer trehalose as an energy source during infection. Experiments with 13C-labeled trehalose and glucose show that hemocytes, during parasitoid infection, increase the uptake of trehalose, which is partially metabolized by glycolysis but mainly by the pentose phosphate pathway. Overall, the metabolism of trehalose after activation of immune cells ensures balance and sufficient energy supply, which is important during immune activation and makes the immune system privileged within organism.

High throughput data acquisition and deep learning for insect ecoinformatics

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Abstract: Insect ecoinformatics is scientifically important and highly applicable, as insects are abundant, speciose, and involved in many ecosystem functions. Yet, insect databases are mostly focused on a small number of pest species, as data acquisition is labor-intensive and requires taxonomical expertise. We describe a high throughput cost-effective approach for monitoring flying insects as an enabling step toward "big data" entomology. We combine "high tech" deep learning with "low tech" sticky traps that sample flying insects. As a proof of concept, we considered three insect invaders of Israel's forests: two hemipteran pests of eucalypts and a parasitoid wasp that attacks one of them. Our deep learning software identifies the three species in images of sticky traps from Eucalyptus forests. This task is difficult as the insects are small and stick to the traps in random poses. The deep learning model discriminated the three focal organisms from one another, and from irrelevant objects (e.g., other insects), with high precision. We used the model to compare the abundances of these species among six sites and validated the results by manual counting. We aim at building an ecoinformatics repository for trap images and generating data-driven models of the populations' dynamics and morphological traits.

Pollinator behavior drives sexual specializations in the hermaphrodite flowers of a heterodichogamous tree

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Abstract: Dioecy, the specialization of individuals into either male-only or female-only sexual function, has multiple evolutionary origins in plants. One proposed ancestral mating system is heterodichogamy, two morphs of cross-fertilizing hermaphrodite flowers that differ in their timing of flowering. Previous research suggested that small specializations in these morphs' functional genders could facilitate their evolution into separate sexes. We tested the possible role of pollinators in driving such specializations. Ziziphus spina-christi is an insect-pollinated heterodichogamous tree with self-incompatible flowers and two sympatric flowering morphs. We compared the flower development patterns, floral food rewards, pollinator visits and fruit production between the two morphs. Male-phase flowers of Z. spina-christi's "Early" and "Late" morphs open before dawn and around noon, respectively, and transition into female-phase 7-8 hours later. Flowers of both morphs contain similar nectar and pollen rewards, and receive visits by flies (their ancestral pollinators) at similar rates, mostly during the morning. Consequently, the Early morph functions largely as pollen donor. The Late morph, functioning as female in the morning, produces more fruit. We developed an evolutionary probabilistic model, inspired by Z. spina-christi's reproductive system, to test whether pollinator visit patterns could potentially play a role in an evolutionary transition from heterodichogamy towards dioecy. The model predicts that reproductive incompatibility within flowering morphs promotes their evolution into different sexes. Furthermore, the pollinators' morning activity drives the Early and Late morphs' specialization into male and female functions, respectively. Thus, while not required for transitioning from heterodichogamy to dioecy, pollinator-mediated selection is expected to influence which sexual specialization evolves in each of the flowering morphs.

Trait change in different insect species from urban and rural habitats, tracked through museum vouchers from the last 100 years.

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Abstract: Increasing human environmental impact leads to rapid transitions from near natural to novel ecosystems. This results in the disappearance of many native species and the invasion of non-native species in such transformed ecosystems. However, some species persist throughout environmental transitions. Mostly it is unclear which adaptations enable these species to persist, whilst others disappear. Furthermore, we usually do not know if these species persist unchanged or adapt to the new conditions. Due to the comparatively long timeframe, during which these transitions occur, direct observations of potential ecological adaptations, such as behavioral and physiological changes, are not possible. However, some insights can be gained from preserved museum vouchers and their morphological traits, the latter can be used as a proxy for a species' ecological and physiological modifications during the transition of an ecosystem. These historical datasets might be completed with recent samples to cover the entire spatio-temporal gradients across environmental transitions. In our study, we investigated morphological trait change in two ground beetle species, one moth and one bumblebee in the Berlin (urban) / Brandenburg (rural) region of north-eastern Germany, collected over 125 years in different habitats, differently influenced by humans.

Classical biological control of Spodoptera frugiperda in Africa and Asia using parasitoids from the Americas

Authors: Kenis Marc, CABI Delemont, Switzerland

Abstract: Since its recent arrival in Africa and Asia, the fall armyworm, Spodoptera frugiperda, has become a major pest of maize and other cereals throughout the two continents, threatening the livelihood of millions of smallholder farmers. So far, emergency responses have consisted mainly in the use of chemical insecticides and more sustainable management methods, such as biological control, are urgently needed. Spodoptera frugiperda could potentially be controlled in Africa and Asia by the introduction of a natural enemy from its area of origin, the Americas, a method named classical biological control. However, in contrast to many other invasive pests, S. frugiperda is also a pest in its area of origin, suggesting that natural enemies alone may not be able to control it. Nevertheless, even a partial control leading to a reduction of yield losses and pesticide use would have, at continental scale, a tremendous effect on food security, health and the economy. The main criteria for the selection of American natural enemies are their efficiency as control agent and their specificity for the target pest. All known predators of S. frugiperda in the Americas are highly polyphagous. Egg parasitism is usually low and the main egg parasitoid, Telenomus remus, is already present in Africa. In contrast, some larval parasitoids could be considered for introduction. In the Americas, larvae are attacked by a large complex of parasitoids and, in areas with no or limited insecticide applications, parasitism rates can be high. Some of the main parasitoids, such as the ichneumonid Eiphosoma laphygmae, are known nearly exclusively from S. frugiperda whereas, for others, specific biotypes or cryptic species cannot be excluded. Some of these species are presently being studied in various quarantine laboratories. At the same time, the parasitoid complex in Africa and Asia has to be investigated to assess potential competitive interactions with introduced parasitoids.

Invasion of the giant pine scale in Australia – first steps towards its biological control

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Abstract: In its native range in Greece and Turkey, the giant pine scale (GPS) Marchalina hellenica (Hemiptera, Margarodidae) has always been considered a rather beneficial insect as it provides honey dew to support pine honey production and has rarely been observed to cause tree mortality. However, very soon after its first detection in Australia in 2014, GPS showed its pest potential by spreading rapidly and causing serious damage to a novel host; the economically important plantation tree Pinus radiata. A preliminary survey of the natural enemy complex of GPS in Greece revealed a broad spectrum of species that influence GPS populations; among the species identified, the predatory fly Neoleucopis kartliana (Diptera, Chamaemyiidae) was recorded at every GPS population studied in Northern Greece. Since N. kartliana also exhibited a predation rate that reached up to 50% in some cases, this predatory fly was quickly selected as having the most potential as a biological control agent against GPS. The first attempts to bring N. kartliana into laboratory rearing have shown that this species responds adequately to the controlled environment conditions; nevertheless, there are still many aspects of the fly's biology, ecology and host-range to be studied before N. kartliana can be introduced to control the invasive GPS in Australia.

Potential for classical biological control of Drosophila suzukii using parasitoids from Asia

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Abstract: The invasive spotted wing Drosophila, Drosophila suzukii, has become a major pest of many fruit crops worldwide. Various methods have been developed to control the pest in conventional and organic systems. However, because of the wide host range of the fly and the high number of generations per year, crops are constantly reinvaded from neighbouring habitats, which complicates management strategies. Classical biological control through the introduction of parasitoids from the native region of D. suzukii in East Asia could provide an area-wide control of the pest. Surveys were carried out in China and Japan to identify the most abundant and most specific parasitoid species in the native range of D. suzukii. These surveys and subsequent research in quarantine in Europe showed that the most abundant and most specific parasitoid is a figitid wasp, Ganaspis cf. brasiliensis. However, cross-mating experiments between populations, molecular studies and behavioural tests revealed the existence of two sibling species, both occurring sympatrically in China and Japan. In specificity tests, one of these species (G1) showed a higher level of specificity than the other (G3). However, studies also revealed that the specificity was not only related to the host species but also to the substrate in which the host larva occurred. Indeed, G1 populations successfully attacked and developed in Drosophila spp. in fresh fruits but not when larvae were offered in fruit-based diets or rotten fruits, In contrast, G3 populations attacked equally well larvae in fresh and rotten fruits and in fruit-based diets. Since, in Asia, G1 is only found in Drosophila spp. in fresh fruits and, in Europe, only D. suzukii attacks fresh, undamaged fruits, G1 should be considered for release in Europe. More generally, this study illustrates the importance of considering the occurrence of biotypes or sibling species varying in host specificity and other traits when selecting agents for classical biological control.

The associational resistance hypothesis in practice: Are mixed Buxus stands more resistant to the box tree moth Cydalima perspectalis (Lepidoptera: Crambidae) than pure stands?

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Abstract: Theory and empirical studies provide evidence of associational resistance to native pests and pathogens in mixed forests when compared pure forests, but there is a lack of data for exotic or invasive species. Based on recent reviews, tree species diversity would be more likely to facilitate alien species establishment at the regional scale (more potential host resources) but based on theoretical studies, mixed forests would reduce the development (at the local scale) and spread (landscape scale) of alien pest or pathogen populations (the “invasion paradox”).

The main idea underlying the associational resistance hypothesis in this context is that non-native pests are often introduced without their co-evolved natural enemies (natural enemy hypothesis), however, mixed forests favour a more diverse community of indigenous natural enemies and if these are generalist enough to spill over onto introduced species, they might be useful to provide a certain resistance of forests to the pests.

Within the framework of the European project on HOlistic Management of Emerging forest pests and Diseases (HOMED) the objectives of this research are to compare mixed and pure natural European box tree (Buxus sempervirens, Buxaceae) stands in terms of defoliation by the invasive box tree moth Cydalima perspectalis (Lepidoptera: Crambidae) and mortality of the pest through predation and parasitism by indigenous parasitoids and predators.

The first year of fieldwork revealed defoliation levels of close to 100% in pure and mixed stands in several locations, showcasing the severe effect of the box tree moth on natural Buxus stands. Parasitism rates and predation were generally low, making it difficult to determine differences between box tree densities. A second year of experiments in additional sites will help to clarify if there is an associational resistance of mixed box tree stands against C. perspectalis.

The Power of Peptides in Crop Protection

Authors: Kennedy Robert, Vestaron Corporation

Abstract: We describe here commercialization of the first peptide for crop protection against insects with a novel IRAC neuromuscular mode of action. We also disclose a pipeline of peptide products each with a path to two additional independent IRAC neuromuscular modes of action.

The role of native, perennial nightshades in shaping the transmission of Candidatus Liberibacter solanacearum by Bactericera cockerelli in California

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Abstract: Psyllid-transmitted bacteria in the genus ‘Candidatus’ Liberibacter pose a growing threat to agricultural production around the globe. However, our understanding of the ecological and biological factors facilitating the emergence and spread of these virulent pathogens in crop plants is still relatively limited. This is due in large part to a lack of research on the natural history of both Ca. Liberibacter and psyllid vectors outside of agroecosystems. We are addressing this critical knowledge gap by studying the genetic diversity and biology of Ca. Liberibacter solanacearum (CLso) and its vector, the native potato psyllid (Bactericera cockerelli), in natural plant communities in California. To accomplish this goal, we screened native, perennial nightshades growing in southern California ecological reserves for both CLso and potato psyllids. We complemented this work with controlled, psyllid-feeding transmission assays to investigate the effects of CLso infection on the health of California native nightshades. The results of this work demonstrate the importance of understanding the genetic diversity and ecology of crop pathogens and their insect vectors beyond the borders of agriculture, in order to accurately infer the origins of insect-transmitted crop diseases and improve their management.

Through Northern Europe to Western Siberia; genetic approach in reconstruction of invasion pathway of Ips amitinus Eich. 1872 (Coleoptera: Curculionidae, Scolytinae)

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Abstract: Ips amitinus is a Central European Highlands origin species which has been considered a secondary pest associated with several species of spruces and pines (Pfeffer, 1995). In last decades, the range of I. amitinus rapidly expanded into Northern Europe (Økland et al., 2019), and fether in Karelia, Leningrad and Arkhangelsk regions in Russia (Mandelshtam, 1999; Voolma et al., 2004; Mandelshtam, Musolin, 2016).

In 2019 it was registered for the first time in Western Siberia, there it became new aggressive pest for Pinus sibirica. The secondary area covers 31.2 thousand km^2 with a tendency for rapid eastward expansion (Kerchev et al., 2019; 2021).

Here we study genetic diversity of I. amitinus collected from native range: Austria, Switzerland, Bulgaria, and from second range: Finland and Russia namely Kaliningrad, Leningrad regions, and West Siberian populations. The analysis revealed that European native populations have high variation of mtDNA haplotypes whereas the populations from secondary range were monomorphic, i.e. observed the founder effect. We conclude that initially there was an invasion into Northern Europe, which became a donor region for the subsequent invasion in Siberia.

This research was supported by the RFBR (grant: 20-04-00587).

Ecological consequences of a shifted phenology in the pine processionary moth

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Abstract: The pine processionary moth Thaumetopoea pityocampa is a pine defoliator with one year life cycle. Typically, mating and egg laying occurs during summer months whereas larval development takes place during winter in gregarious silk nests. Gradual changes in phenology are observed for this species, in particular with earlier flight periods at higher latitudes and altitudes, probably due to adaptation to climate gradients. Here, however, we document an abrupt change in a unique population, possibly caused by mutations in one or more genes regulating life cycle events. In this unique shifted population, the adults mate in the spring and the larvae develop through summer. Such abrupt changes can either cause an eco-evolutionary dead-end, or on the contrary bring ecological opportunities, such as escape from natural enemies, or adaptations to climate change. Here, we report the ecological consequences of the phenological shift for this particular population of the pine processionary moth. Our observations demonstrated ecological implications of the shifted life cycle and ongoing adaptations. Changes in the thermal biology, climatic niche, phenotypic morphological traits, fecundity and egg mortality are evidenced. Feeding constraints imposed by season and host plant physiology are also observed. Finally, the shifted phenology may impose higher risks for human health. Altogether our results show a comprehensive understanding of the implications of phenological changes in the ecology and success of this pine defoliator.

From phenological variability to allochrony: a case study on the pine processionary moth

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Abstract: In temperate species, phenological variability, i.e. the timing of the various stages of the life cycle, can allow adaptation to the local environmental conditions. In particular, insect diapause or quiescence is a classical way of avoiding harsh winter or extreme hot summer conditions.

The pine processionary moth Thaumetopoea pityocampa (Lep., Notodontidae) is a conifer-defoliating species that is found in the Western Mediterranean regions and is currently expanding northwards. It generally has a one-year life cycle, and its phenology is known to gradually vary over its distribution range. Sexual reproduction occurs in summer, and the 5 larval stages usually span from late summer to late winter. When larval development is complete, the caterpillars move from their host tree to their underground pupation site in a typical head-to-tail procession. The pupae enter an obligate diapause, and adult emergence occurs the following summer. As larval development depends on temperature, there is a strong variability in procession date and in diapause duration. Moreover, a fraction of the population may enter prolonged diapause and emerge only a year or more later. Adult emergence and reproduction tend to occur later (in August or September) in warm regions such as the southern part of its range, while it occurs much earlier (June or early July) in northern areas or at high altitude. This pattern is thought to allow the individuals to adapt to the major climatic risk in each region by avoiding extreme heat waves in the South and optimizing resistance to early frost in the North. These general observations suggest that early-reproducing individuals would be counter-selected in the southern part of its range. Nonetheless, a unique population with a shifted life cycle occurs in Portugal and reproduces in spring, and unexpectedly currently shows high population size locally.

To better understand the fine-tuning of phenology in this species, we will document results obtained under two contrasting situations. First, we will report original data based on a historical time series (1970 – 1985) showing how phenology (time of procession and time of adult emergence) varies in space and time over an altitudinal cline in Southern France. The results suggest that local climatic conditions strongly affect the timing of sexual reproduction in this species, but that between-year variations could correspond to different mechanisms than between-site variations. They also show how duration of pupal diapause allows the synchronisation of adult emergence in spite of a very strong variation in the timing of procession. Second, we will present an overview of results concerning the shifted Portuguese population and propose hypotheses concerning its apparent paradoxical success. We will show that the SP probably arose from a sudden phenotypic mutation and experiences allochronic differentiation. We will discuss its fate in front of the current climate change.

Past, present and future potential geographical distribution of Xylosandrus crassiusculus in Europe

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Abstract: Biological invasions constitute one of the main threats to biodiversity. A better understanding of invasive species' biology, ecology and invasion history is necessary to better anticipate and possibly prevent future bark beetles invasions. Species distribution modelling (SDM) is an increasingly important tool to study and forecast biological invasion, helping us determine which areas are suitable for a species to establish. Hence, this tool helps focus prevention, detection and conservation efforts.

Xylosandrus crassiusculus is a successful worldwide invasive ambrosia beetle originating from Southeastern Asia. Storer et al. (2017) showed that X. crassiusculus comprises two genetically divergent clusters, both invasive in various areas.

We assigned specimens from X. crassiusculus' invasive and native area to each genetic cluster and assessed the two clusters' niche overlap. We found that the two clusters had significantly different climatic niches, and thus we performed species distribution modelling on each cluster separately, using the Maxent algorithm. The resulting models were also projected in Europe according to past and future climate datasets. The future projections were performed for two periods, 2041-2070 and 2071-2100, using 3 Shared Socioeconomic Pathways (scenarios of projected socioeconomic global changes up to 2100) and 5 Global Circulation Models (numerical models accounting for the various components of influencing climate).

Our results showed that both genetic clusters could expand their distributions in each continent, and Cluster 1 could establish in Europe, where it is still absent.

Climate change is expected to shift both clusters' range in Europe, decreasing habitat suitability in Southern Europe and increasing it towards Northeastern Europe in 2071-2100. The newly suitable areas would include new points of entry such as major harbours in northern Europe, in regions that are currently climatically unsuitable.

Most of Southern and Western Europe was predicted as already suitable for both clusters in the early XXth century. This suggests that the recent colonisation of Europe by Cluster 2 is not due to a recent change in climate suitability but probably to an increase in propagule pressure via international trade.

Pine processionary moths: promises from genomic developments

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Abstract: The pine processionary moth (PPM) Thaumetopoea pityocampa occurs in the Western part of the Mediterranean Basin. In the last two decades, phylogeographical and population genetic studies have allowed to address evolutionary questions and to partially decipher its geographical structure at different spatial scales. Neutral markers specifically developed for this species were for example used to study its Quaternary history and localize the glacial refugia; to study a case of allochronic differentiation and show how a phenological shift can isolate populations; and identify long-distance dispersal events.

We were recently able to develop genomic resources in this species. We could assemble a high-quality genome that was automatically annotated. Gene prediction was further proposed using transcriptomic data. The results suggest that the PPM genome is composed of 49 pairs of autosomes and one pair of sexual chromosomes. We will discuss how population genomic studies will now be developed based on individual re-sequencing and will open possibilities to question both neutral structure, demographic histories and adaptive evolution. This resource will also allow to study introgression events at fine scale and to explore the genomic evolution of the T. pityocampa / T. wilkinsoni species complex.

Description of a new mite species (Storchia oryzaus) Stigmaeidae: Acari from Pakistan

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Abstract: Experiment was managed to find the predatory mite fauna of family Stigmaeidae (Acari) from Punjab, Pakistan. The holotype adult female (male unknown) of genus Storchia was collected from urban cultivated area of city Gujranwala from rice crop (Oryza sativa) and described here. Eighteen (18) paratypes were collected, among which 12 with same collection data and 6 from another locality of Faisalabad. The description, figures, measurements and discussion of this new species is given here in this manuscript. The collected samples were placed in Acarology Research Laboratory, Department of Entomology, University of Agriculture, Faisalabad, Pakistan.

Climate-adapted push-pull technology: A conservation agriculture technology for food security and environmental sustainability in Africa

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Abstract: Poor yields of cereal crops caused by constraints such as stemborer and fall armyworm pests, parasitic Striga weeds and degraded soils are responsible for the chronic food insecurity in Africa--a situation that is worsening with climate change and human population growth. Push-pull, a climate-adapted conservation agricultural innovation based on companion cropping, effectively addresses these constraints resulting in substantial grain yield increases without the use of any external inorganic inputs. Push-pull involves intercropping cereal crops with moth repellent forage legume, e.g. Desmodium (push), and planting attractive fodder grasses e.g. Napier grass or Brachiaria as a border crop (pull). Desmodium is also effective in suppressing Striga weed while improving soil fertility by fixing nitrogen and improving soil organic matter and biodiversity of arthropods. Both companion plants are valuable fodder plants thus allowing integration of crop and livestock production which diversifies farmers' income sources. Drought-tolerant companion plants are identified and incorporated into the technology,are extending the benefits to drier areas and ensuring its long-term sustainability in view of climate change. The technology provides an opportunity to improve food security, stimulate economic growth, and alleviate poverty in Africa while making agriculture more resilient to climate change.

A little egg lay on a maize leaf… did the plant scream for help?

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Abstract: Herbivore induced plant volatiles (HIPVs) are often emitted when chewing herbivores start biting a plant and these volatiles can function as recruiting signals for predator and parasitoid "bodyguards" in indirect plant defence. Furthermore, it has become apparent that some plants can respond to herbivory at an earlier stage when an egg is laid on a leaf. Our collaborative research, with icipe in Kenya, has revealed that certain maize landraces emit HIPVs in response to stemborer, Chilo partellus, oviposition. We initially found that the two commercially available hybrid maize genotypes tested did not have this trait, whereas, it was widespread in a number of farmer preferred landraces. However, those landraces were not genetically uniform and lacked the yield potential of commercial maize plants. To allow a better understanding of the maize genetics underpinning egg induced HIPV emission, we conducted a genome wide association study (GWAS) of 146 maize genotypes comprising of landraces, inbred lines and commercial hybrids. Plants were phenotyped in bioassays measuring parasitic wasp (Cotesia sesamiae) attraction to volatiles collected from plants exposed to stemborer (C. partellus) eggs. Genotyping-by-sequencing was used to generate maize germplasm SNP data for GWAS. The egg induced parasitoid attraction trait was more common in landraces than in improved inbred lines and hybrids but it did exist in improved germplasm. GWAS identified 101 marker-trait associations (MTAs), some of which were adjacent to genes involved in the JA-defence pathway (opr7, aos1, 2, 3), terpene biosynthesis (fps3, tps2, 3, 4, 5, 7, 9, 10), benzoxazinone synthesis (bx7, 9) and known resistance genes (e.g. maize insect resistance 1, mir1). Intriguingly, there was also association with a transmembrane protein kinase that may function as a receptor for the egg elicitor. We identified maize genomic regions associated with indirect defence and this provides a valuable resource for future studies on tritrophic interactions in maize. The markers identified may facilitate selection of indirect defence by maize breeders. We are also conducting research on maize responses to Spodoptera frugiperda, which has recently invaded Africa, and have found that genotypes that respond to C. partellus eggs with HIPV emission do not necessarily do the same when exposed to S. frugiperda eggs.

Soil-mediated Associational Resistance to an Herbivore due to a novel maize cropping system

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Abstract: Plants can alter structure, nutrients and chemistry of the soil they grow in. These soil changes can positively or negatively influence the growth and metabolism of other plants that co-occur or grow later in the conditioned soil. In this study we investigated the effect of emergent soil properties as a result of push-pull cropping technology on plant defences. Push-pull technology is a pest management strategy that involves attracting cereal stemborers with trap plants; Napier grass (pull) whilst driving them away from the main crop using a repellent intercrop; Desmodium (push). The system has been shown to have ecological and socio-economic emergent properties that go far beyond the effects of efficient insect pest control. Chemicals released by intercrop roots induce abortive germination of the parasitic Striga weed, providing very effective control of this noxious weed. The companion plants provide high value animal fodder, facilitating milk production. Furthermore, soil fertility is improved through nitrogen fixation and increased soil organic matter by the intercrop and soil degradation is prevented as the intercrop acts as a cover crop. We hypothesised that the emergent improved soil quality affected secondary plant metabolites. Maize plants were grown in soil collected from push-pull and non-push pull monoculture fields in the screen house. Volatile organic compounds were collected from 3-week old maize plants through headspace sampling and plant tissue was preserved in 50%methanol. Coupled Gas Chromatography-Mass Spectrometry and HPLC was used for chemical analysis. Volatile analysis showed that maize plants grown in soil from push-pull fields emitted higher amounts defence volatiles. HPLC analysis revealed increase in secondary non-volatile defence metabolites in maize grown in push-pull soil. These results show that push-pull cropping system-associated changes in soil quality affect plant metabolism and increase maize crop metabolite production with effects on plants' direct and indirect defences against herbivores.

Physiological function of immune mediators in ticks

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Abstract: Ticks are obligatory ectoparasites of many animals including human and transmit numerous pathogens such as viruses (SFTS) and bacteria (Lyme disease). During blood feeding, tick salivary secretion is critical for successful tick feeding. Tick saliva containing various bioactive molecules such as immune mediators play a critical role for inhibition of host hemostasis and suppression of host immune system. Limited studies had been conducted to understand the functions of immune mediator in physiological events from hard ticks. Comparative transcriptomic analysis between unfed and partially engorged female ticks revealed that various genes related to the production of immune mediators were differentially expressed. Reverse genetics using RNA interference targeting differentially expressed genes and classic physiological study using pharmacological agents inhibiting or rescuing the production of immune mediator were applied to understand the physiological function of immune mediators in various physiological events such as reproduction and salivation. The understanding of physiological function of immune mediators in tick physiology will provide an insight to the development of novel methods to control tick-borne disease and suppress hard tick population.

Evaluation of the effect of fusion expression of P10 protein to increase productivity of recombinant protein in baculovirus expression system

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Abstract: The baculovirus expression system (BES) is widely used in the protein production industry, but in order to increase the usefulness of the system, it is necessary to further maximize the productivity of the target recombinant protein. There have been reports of various fusion partners for expression enhancement, but there has been no report on the effect of fusion expression of baculovirus P10 protein mass-produced in the nucleus and cytoplasm after virus infection. Based on the characteristic that the P10 protein exists in a stable large matrix form in cells, it was evaluated whether the productivity of the target protein could be increased when expressed in fusion. As a result, it was confirmed that the expression of P10 fusion can increase the production of recombinant protein, and different expression levels were shown according to the P10 fusion regions. These results showed the potential of the P10 protein as a fusion partner to increase the production of the target protein in BES.

Selection of entomopathogenic fungi with acaricidal activity and high environmental stability against the bulb mite Rhizoglyphus robini

Authors: Kim Hyun Soo[1], Lee Jin Yong[1], Woo Ra Mi[1] and Woo Soo Dong[1], [1]Chungbuk National University, Republic of Korea

Abstract: Bulb mites (Rhizoglyphus robini) have recently become a serious problem because of the continuous use of acaricides, which has resulted in resistance among bulb mite populations. Here, we report the results of screening pathogenic fungi for the control of R. robini. The initial screen was performed using 342 isolates of entomopathogenic fungi from soils. As a result, the most effective 11 isolates were selected through comparing the virulence against the bulb mite. In addition to the virulence, thermotolerance and UV-B tolerance of the 11 isolates were further evaluated and compared. Finally, based on all of the above results, three isolates of Metarhizium anisopliae were confirmed to be the most effective for controlling bulb mites, and they can be considered as promising biological control agents against bulb mites.

Colonization of Beauveria bassiana ERL836 on the Monochamus alternatus-infested pine tree logs

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Abstract: Monochamus alternatus is a major forest pest that causes pine wilt disease in pine trees by mediating pine wilt nematodes. The use of chemicals causes pollution of forest ecosystems and toxicity to users. Alternatively entomopathogenic fungi could be considered to control pine sawyer beetle in an eco-friendly way. In this study, a commercialized entomopathogenic fungus, Beauveria bassiana ERL836 strain was used to control the target pest. We investigated the potential of B. bassiana ERL836 to control M. alternatus: the insecticidal activity of ERL836 against M. alternatus adults, the possibility of colonization on pine tree bark, the control effeciency against M. alternatus by fungal pre-treatment on semi-field and field conditions. On the pine trees logs which were pre-treated with the ERL836 fungal suspension in a semi-field condition, the M. alternatus adults were infected and finally dead by the fungus. At the same environmental conditions, a fungal wettable powder (WP) was directly treated on the beetle-infested pine tree logs and it showed a high insecticidal activity, similar to a fungal suspension treatment. Finally in field conditions, the fungal powder treatment showed a high insecticidal activity against M. alternatus.

Establishment and characterization of novel transgenic insect cell line for virus quantification

Authors: Kim Kyu Seek, Chungbuk National University, Republic of Korea

Abstract: The baculovirus expression system is widely used for the production of useful proteins through the generation of recombinant viruses. Therefore, although the virus quantification process is essential for research and industrial purpose, virus quantification has a problem that requires a long time and high skill. To improve this problem, a novel transgenic Sf9 cell line capable of convenient and rapid virus quantification was established. The transgenic Sf9 cells showed a higher cell proliferation rate and virus susceptibility comparing to parent Sf9 cells. In addition, convenient and rapid quantification was possible due to EGFP expression. In particular, it showed high convenience for mechanical quantification using a fluorescence spectrophotometer. The newly established transformed cell line will be able to further increase the utility of the baculovirus expression system by increasing the convenience of virus quantification and shortening the time.

Selection of optimal grain media for mass production of entomopathogenic fungus against the two-spotted spider mite, Tetranychus urticae

Authors: Kim Kyu Seek[1], Woo Ra Mi[1], Lee Jin Yong[1], Kim Hyun Soo[1] and Woo Soo Dong[1], [1]Chungbuk National University, Republic of Korea

Abstract: The two-spotted spider mite, Tetranychus urticae, is the most important spider mite in the family Tetranychidae because it can infest more than 200 host plants, including vegetables, fruit crops, food crops and ornamentals. This study was carried out to select the optimal grain medium for mass production of conidia of the entomopathogenic fungus Beauveria bassiana 331R with high acaricidal virulence against the two-spotted spider mite. As a result of comparative evaluation of production and virulence of conidia according to the medium, characteristics of conidia were different depending on the produced medium. Millet or rice medium showed the highest conidia production, environmental stability, and acaricidal virulence. These results showed that various characteristics including virulence of entomopathogenic fungi are possible through adjustment of the production environment.

Year-round trap capture of the spotted-wing drosophila, Drosophila suzukii (Diptera: Drosophilidae), in Korean strawberry greenhouses

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Abstract: Korean greenhouse strawberries are mostly cultivated from October to May, which includes the cold winter season. During this time, the population size of the spotted-wing drosophila (SWD), Drosophila suzukii Matsumura (Diptera: Drosophilidae), is expected to decrease in the wild, and is also expected to decrease inside the greenhouses, as long as SWD are not already present inside. Field surveys of SWD have been extensively carried out for field-grown agricultural fruits, but no study has been conducted for greenhouse fruits, such as strawberries. Furthermore, strawberries have been shown to serve as one of the most preferred egg-depositing media for SWD. In this study, SWD capture patterns were examined inside and outside of the greenhouse blocks, and in the nearby woodlands in a southwestern locality of Korea using selected traps and attractants for nearly 19 months—in addition to several greenhouse blocks—during the strawberry cultivating periods. The highest capture period was observed from October to mid-December in woodland areas, with a mean capture number per trap of 100–600 individuals. However, capture number subsequently and sharply decreased up to mid-April, resulting in mostly zero-captures or low captures (= 10). During this period, a zero-capture period was observed inside the greenhouse that lasted for nearly three months (late December to late February), while the captures outside the greenhouses were mostly zero or = 5 individuals. An incubation of the fallen strawberries from inside the greenhouses during December to May showed no emergence of SWD adults, supporting the results of trap capture from inside the greenhouses. Taken together, the occurrence of SWD in the strawberry greenhouses is likely to be highly dependent on that of the nearby woodlands. Furthermore, captures were highest in the woodland areas, followed by captures outside the greenhouse and inside the greenhouses. Thus, a sharp winter drop in captures and the subsequent zero- or low-capture periods that were present up to mid-April in the woodland areas were likely responsible for the observed zero-capture periods inside the greenhouses.

Comparison of wild-caught and commercially purchased Orius majusculus

Authors: Kim Jensen, Saltholmsgade, Denmark

Abstract: We find that wild O. majusculus are larger than commercially produces individuals. However, we found no difference in consumption capacity.

Rice grasshopper artificial feeds development

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Abstract: A rice grasshopper has been recognized as a pest damaging crops. However, grasshoppers are raised and then are mixed with flies, mealworm beetles, and grasshopper insect powders to be distributed on the market as feeds for livestock of fish in China and Thailand. Rice grasshoppers are effective to tetanus, asthma and pertussis, and help prevent blood pressure, cholesterol and brain and heart disease. A technique has been established to mass produce rice grasshoppers in Korea all the year round. However, there are some disadvantages in which food plants for rice grasshoppers should be cut and provided. The artificial feeds are developed to compensate for such disadvantages. Corns and hybrid sorghum are used as summer crops, and wheats and IRG are used as winter crops. The growth period is short and their growth is excellent. Whole wheat flour and whole rice powders are used as the source of carbohydrates. Soybeans are used as the source of protein. The mortality rate of fish is low. Thus, these raw materials are mixed to prepare the artificial feeds.

Solid artificial feeds consist of whole wheat flour + whole rice powder + fish + soybeans and are given to 2nd ~ 3rd larvae. When the artificial feeds were provided, the survival rate was 87.9 % (control group 89.1 %) and individual weight of rice grasshoppers was 0.76 g (control group 0.74 g). There was no statistically significant difference.

Novel locomotion mechanisms and leg micro-structures in the world largest semi-aquatic insect, the giant water strider (Gigantometra gigas), as adaptations to its heavy body.

Authors: Kim Woojoo, Seoul National University, South Korea

Abstract: Semiaquatic insects are good organisms to study animals' ability to walk and jump on the water surface with their different types of locomotion and various micro-morphological structures on legs. Their adult body mass varies from about 1 mg to about 500 mg. They use different types of locomotion and developed morphology adapted to locomotion in their species-specific habitats. Researchers mostly focused on a relatively small number of species of medium-body sizes (~8-30mg body weight) from the Palearctic region. It has been recently established that these "typical" water striders use surface-tension-dominated locomotion and are able to control their leg's movements to prevent water surface breaking. We studied mechanisms used for locomotion by the large-bodied water strider from SE Asia: the giant water strider (Gigantometra gigas). We found that, like the "typical" Palearctic species, the giant water striders use near vertical jumps as antipredatory responses. However, their jumps are powered not only by legs' interactions with the water surface, but also by upward drag force created by air-wrapped midlegs moving downward in the water after the surface is broken. Unlike the "typical" waters striders, who use their middle legs symmetrically to thrust themselves forward, the giant water striders use asymmetric gait: an individual extends one midleg forward pointing towards the direction of movement while the second midleg provides power by rowing with counter-movements from the opposite hind leg providing additional thrust. The forward pointing midleg supports their body on the water surface while front legs are lifted and do not touch the surface. This asymmetrical gait results in the insect's forward movement in the direction diagonal to the body axis. The hair structures on legs of G. gigas were also different than those in other water striders. Midlegs' setae in G. gigas are relatively longer than in Aquarius paludum, (after correction for leg size), and they are extended from leg surface at a steeper slope that in A. paludum. This results in an increased functional diameter of a leg, which may be useful to create force in and on the water during jumps and rowing. Finally, the specialized leaf-shaped setae on the ventral side of the hind leg tarsi and tibia were more pronounced and complex than in other species. Those leaf-shaped setae formed a long unified beam structure and contributed to a smooth outline facing water on the ventral side. We hypothesize that these special hair structures of G. gigas are adaptations to novel locomotion mechanisms and are related to the species extreme body size.

Biosynthesis and immunity of epoxyeicosatrienoic acids in a lepidopteran insect, Spodoptera exigua

Authors: Kim Yonggyun, Andong National University, South Korea

Abstract: Eicosanoids mediate both cellular and humoral immune responses in insects. Epoxyeicosatrienoic acids (EETs) are a group of eicosanoids containing epoxide formed by epoxygenase (EPX) activity of cytochrome P450 (CYP). Although EETs have been considered to mediate immune responses in some insects, their synthetic machinery was little understood in insects. This study monitored EETs in a lepidopteran insect, Spodoptera exigua, immunized with bacteria and found all four EETs (5,6-EET, 8,9-EET, 11,12-EET, and 14,15-EET) from larval fat body at 247?1,736 pg/g levels. Then to predict EPXs, 140 CYPs were collected from S. exigua transcriptomes and compared with human EPXs. Four CYPs (SeEPX1-SeEPX4) sharing homologies with human EPXs were chosen and assessed in subsequent expression and functional analyses. All four EPXs were expressed in all development stages. In larval stage, all four EPXs were expressed in immune-associated tissues such as fat body and hemocytes. Furthermore, their expression levels were highly enhanced by bacterial challenge in different tissues. RNA interference (RNAi) using gene-specific double stranded RNA injection suppressed their expression levels by more than 55%. RNAi treatments interfered with hemocyte-spreading behavior and nodule formation upon bacterial challenge except RNAi treatment against SeEPX2. All four EETs stimulated cellular immune response measured by nodule formation in S. exigua. The suppressed immune responses by the RNAi treatments against three SeEPXs were rescued by the addition of 8,9-EET. However, other three EETs gave their specific rescue effect depending on SeEPX types under RNAi. In humoral immune response, all four RNAi treatments suppressed expression of antimicrobial peptide genes. This study reports the presence of all four EETs in larval fat body of S. exigua and suggests that four SeEPXs are associated with immune responses mediated by EETs.

Characterization of the first insect prostaglandin (PGE2) receptor: MansePGE2R is expressed in oenocytoids and lipotheicoic acid (LTA) increases transcript expression

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Abstract: In arthropods, eicosanoids derived from the oxygenated metabolism of arachidonic acid are significant in mediating immune responses. However, the lack of information about insect eicosanoid receptors is an obstacle to completely decipher immune mechanisms underlying both eicosanoid downstream signal cascades and their relationship to immune pathogen-associated molecular patterns (PAMPs). We cloned and sequenced a G protein-coupled receptor (MW 46.16 kDa) from the model lepidopteran, Manduca sexta (Sphingidae). The receptor shares similarity of amino acid motifs to human prostaglandin E2 (PGE2) receptors, and Bayesian phylogenetic analysis supports its classification as a prostaglandin receptor. In agreement, the recombinant receptor was activated by PGE2 resulting in intracellular cAMP increase, and therefore designated MansePGE2R. Expression of MansePGE2R in Sf9 cells in which the endogenous orthologous receptor had been silenced showed similar cAMP increase upon PGE2 challenge. Receptor transcript expression was identified in various tissues in larvae and female adults, including Malpighian tubules, fat body, gut and hemocytes, and in larvae silk glands and female ovaries. In addition to the cDNA cloned that encodes the functional receptor, an mRNA was found featuring the poly-A tail but lacking the predicted transmembrane (TM) regions 2 and 3, suggesting the possibility that internally deleted receptor proteins exist in insects. These shorter transcripts (1.3 kb) were detected in laid eggs and in female tissues (ovaries, Malpighian tubules and fat body), in addition to the complete 1.5kb transcript present in the same. Immunocytochemistry and in situ hybridization revealed that among hemocytes, the receptor was exclusively localized in the oenocytoids. Larval immune challenges injecting bacterial components showed that lipoteichoic acid (LTA) increased MansePGE2R expression in hemocytes. In contrast, injection of lipopolysaccharide (LPS) or peptidoglycan did not increase MansePGE2R transcript levels in hemocytes, suggesting the LTA associated increase in receptor transcript is regulated through a distinct pathway. This study provides the first characterization of an eicosanoid receptor in insects, and paves the way for establishing the hierarchy in signaling steps required for establishing insect immune responses to infections.

Diuretic Hormone 44 Signaling Establishes Levels of Female Mating Drive during Reproductive Maturation and the Post-Mating Responses

Authors: Kim Young Joon[1], Kim Do-Hyoung[1] and Jang Yong-Hoon[1], [1]School of Life Sciences, GIST, Republic of Korea, South Korea

Abstract: Female mating motivation or receptivity in the fruit fly Drosophila melanogaster is an excellent model for understanding reversible modulation of a complex behavioral network. Here, we report the neuropeptide diuretic hormone 44 (Dh44) and its receptor Dh44R1 switch female mating motivation by modulating the functional states of pC1, a subset of the brain's doublesex-positive (dsx) neurons that integrate sensory cues from courting males. Activation of Dh44 or Dh44R1 signaling in pC1 makes immature females and mated females receptive to mating. Our evidence suggests that the Dh44-Dh44R1 pathway integrates the SP signal and switches female sexual motivation by reversibly modulating the functional state of the downstream dsx neurons. Dh44 is orthologous to the vertebrate corticotropin-releasing factor (CRF) family of neuropeptides, which is broadly conserved across taxa, suggesting a role for the Dh44/CRF system in female sexual activity in other animal species.

What effect is the invasive Harmonia axyridis having on the structure of native ladybird guilds and their role in the biological control of aphids?

Authors: Kindlmann Pavel[1], Štípková Zuzana[1], [1]Global Change Research Institute CAS, Brno, Institute for Environmental Studies, Faculty of Science, Charles University, Czech Republic

Abstract: The efficiency of biocontrol agents in aphid-ladybird systems is important in determining the success of biological control. Therefore, it has been the subject of many discussions and empirical studies, which attempt to evaluate the extent to which predators are able to suppress their aphid prey. A very interesting situation occurs when a guild of native ladybirds is invaded by a non-native species (Rosenheim 1993; Hentley et al. 2016). Because of strong cannibalism, the numbers of native ladybirds may be diminished by a non-native invasive species of ladybird, which lowers the biocontrol potential of the former. However, the invader also eats aphids and would also increase the biocontrol efficiency of the new ladybird guild. The question then is what prevails: is the final biocontrol efficiency greater or smaller after the invasion?

A nice example of such a situation is the Pan-European invasion of many countries by Harmonia axyridis (Roy et al. 2016). It is seductive to say that this invader in reducing the abundance of the native ladybirds lowers the biocontrol potential of the whole guild (Pell et al. 2008; Brown et al. 2011; Roy et al. 2012). However, do we really have sufficient data to prove this (Kindlmann and Štípková 2019)? In many cases, the statistical analysis of the data purporting to prove a reduction in biocontrol potential is neither sufficient nor correct.

Here we raise a series of points and warn against improper use of statistics and overemphasis of seemingly persuasive data.

Does aphid colony duration cause low numbers of Harmonia axyridis in the Mediterranean?

Authors: Kindlmann Pavel[1], Štípková Zuzana[1], [1]Global Change Research Institute CAS, Brno, Institute for Environmental Studies, Faculty of Science, Charles University, Czech Republic

Abstract: An enormous amount of knowledge is available concerning factors limiting distribution ranges of species settled in their native areas, but much less information is available on factors limiting potential changes in distribution ranges of species that are currently spreading outside of their present range, especially on factors limiting spread of invasive species. However, this information is often quite essential, as it enables prediction of future spatial distribution and local abundances of invasive species and prediction of potential damages they may cause to people and their crops.

Some individuals of the invasive ladybird, Harmonia axyridis (Pallas) (Coleoptera: Coccinellidae), originating from east Palaearctic, escaped from the glasshouses, where they were reared, and spread massively into natural environment, first in North America and subsequently over most of Europe, which has caused a serious concern. Recent observations show that the spread of H. axyridis towards the equator is limited – for example, it is quite rare in the Mediterranean and its northward spread in South America is also quite slow, as if there were some limit in its spread towards equator. Recent literature indicates it is neither climate, nor the distance of the Mediterranean from the original release location in the Netherlands that is causing the limitation. Therefore, we hypothesized that biotic factors may be the cue. We thought the limiting factor can be the duration of prey colony (= population in one patch, usually one plant) that becomes shorter, as one approaches the equator. This may lead to lowering the fitness of the predator and subsequently to its low population densities. We test here, whether the duration of aphid colony is shorter in the Mediterranean, as compared with the Central Europe. Unfortunately, our data do not support this hypothesis. Therefore, the question of the limitation of H. axyridis distribution towards equator still remains open.

Exploring mechanisms of parasitoid diversification through the lens of chemosensory speciation

Authors: King Kendall[1], Johnson Norman[1], Meuti Megan[1], [1]The Ohio State University, United States

Abstract: Insects are the most diverse multi-cellular organisms on the planet. Parasitoid wasps, in particular, have an incredible species richness and are the second most-described group of insects behind Coleoptera. Their astounding diversity has given rise to questions addressing the mechanisms by which host-associated parasitoids diversify. Over time, parasitoid wasps have undergone adaptive radiations that are seemingly correlated with shifts in host-associations, likely a result of evolving chemical receptor proteins that mediate olfaction of unexploited host groups. Therefore, we believe chemosensory speciation drives parasitoid diversification and may inform mechanisms of evolution of olfactory gene families. To address our long-term goals of mapping the olfactory processes responsible for parasitoid host-finding and acceptance, we have annotated odorant binding protein (OBP) sequences in the Trissolcus basalis genome and modeled their 3D structure. OBPs may act as the first filter in odor coding, as they are responsible for transporting ligands from the environment to the olfactory receptors expressed on the surface of sense cells. Variation in OBP and receptor specificity to ligands may contribute to a parasitoid's ability to shift host groups.

The dorsal eye for phototactic flight in an Asian migratory butterfly, Parantica sita

Authors: Kinoshita Michiyo, SOKENDAI, Hayama, Japan

Abstract: The chestnut tiger butterfly Parantica sita shows seasonal long-distance migration among Asian countries. For orientation flight in its migration, Parantica presumably uses visual cues over the sky, such as polarized light, and spectral and intensity gradient (like in monarch butterflies).

The Parantica compound eye consists of three distinct regions: dorsal rim, dorsal and ventral. These three regions are distinguished by anatomical features. Under epi-illumination microscope ommatidial reflection of the dorsal region appears homogeneously yellowish, whereas yellowish and reddish ommatidia are randomly distributed in the ventral region. The reddish ommatidia contain dense red pigment around their rhabdom at their proximal depth. Ommatidial reflection of the dorsal rim region is the same as in the dorsal region; however, the rhabdoms are relatively large and rectangular shaped, compared to the smaller circular shaped rhabdoms in the ommatidia of the other two regions. These regions also differ in the spectral sensitivity. The sensitivity of the dorsal region is relatively higher in the UV wavelength region than that of the ventral region, which may fit to detect light information over the sky.

The dorsal region would be the best placed for extracting directional cues over the sky. To explore the function of the dorsal region, we investigated phototactic flight as an orientation behavior. When we evenly illuminated a small cage with fluorescent tubes and four halogen lamps, a butterfly naturally flew near the ceiling of the cage. When introducing two additional solar lamps at one side of the cage, the butterfly's flight became biased towards these lamps. This phototaxis persisted when the light of the solar lamps was blue-filtered, and greatly reducing the intensity, while the phototaxis disappeared when the light was yellow-filtered. This phototaxis flight basically persisted even when the dorsal rim region (plus some of the dorsal ommatidia) was occluded. This was also the case when the ventral two-thirds of the eye was occluded. However, butterflies with the dorsal one-third of the eye (= dorsal rim + dorsal region) covered did not fly; instead, they perched on the cage wall. These results indicate that phototaxis in Parantica is most likely mediated by the dorsal region and depends on not only illumination intensity but also spectral composition over the cage.

Inbreeding in Scolytinae, and its consequences for invasive species

Authors: Kirkendall Lawrence, University of Bergen, Norway

Abstract: It is now clear that regular inbreeding (usually, brother-sister matings) is a key factor in the success of invasive alien bark and ambrosia beetles. What are the advantages and disadvantages to regular inbreeding? Are inbreeders better colonizers? Do the relationships with nutritional or pathogenic microorganisms differ, for inbreeders vs outbreeders? What are the short- and longterm genetic consequences of inbreeding—for example, can invasive populations of inbreeders evolve as rapidly as invasive populations of outbreeders? How often do regular inbreeders outbreed, and with what consequences? In my talk, I will address these and other questions about the ecology and biodiversity of inbreeding in Scolytinae.

Scaling up digitization in entomology collections - a new approach initiated and enabled by the Museum fuer Naturkunde Berlin, supported by Naturalis Biodiversity Center and realized by Picturae

Authors: Kirschey Lukas[1], Berger Frederik[1], Grigoryeva Elena[1] and Krause Stefanie[1], [1]Museum fuer Naturkunde Berlin, Germany, [1]Museum fuer Naturkunde Berlin

Abstract: Millions of pins in entomology collections carry valuable information in form of labels that have been described and maintained over generations. Digitizing this information is one of the major challenges of this decade in collection digitization. This will enable direct access to the data of the collection event via databases.

Within the project for collection discovery and development at the Berlin Natural History Museum the requirements for standardized and automated high-throughput collection disclosure were defined in 2020-2021. The aim of this first pilot project is to digitally record 500,000 specimens from the Hymenoptera collection. The project is not limited to mere imaging, but also includes conservational preparation as well as the digital recording of the collection data by collection management.

The first prototype for an automated digitization line was extensively tested at the Naturalis Biodiversity Center in Leiden in mid 2021. After successful trial runs, the system was moved to Berlin and put into operation. Further improvements on all levels followed. In May 2022, the system is about to enter regular operation.

This poster presentation intends to explain the decisions behind this ambitious project, to address the challenges and to present the results so far.

Synergistic interactions of bark beetles and wildfire: post-fire outbreak potential of the Douglas-fir beetle (Dendroctonus pseudotsugae) in dry interior forests of British Columbia

Authors: Kitchens Katherine[1], Carroll Allan[2], [1]University of British Columbia Faculty of Forestry Department of Forest and Conservation Sciences, Canada, [2]University of British Columbia, Canada

Abstract: Douglas-fir beetle (Dendroctonus pseudotsugae) is one of the most significant agents of mortality in Douglas-fir forests. Landscape-scale outbreaks are common following widespread disturbance such as wildfire, drought and/or disease. These events increase the availability of defensively compromised host trees and thereby facilitate beetle population increases. As climate change continues to exacerbate stress in conifer forests, there is concern that Douglas-fir beetle outbreaks will increase in size and severity. Following recent record-breaking wildfire seasons in the dry interior forests of northwestern North America, we initiated a study to elucidate the relationship between Douglas-fir beetle and wildfire. We found the outbreak potential of Douglas-fir beetle to be constrained by pre-fire stand characteristics, burn severity, parasitism and competition from other members of the subcortical insect guild. These relationships varied across three large burn complexes in the dry Douglas-fir forests of British Columbia, Canada. Results will be discussed within the context of future management strategies for changing disturbance regimes in a warming environment.

Identification of the gene responsible for the brown egg 4 (b-4) mutant in the silkworm, Bombyx mori

Authors: Kiuchi Takashi[1], Osanai-Futahashi Mizuko[1], Tomihara Kenta[1], Katsuma Susumu[1], Uchiyama Hironobu[3], Satta Katsuya[1] Yoshitake Kazutoshi[1], Yamamoto Kimiko[2] and Yajima Shunsuke[3], [1]Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan, [2]Insect Genome Research and Engineering Unit, Division of Applied Genetics, Institute of Agrobiological Science, National Agriculture and Food Research Organization, [3]NODAI Genome Research Center, Tokyo University of Agriculture, Japan

Abstract: Ommochrome pigments are widely distributed in invertebrates and involved in body color patterning, screening pigments of compound eyes, and tryptophan metabolism. In the silkworm, Bombyx mori, ommochrome pigments are accumulated in eggs, compound eyes, and reddish markings of larval epidermis. The brown egg 4 (b-4) is a recessive ommochrome mutant, whose eggs and eyes exhibit reddish-brown color, instead of normal purple and black, respectively. The responsible gene for the b-4 mutant is known to be located at 21.9 cM on chromosome 20. Although the mutant and wild-type eggs have similar ommochrome pigment composition, the total amount of pigments significantly reduces in the mutant eggs. Because the amount of 3-hydroxykynurenine, the ommochrome precursor, of the mutant eggs is comparable to that of wild-type, the gene responsible for the b-4 phenotypes is predicted to be involved in the biosynthetic pathway from 3-hydroxykynurenine to various kinds of ommochrome pigments. To well understand the ommochrome biosynthetic pathway, we attempted to identify the responsible gene for the mutant phenotypes.

We obtained backcross progenies (BC1) by crossing a wild-type strain with a b-4 mutant strain. Using genomic DNAs from 92 of these BC1 individuals, their F1 hybrid parents, a parental wild-type and a b-4 individual, we performed double digest restriction-site associated DNA sequencing (ddRAD-seq) and narrowed down the responsible region for the b-4 locus to approximately 1.1 Mb. Sequencing of cDNAs and genomic DNAs from two b-4 mutant strains revealed that exon skipping was induced in one gene due to an insertion of a transposable element. RNA-seq analysis of another b-4 strain indicated that the same gene has a different transcription start site, which leads to a short open reading frame. These results suggested that the mutations in this gene are the cause of b-4 phenotypes. To test this hypothesis, we performed CRISPR/Cas9-mediated gene knockout targeting the candidate gene. Several generation 0 (G0) adult moths displayed totally or partially reddish-brown compound eyes. Generation 1 (G1) individuals with reddish-brown eggs and eyes were obtained from crosses between G0 adults. Genomic sequencing indicated that the G1 individuals had mutations resulting in frameshifts and premature stop codons in the target gene. Furthermore, the eggs from complementation crosses between a b-4 mutant and the candidate gene knockout also exhibited reddish-brown color which was quite similar to the b-4 mutant eggs, demonstrating that the candidate gene is responsible for the b-4 phenotypes.

Genetic engineering of sex-linked genes in the silkworm, Bombyx mori

Authors: Kiuchi Takashi[1] and Katsuma Susumu[1], [1]Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan

Abstract: The silkworm, Bombyx mori, is an economically important domesticated insect, which produces silk as well as recombinant proteins by transgenic or baculoviral technology. To obtain silks and recombinant proteins more efficiently, male- or female-only production system is expected for practical use. We succeeded in identifying both feminizing and masculinizing factors for B. mori (Kiuchi et al., 2014, Nature). In this presentation, we introduce an attempt of silkworm sexual control by genetic engineering of the sex-linked genes.

Distribution of the Japanese beetle, and quarantine and eradication efforts against it

Authors: Klein Michael, The Ohio State University, United States

Abstract: Soon after the Japanese beetle (JB) (Popillia japonica, Newman) was discovered in a New Jersey nursery in 1916, quarantine and eradication programs were started. The eradication effort was abandoned four years later due to “too many beetles”. However, the federal quarantine lasted until the mid-80s, when more states were infested than not. Little was known about P. japonica in its native range in Japan and Russia, and it did not reach pest status because of a lack of turf for larval development, cold temperatures requiring a two year life cycle, and an effective parasitoid. Reports of this species in Korea and China were proven false in the 1990s. In the U.S., the beetle slowly moved out in all directions at a rate of 5-10 miles a year. However, after the national quarantine was eliminated, and a variety of State quarantines put in place, the JB was moved in turf and nursery stock, and infested distant areas more quickly. A national “Harmonization Agreement” protected the three Pacific coast states from nursery shipments, but opened up movement of nursery stock to other uninfested states. This came at a time when there were no insecticides that could eliminate JB larvae in nursery settings. California has the most ambitious JB surveillance and eradication programs, and is the state with the most successful eradications of isolated JB populations. The state deploys two JB traps/mi2 (about 13,000 traps) baited with a “floral lure” and the JB sex attractant (Japonilure). Two beetles in a trap, or beetles in adjacent traps triggers deployment of 50, 25, 5, and 5 traps/ mi2 around the finds. A set eradication program follows the finding of additional beetles. Such programs have been initiated six times between 1961 and 2014, with treatments of Chlordane or imidacloprid for larvae, and primarily carbaryl for adults for 2-4 years, followed by two years of negative trapping at the high density. Acelepyrn is the likely insecticide of choice now for both larvae and adults. Oregon has also had several eradication programs, and just finished the third year of treatment in the only active program in the U.S. Isolated JB populations have also been eradicated in five other western state with treatments of about four years. There are at least six Canadian Provinces with JB infestations, with an eradication/containment effort in only the western most Province. A National Quarantine involving airports and passenger or package carriers remained in existence following the dropping of the nursery program. Package carriers have gone to great expense to keep adult beetles out of their planes, and away from western states. Japanese beetles were discovered on Terceira in the Azores Islands in the mid-80s, but eradication efforts were doomed from the start, and eventually virtually all of the islands became infested. Hopefully, the European community can adapt from past successes and failures to combat the P. japonica infestations now in Italy and Switzerland

Food safety of genetically engineered-insect resistant crops & pesticides

Authors: Kleter Gijs A.[2] and Project team members IUPAC[1], [1]IUPAC, [2]Wageningen Food Safety Research (part of Wageningen University & Research), Netherlands

Abstract: Whereas Bacillus thuringiensis-derived Cry proteins have dominated the scene of crop biotechnology for most of the time since the mid-90s, various other insecticidal agents have started emerging as of lately. A notable development is the introduction of GM crops encoding certain double-stranded RNA (dsRNA) molecules. These may evoke a phenomenon known as “RNA interference”, which eventually leads to the silencing of the gene whose sequence is complementary to the dsRNA. Moreover, applications have appeared for these types of proteins and polynucleotides beyond their expression in GM crops, such as in sprayable formulations with which the protein or dsRNA is sprayed directly onto crop plants that are to be protected. The safety assessment of these active agents expressed in GM crops hosting them is carried out according to the internationally harmonized principles enshrined in FAO/WHO Codex Alimentarius guidelines for recombinant DNA plants. As for the safety of pesticide formulations of proteins and dsRNA, these may be categorized as, for example, biopesticides or other low-risk categories with specific and more specific and risk-proportionate risk assessment requirements than the extensive testing required for mainstream chemical active ingredients and may in some cases also be exempt from action threshold owing to favorable safety profiles.

Development and evaluation of novel spatial repellent delivery devices for the improving adult control strategies of the peridomestic species, Aedes albopictus and Ae. aegypti.

Authors: Kline Dan, USDA/ARS/CMAVE, United States

Abstract: Aedes albopictus and Ae. aegypti are two important invasive species in the United States, which on a worldwide scale transmit several arboviral diseases including dengue, chikungunya, yellow fever and Zika. These mosquitoes are often the dominant species occurring in peridomestic habitats. Even if the threat of imminent disease transmission is lacking their presence causes much annoyance in peridomestic areas, resulting in residents not being able to enjoy performing activities in their yards. Traditional control strategies in the U.S., with heavy reliance on the use of chemical insecticides being delivered by ULV spray trucks is largely ineffective. Therefore, complementary vector control methods are needed to enhance existing control efforts. Several alternative technologies are currently being considered at USDA-ARS, CMAVE, Gainesville, Florida, USA, to improve control of these two species. The use of spatial repellents in the peridomestic environment is one technology being evaluated. Various active ingredients and delivery devices, both active and passive, are being developed and evaluated. Some novel devices target protection of the individual while others target area protection.

Anthropocenic ozone levels can disrupt a fly’s sex communication

Authors: Knaden Markus[1], Jiang Nanji[1] and Hansson Bill S.[1], [1]MaxPlanck Institute for Chemical Ecology, Germany

Abstract: Insect sexual communication often relies upon olfactory signals, the so-called sex pheromones, which can inform about species identity, sex, and mating status of a potential mate. Most insect pheromones, however, contain carbon-carbon double bonds and hence can potentially become degraded by oxidation. Here, we report that the current increased levels of Anthropocenic ozone in the atmosphere oxidize fly pheromones and by that disrupt sex recognition in many drosophilid species.

Invasive host caught up with a native parasitoid: Field data reveal high parasitism of Harmonia axyridis by Dinocampus coccinellae in Central Europe

Authors: Knapp Michal, Department of Ecology, Czech University of Life Sciences Prague, Czech Republic

Abstract: The harlequin ladybird, Harmonia axyridis, is considered to be one of the most invasive insect species worldwide. Its invasion success and extreme speed of range expansion has been partially attributed to weak control of its populations by natural enemies. Previously published data on emergence rates of the hymenopteran parasitoid Dinocampus coccinellae support the enemy release hypothesis: Harmonia axyridis has been consistently less successfully parasitized compared to native ladybird species. In this study, we show that since 2016, i.e. 10 years after its arrival in Central Europe, several populations of H. axyridis in the Czech Republic have a very high prevalence of D. coccinellae parasitism. Dinocampus coccinellae emerged from 46 % of H. axyridis individuals in the most parasitized population. Moreover, H. axyridis was more parasitized than the native Coccinella septempunctata in seven of nine investigated co-occurring populations. The meta-analytically pooled estimate of D. coccinellae emergence rate from H. axyridis across the Czech populations (this study) is thirteen times higher than the pooled estimate for invasive populations of this beetle elsewhere (historical data up to 2016). We hypothesize that some Central European populations of D. coccinellae have evolved to overcome the immune system of H. axyridis, which was previously thought to be responsible for the high larval mortality of D. coccinellae. As parasitism rates are highly variable in time and space, we encourage future research investigating the determinants of parasitoid prevalence in H. axyridis and other large ladybird species on a continental scale.

Winter survival, post-overwintering energy reserves and basic immune parameters in laboratory-reared and field-collected invasive ladybirds

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Abstract: The harlequin ladybird, Harmonia axyridis (Pallas, 1773) (Coleoptera, Coccinellidae) is considered one of the most invasive insect species in Europe and North America. H. axyridis has an effective immune system which was proposed to be partly responsible for its successful invasion. High winter survival is another important factor that can explain the successful invasion of H. axyridis in temperate zones. Using two independent studies, we investigated the effects of overwintering temperature on survival, energy reserves, and basic immune parameters for laboratory-reared and field-collected beetles.

In the first study, we investigated the effect of different winter temperature regimes (warm, average, and cold) on the winter performance of H. axyridis. The warm winter regime increased survival rate and body mass loss and reduced post-winter starvation resistance in both laboratory-reared and field-collected beetles compared to the cold winter regime. Winter survival of laboratory-reared beetles was much lower than that of field-collected beetles. Laboratory-reared beetles lost a larger proportion of their body mass and had a reduced post-winter starvation resistance. Pre-overwintering body mass positively affected winter survival and post-winter starvation resistance in both laboratory-reared and field-collected ladybirds. The differences between laboratory and field individuals indicate that quantitative conclusions derived from studies investigating solely laboratory-reared individuals cannot be directly extrapolated to field situations.

In the second study, we investigated the effects of overwintering on selected physiological and immune parameters of H. axyridis. For laboratory-reared beetles we tested effects of three temperature regimes (cold, average and warm winter) on haemocyte concentration. For field-collected beetles we measured also total protein concentration and antimicrobial activity against E. coli, and all parameters (including haemocyte concentration) were measured for innate as well as for E. coli challenged beetles. Concentration of circulating haemocytes for laboratory-reared beetles decreased significantly in the course of winter. Data for field-collected beetles confirmed the result obtained for laboratory-reared beetles, and haemocyte concentration was also marginally affected by immune challenge. Concentration of circulating haemocytes increased in challenged compared to untreated individuals before overwintering but not after overwintering. Total protein concentration in the haemolymph of H. axyridis increased significantly during the overwintering. Females had significantly higher total protein concentration in their haemolymph compared to males. Antimicrobial activity against E. coli did not changed during overwintering and was unaffected by immune challenge. This research was financed by grant IGA 42110/1312/3145 (FES-CULS Prague).

Do field defects support beneficial arthropods and ecosystem services within arable fields?

Authors: Knapp Michal[2], Kadlec Tomáš[1], González Ezequiel[1] and Seidl Miroslav[1], [1]Czech University of Life Sciences Prague, Czech Republic, [2]Department of Ecology, Czech University of Life Sciences Prague, Czech Republic

Abstract: Non-crop habitats within agricultural landscapes can increase biodiversity and provide important ecosystem services in adjacent fields. Field defects are temporary non-crop patches within arable fields where the crop is poorly developed and other plants can emerge. Despite that these defects can be common, their relevance as habitat for insects is unknown. Therefore, we investigated natural field defects as well as artificial field defects created at field edges and field interiors in collaboration with farmers. We found that natural field defects represent suboptimal habitats for carabids compared to field interiors and the boundaries between them. Similarly, ecosystem services provided by carabids (pest predation and weed seed predation), were slightly reduced in field defects. Low plant cover within field defects probably created hostile conditions for carabids preferring microhabitats with high humidity and moderate temperatures. In artificially created defects within oilseed rape (OSR) fields, we investigated diverse arthropod taxa covering various beneficial groups, e.g., parasitoids, predators, pollinators and decomposers. In general, we found a significant interaction between habitat type and sampling period. During late spring (OSR flowering), similar numbers of species and individuals were found in field defects and field interiors (OSR crop). In summer (when OSR was ripe and desiccated), richness and abundance were much higher in field defects than in OSR crops. Only small differences between defects created at field edges and interiors were detected for many groups. Overall, our results indicate that field defects are important habitats that can enhance abundance and species richness of several groups of beneficial arthropods, especially after crop flowering. This study was funded by grant GACR 18-26542S.

The earliest known occurrence of endophytic herbivory, a Pennsylvanian leaf mine and its evolutionary implications

Authors: Knecht Richard[1], Emma Steve, Benner Jacob[2], Pierce Naomi[1] and Ortega-Hernández Javier[1], [12]Harvard University, United States, [2]University of Tennessee, Knoxville

Abstract: Preserved tissue damage on fossil plants provides valuable insights into the evolutionary and ecological history of plant-insect interactions. Leaf mines, traces of insects whose larval stages feed and live primarily within the parenchymal and mesophyll layers of leaves, are well represented in the fossil record, with the oldest examples dating back to the mid-Triassic (Mesozoic). Several Late Paleozoic leaf mines have been proposed but lack enough defining characters (e.g., stepwise increases in mine width, oviposition site, terminal chamber, etc.) to be generally accepted. Herein, we describe a new fossil leaf mine, with clear defining characters, on a Neuropteris pinnule from the Carboniferous (309.5-315.2 myo) of Massachusetts, USA. This leaf mine is coeval to the oldest known holometabolous insect, an exophytic larva, but extends the oldest occurrence of endophytic larvae by ~65 million years. Leaf mining is only found in the insect orders Coleoptera (8 families), Diptera (18 families), Hymenoptera (3 families), and Lepidoptera (34 families). Phylogenetic evidence along with morphological characters of leaf mines observed in modern leaf mines narrows down the possibilities to an early Lepidopteran or Coleopteran trace maker. This fossil may add additional support to earlier claims of leaf mines in other Paleozoic deposits.

Can bumblebees self-medicate? Investigating secondary nectar metabolite-parasite interactions in the lab and in the field

Authors: Koch Hauke, Royal Botanic Gardens, Kew, United Kingdom

Abstract: Bees can receive medicinal benefits from nectar and pollen secondary metabolites against their parasites. However, many open questions regarding the interaction of secondary metabolites and bee parasites in the host remain. I here present research on the effects and internal dynamics of nectar metabolites on the common intestinal trypanosomatid parasite Crithidia bombi in bumblebees (Bombus terrestris). I identify active secondary metabolites in the nectar of three common foraging sources for Bombus terrestris in Europe: linden trees (Tilia sp.), strawberry trees (Arbutus unedo) and ling heather (Calluna vulgaris).The compound callunene in heather nectar leads to the loss of the parasite flagellum (which is needed for motility and attachment), thereby reducing infection probability. I show that chemical modification through glycosylation or deglycosylation of nectar metabolites from Tilia and Arbutus nectar during gut passage can strongly alter antiparasitic activity. This modification can stem from the host or the bumblebee gut microbiome. I close by presenting experimental field data examining if Crithidia infected bees collect nectar or pollen of different secondary metabolite composition, to test their ability to self-medicate under natural conditions.

Current knowledge and future challenges in the world biodiversity and biogeography of Zygentoma

Authors: Koch Markus[3], Smith Graeme[2], Molero Rafael[4] and Mitchell Andrew[1], [1]Australian Museum, Sydney, Australia, [2]Australian Museum, Sydney, Australia, [3]Institute of Evolutionary Biology and Ecology, University of Bonn, Germany, [4]University of Cordoba, Spain

Abstract: The Zygentoma are an ancient and widely distributed hexapod order but are poorly studied. Almost 660 silverfish species have been described in five families. They can be found in a variety of habitats including free-living, especially in dry environments, in soil and deep subterranean habitats as well as living in the nests of ants and termites. A few species are peridomestic pests. The biodiversity and biogeography of the order is reviewed and a preliminary molecular phylogeny is presented. Some of the open questions and challenges facing us are presented, the most obvious being the lack of experienced taxonomists and the large number of countries whose fauna is almost unknown.

Knowing Microcoryphia (Insecta): Proposal of a standardized description of new taxa

Authors: Koch Markus[3], Gaju Miquel[2], Molero Rafael[5], Bach de Roca Carmen[1] and F. Mendes Luis[4], [1]Barcelona, Spain, [2]Department of Zoology, University of Córdoba, Spain, [3]Institute of Evolutionary Biology and Ecology, University of Bonn, Germany, [4]Museu Nacional de História Natural e da Ciência; Universidade de Lisboa; Lisboa, Portugal, [5]University of Cordoba, Spain

Abstract: Jumping bristletails of the order Microcoryphia (= Archaeognatha) are the most basal lineage of the Insecta. More than 550 species have been described thus far, with fossils from the Triassic, and grouped into two families with different geographical distribution, the Machilidae preferably in the Northern Hemisphere and the Meinertellidae in the Southern Hemisphere. Only a few researchers publish regularly on the taxonomy of the jumping bristletails, although their anatomy and phylogeny regularly attract broad interest in the context of insect evolution. The first fairly precise taxonomic descriptions were made by Silvestri in 1905. However, a revision of the early accounts is necessary, since many of the characters used today to delimit species were not contemplated in the original descriptions. Contemporary accounts are likewise rarely complete as they often omit morphometric values or detailed descriptions of some secondary sexual characters. Our contribution calls for a standardization that homogenizes the taxonomic study of the group, so that the species are described, whenever possible, based on characters that allow proper comparisons between the different taxa. This standardization is currently essential for precise estimation of the global species richness and a prerequisite for accurate phylogenetic analyses.

Pollen preference and nutritional components of pollen collected by honeybees (Apis mellifera) in Murang’a county, Kenya

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Abstract: Several factors have been linked to honeybee population decline globally. Such include limited floral resources, bee pests and diseases, and agricultural pesticides. However, it is largely because of limited floral resources owing to increased land use and fragmentation, contributing to a nutritional shortage. The aim of this study is to investigate the pollen preferences and nutritional component, as well as the levels of pesticide residues of pollen (corbicular) collected by Apis mellifera in three different landscapes (high, medium, and low vegetation diversity) in Murang’a, Kenya over a period of 12 months. Six farms per landscape containing each two colonies of A. mellifera will be used in this research. Bottom fitting pollen traps will be used to collect pollen samples at each hive entrance. The sampling will be done from November 2019 to October 2020. Pollen loads will be analyzed for abundance and diversity of contributing plant species, but also for crude protein content, proline, lipids, as well as the pesticide residues. The findings of this project will improve the knowledge on what crops to cultivate and conserve, the type of pollen or supplement to feed, and the level of pesticide residue contamination. These findings will help guide the government and stakeholders to develop strategic conservation protocols that preserve or restore A. mellifera foraging habitats.

Beetle assemblage across elevations and indicator functioning in Peninsular Malaysian mountains

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Abstract: Community composition, their relative shares, and interactions – largely determines biodiversity responses to environmental variation. Communities also vary according to, among other aspects, latitude and altitude (Ashton et al., 2015). This study assesses the indicator functioning and beetle assemblage across elevations at two mountain slopes in Peninsular Malaysia. The beetle sampling was carried out at elevations: 500m, 1000m, 1500m and 1800 m ASL, where pitfall, Malaise and light traps were used to capture the beetles. The statistical analysis were conducted using GLMM, NMDS and IndVal softwares. The collection was resulted in 198 morpho-species of beetles, from 32 families total number of 3052 beetles. Species richness declined with altitude in light and Malaise but not in pitfall, the two mountains differed considerably in pitfall but less so in light or Malaise data. NMDS showed light traps is distinguished at 1,800 m from lower altitudes. Malaise and pitfall traps reflected primarily variation between the two mountains. IndVal, low altitudes had about twice as many indicators as middle or high altitudes. This research found 83 indicator species for different combinations of Method and Altitude. Light and Malaise trap samples shared about half of the abundant species, whereas pitfall trap samples were distinctive in this respect. Our results are applicable to tropical species conservation, as they provide evidence for many species to be adapted to particular altitudes and, more importantly, differences in beetle samples between collecting methods, which in turn calls caution in analysis interpretations. Therefore, conservation efforts should be based on results obtained using multiple sampling and analysis methods.

Development of conditional sterility system in Aedes aegypti males

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Abstract: Dengue, Chikungunya and Zika, currently, are the most noticeable diseases affecting several countries in the tropical and subtropical areas, and due to global warming and globalization, they are now reaching and spreading very fast to areas without a transmission history. Complementary strategies, in order to contribute with the available methods and fight the disease, are under development or evaluation. These strategies comprise methods to reduce the mosquito populations to levels below the transmission threshold. The well established Sterile Insect Technique (SIT) have proven to be an efficient and effective method against fruit-flies and screwworm, by releasing millions of sterile males on the field and promote the population collapse over time. The sterility is reached by exposing insects to an ionizing radiation source, reducing the general fitness of these males as side effect.

This study proposes the establishment of a transgenic construction to promote a conditional sterility only in males. The advantage of this construction is the possibility to promote sterility without irradiating the insect, resulting in a better performance without compromising fitness.

Embryonic microinjection using a pMos-3XP3-DsRed plasmid carrying an effector gene where, males conditionally express the Apoptosis-Inhibitor-Protein (AIP) antagonist, Michelob_x during embryogenesis, resulted in the establishment of transgenic lines dependent of tetracycline to block sterility. Five out of six strains had mRNA expression of Michelob_x detected by RT-PCR, leading to the challenge of these strains with a mating with non-transgenic virgin females and determining their residual fertility. One out of five strains showed significant reduction in the residual fertility in the absence of the antibiotic, while there was no reduction when they were supplied with antibiotic. This strain had a sterility level of approx. 62% under heterozygosis. This encouraging result led us to the development of another approach to a higher impact on male fertility.

Computer modelling of wing rotation in bumblebees

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Abstract: During hovering and slow forward flight, flapping wings of insects can produce positive upward force on both upstroke and downstoke. This is achieved by large pitching (feathering angle) rotations at the end of each half-cycle necessary for maintaining positive kinematic angle of attack. Prior experiments with robotic flappers have demonstrated similar kinematic patterns produced by wings with only up and downstroke motion being driven directly and elastic hinge attachment permitting passive pitching rotation. Thus, pitching motion of the wings emerges as a result of fluid-structure interaction. In our study, we evaluated the role of fluid-structure interaction for wing rotation of bumblebees Bombus ignitus. Bumblebee hives (Mini Polblack) provided by Arysta LifeScience ltd were maintained at Chiba University from October 2015 to September 2016. The experimental chamber consisted of the hive and a feeding area connected by a flight tunnel with transparent ceiling. The bees were trained to fly through the tunnel. The flights were recorded with three synchronized high-speed cameras (Phantom SA3, Photron), equipped with CCTV lens (B2514D or B5014A, Pentax) at 2000 fps. We used an open-source software DLTv5 to reconstruct the three-dimensional coordinates of the bees. Morphological models of the wings were constructed on a basis of photographic images. Surface density distribution of the membrane was determined by dissecting the wings and measuring the weight of each part. Micro-CT scans (Shimadzu inspeXio SMX-100CT) were used to measure the vein thickness necessary for calculating their linear density distribution. The moments of inertia were obtained by integration of the vein and the membrane density distributions. Subsequently, using the acquired physiological data, computer simulations of the wing motion were carried out. The bumblebee was represented by three rigid elements: the body and two wings, which moved relative to each other. Time-periodic positional angular motion of the wings was prescribed, while the pitching rotation was found by solving an ordinary differential equation with the aerodynamic pitching moment obtained from numerical solution of the partial differential equations governing the surrounding air flow, see an example visualization in the figure. The values of the hinge stiffness coefficient that minimize the mean squared error between feathering angle in the simulation and the experiment were determined by parametric sweep. The results indicate that the hinged plate model provides a reasonably accurate approximation of real bumblebee wing motion. Considering the normalized hinge stiffness as a material parameter, we conjecture that the same optimal value may be adequate for all flight regimes. This would open the perspective of numerical simulation of complex flight maneuvers using only the wing-tip kinematics as input data, which is much easier to measure in the experiments than the full three-dimensional wing kinematics.

Warming alters indirect effects of wolf spiders on litter-dwelling microbial communities in the Arctic

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Abstract: Understanding controls on carbon cycling in the Arctic is critical due to the rapid pace at which this region is warming and its potential feedbacks on the global climate. Despite the importance of the microbial community for driving key soil functions, knowledge of how biotic interactions contribute to microbial community structure and function in this region remains limited. For example, microbial community composition is influenced by the consumer community, which is in turn regulated by litter- and soil-dwelling predators. Wolf spiders are dominant tundra predators that have cascading effects on their detrital prey, decomposition, and soil nitrogen, suggesting that wolf spiders may also influence microbial communities. We tested the effects of wolf spider density and warming on the diversity and composition of litter-dwelling bacterial and fungal communities through a fully factorial mesocosm experiment over two summers in the Alaskan Arctic. We deployed two sets of replicate litter bags at the soil surface and buried in the upper organic horizon and collected the litter bags at the end of the first and second summers. We extracted microbial DNA from subsamples of the litter and prepared Illumina libraries by PCR amplification of bacterial 16S and fungal ITS before processing the sequences via QIIME. After one summer, there were no treatment effects on fungal diversity, but both surface and buried litter in warmed plots had significantly reduced bacterial diversity. After two summers, there were significant interactive effects of wolf spider density and warming on bacterial and fungal diversity. Specifically, under ambient temperature, bacterial diversity increased with increasing spider density, whereas in experimentally warmed plots, higher spider density reduced bacterial diversity both at the soil surface and in buried litter. Treatment effects on fungal diversity varied by location. At the surface, fungal diversity increased with increasing spider density, but this trend was opposite under warming. In buried litter bags, fungal diversity was reduced in low and high spider density treatments compared to the control, whereas under warming, fungal diversity tended to decrease with increasing spider density. There were also interactive effects of wolf spider density and warming on fungal and bacterial community composition after one summer and on the fungal community after two summers. Overall, our results indicate that the effects of wolf spiders on detrital food webs in the Arctic extend to microbial communities but that warming alters these effects. Moreover, these findings suggest that generalist-feeding predators may play an underappreciated role in driving variation in microbial community composition in the Arctic.

The egg-larval parasitoid, Ascogaster reticulata, utilizes ubiquitous volatiles from intact plants to discriminate leaf ages of tea plants

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Abstract: The moth, Adoxophyes honmai, causes serious damage to tea plants, one of the most important crops in the world. Ascogaster reticulata is an egg-larval parasitoid, and one of the principal natural enemies of A. honmai. However, modulation of interactions between parasitoids and the host moth by tea plant odor has not been well studied. Previous investigations have shown that A. honmai prefers to oviposit on mature tea leaves (ML) rather than young leaves (YL). Therefore, we hypothesized that A. reticulata locates host egg masses by searching close to ML when host-derived cues are not available. In this study, we investigated leaf age preferences of A. reticulata and identified attractive volatiles from ML.

A dual-choice bioassay using a 4-arm olfactometer was performed to determine leaf age preferences of A. reticulata. Female wasps preferred intact ML odor over YL. Interestingly, they did not discriminate between YL volatiles and control (clean air). Volatiles from ML and YL were collected using the head-space volatile collection method, and were analysed with GC-MS. Quantitatively, YL emitted greater amounts of volatiles than ML.

We identified 10 compounds from YL and 5 compounds from ML. Although 4 compounds (Z)-3-hexenyl acetate (H), (E)-ß-ocimene (O), linalool (L), and DMNT (D) were found in both, methyl salicylate (M) was detected only in ML. Based on these results, the 5 ML volatiles were regarded as candidate attractants. Blends of 4 or 5 compounds were prepared (HOLDM, HOLD, HOLM, HODM, HLDM, and OLDM), ratios of which were adjusted to match those of ML volatiles. Single componuds (H, O, L, D, and M) were also examined. Parasitoid preferences were tested in comparison with solvent controls using an olfactometer. Parasitoids showed positive responses to HOLDM and HOLM, but not to other blends or to single compounds.

Wasps were attracted to volatiles of ML, supporting our hypothesis. The adaptive significance is that by tracking plant volatiles, parasitoids are more likely to encounter host egg masses in the absence of host-derived cues. Parasitoids preferred blends of H, O, L, and M, indicating that wasps detect tea plant ML based on some of their volatile components. Moreover, the attractive blend components are ubiquitous plant volatiles even though proportions of them may change depending on the species. Such non-specific responses to plant species are necessary for host searching by this parasitoid since the host moth is a generalist. On the other hand, parasitoids distinguish between ML and YL of tea plants, the main host plant of their host moth, by detecitng differences in their volatile components. Taken together, A. reticulata utilizes a blend of volatiles from intact plants to efficiently locate potential habitats of its generalist host. In tea fields, A. reticulata can distinguish appropriate leaf age for host location.

Efficacy of different entomopathogenic fungal isolates against the developmental life stages of three key edible insect species

Authors: Komivi Akutse

Abstract: Globally, the interest to produce black soldier fly (Hermetia illucens L.) and crickets (Gryllus bimaculatus and Scapsipedus icipe) in mass for feed and food, respectively, is gaining attention. Despite their economic importance, there is limited information on the risk of entomopathogenic fungi on the BSF (larval and adult stages) and crickets (nymphal and adult stages), which is vital to the production system. This study evaluated new research on the risk and effects of disease-causing pathogens (Beauveria bassiana and Merthizium anisopliae) on the mortality, egg-laying capacity, and sporulation when the insects were subjected to different concentrations of the fungi species. We showed that adult flies and crickets were more susceptible to the biocontrol agent B. bassiana and M. anisopliae, with high mortality (>70%) than the other life stage in high dose treatment. This confirmed the pathogenicity of both fungal pathogens against BSF and crickets, with potential for significant negative consequences for production.

Multifunctional monoterpenes contribute to the establishment of mutual adaption and restriction relationships between host and Ips typographus L.

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Abstract: Host monoterpenes acting as host defense compounds can be exploited by I. typographus as aggregation pheromone precursors and/or kairomones, and by natural enemy such as predators as a synomones for finding their prey. In the current study, the toxicities of three monoterpenes: S-(-)-a-pinene, R-(+)-a-pinene and myrcene as potential bark beetle pheromone precursors were evaluated on I. typographus adults in both contact and fumigation tests. The in vivo productions of volatile metabolites in the hindguts of males and females when topically treated with these three monoterpenes were analyzed by gas chromatography (GC) and GC coupled with mass spectrometer (MS). The behavioral activities of these monoterpenes when combined with the aggregation pheromone of I. typographus were assayed in the field. These three monoterpenes showed significant insecticidal activities on I. typographus with LD50 values being ca. 247-358 µg/beetle in the topical assay and LC50 values being ca. 3.38-4.54 µl/ml in the fumigation assay, which might be the major host tree defense strategy against the beetles with S-(-)-a-pinene being the most significant. In GC/GC-MS analyses, S-(-)-cis-verbneol, (+)/(-)-trans-verbenol, S-(-)-verbenone, (-)-myrtenal, and (-)-myrtenol were detected in the beetle hindguts when topically treated with S-(-)-a-pinene, and the (+)-trans-verbenol, R-(+)-verbenone, and (+)-myrtenol were detected when topically treated with R-(+)-a-pinene. Productions of these volatile metabolites varied significantly in quantities by sexes of the bark beetles and by chirality of a-pinene [S-(-)- vs. R-(+)-]. E-myrcenol, ipsenol, ipsdienol and their derivatives were not detected in the beetle hindguts when topically treated with myrcene at the dosage tested. S-(-)- and R-(+)-a-pinene showed a significantly synergistic effect on the trap catches of I. typographus, while myrcene revealed a significant antagonistic effect when combined with its aggregation pheromone. The plasticity and multi-functionality of these three monoterpenes might be a part of trade-off strategies in the arms race between the host trees and I. typographus. The S-(-)-a-pinene, as the key monoterpene component of the spruce host trees, might participate in a series of olfactory signal transductions in the tritrophic system of spruce trees – I. typographus – predators, whereas R-(+)-a-pinene and myrcene might also play some roles in host tree defense and behavioral regulations of I. typographus and its predator, Thanasimus substriatus. Our results provided a better understanding of the “trade-off” strategies in the relationship between host trees and bark beetles, and further gained an insight into the co-evolutionary and olfactory mechanisms in the tritrophic system. A deep understanding of all the chemical communication signals used by I. typographus may facilitate an optimal control strategy to combat this economically and ecologically important forest insect pest.

The defense protein MLX56: Its unique structure, its unique mode of function, and its application to produce GM plants resistant to various pests belonging to Lepidoptera, Coleoptera, and Thysanoptera

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Abstract: The Leaves of mulberry, Morus spp. has long been known as a suitable hostplant of the silkworm, Bombyx mori from the ancient time. Recently, we found that mulberry leaves are toxic to insects other than B. mori because of two types of defensive components in mulberry latex, sugar-mimic alkaloids (1-3) and MLX56 family proteins (MLX56 and its close homolog LA-b) (4). MLX56 is a 56 kDa protein consisting of 394 amino acids with a unique sandwich-like structure composed of an extensin domain (Gum Arabic-like domain) surrounded by two hevein (chitin-binding) domains (4). MLX56 inhibited the growth of Spodoptera litura, Mamestra brassicae, and Eri-silkworms, Samia ricini, in 0.01-0.04% concentrations (4). MLX56 has a unique mode of toxic action (5). MLX56 swells the peritrophic membrane (PM, thin chitin-based membrane existing between midgut epithelium and food materials) of Eri-silkworms fed MLX56 into an extraordinary thick gel-like structure by binding to chitin-framework of PM with hevein domains, and swelling PM with extensin domain (5). The thick swollen PM presumably functions as obstacle to digestive processes by decreasing the permeability of digestive enzymes and nutrients through PM, and thereby inhibits the insect growth (5,6). Interestingly, B. mori is resistant to MLX56 as well as to sugar-mimic alkaloids, suggesting the physiological adaptation in the mulberry specialist, and the involvement of the latex components in the evolution of silkworm-mulberry interactions (1-5). We are attempting to make pest-resistant crops using MLX56 (7,8). Tomato, tobacco, and Arabidopsis, transiently (7) or stably (8) expressing mlx56 gene (MLX56 protein) showed strong resistances to various important pests including Spodoptera litura (7,8), Mamestra brassicae (7), Plutella xylostella (Lepidoptera) (7), Henosepilachna vigintioctopunctata (Coleoptera, ladybirds larvae) (8), and Frankliniella occidentalis (Thysanoptera, thrips) (8) suggesting that MLX56 can be a promising substitute/complement of Bt toxin in making pest-resistant crops in future.

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Efficacy of entomopathogenic fungi against Colorado potato beetle (Leptinotarsa decemlineata) under laboratory conditions

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Abstract: The Colorado potato beetle (Leptinotarsa decemlineata) is the most widespread insect pest that causes huge economic losses, especially on potatoes. As a result of the intensive use of insecticides this species has gradually developed resistance to most pesticides and its control is thus currently very difficult. The frequent use of pesticides can have also negative impact on non-target organisms, the environment, and human health. Thereby, the use of biocontrol agents, like entomopathogenic fungi (EPF) is an alternative method for control of this pest. The aim of this study was to assess the efficacy of selected strains of EPF against L. decemlineata adults under laboratory conditions. New EPF strains were isolated from soil samples collected in potato fields in the vicinity of the Czech Republic. Isolation of EPF was performed by a modified method of live traps “Tenebrio bait method” or directly from naturally infected adults of L. decemlineata using selective medium. Fungal species were determined using macroscopic, microscopic, and molecular markers. Totally, 20 strains of EPF isolated from soil samples and 12 strains of Beauveria bassiana isolated from infected adults of L. decemlineata were tested in this study. The highest efficacy against L. decemlineata adults was found in native strains of B. bassiana and the strain of Metarhizium anisopliae (figure) which caused mortality 100 % at the end of the bioassay. The lowest virulence was found in Isaria sp. and Beauveria sp. strains isolated by Tenebrio bait method (ca 80 %). The present study showed that some strains of EPF, especially native strains of B. bassiana and M. anisopliae, might be prospective biocontrol agents against L. decemlineata.

Biologically produced pheromones: Electrophysiological and behavioural responses of Helicoverpa armigera

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Abstract: The detrimental effects of insecticides to human health and the ecosystem has been since long very well documented and the public concern constitutes a significant leverage to public bodies and the scientific community to seek equally efficient but environmentally safe alternatives for pest control using biological or biotechnological methods. In this context pest management systems based on pheromones present a lucrative solution. As an ever-increasing number of chemical insecticides is withdrawn from the market the need for eco-friendly approaches to pest management based on pheromones, such as mating disruption, mass trapping, etc., offers a great challenge to humans and the environment and has the potential of a multiplier effect on the economy.

Currently pheromones are produced by chemical synthesis through an expensive and polluting process, which constitutes a limiting factor to their widespread use.

OLEFINE project (http://olefine.eu/) will produce pheromones from yeast cells in bioreactors through the development of a novel technology that reduces production costs significantly. Biological production of low-cost pheromones will enable the rapid adoption of pheromone-based pest management products that can be used as effective and non-toxic alternatives to insecticides.

Validation and comparison of the efficacy of the in-yeast-produced pheromones with those chemically synthesised, was performed by electrophysiological methods and field tests on the cotton bollworm, Helicoverpa armigera (Hübner) (Lepidoptera: Noctuidae). Specifically, we evaluated the antennal responses to compounds produced by fermentation constituted mainly of Z11-hexadecenal (major component of the sex pheromone) in comparison to commercially available pheromones.

In addition, by electroantennography coupled with gas chromatography (GC-EAD) we investigated whether any impurities left in biologically synthesised pheromones after purification can be perceived by the insect’s antennae and potentially interfere with its normal behaviour.

Laboratory behavioural bioassays and field test in cotton fields in Greece, confirm the activity of the bio-pheromones. The results obtained indicate that there are no differences between the biologically produced pheromones and those chemically synthesised.

Pheromone production from yeasts is an innovative, market disruptive technology and is expected to have a strong impact on the Plant Protection Products (PPP) Industry.

This project is implemented under the framework of Horizon 2020/NMBP-BIO-2017 OLEFINE (OLEaginous yeast platforms for FINE chemicals), which is funded from the European Union’s Horizon 2020 research and innovation programme.

Entomopathogenic nematodes for the management of the Japanese beetle and other invasive white grub species

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Abstract: The larvae of several invasive white grub species are among the most important insect pests of turfgrass and ornamental plants in eastern North America. The Japanese beetle (JB), Popillia japonica, is the most widespread and notorious of these, but species like the oriental beetle (OB), Anomala orientalis, or the European chafer (EC), Rhizotrogus majalis, are regionally more important. White grubs share their natural soil and rhizosphere habitats with entomopathogenic nematodes (EPNs). At least 5 EPN species were originally collected from naturally infected white grubs, and many more have been documented to use white grubs as natural hosts. White grub species differ in their susceptibility to EPNs and the relative virulence of different EPN species also varies among white grub species. Moreover, larval stages of white grubs may also differ in their susceptibility, but the effect varies with white grub and EPN species. Good control (i.e., = 70% in field studies) in turfgrass of JB, has been achieved with the EPNs Steinernema scarabaei (100%), Heterorhabditis bacteriophora (34–97%), and H. zealandica (73–98%). S. scarabaei is the only species that has provided high field control of OB (87–100%) and EC (89%).

EPN efficacy against these pests in ornamental nurseries has been highly variable (0-100%), likely due to factors similar as in turfgrass. However, research has been more limited, and none of the most promising species or strains more recently tested in turfgrass have been tested in nurseries.

EPN persistence beyond a season following application against white grubs has been reported for H. bacteriophora and S. scarabaei. Due to the excellent adaptation of S. scarabaei to white grubs (high virulence, recycling) and outstanding IJ persistence, a single application of this species provided control of OB within 1 month (77–100% at 0.25–2.5 × 109 IJs/ha), provided additional control in the following spring (86–100% at 0.1–2.5 × 109 IJs/ha), and suppressed OB for up to 4 years.

Combining EPNs with other control agents can increase consistency and level of pest control,and lower costs by being able to use reduced rates of chemicals and EPN. Much of the work on combining EPN with other control agents has been conducted in turfgrass with JB and other invasive species. The best studied and most feasible combinations are those of EPNs with the neonicotinoid imidacloprid. Imidacloprid interacted synergistically in combinations of 4 EPN species in third instars of JB and OB. Imidacloprid–H. bacteriophora combinations provided more consistent synergism against third instars but higher control rates against second instars and early third instars using rates as low as 25% and 50% of the full rates for H. bacteriophora and imidacloprid, respectively. Combinations of the anthranilic diamide chlorantraniliprole and H. bacteriophora resulted in mostly synergistic mortality of third–instar JB and OB.

Advances in use of EPNs turfgrass and ornamentals

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Abstract: Turfgrass is one of the best studied commodities regarding use of entomopathogenic nematodes (EPNs). Much of the research has been conducted in the USA. The best studied insect groups for EPN use are white grubs, mole crickets, weevils, and lepidopteran larvae.

The efficacy of EPNs against white grub species varies with white grub species and larval stage and EPN species. Good control of Japanese beetle, Popillia japonica, was observed with S. scarabaei (100%), H. bacteriophora (34–97%), and H. zealandica (73–98%). Only S. scarabaei provided high control of the oriental beetle, Anomala orientalis (87–100%), the Asiatic garden beetle, Maladera castanea (71–86%), and the European chafer, Rhizotrogus majalis (89%). Good control of the northern masked chafer, Cyclocephala borealis, was observed with H. zealandica (72–96%), S. scarabaei (84%), and H. bacteriophora (47–83%). EPN persistence beyond a season following application against white grubs has been reported for H. bacteriophora and particularly the scarab-adapted S. scarabaei.

Invasive mole crickets are important turfgrass pests in the southeastern USA and were controlled with broadcast applications of S. scapterisci and S. riobrave (both 75%). The introduction into the USA of the mole cricket adapted S. scapterisci, isolated from mole crickets in Uruguay and Argentina, was the first successful use of an EPN in classical biological control. It is more effective against the southern mole cricket (S. borellii) than against the tawny mole cricket (S. vicinus) and least effective against the short-winged mole cricket (S. abbreviatus); it is most effective against adult mole crickets and is ineffective against small nymphs. S. scapterisci use in more damage sensitive areas has been limited due to competition from insecticides and by the heavy use of nematicides. In pastures, it has been applied using slit injectors in strips covering 12.5% of the area from which it then spreads over several years.

The bluegrass billbug, Sphenophorus parvulus, was effectively controlled with S. carpocapsae (78%) and H. bacteriophora (74%) in the USA. On golf courses in Japan, S. carpocapsae was very effective for control of the hunting billbug, S. venatus vestitus (84%). Control of annual bluegrass weevil, Listronotus maculicollis, larvae on golf courses with S. carpocapsae, S. feltiae, and H. bacteriophora was variable (0-94%). Split applications of S. carpocapsae were more effective and in combination with the neonicotinoid insecticide imidacloprid provide 84-98% control.

Black cutworm, Agrotis ipsilon, larvae are a pest of golf course greens and tees. S. carpocapsae was the best performing EPN (70–90%). Syringing (twice daily small amount of irrigation) provided limited improvement of S. carpocapsae efficacy under warm, sunny conditions, and split application improved efficacy by around 20%.

The secret of a long, fecund life: why can social insect queens live so long?

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Abstract: Social insect queens can have extraordinary lifespans and at the same time produce many offspring whereas their nestmate workers are often short-lived and functionally sterile. This seems to violate the common life history trade-off between fecundity and longevity which predicts a negative association between these traits. Within the research consortium ‘So-Long’, we study different ants, bees and termites, using the non-social fruitfly Drosophila melanogaster as an ‘outgroup’, to obtain insights into common mechanisms and causes underlying the apparent reversals of the trade-off. To do this we performed a canonical set of experiments across taxa and applied standardized analyses (incl. transcriptomes).
At the mechanistic, molecular level our data suggest that network changes associated with the long, fecund lifespan of queens differ across taxa. Yet, all these mechanisms are connected with the TI-J-LiFe genetic network, which includes the TOR (target of rapamycin) and IIS (Insulin/insulin-like growth factor) signalling pathways, juvenile hormone and downstream pathways such as those involved in immune defence or oxidative stress. At the evolutionary ultimate level, our experimental data indicate that sociality is key to explain the long lifespan of queens. They provide evidence for a superorganismal analogy where workers function partly as disposable soma and queens as germline. Overall, our results provide new insights to the question ‘How and why social insect queens can live so long’.

What happens to fruit-feeding butterfly communities and diversities during tropical forest restoration?

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Abstract: The alarming rate of deforestation of tropical forests has resulted in decline in biodiversity and has compromised ecosystem functioning. The primary aim of forest restoration approaches has been to reinstate the original vegetation. Less emphasis has been placed on other aspects of biodiversity, such as insect communities.

We investigate the recovery patterns of fruit-feeding butterfly communities across a tropical forest restoration project area of Kibale National Park, Uganda. Study sites represent seven restoration areas planted between 1995 and 2011, as well as two primary forest areas. At each study site we used one cylindrical trap baited with fermented banana. The sites were first sampled in 2011-2012 (40 study sites), and the sampling was repeated with five additional study sites in 2020-2021, allowing a direct comparison of how communities and diversities have changed in the nine years.

During the 2011-2012 census we captured a total of 4 588 fruit-feeding butterflies from 67 species, while during the 2020-2021 census 10 015 individuals from 98 species were captured. As a main result, we found that communities in restored forests were becoming more similar to the primary forest communities over time. We conclude that forest restoration also supports the recovery of fruit-feeding butterfly communities

Insect antennae: coupling blood pressure with cuticle deformation to control movement

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Abstract: Insect antennae are hollow, blood-filled fibers with complex shape with muscles only in the two basal segments (scape and pedicel). The distal part of antenna, the flagellum, is muscle-free, but the insect can controllably flex, twist, and maneuver it laterally. To explain this behavior, we performed a comparative study of structural and tensile properties of the antennae of Periplaneta americana, Manduca sexta, and Vanessa cardui. These antennae demonstrate a range of distinguishable tensile properties, responding either as brittle fibers (M.sexta) or strain-adaptive fibers that stiffen when stretched (V.cardui and P.americana). Electron microscopy and high-speed imaging of antennal breakup during stretching revealed complex coupling of blood pressure and cuticle deformation. A solid mechanics model was developed to explain this behavior. The model was validated on artificial antennae with no adjustable parameters. The pressure-cuticle coupling can be controlled through changes of the blood pressure of volume in the antennal lumen and resulted in strain-adaptive behavior. In insects that do not fill the antennal lumen, this blood pressure control is lacking, and the antennae react only by muscular activation; their stress-strain curve is similar to that of a hollow fiber such as a cotton fiber.

Does food enrichment by Hermetia illucens larvae affect overwinter survival and spleen size in the brown trout (Salmo trutta)?

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Abstract: Various enriched rearing methods have been promoted as a possible cost-efficient way to produce fish stockings that show increased survival in the wild. We reared brown trout juveniles in enriched and conventional tanks, provided them novel food enrichment (Hermetia illucens larvae), and finally studied their overwinter survival and relative spleen size. We did not find difference in overwintering survival between the trout that received H. illucens food supplementation and the trout that were not food-supplemented. However, the trout reared under early enriched conditions seemed to show higher feeding performance to forage on these novel prey items, and they had also relatively larger spleens than trout reared in conventional environment. Our results suggest that early enriched rearing provides beneficial and long-lasting effects, but that possible beneficial effects of H. illucens food supplementation remain unclear. Enriched rearing can be recommended especially when fish stockings are produced for conservation purposes.

Suitability of different Amaranthaceae and Polygonaceae species as food sources for the sugar beet weevil Asproparthenis punctiventris

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Abstract: Asproparthenis (Bothynoderes) punctiventris Germar (Coleoptera: Curculionidae) is widely distributed in Eurasia and one of the most important pests of sugar beet. In addition to sugar beet (Beta vulgaris subsp. vulgaris), several Amaranthaceae and Polygonaceae species have previously been described as food sources of the weevil. To find out whether and which plants can maintain or even promote the beetle population outside sugar beet fields, the leaf consumption of A. punctiventris females on sugar beet was compared with different weeds and other plant species. In addition, differences between mated females during oviposition and unmated females during maturation feeding were investigated in the laboratory. Unmated females consumed the greatest amount of leaf mass from B. vulgaris and about a third less from Atriplex species, indicating that these plants have the highest nutritional value for A. punctiventris. Considerably less was fed on Chenopodium spp. and Amaranthus retroflexus. Spinacea oleracea and all Polygonaceae species were hardly or not fed at all. Mated females generally consumed more leaf mass than unmated. Widespread weeds such as Atripex patula and C. album occurring in high densities in sugar beet and other crops could therefore serve as alternative food source in the absence of sugar beet.

Host plant selection and host use in the sugar beet weevil Asproparthenis punctiventris

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Abstract: The sugar beet weevil Asproparthenis (Bothynoderes) punctiventris (Coleoptera: Curculionidae) is one of the most important pests of sugar beet in Eurasia. It is not known which stimuli adult females during maturation feeding use to find the young sugar beet plants or other plants serving as food source after overwintering, and whether the larvae can also develop on plants with a lower nutritional value than sugar beet. The following plants have, in order, a decreasing nutritional value for females: Beta vulgaris subsp. vulgaris, Atriplex hortensis, B. vulgaris subsp. maritima, Amaranthus retroflexus and Chenopodium album. Females were significantly attracted to leaf odours of Beta spp. and responded positively to odours of A. hortensis and A. retroflexus, but not to C. album. The most and heaviest fourth instar larvae developed on sugar beet, while fewer individuals with lesser weight were found on B. vulgaris subsp. maritima and A. hortensis. Very few larvae were able to develop on C. album, and none on A. retroflexus. The analysis of the odour profiles of Beta spp. and A. hortensis could provide information on which plant volatiles act as olfactory attractants for the sugar beet weevil. Such compounds could be integrated into future sustainable control strategies.

Transcriptome analysis of social isolation response in ants Camponotus fellah

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Abstract: Social deprivation can have negative effects on the lives of social animals, including humans, yet little is known about the mechanisms by which social withdrawal affects animal health. In the carpenter ant Camponotus fellah, socially isolated workers have a greatly reduced lifespan relative to ants kept in groups of 10 individuals. By using a tracking system, we found that social isolation resulted in important behavioral changes and greatly increased locomotor activity. The higher activity of single ants and their increased propensity to leave the nest to move along the walls suggested that the increased mortality of isolated ants might stem from an imbalance of energy income and expenditure. This view was supported by the finding that while isolated ants ingested the same amount of food as grouped ants, they retained food in the crop, hence preventing its use as an energy source. Furthermore, we performed the transcriptome analysis to compare the gene expression between grouped and isolated ants that were separated from the mother colony. We found the differential gene expression related with various metabolic process such as nucleotide, fat, or digestion in isolated ants, and the gene expression profile of isolated ants is similar with that of other organisms which show short lifespan in aged or stressed condition. We would like to discuss about the molecular mechanisms how the social environment affects the fitness of ants from the transcriptome analysis.

Comparative Lidar Studies of Mosquito Habitats

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Abstract: Habitats constitute one of the main components of biodiversity and provide possible indicator of diversity at the species level such as mosquitoes, vector of malaria. Four sites of habitats have been selected to monitor mosquitos' activities with a Scheimpflug lidar during campaign measurement inside the National Polytechnic Institute located in the center of Ivory Coast. We detected more than 2000 mosquitoes per day per site.

Telomerase activity in Bombus terrestris

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Abstract: The attrition of telomeres, the ends of eukaryote chromosomes, and activity of telomerase, the enzyme that restores telomere length, play a role in the ageing process and act as indicators of biological age. A notable feature of advanced eusocial insects is the longevity of reproductive individuals (queens and kings) compared to those from non-reproductive castes (workers and soldiers) within a given species, with a proposed link towards upregulation of telomerase activity in the somatic tissues of reproductive individuals. Given this, eusocial insects provide excellent model systems for research into ageing.

We tested telomerase activity and measured telomere length in Bombus terrestris. In somatic tissues, telomerase activity was upregulated only in the fat bodies of pre-diapause queens, and this upregulation was linked to heightened DNA synthesis. Telomere length was shorter in old queens compared to that in younger queens or workers. We speculate that (1) the upregulation of telomerase activity, together with DNA synthesis, is the essential step for intensifying metabolic activity in the fat body to build up a sufficient energy reserve prior to diapause, and that (2) the lifespan differences between B. terrestris workers and queens are related to the long diapause period of the queen. A possible relationship between telomere length regulation and TOR, FOXO, and InR as cell signaling components, was tested.

Effects of urbanisation on woody plant losses to insects

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Abstract: Despite the increasing rate of urbanization, the consequences of this process for biotic interactions remain insufficiently studied. Individual abiotic drivers of global change, which simultaneously affect urban biota, may differently impact plant-feeding invertebrates. In this presentation I briefly summarize the results of two projects, which compared insect herbivory between urban and rural habitats. Our aims were to identify the general pattern of urbanization impact on background insect herbivory, to explore variations in this impact related to characteristics of both urban areas and insect–plant systems, and to uncover the factors governing urbanization impacts on woody plant losses to insects. We also asked whether urbanisation decreased stability (or, more precisely, increased invariability) of plant – herbivore – enemy interactions. The first project compared the foliar damage inflicted on the most common trees by defoliating, leafmining and gall-forming insects in rural and urban habitats associated with 16 European cities. In two of these cities, we also explored quality of birch foliage for herbivorous insects, mortality of leafmining insects due to predators and parasitoids and bird predation on artificial plasticine larvae. On average, the foliage losses to insects were 16.5% lower in urban than in rural habitats. The magnitude of the overall adverse effect of urbanization on herbivory was independent of the latitude of the locality and was similar in all 11 studied tree species, but increased with an increase in the size of the urban area: it was significant in large cities (city population 1–5 million) but not significant in medium-sized and small towns. Quality of birch foliage for herbivorous insects was slightly higher in urban habitats than in rural habitats. At the same time, leafminer mortality due to ants and birds and the bird attack intensity on plasticine larvae were higher in large cities than in rural habitats, which at least partially explained the decline in insect herbivory observed in response to urbanization. The second project, in addition to defoliating, leafmining and gall-forming insects, addressed also sap- and root-feeders, and explored the differences between urban and rural forests during three subsequent years (2017-2019). Already now, our findings suggest that responses of root- and sap-feeding insects to urbanisation may differ from the responses of externally feeding defoliators. We conclude that top-down forces play important role in mediating impacts of urbanization on the background insect herbivory: factors favouring predators may override the positive effects of temperature elevation on plant-feeding insects and thus reduce plant damage.

Effects of climate on insect herbivory, bird attack rate and leaf traits in oak trees revealed by ecologists and school children

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Abstract: Latitudinal patterns in plant defenses and insect herbivory are commonly used to infer the impact of climate change on plant-herbivore interactions. However, despite decades of research, no general pattern has emerged yet. This could be because bottom-up and top-down forces that determine herbivory have rarely been studied concomitantly, making previous attempts to understand the effect of large scale climatic variation on insect herbivory unsuccessful.

We used citizen science to investigate the effect of climate on insect herbivory on the pedunculate oak (Quercus robur) across its complete latitudinal range in Europe. We quantified insect herbivory and the occurrence of specialist herbivores as well as leaf traits and attack rates on artificial caterpillars on 261 oak trees surveyed by both professional scientists and school children in 17 European countries. We further tested whether climate driven variability in insect herbivory was determined by joint variation in bottom-up (plant defenses and nutritional quality) and top-down (bird attack rates) forces acting upon herbivores.

Although there was no clear relationship between climate and total herbivory, the proportion of oak leaves with insect galls increased with increasing spring temperature and peaked at intermediate level of spring precipitation; and the proportion of leaves with insect mines peaked at intermediate spring temperature. Among the leaf traits examined, leaf soluble sugar content decreased with increasing precipitation while leaf C:N ratio increased non-linearly with temperature. Leaf defenses and bird attack rates on artificial caterpillars were unrelated to climate. The proportion of leaves with mines was positively related to the concentration of hydrolysable tannins, but neither other traits nor bird attack rates affected insect herbivory.

Our study shows that although insect herbivory on oak leaves, leaf traits and bird attack rates were all highly variable across Europe, they were weakly influenced by climate variation and were not related to each other. These findings urge for further examination of the drivers of insect herbivory on trees.

Does winter cold really limit the dengue vector Aedes aegypti in Europe?

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Abstract: The mosquito Aedes aegypti is a potential vector for several arboviruses including dengue virus. The arboviral vector seems to be restricted to their subtropical/tropical habitats and may have difficulties to overwinter and establish permanent populations in Europe. The aim of this study was to clarify if cold winter temperature limits the re-establishment of the dengue vector Ae. aegypti in Europe. At first, we performed a systematic literature review of the cold tolerance of eggs of two major arbovirus mosquito vectors Ae. aegypti and Aedes albopictus. At second, we added experimental data to close knowledge gaps from literature. We conducted a cold tolerance experiment with eggs of non-diapausing subtropic populations of both species (egg exposure to 0°C & -2°C: <8 days; -6°C: <2 days). The meta-analysis of literature data clearly showed the lack of studies testing zero and subzero temperatures of Ae. aegypti in comparison to Ae. albopictus, though those few studies implied a certain cold tolerance in Ae. aegypti eggs. We confirmed the reported cold tolerance of Ae. aegypti eggs experimentally (16.71% hatching after exposure to -2°C for 8 days; 10.3% hatching after exposure to -6°C for 2 days). The bibliometric and experimental data clearly indicate that subtropical populations of both species can survive low and sub-zero temperatures for a short time period, though the success rate to reach adulthood strongly decreases over exposure duration. Three Ae. aegypti adults emerged after a 6-day exposure to -2°C, and one Ae. albopictus adult emerged after a 1-day exposure to - 6°C. Emergence of adults after longer exposure duration did not occur. One may suspect, that Ae. aegypti eggs are likely to overwinter in Southern Europe especially with regard to climate warming.

Seasonal patterns in high-altitude insect movement over Texas revealed by radar

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Abstract: Aerial insect migration is widespread and has enormous impacts on terrestrial landscapes. Yet, these vast flows of biomass, involving trillions of individuals globally, are generally not well characterized. In North America some migratory insects are significant agricultural pests and characterizing their movements, particularly cultivated areas, is of great interest. Although numerous factors may govern these movements, including seasonal and geographic variation in species and behaviors, many movements are facilitated by favorable winds and thought to occur in altitudinal layers in which insects can employ these winds to migrate and disperse. We analyzed data from a vertical radar installed over three seasons during 2018 in southern Texas, as well as data from a nearby weather radar, to identify patterns in aerial insect flows. We report distributional patterns of these flows, with discussion of species involved and comparisons with movements of other aerial biota through this airspace.

A Decade of Biological Control: The Success Story of Liloceris cheni in Florida

Authors: Kraus Emily, Florida Department of Agriculture and Consumer Services, United States

Abstract: Florida is home to hundreds of exotic species. Some of these invaders have serious consequences for the native flora and fauna. The air potato vine, Dioscorea bulbifera, is one such plant. The invasive vine eventually reached all 67 counties in Florida as well as counties in five other states. The vine is known for crowding out native species and becoming a major nuisance for landowners. Biological control was considered for this pest as mechanical and chemical controls were labor intensive and costly. The air potato beetle, Liloceris cheni, was selected as a potential agent. The beetle was tested for host specificity against 41 non-target plant species and determined to be sufficiently host specific. Air potato beetle individuals were released into conservation areas in Florida in 2011 and subsequently provided to residents for release on private properties. Since then the beetle has reduced propagule production, vine mass, and overall improved control of the pest vine.

Individuals were collected from both China and Nepal. There was some apprehension that release of the two biotypes would hinder biological control through reduced fecundity of hybrids. Fortunately, this was not an issue as the beetles showed no preference between biotypes and fecundity was promising in all crosses. Concern again arose when biological control of a closely related beetle, Liloceris lillii, using a larval parasitoid was suggested in the northern US. Subsequent investigations revealed the larval parasitoid displayed clear preference for L. lillii and fortunately posed no threat to L. cheni.

Regarding the vine itself, multiple pathogens and arthropods have been found associated with the plant in Florida. It is not surprising that there would be associations as Florida has several native Dioscorea spp. As the vine continues its' spread further north it is likely there will be newly formed interactions with organisms in those areas. In addition to these potential interactions there are several questions which must be answered to predict the efficacy of the beetle in these areas. The beetle's tolerance responses to temperature and ability of the beetle to withstand cold temperatures is of major concern. Additionally, the ability of the beetle to successfully diapause and emerge in sync with the vine is vital to the effective control of the vine. Finally, it must be determined if the beetles will produce self-sustaining populations or if continued rearing efforts be required to promote management via biological control. Several entities have been in collaboration to answer these questions. Preliminary results will be presented.

Bio-rational management of Halyomorpha halys in fruit orchards in Pennsylvania, USA

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Abstract: Since the 2010 season, many successful IPM programs in Pennsylvania fruit orchards were disrupted due to the severe outbreaks of the brown marmorated stink bug (BMSB) Halyomorpha halys (Stål) (Hemiptera – Pentatomidae). Broad spectrum insecticides, mainly pyrethroids and some neonicotinoids, were identified as the most effective tools for emergency treatments against BMSB, and consequently wide-spread overuse of such products by farmers was frequently observed. Over a time, research on BMSB monitoring strategies and alternative management methods has helped to decrease the number of insecticide sprays throughout the season. The BMSB monitoring studies which included lure and trap design comparisons, documented the viability of BMSB field monitoring practices for accurate assessment of the actual BMSB pest pressure at least from mid-July until October. During the 2017 - 2019 seasons we also tested insecticide treated nets baited with commercially available BMSB monitoring lures to monitor BMSB populations around commercial apple orchards. Starting from mid-July, the treated nets were placed outside of the apple blocks, with a higher number of nets placed in the direction of potential influx of BMSB from the outside vegetation such as woods. The standard BMSB monitoring sticky or container based traps were used to assess the pest population in the orchards surrounded by the net traps and control blocks. At the peak BMSB activity periods very high numbers of BMSB adults and nymphs, as well as native stink bugs were collected from under the BMSB net traps.

Reduction in the usage of insecticides enhances practical effective biological control of BMSB. During the 2016 and 2017 field seasons we found species of native egg parasitoids attacking BMSB eggs in Pennsylvania from three native genre Anastatus spp., Telenomus spp., and Trissolcus spp. Additionally, populations of the samurai wasp (Trissolcus japonicus Ashmead), a highly successful parasitoid of BMSB in Asia, have been recently found on sticky traps located in and around fruit orchards in Pennsylvania. During the 2018 and 2019 seasons for the first time we also found the samurai wasp attacking sentinel and wild BMSB eggs. With the samurai wasp being widely present in Pennsylvania fruit orchards, this parasitoid has now become an important candidate for potential biological control of BMSB alongside its native “cousins.”

Reductions in the number of insecticide applications combined with BMSB aggregation pheromone baited insecticide nets and potential broad distribution of samurai wasps should lead to a wide utilization of effective alternative BMSB management method(s).

The development and application of novel molecular tools to study prey-predator interactions in arthropod communities

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Abstract: Recent developments in DNA sequencing technology have greatly contributed to our understanding of the taxonomic diversity and species interactions in biological communities. This is particularly true for arthropod communities, where interactions are often cryptic and difficult to observe. Molecular gut content analysis using high throughput amplicon sequencing now enables the reconstruction of even rare and elusive prey-predator interactions in unprecedented detail. However, the routine application of high throughput molecular gut content analysis of predatory arthropods still faces significant challenges. A particular issue is the overabundance of predator DNA sequences. Here we highlight two novel molecular tools to enrich prey DNA from DNA extractions of predatory arthropods. The first approach is based on a separation of intact predator DNA and degraded prey DNA, while the second utilizes PCR primers targeting lineage specific SNPs, to prevent predators from amplifying. Using these protocols, we show two exemplary applications in the study of arthropod communities in Hawaiian rainforest ecosystems. We first focus on an adaptive radiation of Hawaiian spiders, in which dietary niche partitioning may have played a critical role in diversification. Different sympatric species of the genus Tetragnatha are not only distinguished by different substrate use and web architecture, but also by clearly distinct and specialized prey niches. Moreover, we show how the invasion success of introduced arthropod taxa on Hawaii may be directly associated with a release from predation by endemic arthropods.

Targeting the molecular basis of pheromone detection in the desert locust Schistocerca gregaria

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Abstract: In insects, pheromone signals are detected by specialized olfactory sensory neurons (OSNs) mainly residing in chemosensory sensilla on the antenna. In moths and Drosophila, these OSNs express pheromone-specific odorant receptors (ORs) and are characterized by the CD36-related “sensory neuron membrane protein 1” (SNMP1) that is supposed to act as a co-receptor involved in the transfer of pheromones to adjacent ORs.

In search for pheromone receptors in the desert locust Schistocerca gregaria, we have analyzed via fluorescent in situ Hybridization a potential co-expression of SNMP1 with a variety of the 119 ORs that we recently identified in this species. For a substantial portion of the ORs tested, this revealed co-expression with SNMP1 in OSNs, suggesting that not only ORs for pheromonal but also ORs for non-pheromonal compounds are co-expressed with SNMP1. To evaluate a possible role of the SNMP1-co-expressed ORs in pheromone detection, we utilized the S. gregaria pheromonal compounds phenylacetonitrile (PAN) and acetophenone in so-called “DREAM-experiments” to assess a subset of the co-expressed ORs for their response to these substances. These approaches indicated that some of these ORs were activated by either PAN or acetophenone.

In order to scrutinize the possibility that SNMP1 is involved in the detection of pheromonal as well as non-pheromonal compounds, we knocked-down its expression by RNAi and are currently analyzing the consequences for the responsiveness of the antenna to PAN and plant volatiles using electroantennogram recordings. The results may shed some new light on the role of SNMP1 in insect olfaction.

Sixty years of wheat germ in insect artificial diets: history, cautionary tales of trade-offs and contamination, and a look ahead

Authors: Krishnan Natraj, Department of Biochemistry, Molecular Biology, Entomology and Plant Pathology, Mississippi State University, United States

Abstract: Insects reared on artificial diets have many uses such as feed for other animals, agents of biological control in sterile insect techniques, food for people, bioreactors for production of pharmaceuticals or recombinant proteins for human medicine and research material in entomology and other biological sciences. Incorporation of wheat germ represented a quantum leap in the development of artificial diets for lepidoptera. Insect biochemist Erma Vanderzant (1920-1999) used wheat germ in a diet for the boll weevil (Anthonomous grandis) in 1959 at the USDA, ARS laboratory at Texas A&M. While this diet showed some promise for rearing the boll weevil, the Vanderzant group achieved remarkable success incorporating wheat germ into an artificial diet for the pink boll worm (Pectinophora gossypiella) a year later. Since then, wheat germ has proven to be a vital component in successful artificial diets of numerous lepidoptera plus some coleoptera and orthoptera. In this presentation, I will review the history of various diet formulations involving wheat germ with a focus on why wheat germ is such a suitable diet component for lepidoptera and the trade-offs one experiences when the percentage wheat germ in a diet is varied. In addition, I will present the cautionary case of the Yamamoto diet for the tobacco hornworm (Manduca sexta), in which the wheat germ was contaminated with the insect growth regulator methoprene. Finally, I will briefly discuss the possible future of wheat germ in insect artificial diets.

Animal Hosts of Tunga penetrans in Uganda

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Abstract: Tungiasis is a zoonotic ectoparasitic disease which is caused by T. penetrans in Africa. In addition to humans, T. penetrans affects a wide range of domestic and wild mammalian species including pigs, dogs, cats and rodents. Animal reservoirs have been described in South American transmission settings but little is known about the role of animals in the disease in Africa. A Cross sectional survey conducted among animal keeping households in 10 endemic villages in Uganda during a dry season revealed pigs, dogs, goats and cats as animal hosts of T. penetrans. Among villages, the prevalence of households with at least one case of animal tungiasis could be as high as 71% (median 22%). Pig infections were most common and were found in 9 out of 10 villages surveyed, with a household prevalence of up to 64% (median 16.2%). Dog tungiasis was detected in five of the 10 villages but at low median prevalence of 2%. Only two goat kids from two villages and a single cat were affected. There were strong correlations between animal and humans tungiasis at village ($rho=0.89$, $p<0.001$) and household ($rho=0.4$, $p<0.001$) level. Pigs presented with the highest intensity of infections and thus severe morbidity. These findings call for regular ectoparasite control among animals targeting T. penetrans as part of an integrated One Health control strategy.

Thrips vision: a morphological, functional and ecological view

Authors: Krueger Stephanie[1] and Moritz Gerald[1], [1]Martin-Luther-University Halle-Wittenberg

Abstract: How a thrips can see the world depends on the functional morphology of their eyes and behavioural ecology. A focus on pest thrips may illuminate the behavioural and pest potential of a few species, but it leaves out the ecological and evolutionary framework. Thousands of species of Thysanoptera show different abilities in the use of the optical sensory organs. Some are plant sap suckers (flower, leaf, pollen), others feed on fungi (hyphae, spores), and still others are predators. Visual system requirements differ between species. Finding of host plants or food, dispersal behaviour, spatial orientation or partner findings are crucial and specific for every species.

This becomes already evident by the different eye characteristics. Whereas some apterous species possess only up to 10 Ommatidia, others have over 100. Especially the Phlaeothripidae with the eucon dioptric apparatus seem to have a far more efficient visual system. Also, the species-specific manner of pigmented ommatidia is much more expressed in this family by forming stripe patterns of pigmented ommatidia, compared to 2 to 7 individual darkened ones in Thripidae.

All of them need special solutions for efficient analysis of their environment, which will be presented in the lecture.

Piecing the puzzle of the sex determination and dosage compensation pathways in Anopheles

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Abstract: In the African malaria mosquito, Anopheles gambiae, two sex determination genes have been described: the male-determining gene Yob and the dsx. It is unclear how the instruction from Yob is mediated to dsx. Here we show that Drosophila tra2 ortholog is an element of the sex determination pathway necessary for splicing of dsx into the female form in A. gambiae. Mild stable knockdown of tra2 in transgenic mosquitoes leads to partial masculinization of females, whereas stronger knockdown leads to female lethality. Moreover, knockdown of tra2 through ectopic delivery of double-stranded RNA in embryos kills the females prior to hatching. These results indicate that, in addition to having a role in sex determination, tra2 is involved in regulating dosage compensation in A. gambiae.

A phylogenomic analysis of the hyper-diverse avian louse family Heptapsogasteridae (Phthiraptera, Ischnocera): a test of historical taxonomic hypotheses

Authors: Kuabara Kamila, Drexel University, United States

Abstract: The tinamous (Aves: Tinamiformes: Tinamidae) are Paleognathus birds endemic to the Neotropics, and one of the oldest extant avian lineages with fossils dating to the Miocene. Most bird species harbor two or three species of lice, but the tinamous possess the most diverse community of louse genera and species known, and typically have high-intensity infections of parasitic lice as well. This highly replicated parasite diversity on only one host lineage may be a product of tinamous' ancient evolutionary history, providing extensive time for parasite speciation, colonization, and back colonization, as well the high diversity of feather types. Tinamous are parasitized by the families Menoponidae (suborder Amblycera), Philopteridae, and Heptapsogasteridae (suborder Ischnocera), and the latter includes the bulk of the louse fauna found on tinamous. Over the years (1936-2022), the validity of the family Heptapsogasteridae was the focus of many studies, and nowadays it is not formerly recognized. Here I provide the first species-level molecular phylogenetic tree for the family Heptapsogasteridae, testing the monophyly of the genera and subfamilies using genomic data, as well analyzing some morphological characters (such as the shape of the head, thoracic features, chaetotaxy, and genital armature).

Could household use of mosquito coil be responsible for selecting F1534C insecticide resistance mutation in Aedes aegypti?

Authors: Kudom Andreas[1], Mensah Ben[1], Ayettey Joana[1] and Cofie Sarah[1], [1]University of Cape Coast, Ghana

Abstract: Mosquito coil is one of the heavily used domestic insecticides in many African countries. Aedes aegypti, the vector for yellow fever, dengue fever and other arboviral infections, breeds, rest and seek hosts in houses where mosquito coils could be in use. Thus, immediately from emergence through to oviposition, adult Ae. aegypti could be exposed to either sub-lethal or lethal doses of mosquito coil. The question is, could such an exposure select for resistance in Ae. aegypti population? This laboratory investigation was conducted to assess the impact of sub-lethal dose of mosquito coil on the selection of F1534C insecticide resistance mutation in Ae. Aegypti. Larvae collected from the Central Region of Ghana were reared to adult and exposed to sub-lethal or full doses of mosquito coil in a Peet-Grady chamber. Susceptibility to Deltamethrin (0.05%, 0.25%), and Permethrin (0.75%, 3.75%) was also determined using WHO test kits. The dead and alive mosquitoes from the two bioassays were screened for F1534C mutation using AS-PCR technique. The mosquito was resistant to permethrin 0.75% (71.7 ± 16.3) and deltamethrin 0.05% (75 ± 19.5) but susceptible to the coil (99.3 ± 1.2). A total of 250 mosquitoes were genotyped for the F1534C mutation with the overall resistant allele frequency of 80.4%. None of the wildtypes survived the sub-lethal dose of the coil. Mosquitoes with susceptible alleles had about a 5% chance of surviving the exposure compared to mosquitoes with resistant alleles (OR=0.0519, 95%CI=0.01-0.2, p=.0001). The result may suggest that in houses, Ae. aegypti with susceptible allele may likely die leaving behind those with resistant allele when exposed to sub-lethal doses of mosquito coil. Thus, mosquito coils could contribute to the selection of F1543C resistant population.

Novel delivery method of dsRNA to Japanese beetles assisted by peptide nano-capsules

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Abstract: Gene silencing by introducing doubled-stranded RNA (dsRNA) through feeding can provide target specific control of pests like Japanese beetles. The use of dsRNA to trigger RNAi effects by downregulating essential gene functions in insect herbivores has been recognized for many insect species, but the stability of dsRNA during or after oral delivery remains a problem for this approach. Peptide nano-capsules are being evaluated to increase the stability of dsRNA and enhance cellular uptake by gut cells. To understand how transcytosis in midguts of larval and adult stages may influence the translocation of the dsRNA–nanoparticle complexes, we used isolated midgut tissues mounted into an Ussing chamber. Also, candidate sequences were identified from existing transcriptome data for Japanese beetles, and dsRNA produced. In lab experiments, delivery of those dsRNA to third instar larvae via injection and ingestion were evaluated. Similarly, dsRNA were delivered to adults in laboratory feeding assays. The results of these experiments will be presented. The application of nanotechnology has utility to produce sprayable forms of dsRNA for target specific control of Japanese beetles. This proof of concept work can support the biosecurity concerns with the ongoing range expansion of P. japonica. The identification of dsRNA and evaluation of novel delivery via nano-capsules can reduce reliance on insecticides for eradication efforts.

Comparative analysis of insect developmental responses to temperature

Authors: Kutcherov Dmitry, Saint Petersburg State University, Russia

Abstract: Temperature is an omnipresent ecological factor that exerts profound and diverse effects on insects. Low and high temperature extremes are among the key determinants of species distribution, and so there has been considerable effort in measuring insect performance under stressful conditions to identify the corresponding lower and upper limits and thresholds. Although immature development time and final body size are also among the most frequently measured temperature-dependent insect traits, surprisingly little is known about the patterns of their interspecific variation. The first attempts to discern evolutionary patterns in the thermal requirements for development in insects were undertaken almost 30 years ago. Since then, ecophysiologists have shifted from viewing the thermal phenotype as a set of species-specific parameters towards viewing it as a plastic continuum of thermal reaction norms. Further, it is now widely understood that multispecies datasets carry a genealogical structure that has to be accounted for in comparative analyses. Thus, the time is ripe to revisit the question of the evolution of insect developmental responses to temperature with the use of modern concepts and tools. During my talk, I will briefly show how phylogenetically informed comparative methods can be used for testing various hypotheses regarding the variation and evolution of development time in insects: Does phylogenetic inertia constrain the evolution of insect thermal phenotypes? Is developmental rate least variable at the temperatures which are most commonly experienced in nature? Is it true that adaptation to low temperatures encumbers the ability to develop quickly? Are the temperature optima for insect development, survival, and body size tightly linked or decoupled? All these questions are important both for our understanding of the evolution of insect life-histories in the past and for predicting insect responses to the consequences of human activity in the future. The study was supported by the Russian Foundation for Basic Research (grant no. 20-04-00185).

Drosophila melanogaster female pheromone induces oviposition aversion in D. suzukii

Authors: Kwadha Charles[1], Rehermann Guillermo[1], Bengtsson Marie[1], Witzgall Peter[1] and Becher Paul[1], [1]Swedish University of Agricultural Sciences, Sweden

Abstract: The spotted wing drosophila, Drosophila suzukii, infests ripening soft-skinned fruits causing economic damage. Recently, studies revealed that exposure of oviposition substrates to D. melanogaster, induces egg-laying aversion in D. suzukii. We hypothesized that pheromones of D. melanogaster could partly account for the aversion observed in D. suzukii. In dual-choice oviposition assays, we tested this hypothesis by firstly, exposing blueberries to D. melanogaster and secondly treating blueberries with D. melanogaster pheromones. We report that exposing blueberries to D. melanogaster, invoked consistent avoidance of egg-laying in D. suzukii, and that when berries were treated with female pheromone, it induced egg-laying aversion in D. suzukii. Additionally, using a flight assay, we show that the pheromone antagonizes attraction of D. suzukii to the yeast Hanseniaspora uvarum. Our findings are relevant in the context of finding sustainable ways of managing the invasive pest, particularly by manipulating D. suzukii behavior.

Control of the vector insect of Pinewood Nematode by Neonicotinoid insecticide trunk injections

Authors: Kwon Gunhyung[2], Lee Jinheung[2], Souvic Sarker[1] and Kwon Youngdae[2], [1]Department of plant medicals Andong National University, South Korea, [2]Gyeonggi-do Forestry Enviroment Research Center, South Korea

Abstract: Trunk injections to prevent pine wilt disease was made in a preventive way by using nematocide. This study was conducted to prevent insecticides by injecting trunk into pine trees and then feeding on new shoots containing drugs during the process of the fable insectivore's dessert. This method of insecticide tree injection minimizes the environmental impact compared to conventional aviation controls by only polluting sky bullion, which eats fresh herbs. In order to select the most suitable drug for insecticide tree injection, seven types of neonicotinoid insecticide were diluted indoors by 2,000 dilution each, and then 2µl was injected into the solider sky, and Clotianidin SL and Thiamethoxam DC had the best pesticide effect from digestive poisoning. They were installed in pine trees, and then they were installed in the mash pocket. In addition, the Japanese pine sawyer were installed in pine trees for site application and compared to the untreated tools, and the possibility of applying them to the site prevention system was found because there was no scattering in the scattered trees of the pesticide tree injection test sites.

Molecular and behavioral analysis of gustatory receptor neurons in Drosophila larvae

Authors: Kwon Jae Young[1], Choi Jaekyun[1], Sung Choi Min[1] and Yu Seungyun[1], [1]Sungkyunkwan University, South Korea

Abstract: Finding and feeding on food sources is necessary for the survival of all animals. This behavior is mainly influenced by the taste and nutrition of a food source, as well as the nutritional status of an individual organism. Sweet substances generally cause attractive behavior, and bitter substances generally cause aversive behavior. Feeding behavior can be defined as the entire process that encompasses searching for food to digestion and nutrient absorption. We use Drosophila larvae as a model system to study the process of choice, in which the quality of food is judged, and the process of ingestion, in which the selected food is ingested into the digestive tract. We examined larval behavioral responses to 23 bitter compounds, testing for choice and ingestion as separate processes. Several compounds caused differential responses for choice and ingestion behavior. For example, denatonium causes an aversive response in a choice assay, but has a neutral effect on ingestion behavior. We found that pharyngeal gustatory receptor neurons (GRNs) have a major role in regulating ingestion, and we constructed a Gr-GRN map of the pharyngeal sense organs.

Interspecific hierarchies from aggressiveness and body size among the invasive alien hornet, Vespa velutina nigrithorax, and five native hornets in South Korea

Authors: Kwon Ohseok[1], Choi Moonbo[1], [1]Kyungpook National University, South Korea

Abstract: The range of the invasive alien hornet, Vespa velutina nigrithorax, has been continuously expanding since its invasion of Korea in 2003. Here, we compared the aggressive behaviors and body size of V. velutina nigrithorax with five native hornet species to identify the interspecific hierarchies that contributes to the spread of this species. Aggressive behaviors were classified into 11 categories and each interaction was scored as a win, loss, or tie. As a result, V. velutina was superior to V. simillima in 153 fights where V. velutina won 71% and showed a high incidence of threatening behavior. V. mandarinia outperformed V. velutina in 104 fights where V. mandarinia won 91% and grappling behavior was common. V. analis was superior to V. velutina in 67 fights where V. analis won 76% and showed a high amount of threatening behavior. V. crabro was superior to V. velutina in 93 fights where V. crabro won 73% and showed a high rate of threatening behavior. V. dybowskii was superior to V. velutina in 132 fights where V. dybowskii won 91% and showed a high rate of threatening and grappling behaviors. The body size of V. velutina was larger than V. simillima (although not statistically significant) and smaller than all other Vespa species. Therefore, according to the results of this study, the low interspecific hierarchies of V. velutina seems to be a major cause of slower spreading rates than it has shown in Europe. However, over time, its density has gradually increased within the forest, in which it seems to be overcoming its disadvantages and expanding its range, possibly as large colonies and good flying abilities make it easier to secure food.

War in the darkness: the use of volatile organic compounds as biological alternatives to control wireworms

Authors: La Forgia Diana[2] and Verheggen François[1], [1]Chemical and Behavioural Ecology, Gembloux-Agro-Bio-Tech, TERRA, University of Liege, [2]Agroscope, Switzerland

Abstract: Wireworms (Coleoptera: Elateridae) are polyphagous soil-dwelling pest that feed on roots and tubers of crops of high economical value. This work was focused on the VOCs quantification from the roots of two maize varieties having experienced contrasted levels of wireworm infestation in the field. We showed that the least susceptible variety released a more diverse blend of VOCs. We also investigated whether wireworms are attracted by conspecifics. The compound 2-Pentylfuran was present in high quantity, particularly in treatments where larvae were present. Behavioral assays in dual-choice olfactometer showed a significant attraction to 2- Pentylfuran. The larvae aggregation with conspecifics on plant roots was highlighted for the first time, opening an important research path. Finally, we developed an attract-and-kill system proposing alginate beads filled with EPNs and spiked with potato extract to larvae. We found that the ingestion of these beads led to higher mortality rates. This method demonstrated some signs of reduction of the wireworms metabolism. Finally, the development of the attract-and-kill system combining VOCs with EPNs showed a long-term reduction of wireworms activity that needs to be tested in the field. The results obtained may open new paths in the study of the aggregation, the host selection and preference.

The Transition from a Gymnosperm to an Angiosperm Dominated Flora: What Happened to Herbivorous and Pollinating Insects at the Aptian-Albian Gap?

Authors: Labandeira Conrad, National Museum of Natural History; University of Maryland, United States

Abstract: Around the 1990s three studies determined that total insect diversity at the family level did not increase during the early ascendancy of angiosperms. These studies were controversial because they contravened the canonical expectation that the evolutionary and ecological expansion of early angiosperm lineages would have favored a similar expansion of their associated, trophically dependent, insect lineages. However, these studies were followed by additional examinations of data that also arrived at the same conclusion: at the family level, there was no increase in insect diversity that was synchronous with angiosperm expansion. What was the reason for this? A recent, separate analysis of 280 insect families that were associated with ferns, gymnosperms and angiosperms during most of the Mesozoic and Cenozoic, including the formative time interval in the Early Cretaceous from 120 to 100 million years ago, provides some clues. First, insect families dominated by fern host associations that made the switch to angiosperms were few and contributed little to a diversity increase through this time interval. Second, insect lineages with dominant gymnosperm hosts reached a level of 95 families in the 35 million years preceding the angiosperm radiation. Third, insect lineages dominated by gymnosperm-to-angiosperm host shifts and insect lineages newly originating with early angiosperms reached a level of 110 families after the early phase of the angiosperm radiation. Fourth, these two insect diversity maxima are separated by an approximately 20 million-year-long interval of the Early Cretaceous known as the Aptian–Albian Gap. The Aptian–Albian Gap indicates a major lull that is characterized by extinction of insect lineages with obligate gymnosperm associations that overlapped with the origination of new lineages having obligate angiosperm associations. This time interval indicates a period of heightened taxic turnover. Last, these taxic data are best demonstrated both for herbivores and pollinators. However, during the past decade, numerous studies of insect pollinators associated with instances of abundant gymnosperm and rare angiosperm pollen document the prolonged delay in this transition across the Aptian–Albian Gap. A preliminary and ongoing study is using a different approach by characterizing the pattern of herbivory, using damage types (DTs), on the latest, well-preserved, gymnosperm-dominated flora and the earliest, well-preserved, angiosperm-dominated flora. This study of involving DTs of insect herbivores immediately before and after the Aptian–Albian Gap suggests a similar pattern. These three approaches of examining plant-associated insect taxa immediately before, during and after the Aptian–Albian Gap-the (i) family-level taxic diversity of plant-associated insect families, (ii) the various insect pollinator studies, and (iii) examination of insect herbivory on diverse floras-collectively provide a compelling ecological explanation for the fla

BeeScanning

Authors: Lagerman Björn, BeeScanning Global AB https://beescanning.com, Sweden

Abstract: BeeScanning - monitors bees health

BeeScanning is an app that analyses images, taken with the smartphones camera. Knowledge when needed to discover parasite varroa, dwv, queen and colony strength.

With a smartphone using the camera and the BeeScanning app, beekeepers can instantly diagnose the parasite mite varroa destructor as well as other features in the hive. Images are taken on living bees on the comb. The tool will also form basis for selection in breeding programmes as well as the basis for population modelling research in the colony. New features are added including brood diseases and bee behaviours, evolving technology using video and sound. Enabling a tool for enhanced knowledge.

BeeScanning is funded by the European Innovation Program, the Swedish Board of Agriculture, The Swedish Agency of Innovations, via Kickstarter and 10 national and international awards.

The app is free to download and free to use for finding varroa. There are 6 000 users, 35 000 images and more than 15 000 manually annotated regions in 15 classes. View http://tagger.beescanning.com Analysed images are stored and used for furhter training the AI. Images are instantly analysed in the following classes :

Bees with varroa
Queen
Deformed wings
Number of bees
Mean average precision: 83% Recall 67%

Results are presented to the user in absolute figures and as mean varroa infestation level %.?Found objects are labeled and displayed to the user for review. Histograms indicates trends of the colony performance as a tool for decisions on treatment and/or breeding purposes.

The Beescanning technology is based on proprietary convolutional neural network, NN, and deep learning. Not by classification or algoritmic image analysing. This means results will continue to improve as the artificial intelligence learns from the ever increasing data its fed by the users.

Metadata as time, geopostion, breed is collected from growing the worlds largest database of images of bees on combs. We aim for a tool that can monitor events, nutritional status, health and make prognoses.

BeeScanning is based on our findings that there is a correlation between the actual varroa infestation level, as measured by alcohol washing or Apistan, and varroa that is optically detectable. https://beescanning.com

Björn Lagerman, founder BeeScanning Global AB

Arthropod pest management for winter strawberry production in USA

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Abstract: Winter strawberry production in Florida is a unique system, owing to the small window of economic opportunity, extent of global market demand, and the pest management challenges faced by the open-field production conditions. While, the Florida strawberry industry is working hard to adapt to the pest management and economic constraints, organic strawberry production is on the rise, due to public demand. Key pests including the invasive Scirtothrips dorsalis Hood, Frankliniella occidentalis (Pergande), and F. schultzei Trybom (Thysanoptera: Thripidae), and twospotted spider mite, Tetranychus urticae Koch (Arachnida: Acari: Tetranychidae) are managed using conventional pesticides, while 88% of Florida strawberry growers have integrated augmentative biocontrol tactics for management of T. urticae. Techniques such as the application of ultra-violet C (UV-C) spectrum are also being examined to facilitate pest management in strawberries. A greenhouse study was conducted to examine the efficacy of a capsicum oleoresin extract based biopesticide, a predatory mite, Amblyseius swirskii Athias-Henriot (Arachnida: Mesostigmata: Phytoseiidae), and a conventional insecticide spinetoram, to control S. dorsalis. Additionally, strawberry field studies were conducted to assess the spatial and temporal distribution of S. dorsalis and F. occidentalis and the efficacy of UV-C application to suppress key pests. Results showed that the biopesticide was as effective as spinetoram to suppress adult S. dorsalis populations in the greenhouse. The predator, A. swirskii, on the other hand was as effective as spinetoram to suppress plant damage and S. dorsalis larval populations. Further results and implication for future research will be discussed.

Regional population dynamics of northern geometrids: A Fennoscandian collaboration

Authors: Laksforsmo Vindstad Ole Petter[1], Bylund Helena[3], Uhd Jepsen Jane[2], Ruohomäki Kai[7], Gilles Yoccoz Nigel[4], Tenow Olle[3], Anker Ims Rolf[1] and Klemola Tero[7], [1]Department of Arctic and Marine Biology University of Tromsø (UiT) Tromsø, Norway, [2]Norwegian Institute for Nature Research, Norway, [3]Swedish University of Agricultural Sciences, Sweden, [4]University of Tromsø - The Arctic University of Norway, Norway, [5]University of Turku, Finland

Abstract: Population cycles of geometrid moths (Operophtera brumata and Epirrita autumnata) in northern Fennoscandia have received substantial attention in the ecological literature. This reflects a long-standing Fennoscandian tradition for research on the causes and consequences of moth population cycles. However, most of this research has been conducted with relatively minor cooperation between research groups in Finland, Norway and Sweden. Here, for the first time, we draw together moth population time series from all three Fennoscandian groups. This enables us to elucidate macro-scale regional patterns in key descriptors of cycle dynamics, including periodicity, amplitude, density-dependence and spatial synchrony.

Effects of Hosts on the Phenacoccus Solenopsis Tinsley

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Abstract: Phenacoccus solenopsis Tinsley, a worldwide distributive malignant invasive pest. For its wide host range and strong adaptability, P. solenopsis has caused devastating effects to farm crops, cash crops and horticultural plants. In China, the pest has spread to 15 provinces and districts, which brings about enormous realistic harm and potential threat to agricultural production. There were obvious differences and preference for each instar in choosing seven different hosts. To further understand the population dynamics and adaptive capacity to different hosts, the work systematically studied the influences of hosts on the growth, survival, fecundity and longevity of P. solenopsis. The results showed the order of feeding preference of each instar was as follows. 1st instar: Bidens pilosa = Gossypium spp. >Solanum tuberosum > Malvaviscus arboreus > Ipomoea batatas > Hibiscus rosa-sinensis > Lycopersicon esculentum. 2nd instar: Gossypium spp. > M. arboreus = B. pilosa > L. esculentum > S. tuberosum = H. rosa-sinensis > I. batatas. 3rd instar: Gossypium spp. = M. arboreus > H. rosa-sinensis =B. pilosa > S. tuberosum = I. batatas > L. esculentum. Adult female: Gossypium spp. = H. rosa-sinensis = M. arboreus > B. pilosa > S. tuberosum > I. batatas = L. esculentum. The survival rate, developmental duration, female ratio, longevity and fecundity of females were different on different hosts. Nymphs survival rates were higher on M. arboreus, I. batatas and B. pilosa, the lowest was on L. esculentum. The longest nymphal developmental period was on B. pilosa (16.5 d), the shortest was on M. arboreus (11. 7 d). The entire lifespan of female on B. pilosa was the longest (62.1 d), the shortest were on I. batatas and L. esculentum (40.9 d and 41.0 d, separately). Female rations were the highest on L. esculentum and S. tuberosum (69.08% and 69.00%, respectively), on M. arboreus was the lowest (53.55%). The fecundity was the highest on M. arboreus, up to 647.92 nymphs per female, followed by S. tuberosum (503.33 nymphs per female), the lowest was on I. batatas, only 171.09 nymphs per female, followed by B. pilosa (195.33 nymphs per female). Experimental population life table parameters indicated that, M. arboreus was the most suitable host for P. solenopsis, S. tuberosum was the second, followed by Gossypium spp. However, B. pilosa, mealybug favorite host was not suitable for its growth and development. This study indicated P. solenopsis potential threat to different hosts.

Hormonal and neural control of egg production in the historically important model insect, Rhodnius Prolixus

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Abstract: Rhodnius prolixus, the blood gorging kissing bug, is the model insect used by Sir Vincent Wigglesworth and others, upon which the foundations of insect physiology, endocrinology, and development have been built. R. prolixus is also medically important, being a principal vector of Trypanosoma cruzi, the causative agent of Chagas disease in humans. The blood meal stimulates and enables egg production, and since an adult mated female can take several blood meals in her lifetime, each female can produce hundreds of offspring. Understanding the reproductive biology of R. prolixus is therefore of some critical importance for controlling the transmission of Chagas disease. The R. prolixus genome is available and so the post-genomic era has arrived for this historic model insect. This talk focuses on the female reproductive system and coordination over the production of eggs, emphasizing the classical (neuro) endocrinological studies that led to a model describing inputs from feeding and mating, and including the neural control of egg-laying. Recent insights brought about by molecular analyses, including transcriptomics, confirm, support, and considerably extends this model.

Acknowledgements: This research is supported by the Natural Sciences and Engineering Research Council of Canada.

Tracking thrips

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Abstract: Developing effective traps for insect control requires knowledge on attraction and repulsion of different kinds of stimuli, in combination with their effects on flight behaviour. For thrips this is especially challenging, due to their small size and irregular flight behaviour. Discrimination experiments, therefore, mostly use sticky plates for registering landing sites disregarding many possible differences in behaviour dynamics. Measuring the dynamics of behaviour typically requires high-speed and high-resolution videos leading to extremely large data sets, which makes the whole procedure cumbersome and unattractive.

Here we describe a tracking system detects multiple thrips in video footage on the fly in high-speed video footage from two cameras in a three-dimensional configuration. Rather than raw images we save the locations of all visible thrips, from which the 3D paths of individual thrips are reconstructed off-line. We show several, dedicated steps to boost sensitivity for detecting thrips that are barely visible by the human eye. The methods will be illustrated with results from colour preference experiments where attractiveness is measured for single colour patches and for patches with different colour contrasts. The system allows for high-throughput measurements, providing dynamics of behaviour that would get lost when just counting the number of landings.

Where the wild rose galls grow: the phylogenomics and biogeographic history of Diplolepis (Hymenoptera: Cynipidae)

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Abstract: Gall wasps of the genus Diplolepis induce structurally distinct galls on wild roses, which provide gallers with food and shelter. Currently many Diplolepis species are distinguished by their galls in addition to adult morphology. Previous work using mitochondrial gene COI has revealed discordance between gall morphology and DNA barcodes. To address these problems, we generated the first genus-wide genomic dataset of Diplolepis using ultraconserved elements (UCEs) to resolve phylogeny among hypothesized lineages, determine the age and biogeographic origin of the genus, and describe global biogeographic patterns.

Diplolepis species (Cynipidae) found in Siberia, Kazakhstan and the Caucasus region

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Abstract: The tribe Diplolepidini Latreille, 1802 is the only group from Cynipidae family (Hymenoptera) which causes galls on wild roses (Rosa sp.). It comprises two genera: Diplolepis Geoffroy, 1762 and Liebelia Kieffer, 1903. The Holarctic genus Diplolepis is more speciose in the Nearctic, while Liebelia is restricted to the Palearctic. Diplolepis is represented by cca. 12 species in Asia, while around 30 species are described from the Nearctic. However, many more wild rose species are known from Asia than from the Nearctic, and there is a probability that many Asian rose gall inducers have been overlooked until now. From the Siberian region data regarding Diplolepis species are especially scarce, and no species have been previously recorded in Georgia. In 2018, as part of the RO-CRES expedition (CNFIS-FDI-2018-0104), we collected samples of rose galls along a wide geographical range from Eastern Europe to Primorsky Krai, including Kazakhstan, North-Ossetia, and Georgia. Several samples were taken from Siberia. The species usually appeared on Rosa majalis and R. acicularis, but in Kazakhstan and Georgia also on R. rapini and R. oxyodon. In Siberia the most abundant and common Diplolepis species was D. spinosissimae. Based on mtCOI barcode sequences we identified two undescribed species, one from Novosibirsk Oblast and one from the eastern part of Kazakhstan, near Pavlodar. Furthermore, reared specimens of D. mayri and D. fructuum collected in North-Ossetia and Georgia differed from western European specimens based on mtCOI barcodes and morphometry. This information supports the assertion that Diplolepis diversity in the eastern Palearctic is poorly known and that more new species are likely to be discovered.

The parasitoid community of Diplolepis abei Pujade-Villar & Wang, 2020

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Abstract: The genus Diplolepis Geoffroy, 1762, has a Holarctic distribution and causes galls on wild roses (Rosa sp.). Diplolepis is more speciose in the Nearctic than in the Palearctic, being represented by cca. 12 species in Asia, and cca. 30 species in the Nearctic. Diplolepis abei Pujade-Villar and Wang, 2020, is the first known rose gall-inducer of economic importance. It causes galls on the Chinese Kushui rose, a hybrid of Rosa sertata Rolfe × R. rugosa Thunb. which is cultivated mainly in Gansu Province (China) for its oil. Where the R. sertata × R. rugosa hybrid is commonly planted, gall-infected shrubs may suffer up to 70% yield loss according to rose oil farmers. Because in infected plantations D. abei is considered a significant pest, its parasitoid community is of great importance. Torymus bedeguaris is the only previously recorded parasitoid of D. abei. Here we report other parasitoid species belonging to the genera Pteromalus, Eupelmus, Eurytoma, and Orthopelma. Only half of the collected galls yielded gall inducers and parasitoids. In the galls with emerged inhabitants the parasitism ratios reached above 85%. This parasitism ratio is not significantly different from those found in the case of European uni- and multilocular species, which suggests that the parasitoid community and the gall inducer are not adventive, as was hypothesized by regional farmers.

Stink Bugs: Biorrational Control Based on Semiochemicals and Vibrational Communication

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Abstract: Olfaction is the main channel used by several organisms to transmit and receive information. Stink bugs use semiochemicals to communicate inter- and interspecifically for different purposes, for example to aggregate, to locate a mate, food, plant hosts, or to identify danger, such as the presence of predators and parasitoids. The chemical signals are essential for their reproductive success. In most organisms, communication does not occur using only one channel, but in general, more than one channel is used simultaneously or successively to transmit information to another organism. The pivotal study with Nezara viridula (L.) indicated that stink bugs use vibrational and chemical signals during their reproductive behaviour. Laboratory studies showed that vibrational signals can be used to attract different conspecifics for mating purpose and, that heterospecific vibrational signals can disturb the reproductive behaviour of conspecifics. Recently, field experiments, conducted in Brazil, combining pheromone traps with vibrational signals enhanced the attraction of Euschistus heros (F.) females compared to traps baited only with the sex pheromone. In this presentation, we will summarize the main advances on pheromone studies on Neotropical stink bugs, and also the new tools that are been aggregated to pheromone traps, like vibrational signals and electronic sensors, to monitor stink bugs in arable crops.

The effect of intercroping on the assemblage of primary and secondary parasitoids of aphids of plum orchards

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Abstract: The use of intercropping to decrease herbivorous populations, through the increase and consequent effect on natural enemies' populations, can be considered as a remedy for agricultural intensification. Non-crop or alternative-crop resources could affect natural enemy diversity and activity by providing refuge, in which they may seek shelter from deleterious environmental factors, different food resources and habitat for alternative prey or hosts. Parasitoids are frequently used in biological control given that they are considered as specialist and efficient agents of control. The presence of alternative hosts in habitats adjacent to crops may provide a source of parasitoids at the beginning of the growing season, thereby maximizing biological control. The aphid species Brachycaudus helichrysi, Aphis spiraecola and Myzus persicae on plum orchards and Rhopalosiphum padi in cereals share parasitoid species. During the winter months in Chile, R. padi is parasitized by the same species during the first stages of winter cereals, that also attack plum aphids. We studied the effect of alternative hosts surrounding plum orchards on the control of plum aphids by parasitoids. We hypothesized that alternative hosts on an intercrop of oats represent a source and refuge for natural enemy populations to ensure the early arrival of parasitoids to plum orchards for the control of aphids in spring. To test this hypothesis, we compared the composition and abundance of parasitoids and aphids between plum orchards with an interow of Avena sativa and a control without the interow crop. The most abundant aphid species during the winter on the cover crops was R. padi and the parasitoid A. platensis, the most abundant parasitoid. On the other hand, during spring, the abundance of aphids on plums was higher on the controls compared to treatments. We examine the parasitism rates of all species, the species composition of primary and secondary parasitoids and the links between these and three most abundant aphid species of plum. The use of an oat interow although increased parasitoid abundance, reduced the overall diversity when compared to the parasitoids present on weeds in the control plots. The secondary parasitism events and unemerged mummies was greater than expected, the effects of these on the overall parasitism rates are discussed as well as the alternative hypotheses to explain aphid decline in treatment plots.

Host quality induces phenotypic plasticity in a wing polyphenic insect

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Abstract: The availability of food is a critical environmental condition that impacts an animal's growth and development. Many insects facing this challenge have evolved a phenotypically plastic, adaptive response that allows them to develop into adults that will face the appropriate environmental condition. For example, many species of insect exhibit facultative wing growth, which reflects a physiological and evolutionary trade-off between dispersal and reproduction, triggered by environmental conditions. What the environmental cues are and how they are transduced to produce these alternative forms, and their associated ecological shift from dispersal to reproduction, remains an important unsolved problem in evolutionary ecology. In our work, we investigate the role that host quality has on the induction of wing development in wing polyphenic insects exhibiting strong tradeoffs in investment between dispersal and reproduction, the brown planthopper, a serious pest of rice in Asia. As rice plants grow, the short-winged brown planthopper dominates the population, but a shift occurs as the plants mature and senesce in the field such that long-winged brown planthoppers emerge and migrate. It remains unknown how changes in the rice plant induce development of the long-winged morph, despite recent discoveries on the role of the insulin and JNK signaling pathways in wing development. We found that by mimicking the glucose concentration of senescing rice plants, we significantly increased the proportion of long-winged female planthoppers. The effects of glucose on wing morph are additive with previously described effects of density. Our results show that host quality both directly regulates phenotypic plasticity and interacts with other factors such as density to produce the appropriate phenotype for specific environmental conditions.

Global change and locust swarms: a synthesis of climate change and land degradation effects on insect populations booms

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Abstract: Locust (Orthoptera: Acrididae) swarms have plagued human history by posing significant threats to global food security. For example, the Australian Bureau of Agricultural and Resource Economics estimated that there would have been USD $963 million in damage during the 2010-2011 Australian plague locust (Chortoicetes terminifera) plague without control. Therefore, understanding how global change may influence the probability of locust outbreaks is important for economies and food security. However, the effect of multiple aspects of global change on insect population booms remain difficult to predict. In this talk, I will synthesize our current research on the ecological underpinnings of Australian plague locust outbreaks with regards to global change.

To gain insight on possible factors that induce outbreaks, we constructed hierarchical additive models using a 30-year data set of Australian plague locust outbreaks. We found that outbreaks were overwhelmingly dictated by the lag effects of rainfall and temperature and were negatively correlated with soil nitrogen. Land degradation through overgrazing can lead to nutritionally optimal grasses for locusts and increase population sizes. Indeed, this has been shown in three other locust species and is anecdotally reported with the Australian plague locust. I will share data testing how land degradation can affect locust outbreaks through altering both the spatial distribution of the nutritional environment and the distribution of woody vegetation. To understand how climate change will impact locusts, we constructed random forest models using the same data set and predicted the effects of climate change under Representative Concentration Pathway 8.5 using BIOCLIM variables. We predicted that locust outbreak probability will decrease as much as 90% by 2071-2090 and become more localized in Southern Australia.

Climate change will influence how land is used around the world by allowing agriculture in new areas (e.g. northern latitudes) while preventing it in other areas (e.g. drylands). Therefore, climate change will have both direct and indirect impacts on insect population dynamics. Understanding these effects are important in making predictions on where and when the Australian plague locust and other insects will go through population booms.

Mosquitoes anticipate feeding by modulating their thermal tolerance

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Abstract: Each time they feed on a warm-blooded vertebrate host, blood-sucking arthropods undergo thermal stress, due to the rapid entry of a relatively large amount of a hot fluid into their body. To cope with this stress, two mechanisms have been uncovered in recent years: physiological thermoregulation and thermotolerance based on molecular protective measures. Until now, both strategies have been documented as triggered by the ingestion of warm blood. Yet, physiological thermotolerance can be anticipatory and endogenously controlled. Desert ants, for instance, synthesise heat-shock proteins not only as a response to heat but also at low temperature, anticipating midday excursion. We investigated whether or not Aedes aegypti mosquitoes, who do not thermoregulate, modulate their thermal tolerance along the day. We analysed the daily modulation of spontaneous activity, aggressiveness, maximal critical temperature, lethal time at critical temperature and HSP expression. Our results indicate that mosquitoes anticipate probable feeding opportunities by heightening their thermal tolerance.

Daily and circadian rhythms in disease vector mosquitoes

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Abstract: Aedes aegypti mosquitoes are the primary vector of Zika, dengue, and yellow fever viruses, for which treatment options are limited and infection can be deadly. In light of rising insecticide resistance among mosquito populations, novel approaches based on an improved understanding of mosquito biology are needed to reduce disease transmission. Mosquito host-seeking behavior largely depends on olfactory host detection, identification, and localization. Similar to other biological and physiological processes such as mosquito locomotor activity and gene expression, host-seeking and blood-feeding behaviors are modulated by biological clocks. However, there remains little known regarding the rhythmic modulation of fine-scale molecular olfactory processes. Here, we combined behavioral assays with biochemical and molecular approaches to address this knowledge gap. Electrophysiological and behavioral responses to host and plant odors were assessed throughout the day in Ae. aegypti females, revealing odorant specific patterns in sensitivity and responses. Because mosquito-host interactions are not limited to host-seeking, we next analyzed the interaction between time-of-day and blood-feeding. At this stage, female mosquitoes must cope with multiple stressors in order to obtain nutrients necessary for reproduction. They are subjected to extreme thermal stress and, upon digestion of the blood, they must cope with high levels of oxidative stress. We analyzed daily variations in the transcriptome of female Ae. aegypti heads and investigated rhythms in the metabolism of blood digestion using state-of-the-art respirometry methods. These are the first measurements reported on carbon dioxide release from individual Ae. aegypti female mosquitoes and provide new insights regarding mosquito respiratory and metabolic physiology. This work identifies mechanisms that represent novel potential targets for mosquito control.

Host-Pathogen Interplay Determines the Outcome of Bacterial Infection in Drosophila

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Abstract: Bacterial infection in Drosophila can result in two dramatically different outcomes, even for genetically identical, co-housed fruit flies given experimentally identical infections. Some individual flies die with high bacterial burden while others control the pathogen into a fairly asymptomatic chronic infection. The probability of death from infection can then be considered as the probability of entering into either the lethal state or the chronic state. We have identified multiple, diverse bacteria that are capable of establishing both classes of infection, and have demonstrated that the probability of entry into the lethal versus the chronic state is a combined function of bacterial and host physiology. While classical virulence and immunity are crucial determinants of infection outcome, the probability of state entry is also influenced by physiological factors that are outside these stereotypical determinants. Our findings suggest a mechanistic basis for individual variation in susceptibility to infection and for environmental effects on resistance.

The CYP9A cluster in Spodoptera frugiperda, implications in adaptation and resistance

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Abstract: Spodoptera frugiperda is a polyphagous lepidopteran, a major crop pest. Although it originates from the American continent, in recent years it has gradually invaded the world. Moreover, it is ranked in the top 15 of the most resistant arthropods. It has therefore developed an efficient detoxification system to eliminate xenobiotics (plant secondary metabolites and insecticides) that it encounters in its environment. Cytochromes P450 (CYP) play a major role in these detoxification mechanisms. The S. frugiperda genome encodes 14 genes of the CYP9A family, twelve of which are organised in a cluster and have evolved rapidly in lepidopterans. These genes are inducible when the insect is exposed to xenobiotics and are found over-expressed in resistant populations. We set out to use the Sf9 cell model to investigate the role of these genes in adaptation and resistance using the CRISPR/Cas9 technique.

Characterization of the tick Ixodes ricinus nicotinic acetylcholine receptors expressed in the synganglion using membranes microtransplantation

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Abstract: Ticks are known as harmful parasites and vectors of many pathogenic viruses, bacteria, and protozoa of medical and veterinary importance. Studies demonstrated that Ixodes ricinus nicotinic acetylcholine receptors (nAChRs) are particularly expressed in the central nervous system which is a condensed mass of fused nerve fibers known as the synganglion. But, studies are difficult to perform in I. ricinus nAChR subtypes because genes coding for nAChR subunits are not characterized. In the present study, we use the microtransplantation of purified membranes from neuronal tissues in Xenopus oocyte. Acetylcholine and nicotine-evoked currents were characterized in oocytes. We found that acetylcholine and nicotine currents are inhibited by alpha-bungarotoxin and sensitive to the neonicotinoid insecticides clothianidin, imidacloprid, acetamiprid and thiamethoxam. We also tested the effects of the nicotinic acetylcholine positive allosteric modulator, PNU-120596. The results obtained indicate that PNU-120596 strongly increase acetylcholine and nicotine-evoked currents. We conclude that microtransplantation of purified membrane from the tick synganglion could be a valuable tool for the development and screening of new acaricides targeting the tick I. ricinus nicotinic acetylcholine receptors.

Insecticide treated cattle as a One Health approach to tackling trypanosomiasis in Tanzania

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Abstract: Tsetse transmit trypanosomes which cause human and animal African trypanosomiasis. The WHO aims to eliminate sleeping sickness as a public health problem by 2020, however the existence of Rhodesian HAT foci in conservation areas of east and southern Africa threaten this aim. In three wildlife-livestock interface areas of northern Tanzania, we are quantifying the (i) distribution and abundance of tsetse; (ii) proportion of tsetse and cattle testing PCR-positive for trypanosome DNA; and (iii) tsetse and trypanosomiasis control measures implemented by livestock farmers. The study areas in Mara, Simanjiro and Tanga regions provide a contrast in livestock production systems with mixed crop-livestock farming, traditional pastoralism and zero-grazing herds predominating respectively.

We have found that the abundance of tsetse declines by >99% from inside conservation areas to >6km into farming areas. The decline was correlated, in part, with farming-related degradation of natural habitat but also likely due to the presence of insecticide treated cattle. Questionnaire surveys of Serengeti livestock farmers suggested that 68% of herds were treated regularly with pyrethroids, and chemical analysis of cattle hair showed that ~27% of herds had detectable levels of pyrethroids. Surveys of cattle showed that Trypanosoma brucei rhodesiense was present in wild tsetse (0.03% (CI 0.004 – 0.12%)) caught inside the conservation area but not in cattle. Trypanosoma congolense was present in 5.3% (CI 4.8 – 5.9%) of tsetse and 16.7% (CI 14.1 – 19.5%) of cattle in the Serengeti study area. Data from around the Tarangire National Park is currently being analysed with preliminary data indicating livestock keepers are also using insecticides regularly.

Our results suggest that farmer-led interventions could reduce the risk of T. b. rhodesiense amplification in cattle at the wildlife-livestock interface, but that AAT will persist even in the presence of low numbers of tsetse. Our work also confirms that the difficulty of reducing AAT is related to teneral tsetse being more susceptible to T. congolense and T. vivax than T. brucei. Widespread treatment of cattle with pyrethroids is being promoted through government subsidy for pyrethroids and a national programme to rehabilitate dip tanks. Further improvements to control tsetse and AAT might be achieved through better provision of information to livestock keepers to improve their use of pyrethroids in combination with trypanocides. Our findings in Tanzania could provide a model for other countries aiming to promote One Health solutions to African trypanosomiases.

Outreach and education in the response to spotted lanternfly outbreaks in the United States

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Abstract: Since it's detection in the U.S. in 2014, the invasive pest spotted lanternfly (SLF) has raised alarm among agricultural commodities, transport businesses, and homeowners alike. In part, this can be attributed to the large host range of SLF, feeding on over 70 different plant species, causing it to become a landscape-level pest. SLF is also a state-regulated pest under quarantine in several states within the Northeastern U.S. High populations of SLF combined with their high mobility and broad host range cause concern among business owners, nurseries, and fruit growers trying to remain SLF-free. High levels of feeding by SLF in both backyards and vineyards cause the build-up of honeydew and subsequent sooty mold, accumulating on patio furniture, cars, backyard plants, vines, and the fruit itself. In vineyards, SLF damage has led to yield losses and vine death, and growers struggle to maintain control with frequent reinvasion from the surrounding landscape. While research on SLF to better understand its biology and behavior is ongoing, public and industry outcry and demand for management strategies is increasing. The invasion response and extension efforts, SLF reported damage on key agronomic industries, and current strategies for addressing the needs of affected stakeholders will be highlighted.

Intrareceptor and intraneuronal inhibition in mosquito olfaction

Authors: Leal Walter, Department of Molecular and Cellular Biology, University of California-Davis, United States

Abstract: The integration of chemical signals at the peripheral sensory system (antennae, maxillary palps, and proboscis) is one of the least understood mechanisms of insect olfaction. We found odorants receptors in the southern house mosquito Culex quinquefasciatus and the yellow fever mosquito Aedes aeygpti that, when expressed in Xenopus oocytes, responded to some compounds with regular inward currents, whereas other compounds (inhibitors) elicited outward currents. Additional support for these regular and reverse currents was obtained with electroantennogram (EAG) and single sensillum recording (SSR) from mosquitoes as well as from transgenic vinegar fly, Drosophila melanogaster, carrying an "inhibitory receptor" whose expression was driven by DmelOrco promoter. Both in the Xenopus oocyte recording system and in vivo, inhibitory compounds attenuated responses elicited by excitatory compounds (odorants) in a dose-dependent manner. These intrareceptor interactions were also manifested in mosquito behavior as the response to a repellent odorant was attenuated by an inhibitory compound that acts on the same receptor as the repellent. SSR from OrcoGAL4/UAS-CquiOR32 flies provided evidence for possible intraneuronal lateral interactions. Hyperpolarization caused by interactions of inhibitory compounds with CquiOR32 attenuated responses of colocalized native receptors from the vinegar fly to their cognate ligands. In this presentation, we will address the following questions (Leal, in press): Do inhibitors bind to orthosteric or allosteric binding sites? Do they shift the equilibrium between the active and inactive states of a receptor thus reducing the probability of firing? Or do they form a different channel (e.g., Cl- channel) than the cation channels opened by agonists thus causing hyperpolarization?

Research data included in this presentation were supported by the National Institute of Allergy and Infectious Disease of the National Institutes of Health under award number R01AI095514.

Leal, W. S. (in press). Mechanism of action of insect pheromones and other semiochemicals in Comprehensive Natural Products III: Chemistry and Biology, J. Piel, W. Boland, J. Clardy, Eds., Elsevier.

Investigating the role of wheat variety on host plant selection and fitness of aphid BYDV vectors to improve the integrated pest management in cereal crops

Authors: Leandro Maria Elisa[1], Roberts Joe[1], Pope Tom[1] and Dickin Ed[1], [1]Harper Adams University, United Kingdom

Abstract: Transmission of barley yellow dwarf virus (BYDV) is economically the most damaging outcome from aphid infestations in autumn sown cereal crops (Walls et al., 2019). The most important vectors of BYDV in the UK are the bird cherry-oat aphid Rhopalosiphum padi (Linnaeus) and the grain aphid Sitobion avenae (Fabricius) (Hemiptera: Aphididae) (Dewar and Foster, 2017). Among cultural management approaches, trap crops are considered a useful strategy for insect pest control. Trap crops are plants that are grown alongside the main crop to attract insects or other pests that would otherwise cause economically important crop damage (Hokkanen, 1991). Furthermore, by providing a habitat for natural enemies and helping to conserve the soil, these crops can support the broader ecosystem (Cavanagh et al., 2009; Holden et al., 2012). This project tests whether the use of wheat varieties grown around the perimeter of the field that are more attractive to aphid BYDV vectors are effective as trap crops in reducing the numbers of aphids entering the main crop. In order to select suitable trap crops, we must understand host selection behaviour and fitness of aphid vectors. We are currently investigating the landing behaviour and fitness (development and fecundity) of BYDV vectors on different winter wheat varieties, including old genotypes associated with aphid outbreaks in the past, such as Maris Huntsman. With these results, we aim to identify varieties which are more attractive to aphids with the potential to be used as trap crops and investigate the olfactory basis for host selection in order to develop a better monitoring tool for BYDV vectors.

Why I Joined the Twitteratii – Tweeting and blogging for entomology

Authors: Leather Simon, Harper Adams University, United Kingdom

Abstract: Come and listen to me describe my journey from social media sceptic to evangelist Tweeter. I was always interested in science communication but realised that the 'traditional' ways of reaching the public and other scientists was, although comfortable, not very efficient. Being on Twitter and starting a Blog, has not only expanded my reach far beyond the scientific community, but has at the same time increased my scientific collaborations and taken my research into new and exciting directions. Come and be converted to the wonderful world of EntoTwitter????

Biological Crop Protection: A New ‘Slow Down-Speed Up’ Strategy for Aphid Management

Authors: Leather Simon[1], Pope Tom[1], Roberts Joe[1], Bruce Toby[2], Ali Jamin[2], Chandler Dave[3], Prince Gill[3], Teakle Graham[3] and D. J. Kirk William[2], [1]Harper Adams University, United Kingdom, [2]Keele University, United Kingdom, [3]University of Warwick, United Kingdom

Abstract: Aphids are important insect pests of a wide range of crop plants, causing over $1billion of crop losses annually. For field crops, the ‘standard’ method of managing aphids has been to apply synthetic insecticides. While this approach has been an effective control method for many years, overreliance on insecticides has led to the evolution of insecticide resistance in several key aphid pests. Compounding resistance issues are environmental concerns regarding insecticide use, leading to legislation changes and many products being withdrawn from sale. This has left farmers with few effective options for controlling the aphid pests that have now become a major threat to global crop production. A sustainable aphid management strategy that can help to protect harvests from pests is urgently needed to address this threat.

The project aims to develop the tools and knowledge needed for an effective IPM system to manage aphid pests of field crops using a model system comprising of Brassica spp. plants, the peach potato aphid (Myzus persicae) and parasitoid wasps such as Diaeretiella rapae. This model system will be used to test the hypothesis that plants with partial resistance ‘slow down’ aphid development and increase their susceptibility to biological control agents, while pest control can be ‘sped up’ using cis-jasmone to induce plant defence priming to attract and retain parasitoid wasps within a Brassica crop. Results so far indicate that several Brassica spp. genotypes from the Vegetable Genetic Improvement Network (VeGIN) exhibit partial aphid resistance, characterised by reduced intrinsic rate of increase (rm), fecundity, and mean relative growth rate (MRGR). Experiments will now focus on enhancing biocontrol and integrating it with this partial resistance to increase efficacy of pest management.

To achieve more sustainable crop protection methods that are less prone to resistance, farmers should not over-rely on any one intervention. Diversification of crop protection can be achieved through integrated pest management (IPM), which promotes the use of an appropriate combination of environmentally sustainable methods of pest control. Unfortunately, as farmers have been so reliant on synthetic insecticides as their principal form of pest control, there is currently no effective IPM system in place for most aphid pests in field crops but our ongoing research aims to develop an IPM system.

Integrating GWAS and transcriptomics to identify the molecular underpinnings of thermal stress responses in Drosophila melanogaster

Authors: Lecheta Melise[3], Powers Beck[5], Lockwood Brent[4], Awde David[3], Axen Heather[2], Waters James[1], Bora Katie[5], Unfried Laura[3], Whitlock Miles[3], Jacobs Nicholas[3], Teets Nicholas[3], Cahan Sara[4] and Frietze Seth[4], [1]Providence College, United States, [2]Salve Regina College, United States, [3]University of Kentucky, United States, [4]University of Vermont, United States

Abstract: Temperature is one of the primary abiotic factors affecting performance, survival, fitness, and consequently the geographic distribution of species. Knowledge of the critical thermal limits of an organism provides important insights about local adaptation and is essential for predicting changes in geographic distribution in response to climate change. Response to thermal stress involves dynamic shifts in gene expression, but previous work has not characterized the extent to which genetic variation in whole-organism thermal tolerance is associated with the transcriptomic response to temperature stress. Here, we use a combination of Genome Wide Association mapping (GWAS) and transcriptomic profiling to investigate whether molecular physiological phenomena, such as gene expression, underlie the mechanisms by which genetic variation causes variable responses to temperature. We measured the critical thermal maximum (CTmax) and critical thermal minimum (CTmin) of 100 lines of the Drosophila Genetic Reference Panel (DGRP) to estimate the thermal breadth of each line. Phenotypically, we observed greater variation in the lower thermal limit, with CTmin ranging from 1.8 to 8.5 °C, while CTmax ranged from 38.75 to 40.65 °C. GWAS identified candidate thermal limit loci in over 300 and 55 genes that were significantly associated with upper and lower thermal limits, respectively. RNA-seq analyses of transcriptional responses to acute heat or cold shock revealed that many of these candidate thermal limit genes exhibit dynamic changes in expression in response to acute thermal stress. Notably, these genes belong to developmental, metabolic, and neuronal pathways. Overall, our results suggest that transcriptional responses to acute thermal stress are a key aspect of the physiological basis for genetic variation in thermal tolerance in Drosophila.

Modulation of defense response in rice by the bacterial microbiota of the Spodoptera frugiperda oral secretions

Authors: Leclerc Laëtitia[1], Gaudriault Sophie[2], Negre Nicolas[2], Champion Antony[3], Duval Pénélope[2], Blanchot Amélie[2], Nguyen Trang Hieu[3], Petitot Anne-Sophie[3], Orjuela Julie[3] and Ogier Jean-Claude[2], [1]DGIMI INRAE - DIADE IRD - Univ Montpellier, France, [2]DGIMI, Univ Montpellier, INRAE, Montpellier, France, [3]DIADE, Univ Montpellier, IRD, Montpellier, France

Abstract: Spodoptera frugiperda is an insect pest native to America, which has recently spread throughout the world. Its polyphagous caterpillar attacks a wide variety of host plants, including some of great economic interest such as corn (Zea mays) and rice (Oryza sativa). These plants recognize herbivorous insects thanks to Herbivore Associated Molecular Patterns, present in the insect oral secretions (OS). Our objective is to study the activation of the rice defense response following herbivory and evaluate the role of the insect bacterial microbiota in this process. To this end, we used Spodoptera frugiperda larvae fed with antibiotic-treated artificial diet and showed that the treated OS (OS-) is cleared of cultivable microbiota compared to not treated larvae (OS+). We then mimicked a caterpillar attack on rice leaves using a mechanical wounding followed by deposition of OS+ or OS- and analyzed the modulation of rice defense responses by global transcriptomic analysis. We identified a set of genes involved in defense responses whose expression is specifically induced by the OS+ in comparison with the OS- treatment. These rice genes are interesting candidates for further analysis of the dialog between the OS microbiota and the plant.

Regulating mechanisms underlying sex-dimorphic circadian expression of mate-finding locomotion of the German cockroach

Authors: Lee How-Jing, Department of Entomology, National Taiwan University, Taiwan

Abstract: The German cockroach is a nocturnal species that displays active locomotion at night. The male adults show circadian rhythm in mate-finding locomotion, but the females do not express the matching circadian rhythm. Since the females possess cyclic reproduction, the mating window is limited within 3-4 days per reproductive cycle. The cost of unsuccessful mating is so high that forces the sexual mature female to actively search for mate regardless day or night during mating window. This sexual dimorphic phenomenon is regulated by a masking factor on the female reproduction. The endogenous circadian clock is running in female adults even though its expressing rhythm is masked by the developing ovaries. The developing ovaries can exert its masking effect through hormonal pathway. The hormone(s) involved in this regulation is not yet demonstrated. But, dopamine has been proved to be the neurotransmitter in the regulation of locomotion and reproduction. In the synthesized cascade of dopamine, tyrosine hydroxylase and dopa decarboxylase are the essential enzymes, and circadian rhythmicity of their mRNA expression levels are consistent with locomotor activity patterns of male and female adults. The mRNA expression level of tyrosine hydroxylase and dopa decarboxylase in male adults displayed circadian rhythm, but none of them displayed circadian rhythm in virgin female adults. Although the effect of extra dopamine and antagonist (cis(Z)-flupenthixol) on locomotor activities of male and female adults only last for one day, the injection does not alter the expression of circadian rhythm in both male and female adults regardless the changes in total amount of locomotion. These results suggest that dopamine does participate in downstream regulation of locomotion without affecting the circadian clock. The dopamine does not serve as a masking factor on the locomotor circadian rhythm.

Diversity pattern of moths in agricultural ecosystem with the effect of landscape composition and configuration

Authors: Lee Jae-Young[1] and Choi Sei-Woong[1], [1]Mokpo National University, South Korea

Abstract: This study is to investigate the response of the moth community according to the composition and configuration of the agricultural landscape in the southwestern part of Korea. We predicted that the diversity would increase as the landscape composition and configuration were more complicated.We also predicted that the composition of moth community based on moth's size would differ depending on the habitat type since species with high mobility respond better to environmental changes, whereas species with low mobility may or may not respond slowly. We found that the habitat type with more complex in composition and configuration possess the higher species richness and abundance. We found that there was a difference between moth groups and forest type: middle and large species than small species were more common in the complex landscape. Habitat size and number of patches have been shown to affect moth abundance, which is interpreted as one of major factors for maintaining species abundance. In addition, when considering mobility, small species group in less-complex landscape was predicted to be more vulnerable to population change and extinction risk because the small moths are slower to respond to environmental changes than relatively larger species.

Characterization of entomopathogenic fungal metabolites with high insecticidal activity against the green peach aphid, Myzus persicae

Authors: Lee Jin Yong[1], Woo Rami[1], Kim Hyunsoo[1] and Woo SooDong[1], [1]Chungbuk National University, Republic of Korea, South Korea

Abstract: It is known that entomopathogenic fungi not only infect and directly kill insects, but also inhibit the physiological function of insects through various secondary metabolites during the proliferation process. In this study, the insecticidal metabolites were investigated from the culture medium of Metarhizium anisopliae 15R strain, which has high insecticidal activity against the green peach aphid, Myzus persicae. The virulence of the culture medium produced in various culture media was compared, and insecticidal substances were elucidated by analyzing the properties and evaluating the stability of the produced insecticidal metabolites. As a result, specific substances showing high virulence were identified from the culture medium, and these results are expected to provide basic data to understand the insecticidal mechanism by metabolites, as well as help in the development of biochemical insecticides using metabolites.

Evaluation of the stability of recombinant baculovirus according to the transposition location of the target gene in the viral genome

Authors: Lee Jong Ho[1], Kim Hyun Soo[1], Woo Soo Dong[1], [1]Chungbuk National University, Republic of Korea

Abstract: The baculovirus expression system (BES) is widely used for the production of useful proteins through the generation of recombinant viruses. Recombinant viruses are generated using a method of homologous recombination or transposition between a target gene and viral DNA. In particular, a bacmid is conveniently used in BES because it can easily produce a recombinant virus by transposition of a target gene in Escherichia coli, but the low stability of the recombinant virus by this method is pointed out as a problem. In this study, the stability of the recombinant virus according to various transposition locations of the target gene in bacmid was evaluated, and the transposition site of the target gene was determined to produce a recombinant virus with increased stability.

Evaluation of insecticidal and antimicrobial activity of entomopathogenic fungal metabolites against the green peach aphid, Myzus persicae

Authors: Lee Jong Ho[1], Woo Ra Mi[1], Kim Hyun Soo[1] and Woo Soo Dong[1], [1]Chungbuk National University, Republic of Korea

Abstract: Entomopathogenic fungi are widely used for controlling various pests as representative biological control agents, and their metabolites have also reported various biological activities such as plant growth promotion, antioxidant activity and antibacterial activity. This study was conducted to

evaluate the possibility of simultaneous control of pests and plant diseases using fungal metabolites. The insecticidal activity and antimicrobial activity against plant pathogens were evaluated for metabolites of entomopathogenic fungi with high insecticidal activity against the green peach aphid, Myzus persicae. As a result, the metabolites of these fungal isolates showed antibacterial and antifungal activity against various plant pathogens such as Botrytis cinerea and Colletotrichum acutatum as well as insecticidal activity against the green peach aphid. The possibility of simultaneous control of pests and plant diseases using fungal metabolites was confirmed.

Effect of 385 nm wavelength LED light on Nesidiocoris tenuis (Reuter) (Hemiptera: Miridae) and Bemisia tabaci (Gennadius) (Hemiptera: Aleyrodidae)

Authors: Lee Joon Ho[2], Park Young-gyun[1], [2]Seoul National University, South Korea, [1]Entomology program, Department of Agricultural Biotechnology, Seoul National University, 1, Gwanakro, Gwanakgu, Seoul 08826, Republic of Korea, South Korea

Abstract: Nesidiocoris tenuis is a competent biological control agent for controlling Bemisia tabaci, which is a major pest of greenhouse crops. Successful establishment of predators in the target area in greenhouses is essential for effective biological control. In this study LED light was tested for enhancing the establishment rate of N. tenuis and successful control of B. tabaci in the greenhouse. The 385 nm wavelength, that showed high attractiveness to N. tenuis in the Y-tube test, was applied. The 385 nm wavelength LED light positively affected populations of N. tenuis and B. tabaci, and combination of N. tenuis and 385 nm wavelength LED light was successful for suppressing the B. tabaci population. Life history characteristics of N. tenuis and B. tabaci under the 385 nm wavelength LED light are currently being investigated and will be presented.

Models for predicting immigration and emigration of Metcalfa pruinosa (Hemiptera: Flatidae) in crop fields

Authors: Lee Joon Ho[1], Kim Min-Jung[1], [1]Seoul National University, South Korea

Abstract: Since the polyphagous hemipteran insect, Metcalfa pruinosa (Say), was introduced in Korea in 2009, it has caused serious damage to various herbaceous corps and fruit trees. M. pruinosa hibernates under barks of trees as eggs, and hatched nymphs persistently dispersed to surrounding vegetation from their overwintering habitats. In this study, dispersal of hatched nymphs of M. pruinosa from trees and their immigration into crop fields were monitored for two years. Hatching and dispersal models of first instar nymphs were developed and validated, and their immigration pattern was also modeled. The infestation risk of M. purinosa nymphs in herbaceous crops fields was gradually decreased as time goes by. The optimal management time in orchards was estimated as 423 DD to 474 DD (base temperature, 10.1 ?C) through simulation of population size on trees, with egg hatching model and dispersal model of first instar nymphs. The management time of M. pruinosa in herbaceous crop fields were also suggested according to different growing seasons of crop plants. In addition, models of adult occurrence and emigration were developed.

Relationship of population genetic structure of Bemisia tabaci MED (Hemiptera: Aleyrodidae) with its fitness and insecticide resistance in Korea

Authors: Lee Joon Ho[1], Park Yujeong[1], [1]Seoul National University, South Korea

Abstract: The sweet potato whitefly, Bemisia tabaci (Gennadius) (Hemiptera: Aleyrodidae) is a major pest that causes serious economic damage worldwide. In Korea, B. tabaci MED (Mediterranean) was first detected in 2004. Our previous study showed that most of B. tabaci MED populations converged into one genetic cluster during one year even in the same tomato greenhouses. To explore the factors responsible for this phenomenon, study was conducted to compared the fitness of the two different genetic cluster of B. tabci MED, and to reveal the three type of major insecticide resistance (organophosphates, pyrethroid, and neonicotinodids) among B. tabci MED populations. Our result indicated that the rapidly converged phenomenon of genetic cluster in B. tabaci MED populations appeared to be related with their fitness parameters and insecticide resistance revel.

Kind of Blue: the gene makes lepidopteran larval integuments blue

Authors: Lee Jung[1] and Shimada Toru[1], [1]Gakuhusin University, Japan

Abstract: The larvae of lepidopteran insects show bluish-green body colours in many species, as indicated by their Japanese description as ‘Aomushi,’ which literally means blue caterpillar. A mixture of yellow pigment carotenoids and blue pigment bilins in varying proportions forms the green colours of Aomushi.

The eri silkmoth (Samia ricini) have strains with the different body colour: blue and white strains. We determined the whole genome sequences of the white strain to locate the responsible gene for the difference in larval body colour (Lee et al., 2021). We found that a point mutation in a gene located on chromosome 8 causes the loss-of-function of the protein, resulting in the absence of Biliverdin IXγ, a member of the bilins, in epidermal cells of white strain. Therefore, we designated this gene as BVT, Biliverdin transporter. Interestingly, functional analysis of BVT orthologues in Chinese oak moth (Antheraea pernyi) and Asian swallowtail butterfly (Papilio xuthus) revealed that BVT is responsible for the transport of bilins to the epidermal cells in both A. pernyi and P. xuthus. Currently, we quantitatively assess the ability of BVT using Xenopus laevis oocytes.

Divergence history and high-altitude adaptations of Alpine geometrid moths (Lepidoptera)

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Abstract: Many unique high-altitude mountain habitats have been declining due to climate change, threatening their flora and fauna, which have adapted well to these ecosystems. We study how high-altitude adaptations such as wing length reduction and daily activity have evolved in the European Alps using geometrid moths in the tribe Gnophini as the study group. These moths are an excellent insect group for studying such questions because of well-researched life histories and taxonomy, many with narrow ecological niches including restricted altitudinal ranges, and short life cycles. Using molecular data, we built a phylogenetic hypothesis for Gnophini moths to understand whether the various high-altitude habitats have been colonised by a single moth lineage and they share a common ancestor through adaptations, or whether there have been several colonisations by non-related lineages and the adaptations are a result of convergent evolution. Our results also provide a robust basis for classification of these moths and we demonstrate how phylogenies can be used to make more informed conservation prioritisation decisions.

Population Genetic Structure of Anoplophora glabripennis in South Korea: Invasive Populations in the Native Range?

Authors: Lee Seunghyun[2], Lee Seunghwan[2] and Lee Yerim[1], [1]none, South Korea, [2]Seoul National University, South Korea

Abstract: Native to China and the Korean Peninsula, the Asian longhorned beetle (ALB), Anoplophora glabripennis, has spread to North America and Europe. In both its native range and the territory it has invaded, ALB is responsible for the death or removal of millions of urban, roadside, and forest trees. Here, we present the population genetics of ALB in South Korea, using 801 bp of mitochondrial DNA and the most comprehensive sampling to date. ALB populations in South Korea are divided into three distinct geographical subgroups: the northeastern natural forest and the western and southern urban areas. Historical records suggest that the forest-dwelling subgroup is native, as does the moderate genetic diversity of this population. Meanwhile, the fact that ALB was first observed in the western and southern areas only recently, the extreme genetic bottleneck status of these populations, their distribution in large port cities and adjacent areas, and the difference in observed host plants used by the forest subgroup and the urban subgroups suggest that the urban populations are non-native recent invaders. Approximate Bayesian computation suggested that the western and southern subgroups most likely originated from northeastern and northwestern China, respectively. Therefore, our study demonstrates that ALB invasion has occurred even within the species' native territory. This finding alters our perception of biological invasion by providing a unique example of a species that has invaded its own native range.

Identification of a sex pheromone of Anomis privata (Lepidoptera: Noctuidae)

Authors: Lee Sujin[1] and Kim Junheon[1], [1]National Institute of Forest Science

Abstract: Anomis privata (Lepidoptera: Noctuidae), is one of the primary defoliator insects on Hibiscus spp. in Korea. The moths of this family are difficult to detect without pheromone traps due to being active at night. To develop a suitable tool for monitoring this pest in Hibiscus syriacus, we investigated the attractiveness of sex pheromone to A. privata adults. We performed gas chromatography-mass spectrometry (GC-MS) analysis of female abdominal tip extracts and identified 7-methylheptadecane (7-MeC17) as a major component of sex pheromone candidate. 7-MeC17 was chemically synthesized and were tested for field attractancy. Male A. privata were captured in 7-MeC17 baited traps from April to August in Seoul and Suwon, Korea in 2021. In field tests, traps baited with 7-MeC17 attracted significantly more males than those with hexane as control. Based on these results, it was revealed that 7-MeC17 is one of pheromone components of A. privata. And it suggests that 7-MeC17 could be useful in a monitoring strategy, which can determine an accurate assessment of the threshold for insecticide applications of target insects.

Volatile disease markers derived from American foulbrood as putative hygienic cues in Apis mellfiera

Authors: Lee Sujin[1], Han Giyoun[1], Noh Gwangrae[1], Wook Kwon Hyung[1], Lee Myeong-Lyeol[1], Lim Sooho[1], [1]Department of Life Sciences & Convergence Research Center for Insect Vectors, Incheon National University, Republic of Korea

Abstract: The honey bee, which lives in a crowded environment of a social hive, is vulnerable to disease infection and spread. Hygienic behavioral responses are especially important for honey bee resistance to American foulbrood (AFB), a fatal bacterial disease of honey bee brood among honey bees worldwide. Successful resistance relies on early detection and removal of infected larvae before they serve as a source for disease propagation within the colony. Here we investigated the volatile disease markers (VDMs) of AFB as well as differences in olfactory responses in hygienic-aged bees and foragers. Upon the inoculation of AFB pathogen to honey bee larvae in lab condition, we identified propionic acid, valeric acid, and 2-nonanone as VDMs of AFB infection using GC/MS. Electrophysiological recordings demonstrated that middle-aged bees, the hygienic-aged bees, are more sensitive to these VDMs than foragers, indicating that these VDMs are efficient and significant for detecting sick honey bee larvae in bee hives. Our finding shows that these VDMs might be exploited by adult workers seeking to removed diseased larvae as putative hygienic cues. This study is considerable value both in understanding VDMs associated with honey bee to study the molecular and neural correlates of given hygienic behaviour detecting these volatile chemicals by honey bees.

Transcriptome studies of the floodwater mosquito, Aedes vexans (Diptera: Culicidae) with potential as secondary vectors using Illumina HiSeq 4,000 sequencing

Authors: Lee Yong Seok, Soonchunhyang University, South Korea

Abstract: Aedes vexans is the inland floodwater mosquito widely distributed in every continent excepting Antarctica and South America. They are opportunistic feeders preferring blood meal of larger animals including cattle, horses, deer, and humans. Further, the mosquito species is a compatible vector of several diseases, including West Nile virus and dog heartworm. In this study, we performed transcriptome characterization of Ae. vexans using Illumina HiSeq 4,000 sequencing and assembly of sequenced reads using Trinity. A total of 55,813,852 raw read and 54,630,771 clean reads (97.88% of raw reads) were obtained after Illumina paired-end sequencing and pre-processing steps. After Trinity de novo assembly, TransDecoder and TGICL clustering, a total of 37,111 unigenes were obtained. Out of the total unigenes count, 28,733, 17,893, 14,626, and 17,055 showed homologous matches against the PANM, UniGene, SwissProt, and KOG databases. A total of 9,483 unigenes were assigned to Gene Ontology (GO) terms, and 3,741 unigenes were mapped to 483 KEGG pathways. The zinc finger (C2H2-type), reverse transcriptase, integrase (catalytic core), protein kinase, and RNA recognition motif domain among others showed as the top InterProScan domains. The obtained datasets serves as a basis for future studies towards understanding ecology, metabolism, and parasitism potential of Ae. vexans.

Characterization of Haemaphysalis longicornis microbiome collected from different regions of Korean Peninsula

Authors: Lee Yong Seok[9], Sang Min Kyu[8], Park Jie eun[8], Lee Hee Il[4], Song Dae Kwon[8], Hwang Hee Ju[5], Kim Hyun woo[4], Kim Tae Yun[4], Park So Young[7], Kang Se Won[6], Bharat Bhusan Patnaik[2], Cha Sung-Jae[3] and Han Yeon Soo[1], [1]Chonnam National University, [2]Fakir Mohan University, [3]Johns Hopkins Bloomberg School of Public Health, [4]Korea Disease Control and Prevention Agency, [5]Korea Native Animal Resources Utilization Convergence Research Institute , [6]Korea Research Institute of Bioscience and Biotechnology, [7]Nakdonggang National Institute of Biological Resources, [8]Soonchunhyang university, [9]Soonchunhyang University, South Korea

Abstract: Ticks are vectors that cause disease by transmiting bacteria, viruses, and protozoa to humans or animals. The Asian longhorned tick Haemaphysalis longicornis, a vector of medical and veterinary importance is widely distributed in Korean peninsula and can transmit various pathogens including Rickettsia spp., Borrelia spp., and severe fever with thrombocytopenia syndrome virus (SFTS virus). Despite the abundance and importance, studies on the microbiome of H. longicornis in Korea are limiting. Here we first report the microbiome diversity of H. longicornis in terms of region, stage and sex. H. longicornis used in this study were collected from 16 different regions of the Korea Centers for Disease Control and Prevention's Climate Change Media Monitoring Center from June to July 2019. The V3-V4 region of the 16S rRNA gene was amplified by PCR, and sequenced using the Illumina MiSeq platform. The microbial diversity analysis was performed using Qiime2. A total of 1,754,418 non-chimeric reads were obtained from a total of 46 samples, and an average of 126 operational taxonomic units (OTUs) and a total of 1,398 OTUs were identified. Our results were used for H. longicornis microbial community database construction for each region that enables to identify singularities in each region.

Leveraging genomics for integrated mosquito control in the Dutch Caribbean

Authors: Lee Yoosook[5], Weakley Allison[5], Cornel Anthony[5], Blosser Erik[5], Davelaar Gerald[4], Lanzaro Gregory[5], Bargielowski Irka[5], Hulshof Koen[2], Braks Marieta[1], Leslie Teresa[3] and Collier Travis[5], [1]Centre for Zoonoses and Environmental Microbiology, National Institute for Public Health and the Environment (RIVM), Netherlands, [2]Public Entity Saba. Public Health Department, Saba, Netherlands, [3]The Caribbean Public Health Agency, Sint Eustatius, Netherlands, [4]the Sint Maarten Ministry of Public Health, Netherlands, [5]University of California - Davis, United States

Abstract: The Aedes aegypti mosquito is a vector of several arthropod-borne viruses (arboviruses), such as dengue, Zika, yellow fever, and chikungunya. Dengue alone causes 96 million clinical cases annually and 50% of world population lives under the risk of contracting dengue viruses, including Saba Island residents (Bhatt et al., 2013). In order to reduce this arboviral disease transmission risk as much as possible, the Public Health Department of Saba started conducting genetic studies on Saba and surrounding Dutch Caribbean islands to collect data that could be used in application for both novel and conventional vector control strategies. The ultimate goal is to develop an effective control strategy to reduce and possibly eliminate Ae. aegypti populations from Saba island. To accomplish this long term goal, we first investigated on the population structure of Ae. aegypti within Saba and between Saba and its neighboring two islands. Recent advances in genetic and genomic tools in Ae. aegypti (Lee et al., 2019) allow estimating dispersal from genomic data, which will inform the design and use of genetic and other control systems. Genetic information from this study provides knowledge on several issues critical to the design of novel elimination strategies. For example the data inform: a) the overall population structure and whether population bottlenecks occur; b) trapping network requirements for population assessment and surveillance when the control or elimination intervention is being applied; and c) the extent of migration between locations within Saba and between Saba and the neighboring islands.

Survival Rate Variation According to Winter Temperature of Lantern Fly, Lycorma delicatula (Hemiptera: Fulgoridae) and Selection of Organic Farming Materials in South Korea

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Abstract: Lantern fly, Lycorma delicatula is the invasion insect pests introduced to South Korea in 2006. There are 41 species of insects known as host plants, and nymphs and adult suck the plant and emit nectar in the process, causing damage to grapes, a major fruit tree in Korea. In terms of predicting the occurrence of outdoor wintering populations, it is necessary to investigate the survival rate of populations exposed to low temperatures during wintering conditions under outdoor conditions. We have analyzed the survival rate and weather data of this wintering pest and share the findings from 2011 to 2019. This pest responds sensitively to Korean weather conditions, especially winter temperatures. In addition, as eco-friendly cultivation of crops is expanding, we will introduce organic farming materials that can effectively control this pest.

Plant breeding strategies to improve integrated pest management of the tomato russet mite

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Abstract: Biological control of the tomato russet mite is still difficult on tomato. Two main factors play a significant role: 1) the small size of the mite allows it to seek refuge in between plant trichomes; and 2) the tomato leaf hairs make it a hostile environment for many natural predators, such as phytoseiid mites. As a strategy to improve the control of the tomato russet mite using predatory mites, we assessed biological control on a tomato mutant (hairless: LA3556) that shows a distorted trichome phenotype.

We first described the interaction between the herbivore and the hairless tomato accession. To our surprise, we found that a genotype with distorted constitutive defences (i.e. trichomes) deployed an increased resistance against the tomato russet mite. Secondly, we observed that the fecundity of predatory mites was higher on hairless (with a surplus of russet mite prey) than on the normal accession. Finally, population dynamics experiments showed that biological control of the russet mite was most effective on the hairless tomato genotype. Overall, we show that removing a resistance plant trait can promote biological control agents, and consequently achieve a better control of a challenging pest, such as the tomato russet mite.

Whole genome sequencing reveals conserved and specific features of endogenous polydnaviruses in ichneumonid wasps

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Abstract: Polydnaviruses (PDVs) are mutualistic endogenous viruses associated with some lineages of parasitoid wasps that allow successful development of the wasps within their hosts. Bracoviruses are PDVs associated with braconid wasps whereas ichnoviruses are associated with ichneumonids. These viruses result from separate events of integration of an ancestral viruses into the wasp genome, but share some common features. Polydnaviruses are unusual viruses in that their relatively large genomes are divided into separate, circular DNA molecules (hence the name "poly-dna virus"). Furthermore, their genomes are fully incorporated into the wasp genomes and comprise two major elements: (1) virulence genes located on proviral segments that are packaged into the viral particle, and (2) genes involved in the production of the viral particles, which are found in the wasp genome but not encapsidated. Whereas the genomic organization of bracoviruses within the wasp genome is relatively well known, the architecture of endogenous ichnoviruses remained poorly understood. We sequenced the genome of multiple ichnovirus-carrying ichneumonid wasps. Assemblies with long scaffold size allowed mapping of the integrated ichnovirus sequences against the wasp genome. We found that proviral segments are widely dispersed across the wasp genome, with their position widely variable between the two wasp species. Conversely, the replication genes in both species were grouped in clusters harboring a conserved organization in terms of gene content and gene order. This distinction is consistent with the biological properties of these two viral elements: proviral segments need to be fine-tuned to the host physiology, while viral architecture genes should have largely conserved biological function. This genomic architecture, however, is entirely diverse from that found in bracoviruses, highlighting different evolutionary pathways for the domestication of mutualistic viruses in the two lineages.

Deciphering the genetic programs defining the sexual and parthenogenetic reproductive modes of the pea aphid

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Abstract: In aphids (Hemiptera), there are several morphs of females, mainly sexual oviparous females and parthenogenetic viviparous females. Those morphs alternate in a season-dependent manner by phenotypic plasticity. This involves the capacity of embryos to sense external local environmental cues during their development with alternative routes providing a final phenotype adapted to those new cues. In our lab, we currently describe and analyse the gene expression regulation patterns during the establishment of the phenotypic plasticity of the reproductive mode in aphids due to the shortening of the photoperiod at autumn arrival. The development of sexual and asexual embryos that differ mainly by their production of haploid meiotic gametes or diploid non-recombinant gametes is thus compared. We developed an integrative genomics approach that aims at defining most of the functional DNA elements associated with the formation of alternative morphs. For this, we sequenced the long (containing mRNAs and lncRNAs) and small RNAs (focusing on miRNAs) of embryos at different stages of development from the pea aphid A. pisum individuals in the course of selecting the sexual or parthenogenetic reproductive mode. We described a new repertoire of 19387 mRNAs, 2720 lncRNAs and 276 miRNAs (with 786 new mRNAs, 1124 new lncRNA and 173 new miRNAs identified from this study). Then we analysed the differential expression of these different RNA types during the development of sexual or asexual embryos, as well as during key decision points for the entry in the sexual or parthenogenetic development of the embryos. We combined genomics, bioinformatics and mathematic modelling to construct gene networks describing and modelling the molecular processes associated with the phenotypic plasticity of the reproductive mode. We predicted their putative interactions and modelled their network functioning. We analysed more deeply some of the candidates to fill the gap between prediction, hypotheses and biological observations.

3-D wing structure determines aerodynamic efficiency in flapping fly wings

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Abstract: The aerial performance of flying insects largely depends on how flapping wings interact with the surrounding air. It has been suggested that the wing's mechanical properties governed by three-dimensional camber and corrugation stiffen the wing against aerodynamic and inertial loading during flapping motion. However. there is an ongoing controversy on the benefit of wing corrugation and camber for vertical, weight-supporting force production. Some authors reported an improvement in performance owing to corrugation, while others argue that corrugation attenuates performance. To solve these opposing findings, we investigated the potential benefit of 3-D wing shape in three different-sized species of flies using models of microCT-scanned natural wings and wings, in which we numerically removed either camber, corrugation, or both properties. Aerodynamic forces and power requirements during flapping were derived from computational fluid dynamic modeling. Our data show that 3-D camber has no benefit for lift production and attenuates Rankine-Froude flight efficiency compared to a flat wing. There is no evidence for lift-enhancing trapped vortices in corrugation valleys of fly wings. As the size of flow structures depends on Reynolds number, we suggest that corrugation structures should be more coarse in small insects than in larger animals for pronounced wing-vortex interaction. Altogether, our research strongly supports the assumption that the wing's three-dimensional structure provides mechanical support against external forces rather than improving lift or saving energetic costs associated to active wing flapping.

The effects of microclimate variability on overwintering dynamics in the butterfly Pieris napi

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Abstract: Studies on overwintering dynamics generally use climate chambers and low temperatures to simulate winter conditions. However, diapause in the field occurs in varying microclimates, and fitness of overwintering insects is dependent on both conditions before winter, during winter and after winter.
We have delineated an area of around 1.5 km2 in a fenced field site characterized by a variation of open field, wetlands and open forests in southern Sweden, where we have established a dense network of 120+ near-ground climate loggers. In this area, we are now performing a range of experiments where we test effects of microclimate variability on overwintering dynamics in a butterfly with facultative pupal diapause, Pieris napi.

Many studies on thermal performance biology focus on single life-stages, often the one with the longest duration. Since life-stages can differ dramatically in thermal sensitivity, and coincide with seasonal variability in temperature, we tested thermal performance in both single life-stages as well as across the whole ontogeny. To our surprise, we found that thermal dependence was mostly additive and that conclusions drawn from experiments with single life-stages are surprisingly similar to those where the whole life-cycle is exposed.

There is a general appreciation of relatively warm temperatures being optimal for ontogenetic development in insects. At the same time, there is a general appreciation of relatively cold temperatures being optimal for diapause, for both for energetic and timing reasons. How, then, do these integrate into overall fitness for an individual insect that experiences both summer and winter thermal variability? Our data suggests large idiosyncratic effects of temperature on fitness that varies in a life-stage dependent manner. Sites that are optimal during summer are not likely to be optimal during winter.

Finally, while larvae can to some extent choose microhabitat and manipulate their thermal range, adult females have a much larger potential to control the microhabitat available for their offspring. Females flying early in the season lay eggs that will develop without diapause, while females flying late in the season lay eggs that will undergo diapause. Since we know that thermal optima differ for these two groups of offspring, for a large part of their life span, we ask if females optimize fitness by selecting different oviposition microhabitats during different parts of the season. Our preliminary data suggest that this is not the case, females choose warm sites regardless of time of year, and are more likely to make choices based on host plant quality than microhabitat quality.

Together the studies suggest that winter and summer fitness optima are poorly correlated, and that females show little appreciation for winter dynamics when making choices for their offspring.

Diapause in the pine processionary moth (Thaumetopoea pityocampa): ecological and applied significance

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Abstract: Several studies reporting incidence of pupal prolonged diapause across the species range were reviewed, indicating a U-shaped relationship between incidence of prolonged diapause and winter temperature, and a negative correlation between overall pupal survival and the proportion of diapausing individuals. There is evidence of at least 7-year long prolonged diapause in one alpine population, with important consequences on population dynamics and pest management.

Diapause termination mechanism in both univoltine (emerging in the same year) and prolonged diapausing (returning to diapause) individuals has been previously hypothesized based on the occurrence of a key period during the pupal stage. By using two measures of metabolic activity, such as body temperature and O2 consumption, the existence of a transient restoration of activity (termination) has been confirmed in both univoltine and prolonged diapausing pupae. The two methods clearly detected simultaneous diapause termination through increased metabolic rate in both types of pupae before any morphological or behavioural changes could be observed, but univoltine individuals were characterized by a continuous increase until emergence while prolonged diapause individuals later returned to previous activity levels. This finding is a starting point for the study of diapause development in PPM from an ecological point of view.

In addition to pupal diapause, there is evidence of a prepupal dormant stage implicated in synchronizing of emergences. Through a weekly sampling spanning a two-month procession period, prepupae were found to differentially regulate their development time in such a way that adult emergences were concentrated and synchronized in less than one month. Early-descending larvae don't pupate immediately whereas late-descending prepupae develop into pupae much faster. The finding of prepupal diapause and its significance in synchronization of emergence may improve phenological models and provide managers with a new tool to handle this pest.

Wireworm control with Metarhizium- what factors influence the success?

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Abstract: Among the main subterranean pests of potatos in Europe are the wireworms. With more than 15 different species often occurring in mixed populations in single fields, they pose a difficult problem for the grower. As in potato no chemical alternatives are abvailable in in many European countries, the interest is turning to entomopathogenic fungi. Metarhizium spp. strains can exhibit good efficacy in the lab, but the efficacy of Metarhizium formulations in the field is often not sufficient so far.
In the project „AgriMet“ new Metarhizium formulations, based on coated autoclaved millet grains and on a wettable powder, were developed for use in potato and subsequently tested with different wireworm species and under different environmental conditions in field and lab. Also the distribution of wireworms in-field and wireworm behaviour of different species is assessed. Results show that the use of entomopathogenic fungi and also of entomopathogenic nematodes is on the one hand very dependent on environmental conditions, but additionally also very much species dependent. This challenges the idea that a single antagonist may always be enough to control wireworms.

Sublethal Effects of Entomopathogenic Fungi, Beauveria bassiana, on Group-Reared Life Table of Delia antiqua

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Abstract: We assessed effects of parental exposure to Beauveria bassiana on life history traits of subsequent generations of Delia antiqua (Meigen) on Group-Reared Life Table with a sublethal concentration (LC10) of B. bassiana (isolate XJWLMQ-32). The developmental time of progeny larvae and male longevity were shorter at fungal-treated group than at control group values. The male to female ratio and fecundity were reduced in fungal-treated group offspring flies. We calculated life table parameters for the progeny and found the intrinsic rate of increase (r), the finite rate of increase (?) and the net reproduction rate (R0) of fungal-treated group were significantly less than the progeny of untreated parents. These results demonstrate that B. bassiana has sublethal effects that reduce the reproductive success of onion maggot and these effects should be taken into account when evaluating its use in management programs for onion maggot.

Utilization of trap nest in the breeding environment of hole-nesting aculeates (Hymenoptera, Aculeata) in Finland

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Abstract: The populations of hole-nesting stinging wasps and bees have been decreasing during the last years and many species have become very endangered. The main reason has been the drastic change in agricultural surroundings. The amount of suitable nesting holes has decreased strongly due to the fact that wooden building materials have been changed to stone or metal. At the same time various meadow and dry meadow vegetation types have been modified into monotonic hayfields. Consequently, the so called edge areas have also decreased dramatically. During the years 2001-2019 I studied the suitability of various materials as artificial nests for aculeate wasps and bees. I tested the suitability of different sized plastic straws, reed, cow parsley, pieces of logs and laths, with drilled holes of differing diameter. Based on these results I tested an artificial combination nest with natural straws and a wooden cubic with drilled holes of differing sizes. In total, 92 test objects and 362 artificial nests resulted 7516 individuals representing 121 aculeate species.
Based on the present study, the use of artificial nests is most succesful in natural surroundings. Natural materials (reed, cow parsley, wood with holes) are better building materials of artificial nests in comparison to plastic straws. Humidity concentrating into the walls of plastic straws makes the walls between cells of nests to collapse. The smallest plastic straws seem to be too small, because no nesting was observed in them. A clear difference was observed between reed and cow parsley in favor for reed what comes to the number of species nesting in them. In birch blocks there were significantly more nests in holes of six mm in diameter as compared to smaller ones (diameter 4 mm).
Most species nested in birch block in alder forest. These habitats are diverse rural landscapes dating back to swidden culture and pastures. I did not observe any significant differences in species compositions between birch, aspen and alder habitats. In addition, I did not find any significant difference between birch blocks in cultural surroundings differing from each other in land use (fallow, pasture area and cereal field).
Based on the present study, artificial nests made of natural materials (straws, blocks, combination nests and laths) may be used as nesting sites for all hole nesting wasps and bees in Finland. The placing of nests is crucial for the success of nesting. The artificial nests must be placed in warm places. In addition, the nesting holes must be drilled horizontally and directed to morning sun.

Distributional changes in Finnish moth fauna during 1993-2012

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Abstract: The Finnish moth monitoring scheme (Nocturna) was launched in 1993 as a long-term monitoring project of biodiversity covering a species-rich taxon, nocturnal moths, with ca. 900 species observed in the country. Since the late 1990s the monitoring has mainly focused on forested environments. The monitoring network included at highest 152 light traps in 1996, but later the number of trap sites decreased so that in 2010s the trap number has varied between 40 and 45. Previously, the regional environmental authorities were responsible for maintaining the traps, but this changed after 2015 and now traps are increasingly maintained by voluntary lepidopterists. In 2017, the trap network consisted of 60 sites. Voluntary lepidopterists have also identified the moth samples and saved the observations into a database. The monitoring scheme is currently coordinated the Finnish Environment Institute (SYKE).

Several significant large-scale changes have been observed in the Finnish moth communities during the period 1993-2012. The annually observed species richness and community evenness, as described by Fisher's alpha index, have increased. These increases are most pronounced in Southwestern Finland. Incidence of multivoltinism, i.e. production of more than one generation during the season, has also increased with the strongest change again in the SW parts of the country. Several moth species of southern origin have strongly increased in abundance, whereas a lower number of northern species, typical of the boreal climate, have declined. Following changes in the abundance of individual species, community composition has shifted towards predominance of southwestern faunal elements. Total abundance of all moth species has varied periodically so that abundance peaks have occurred during 1995-96 and 2005-06, i.e. with intervals of ten years.

The most likely explanation for most of the observed changes in the Finnish moth communities is the climate warming that has occurred across Northern Europe during the monitoring period. Moths feeding on nitrophilous plant species, i.e. plants benefiting from high soil nitrogen contents, have also become more abundant due to nitrogen deposition. In addition, Decrease in the acid rain has probably affected positively populations of moth species feeding on lichens in the larval stage.

Layers of immunity: Deconstructing the Drosophila effector response

Authors: Lemaitre Bruno, EPFL, Lausanne, Switzerland

Abstract: We are currently dissecting the Drosophila innate immune response with a focus on effectors. Since immune effectors are members of multigene families, their function cannot be adequately addressed by the single mutant approach that still prevails today. Thus, we are generating flies carrying single and multiple mutations of immune effectors in a defined genetic background, which will allow comparative analysis of gene function either individually or collectively at the level of gene families. Our study will be done both at the level of individual effectors and immune modules. Recently, we have characterized how antimicrobial peptides individually or collectively contribute to host defense. Our studies reveal an unexpected level of specificality at the effector level as a single antimicrobial peptide can determine survival or death to a defined pathogen. We also address the role of immune effectors beyond immunity in contexts that have been implied but not well demonstrated, notably in the control of the gut microbiota and the elimination of tumor cells, neurodegeneration, and aging. By deciphering how immune effectors combat infectious microbes and impact non-immune processes, our work will illuminate critical aspects of Drosophila host defense, and will be instrumental in comprehension of innate immunity in general.

The Drosophila antimicrobial response: deconstructing the immune effector program using CRISPR/Cas9 technology

Authors: Lemaitre Bruno, EPFL, Lausanne, Switzerland

Abstract: While neglected during the decades where adaptive immunity captured most of the attention, innate immune mechanisms have become central to our understanding of immunology. The recent emphasis on innate immunity has, however, mostly focused on the first two phases of the immune response: recognition and signaling. In contrast, how innate immune effectors individually or collectively contribute to host resistance has not yet been investigated to the same extent. The existence of multiple effectors that redundantly contribute to host resistance has hampered their functional characterization by genetic approaches. As a consequence, the logic underlying the role of effectors is only poorly defined, and exactly how immune parameters contribute to survival is not well characterized. To fill this gap, ware currently studying the deployment of the immune response with a focus on immune effectors taking advantage of the CRISPR/Cas9 editing approach. To carry out this ambitious program, we systematically inactivate putative immune effector genes and generate compound mutants with mutations in various effector genes. This approach allows us to overcome functional redundancy, and to disentangle the respective contribution of each effector to host resistance. We are currently characterizing the role of antimicrobial peptides in immunity and beyond infection, notably aging. We are also studying the metabolic and physiological landscape required to mount an effective immune response while preserving vital host functions. Collectively, our study aims at providing a high-resolution map of the Drosophila immune response by deciphering the relative contribution of each immune effector to combat infectious microbes. Taking into consideration the key role that the immune system plays in many processes including microbiota control, neurodegeneration, and aging, our study is likely to have a global impact.

Effects of trans-generational immune priming on honeybee colonies

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Abstract: The health of managed honeybee (Apis mellifera) colonies has decreased, along with decreasing numbers of many pollinators. Pathogens are one of the many reasons for the decline, so studying the responses of honeybees against pathogens could provide ways to help these important pollinators. Immune priming is a function of the invertebrate immune system that can improve resistance against a previously encountered pathogen, and the priming effect can even extend to the next generation. While trans-generational immune priming (TGIP) has been shown to increase the pathogen resistance of the honeybee larvae in the lab, potential tradeoffs or behavioral changes related to TGIP have not been studied in honeybees. Working with Finnish beekeepers, we plan to set up experimental beehives with immune-primed and control queens. The foraging preferences, foraging efficiency and general performance of these colonies is then compared by specifying the sources of collected nectar and pollen, measuring colony growth and the quantity of produced honey, and further by contrasting the forage to the available floral resources in the surrounding landscape. Benefits of TGIP will be assessed by following colony survival and pathogens in the hives. The findings will shed light on potential behavioral changes and tradeoffs related to TGIP on the level of the honeybee colony.

Insect Rearing Science and Education Development and Applications

Authors: Leppla Norman, University of Florida Institute of Food and Agricultural Sciences Entomology and Nematology Department, United States

Abstract: Insect rearing has advanced from using relatively crude small-scale methods and natural diets prior to the 1960s to an industrial scale that includes specialized facility design and management, complex production systems that incorporate artificial diets and automated equipment, effective microbial management, and sophisticated production, process and product quality control. These advancements depended on the development of supporting insect rearing science and technology, along with unique education and training. The symposium on “Principles and procedures for rearing beneficial and other economically important arthropods” will address the following: Nutrition and diets, microbial management, quality control, population genetics, environmental biology, and facility design. These topics will be presented by the instructors for them at the International Insect Rearing Workshop conducted annually at Mississippi State University. Thus, the field of insect rearing and its associated profession have been created and advanced. This, in turn, has made possible a wide range of applications that require a dependable supply of high-quality insects. Included are the sterile insect technique, biological control, insecticide development, pheromone identification and synthesis, educational displays, conservation, human food and animal feed, and many other important purposes for colonized insects. Recently, an unprecedented increase in the magnitude of insect mass rearing for animal feed and human food has resulted in the maximum output of a facility extending from billions to tons per week. Due to this scale of insect mass rearing, renewable sources of feed are available for farm-raised fish and other farm animals. Regardless of the purpose and magnitude of insect rearing, the capability now exists to provide a reliable supply of high quality and affordable insects.

Hoverflies as ecosystem service providers in an urbanizing world

Authors: Lequerica Manuel[1], Threlfall Caragh[1], Hochuli Dieter[1] and Latty Tanya[1], [1]The University of Sydney, Australia

Abstract: Australian hoverflies (approximately 180 species) provide important ecosystem services such as pollination and control of phytophagous pests. The role of hoverfly larvae as predators of aphids has the potential to reduce pesticide use while the role of adults as pollinators can benefit the conservation of native vegetation. Although 86% of Australia’s population is urban, little is known about the impact of urbanization on hoverfly diversity and distribution. We surveyed hoverflies from 30 urban sites in four consecutive seasons during one year. We used a multi-scale approach to quantify habitat attributes and compared hoverfly richness and diversity to the measured environmental variables. Multiple regression analyses revealed that hoverfly diversity was higher on less frequently mowed sites and in sites with higher abundance of flowers, regardless of human population density. Hoverfly abundance was positively related to sunshine, but it was not related either to temperature or honey bee (Apis mellifera) abundance.

The ability of hoverflies to stay active during the coldest months, inhabit densely populated urban areas, and having a generalist flower diet are characteristics that make them suitable candidates for the provision of multiple ecosystem services in cities. Cities can be transformed into reservoirs of hoverfly diversity with simple interventions such as assuring a constant flower supply throughout the year or decreasing the frequency in which ground cover is mowed. We suggest a series of environmental practices that can increase the diversity and abundance of native hoverfly species in urban areas, thus enhancing the provision of important ecosystem services such as pollination and control of hemipteran pests.

Responses of hover fly diversity and abundance to local and landscape attributes of urban greenspaces in Sydney, Australia

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Abstract: Urban greenspaces are vital refugia for insect biodiversity, but seasonal responses of insect taxa to landscape and local attributes of urban greenspaces are not well known. Regions with mild temperate climates and winter-flowering plants have active winter pollinators that are often neglected. A thorough knowledge of the seasonally fluctuating ecological needs of insects is essential for insect-friendly greenspace management. Hoverflies are cosmopolitan inhabitants of urban greenspaces where they provide multiple ecosystem services. We used a multi-scale approach to determine the seasonal effects of urbanisation on hover fly populations. We selected 30 sites along an urbanisation gradient in Sydney, Australia and sampled each site over a year across seasons. We found that hover fly species richness was higher in winter and spring than in summer, while abundance was highest in winter and lowest in summer. Our results also show that a combination of local and landscape attributes of urban greenspaces affect hover fly species richness and abundance in seasonally dependant ways. Hover flies are especially abundant and diverse during winter- a time of the year when other native floral visitors are less active. Thus, hover flies may be important pollinators of the large community of winter-flowering plants in Australia.

Feeding patterns of an aphid parasitoid: influence of host presence and of the distance between host and extrafloral nectar

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Abstract: Extrafloral nectar (EFN) is one of the principal carbohydrates resources used by many parasitoid species, including Aphidius ervi Haliday [Hymenoptera: Braconidae], in order to extend its lifespan and, for a female, to increase its egg load. Providing parasitoids with EFN sources can improve their efficiency as biological control agents against aphid pests. The frequency at which parasitoids such as A. ervi females need to feed in order to optimize their time between ovipositing or re-strengthening through nectar uptake is unknown: no study using video recording to observe the feeding patterns of parasitoids has been found so far. In this study, we used a movement detection software in order to estimate EFN uptakes and the duration of every uptake by A. ervi females, either in the absence of its host or in its presence, successively at two distances from the EFN providing plant, under controlled conditions. A segmentation/clustering method identified a tendency of feeding twice a day for females in the absence of its hosts. Interestingly, they tended to feed only once a day in the presence of aphids (next to the providing plant or 80cm away). Our results give valuable information on the effect of hosts on parasitoids feeding behaviour

Access and benefit-sharing for genetic resources for food and agriculture

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Abstract: It is widely acknowledged that genetic resources for food and agriculture (GRFA) are in many respects different from 'wild' biodiversity. In fact, the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity (Protocol) recognizes "the special nature of agricultural biodiversity, its distinctive features and problems needing distinctive solutions." The Protocol also requires its Parties to consider "in the development and implementation of its access and benefit-sharing legislation or regulatory requirements […] the importance of genetic resources for food and agriculture and their special role for food security" – a complex challenge for governments and administrators alike.

The Commission on Genetic Resources for Food and Agriculture that once negotiated the International Treaty on Plant Genetic Resources for Food and Agriculture, a special agreement that provides a tailor-made multilateral ABS system for a particular subsector of GRFA, prepared "ABS Elements"(*). The ABS Elements aim to assist governments considering developing, adapting or implementing access and benefit-sharing measures to take into account the importance of GRFA, their special role for food security and the distinctive features of the different subsectors of GRFA, including micro-organism and invertebrate genetic resources (MIGR).

The ABS Elements stress the importance of assessing the use and exchange mechanisms of concerned subsectors of GRFA and of consulting relevant governmental and non-governmental entities holding, providing or using specific genetic resources. Many agricultural stakeholder have not paid much attention to the development of the Protocol. It is therefore important to inform them, seek their views and involve them in the decision-making process prior to the adoption of national ABS measures that may have significant impact on the different subsectors and how they may utilize and exchange genetic resources for research and development.

The ABS Elements indicate a significant amount of flexibility Governments have in the design of ABS policies. A whole range of options is available to adequately reflect the distinctive features of specific subsectors of GRFA in ABS regimes. None of the international instruments require to restrict access to micro-organism and invertebrate genetic resources. Governments may also opt for specific provisions addressing research and development of genetic resources for the purpose of developing biological control agents. The presentation will provide an overview of options and elements, governments and stakeholders may take into account when considering policy, administrative or legislative measures on ABS.

(*) FAO. 2019. Elements to facilitate domestic implementation of access and benefit-sharing for different subsectors of genetic resources for food and agriculture – with Explanatry Notes.

Silencing immunity to determine how pathogens influence invasion success

Authors: Lester Phil[1], Felden Antoine[1], [1]Victoria University of Wellington, New Zealand

Abstract: Pathogens have been proposed as a cause of boom-and-bust dynamics in invasive species. The globally invasive Argentine ant (<i>Linepithema humile</i>) forms large “supercolonies” within which pathogens have the potential to quickly spread. Here, we used a RNAi approach to target core components of the ants’ immune system in order to manipulate their immunity. We effectively disrupted expression of genes across multiple immune signalling pathways, and present data on phenotypic changes associated with dsRNA treatment. Through a range of behavioural and molecular assays, we investigate how pathogens might influence invasion success, and explore the possibility of using RNAi targeted at the immune system as a pest control strategy.

Transcriptomic signatures associated with social behaviour in the Argentine ant reveal variation in genes associated with biogenic amines, hormones and chemoreception

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Abstract: Social behaviour is considered as a key factor in the success of social insects, including invasive ants that often have substantial disruptive effects on ecosystems. Beyond the reproductive division of labour between workers and queens, social insect worker castes are also often characterised by behavioural variation, with different individual workers engaging in different tasks. Here, we used high-throughput RNA-Sequencing to investigate transcriptome-wide variations associated with morphological castes (i.e. queens versus workers), as well as worker age and worker foraging propensity in the globally invasive Argentine ant (<i>Linepithema humile</i>). We found that morphological castes, worker age and foraging propensity were associated with distinct transcriptomic signatures, including variation in genes associated with biogenic amines, hormonal control and chemoreception. JH-related genes (e.g. gonadotropin-releasing hormone, farnesol-dehydrogenase, hexamerin, ecdysteroid-regulated protein) were differentially regulated in queens versus workers, but also associated with worker foraging propensity. Gene co-expression network analysis (WGCNA) also indicated significant enrichment of hormone-signalling pathways in gene modules associated with worker age and foraging propensity. Overall, our results indicate that variation in social behaviour has a molecular basis in Argentine ants, and provide directions to further investigate the complexity of their social organisation.

Do invasive Argentine ants affect viral infection dynamics in honey bee colonies?

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Abstract: Determining what effect invasive species have on local disease dynamics is critical to understand disease emergence. Honey bee-associated viruses, which are linked to colony collapses are found in many arthropod species, including invasive ants. The invasive Argentine ant, which reaches high densities and infests beehives possibly exposes bees to viral pathogens. We monitored viral and non-viral infections in honey bees in the presence and absence of Argentine ants over seven months. Black queen cell virus and deformed wing virus (DWV) levels, but not prevalence, in bees significantly increased with ant presence. Kashmir bee virus infected only a few colonies from ant-infested sites. All three viruses were found in ants throughout the experiment. Microsporidian and trypanosomatid infections, which are more bee-specific, were not affected. An analysis of the bee virome in autumn found that DWV had the highest infection levels and that no ant-associated viruses were infecting bees. Virus spillback from ants could increase infections in bees and indicates that ants vector bee pathogens. In addition, stress from ant attacks may affect viral susceptibility. Our study contributes to unravel how a globally invasive species is associated with disease emergence in an economically important pollinator.

CRISPR gene drives to eradicate or suppress globally invasive social wasps?

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Abstract: CRISPR gene drives are a novel technology with the potential for widespread and cost-efficient pest control, but are also highly controversial. We examined a potential gene drive targeting spermatogenesis to control the invasive common wasp (Vespula vulgaris). Vespula wasps and many other globally invasive pests are haplodiploid and widespread in native ecosystems. Their life cycle makes gene drive production challenging. We show that different spermatogenesis genes have different levels of variation between introduced and native ranges, enabling a potential ‘precision drive’ that could target the reduced genetic diversity and genotypes within the invaded range. In vitro testing showed guide-RNA target specificity and efficacy that was dependent on the gene target within Vespula, but no cross-reactivity in other Hymenoptera. Mathematical modelling incorporating the genetic and life history traits of Vespula wasps identified the necessary characteristics for a male sterility drive to achieve population suppression or eradication. There was a trade-off between drive infiltration and impact: a drive causing complete male sterility would not spread. Partial sterility could be effective in limiting or suppressing population size if the homing rate is sufficiently high. Our results indicate that gene drives may offer viable suppression for wasps and other haplodiploid pests, when homing rates are sufficiently high, but pest eradication is likely to be challenging.

New findings on biology and ecology of entomopathogenic nematodes inform the development of new formulation and application methods

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Abstract: Entomopathogenic nematodes are applied to numerous crops to control insect pests. Two claimed advantages of using entomopathogenic nematodes have been that they are formulated in ways that resemble other insecticidal products, and they can be applied using equipment that most growers currently use with only minor modifications. But these aspects of using entomopathogenic nematode-based products often fail to exploit new findings of nematode biology and ecology, nor do they encourage customizing formulations and application methods to specific characteristics of cropping systems. Our efforts to incorporate new biological findings into formulation and application methods, especially in terms of behavioral modification, can lead to increased efficacy of entomopathogenic nematodes.

JHSB3 signaling and egg production in the classical insect model, Rhodnius Prolixus

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Abstract: Juvenile hormones (JH) are sesquiterpenoids secreted from the corpus allatum. In female adults of several insect species, JH acts as a gonadotrophic hormone, regulating vitellogenesis and oogenesis. JH binds to its nuclear receptor, the bHLH-PAS protein Methoprene tolerant (Met), triggering its dimerization with the protein Taiman (Tai). The resulting active complex induces transcription of JH response genes, such as the transcription factor Krüppel homolog 1 (Kr-h1). Although the kissing bug, Rhodnius prolixus, has been widely used as a model to study endocrine signaling in insects, the mechanisms and target genes underlying JH action are not fully understood. In this study, we report for the first time the participation of JH III skipped bisepoxide (JHSB3) signaling (the JH isoform shown by Noriega and colleagues to be present in the hemolymph of R. prolixus) on the synthesis of yolk protein precursors (YPPs) by the fat body and the ovaries, and impact on reproductive fitness. By RT-qPCR we find that RhoprMet and RhoprTai transcripts are not regulated nutritionally by blood feeding, as the YPPs are. We also show that topical application of synthetic JHSB3 on insect females increases transcript and protein expression of YPPs, mainly by the fat body but also by the ovaries, a second YPPs source. These results are confirmed by ex vivo assays and by downregulating RhoprMet and RhoprTai transcripts using RNA interference (RNAi). When the JHBS3 signaling cascade is impaired by RNAi, the synthesis of YPPs decreases and ovarian follicles do not take up nutrients, thereby inhibiting egg production. Interestingly, we also observe that expression of RhoprKr-h1 transcript is highly dependent on JHSB3 signaling, which opens doors to study the role of this transcription factor in R. prolixus reproduction. Overall, the results suggest that follicular synthesis of YPPs is dependent on JHSB3 signaling, and indicate a major participation of not only RhoprMet but also RhoprTai in successful reproduction. This research contributes some missing pieces in JH action in the insect model in which a JH was first reported almost 100 years ago.

Research supported by the Natural Sciences and Engineering Research Council of Canada.

Pathogen prevalence in the blacklegged tick Ixodes scapularis: does pathogen infection alter tick behaviors

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Abstract: The blacklegged tick Ixodes scapularis is the vector of various pathogens that cause serious human and animal diseases. Over 30,000 human cases of Lyme disease are reported to CDC annually and Borrelia burgdoferi is the causative disease agent that is transmitted to humans by the blacklegged ticks. It is known that pathogen infection can alter host-seeking behaviors in mosquitoes. The objective of this study is to determine pathogen prevalence in questing Ixodes scapularis ticks collected from parks and natural areas in Maryland and test if pathogen infection alters tick behaviors. Each tick was subjected to laboratory repellent tests involving a series of ascending DEET concentrations to determine the concentration of DEET that repels the tick. DNA extractions were obtained from individual ticks after behavioral assays. RT-PCR was used for detection of various tick-borne pathogens, including Borrelia burgdorferi (sl), Borrelia miyamotoi, Babesia microti, and Anaplasma phagocytophilum. Statistical analysis was performed to determine if there is a correlation between tick's response to DEET and the pathogen infection status of the tick. Preliminary analysis of data indicate pathogen-infected and non-infected adult ticks may be equally sensitive to DEET in laboratory bioassay. Research are currently being conducted to evaluate the responses in nymphs, and to study the potential impact of pathogen infection on tick's host-seeking behaviors.

Monitoring and control of Colorado potato beetle: from field to large–scale region

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Abstract: Colorado potato beetle (CPB) is internationally recognized as not only the devastating quarantine pests, but also the major foreign quarantine objects and invasive alien species. Natural migration is the major dispersal strategy of its spreading. It spread to Kazakhstan of Central Asia in 1980s where near from Xinjiang of China. And then CPB was found for the first time in 1993 in Xinjiang. Since then, it continued to spread from west to east. And the risk of its further spread eastward into Gansu, Inner Mongolia and other potato main producing areas of China is increasing. In the other side, in recent years, invasions of CPB from Russia to China have become a threat in northeastern China.

The spatial distribution pattern of CPB is affected by temperature, moisture, topography and human activities. The temperature factor is mainly the main temperature of the wettest quarter and the warmest quarter, due to the warmest quarter in Xinjiang, China. The wettest quarters are basically coincident, all in the summer of June-August, so we can think that the average temperature in summer is the most critical factor affecting the distribution of CPB. The main factor of the moisture factor is the lowest temperature in the coldest month and the average precipitation in the coldest month. The lowest temperature in the coldest month can be regarded as a part of the temperature factor, that is, the influence of low temperature. However, the temperature, especially the low temperature in winter, also plays a role in the use of water by insects. Among the topographic factors, the ratio of altitude, day and night temperature difference to annual temperature difference reflects the influence of terrain. In human activities, the distance from the settlement point is the main advantage. The four main factors have different effects on the spatial distribution pattern of CPB because of their different contribution rates. They are ranked according to the contribution rate: temperature factor>water factor>topographic factor>human activity factor.

To further clarify the role of airflow in the spread of CPB in Xinjiang, the direction and speed of airflow were analyzed in Northwestern China from June to September in 2007-2014 in 850 hPa with the method of atmospheric background field analysis by using GrADS software and NCEP and NCAR joint meteorological reanalysis data; In the colonized regions of CPB in Xinjiang, the direction of airflow was same as the CPB spread direction in the early years of its invasion in China. And the airflow played an important role in the invasion process from Kazakhstan. While in the current frontier regions, the airflow direction was not conducive to CPB dispersal from west to east, and the airflow intensity and duration were not enough to make CPB spread into Hexi Corridor of Gansu Province; The role of airflow carrying for CPB had a certain effect on it invaded China and dispersal in the early year of its invasion.

Survey of household termite species composition and dispersal flight season with synergy of citizen science project in Taiwan

Authors: Li Hou-Feng[1], Huang Shih-Ying[1], Li Wei-Jie[1] and Tsai Yi-Ying[1], [1]Department of Entomology, National Chung Hsing University, Taiwan

Abstract: The Formosan subterranean termite, Coptotermes formosanus Shiraki, and Asian subterranean termite, C. gestroi (Wasmann) are both destructive economic pests worldwide. Their alates have swarming behavior during late-spring to early-summer to establish new colonies and to extend their distribution. In 2008, a questionnaire survey to local pest control operators indicated that C. formosanus and C. gestroi were major household pests in Taiwan. However, quantitative infestation data was unavailable. Conducting termite infestation surveys is difficult because access to private constructions is limited. In addition to infestation surveys, estimation of the nationwide swarming season is also challenging, since termite swarming occurred unpredictably and usually lasted for less than an hour.

In this study, we launched a citizen science project to collect household termite samples by cooperating with homeowners and local pest control operators. A species identification service website, termite.nchu.edu.tw, was established for acquiring information, including collection date, address, and infested items. In addition, a Facebook group was used for advertisement and to recruit more people to collect and send termite samples to our laboratory. Species identification results were provided to collectors through e-mails, with all termite samples preserved in the NCHU Termite Collection for further biological studies.

In the past five years, 2015-2019, > 3,000 termite samples were sent to our laboratory. A total of 1,296 household termite samples showed C. formosanus and C. gestroi, were responsible for 95% of the termite infestations, but species compositions were significantly different in Northern and Southern Taiwan. C. formosanus and C. gestroi are dominant in Northern and Southern Taiwan, respectively, with >90% infestation rates in the respective areas. In Central Taiwan, infestation rates were similar. Three other minor household termites, Odontotermes formosanus (Shiraki), Reticulitermes flaviceps (Oshima) and Cryptotermes domesticus (Haviland), were together responsible for <~5% termite infestations in each county. A total of 363 termite alate collections showed C. formosanus’s and C. gestroi‘s swarming peaked in April and May, respectively. The sympatric distribution and overlapped swarming seasons of the two Coptotermes spp. were observed in Central Taiwan between late-April and mid-May.

This study showed that a citizen science project can help scientists access household pest samples, infestation status, and pest biological information with the help of homeowners and pest control operators. Citizen science projects also provide an extension platform for citizens, industry, and academia, which will further facilitate pest management in urban environments.

Multiple bacterial symbionts affect the metabolism of insecticides by brown planthopper (Nilaparvata lugens)

Authors: Li Jianhong[2], Wan Hu[1], Zhang yunhua[1], Tang Tao[1], [1]College of Plant Science and Technology, Huazhong Agricultural University, Wuhan, China, [2]Huazhong Agricutural University, China

Abstract: Symbionts participate in various physiological activities of their insect hosts, including detoxification metabolism. Emerging evidence indicates that the bacterial symbiont Arsenophonus is involved in insecticide detoxification metabolism in N. lugens, which harbors diverse symbionts. Whether other bacterial symbionts play a role in this process is still unknown. The present study showed that the toxicity of imidacloprid, chlorpyrifos and clothianidin to N. lugens was significantly increased in N. lugens pretreated with antibiotics, and the detoxifying enzyme activities of cytochrome P450 enzyme (P450) and glutathione S-transferase (GST) were significantly weakened. In addition, three GST (NlGSTd2, NlGSTe1, and NlGSTs1) and five P450 (NlCYP303A1, NlCYP306A2, NlCYP4DD1, NlCYP425A1, and NlCYP3115A1) genes were both significantly downregulated in N. lugens treated with antibiotics (tetracycline or ciprofloxacin). Furthermore, the expression levels of various detoxifying genes were significantly correlated with Wolbachia, Arsenophonus, Acinetobacter, and Staphylococcus. These results suggested that multiple bacterial symbionts affect the metabolism of insecticides by N. lugens by regulating the expression of the GST and P450 genes. The present study enriched the theory of insect toxicology, laying the foundation for further study on the mechanism of host detoxification metabolism mediated by symbionts in insect pests.

Transcriptional response of ATP-binding cassette (ABC) transporters to insecticide in the brown planthopper, Nilaparvata lugens (Stål)

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Abstract: ABC transporter superfamily is one of the largest group of proteins and play a non-negligible role in the phase ? of the detoxification process, which is an important mechanism for insects to defend against environmental stress (toxic secondary plant metabolites and insecticides). In the present study, we have identified 32 ABC transporters in the Nilaparvata lugens, which are grouped into eight subfamilies (ABCA-H) based on phylogenetic analysis. The temporal and spatial expression profiles suggested that the first-instar, second-instar, third-instar, fourth-instar, fifth-instar and male showed a certain similarity, which was different from egg and female. The spatial expression profiles showed that NlABCA1, NlABCA2, NlABCB6, NlABCD2, NlABCG4, NlABCG12, NlABCG15, NlABCH1 were highly expressed in the midgut and the Malpighian tube. In addition, ABCG12, which belongs to the ABC transporter G subfamily, was significantly up-regulated after exposure to sulfoxaflor, nitenpyram, clothianidin, etofenprox, chlorpyrifos and isoprocarb. Moreover, verapamil significantly increased the sensitivity of N. lugens to nitenpyram, clothianidin, etofenprox, chlorpyrifos and isoprocarb. This study was conducted to provide a basis for further studies on ABC transporter genes in N. lugens, and for more comprehensive understanding of the response of N. lugens under environmental stress such as insecticides.

Horizontal Transfer of a Retrotransposon from the Rice Planthopper to the Genome of an Insect DNA Virus

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Abstract: Horizontal transfer of genetic materials between virus and host has been frequently identified. Three rice planthoppers, Laodelphax striatellus, Nilaparvata lugens, and Sogatella furcifera, are agriculturally important insects because they are destructive rice pests and also the vector of a number of phytopathogenic viruses. In this study, we discovered that a small region (~300 nucleotides [nt]) of the genome of invertebrate iridescent virus 6 (IIV-6; genus Iridovirus, family Iridoviridae), a giant DNA virus that infects invertebrates but is not known to infect planthoppers, is highly homologous to the sequences present in high copy numbers in these three planthopper genomes. These sequences are related to the short interspersed nuclear elements (SINEs), a class of non-long terminal repeat (LTR) retrotransposons (retroposons), suggesting a horizontal transfer event of a transposable element from the rice planthopper genome to the IIV-6 genome. In addition, a number of planthopper transcripts mapped to these rice planthopper SINE-like sequences (RPSISs) were identi?ed and appear to be transcriptionally regulated along the different developmental stages of planthoppers. Small RNAs derived from these RPSISs are predominantly 26 to 28 nt long, which is a typical characteristic of PIWI-interacting RNAs. Phylogenetic analysis suggests that IIV-6 acquires a SINE-like retrotransposon from S. furcifera after the evolutionary divergence of the three rice planthoppers. This study provides further examples of the horizontal transfer of an insect transposon to virus and suggests the association of rice planthoppers with iridoviruses in the past or present.

Can we pyramid Bt toxins and plant allelochemicals to combat pests?

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Abstract: Genetically engineered crops that simultaneously produce Bacillus thuringiensis (Bt) toxin proteins and higher concentration of defensive allelochemicals may act synergistically to kill devastating insect pests and delay their resistance to either of the two types of toxins. To evaluate the possibility of pyramiding Bt toxins and plant allelochemicals to mange pests, we examined the toxicological interactions between Cry1Ac, a major Bt toxin protein expressed in the current Bt crops, and flavone, a representative of the ubiquitous flavonoid allelochemicals, in Helicoverpa armigera, a world-wide devastating pest targeted by Bt cotton and Bt corn. Two lethal (LC25 and LC50) and one sublethal (LC10) doses were selected from the dose-response lines of the two toxins to reveal the nature of their interactions. Simultaneous exposure of H. armigera neonates to Cry1Ac and flavone of the LC25 dose caused a mortality significantly higher than that of either toxin alone and their expected additive mortality. Preexposure for 24 h to the sublethal dose of Cry1Ac followed by 6-day simultaneous exposure to the LC50 dose (1.6 mg/g diets) of flavone plus the sublethal dose of Cry1Ac resulted in a mortality significantly higher than that of the LC50 dose of flavone alone and the expected additive mortality of the LC50 dose of flavone plus the sublethal dose of Cry1Ac. One-day preexposure to the sublethal dose of flavone followed by 6-day simultaneous exposure to the LC50 dose (6 ng/cm2) of Cry1Ac plus the sublethal dose of flavone, however, did not enhance the mortality of the LC50 dose of Cry1Ac. The results suggest that Cry1Ac and flavone synergistically enhance each other's toxicity when H. armigera larvae ingest lethal doses of both toxins from Bt crops. The results also show that when only one of the two toxins reaches its lethal doses in Bt crops, sublethal dose of Cry1Ac induces the toxicity of flavone, whereas sublethal dose of flavone has no impacts on the toxicity of Cry1Ac.

Comparative analysis and functional study of microRNA of the testis and ovary of the Helicoverpa armigera

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Abstract: MicroRNAs (miRNAs) are a class of short (18-24 nucleotides), small non-coding RNAs that bind to 3'UTR to regulate gene expression by post-transcriptional suppression of mRNA. Several studies have demonstrated that miRNAs are involved in the development of testis and ovary of Drosophila melanogaster and Bombyx mori but there are few studies of Helicoverpa armigera. In this study, two small RNAs libraries of H. armigera ovary and testis were constructed using deep sequencing technology. The results showed that the types of small RNA enriched in the testis and ovary were different. MiRNAs are mainly found in testis and piRNAs in ovary. Two miRNAs (miR-252a-5p and miR-263b-5p) were selected from the libraries and qRT-PCR showed that they had different expression profiles in other tissues (head, throax, abdomen, foot, wing and fay body) and different development stages. Target prediction showed that a total of 2,134 candidate genes of miR-252a-5p and 5,474 of miR-263b-5p were found respectively. Among them, we chose 3 of miR-252a-5p (DPP, OVOL and JHEH) and 4 of miR-263b-5p (FOXO, BTB, EGFR and JHEs) as target genes. Furthermore, injection of two miRNAs mimics/inhibitors lead to the opposite expression profile with their target genes. Using a dual luciferase reporter assay in S2 cells, we confirmed that miR-252a-5p and miR-263b-5p suppressed transcription of their target genes suggesting that these miRNAs as minor regulators play vital regulatory roles in H. armigera. Taken together, this study provides insights into reproductive development in miRNA expression of H. armigera.

Insect Identification Based on Spectral Fringes Produced by Clear Wings

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Abstract: Due to the growing awareness that insects' diversity and populations are in decline, there is an increased need for monitoring insects. Entomological lidars and photonic sensors can monitor and remotely identify flying insects based on their back-scattered signal in terms of modulation-, polarization, and spectral content. The back-scattered light from insects is predominantly oscillatory and derives from the wings. This part of the signal is also more coherent and co-polarized than the light reflected from the insect's abdomen. Clear membranes display soap-bubble colors due to thin-film interference, a feature that associated with the thickness of the wing. A hyperspectral camera can capture these wing interference patterns and accurately identify the wing thickness. Here we investigate whether the spectral fringes can provide complementary information to aid remote insect identification. We demonstrate that we can extract wing thickness and modulation depth information from spectral fringes of 87 species of common insect pollinators in Skåne, Sweden. The modulation depth of a fringe provides information related to insect wing thickness homogeneity, wrinkleness, or anti-reflectance features. Our results show that examined species display distinct modulation and wing thickness, and therefore such features can be used to improve the specificity of species identification of photonics sensors.

W chromosome and sex determining genes in Bombyx mori

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Abstract: Deciphering the regulatory factors involved in the sex determination Bombyx mori, has been a puzzle challenging researchers for nearly a century now. Femaleness in B. mori is determined by the presence of a single W chromosome, irrespective of the numbers of autosomes or Z chromosome. We still lack the complete sequence of a W chromosome in a system of female heterogamety and, obtaining this information will be central to the understanding of the evolution of non-recombining sex chromosomes. We sequenced W chromosome of B. mori using different molecular biological and computational tools. The combination of molecular biological tools like 3D BAC pools, Laser Microdissection of W bodies, NGS, HI-C, PacBio and nanopore ultra-long sequencing coupled with computational analysis of large sequence data, provided us with a good coverage of W chromosome sequence. We de novo assembled 9 W-derived genome contigs of 19.8 Mb which contains Fem-piRNA cluster gene and CCCH-type Zn-finger protein genes. W sequencing of sex-limited yellow cocoon W mutant and sex-limited Zebra W mutant was also performed confirming the presence of Fem-piRNA cluster gene and CCCH-type Zn-finger protein genes, Now we are studying the function of Zn-finger protein expressed on W on Fem-piRNA gene expression and sex-determination pathway.

Effects of warming on insect herbivory and herbivore-induced plant volatiles in the Arctic tundra

Authors: Li Tao[1], Michelsen Anders[1], Rieksta Jolanta[1] and Rinnan Riikka[1], [1]University of Copenhagen, Denmark

Abstract: Climate change is altering plant-herbivore interactions with ecosystem-level consequences. This is particularly the case in the Arctic, which is warming at twice the global average. In the boreal mountain birch forest, for example, distribution shifts towards higher elevations have been observed for notorious geometrid moths such as Epirrita autumnata and Operophtera brumata. One important mechanisms underlying insect range expansion involves climate-driven changes in host plant defensive chemistry, such as emissions of volatile organic compounds (VOCs). Plant VOCs are known to play multiple roles in plant-insect interactions, including attracting/deterring insect herbivore and attracting predators and parasitoids of the attacking herbivores. However, it remains largely unexplored how insect herbivory in the Arctic influences plant VOC emissions, particularly with ongoing climate warming. This presentation will attempt to address this issue. We employed short-term (one month), medium-term (9 years) and long-term (19 years) experimental warming in an arctic heath ecosystem (Abisko, Northern Sweden) to 1) investigate the impacts of in situ warming on insect herbivory and 2) assess the importance of herbivore-induced plant VOCs and interactions with warming in the Sub-Arctic tundra. We will present these data and discuss the ecological consequences.

Screening, evaluation and optimization of artificial diet for Neoseiulus barkeri

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Abstract: Neosuiulus barkeri is an effective commercial biological control agent on the sustainable pest management on spider mites, whiteflies and thrips. Its mass rearing procedures based on alternative prey like storage mites involved space and labor to maintain large parallel cultures of the factitious prey. Further, storage mites may cause potential health problems for workers in production facilities or application fields caused by allergy or asthma associated with the storage mites. The availability of an effective artificial diet for predatory mites provides an opportunity to avoid such problems for the mass and standardized production. This study screened a better artificial diet formula by adding different animal source components to the basic artificial diet. The life table parameters, predation functions and cannibalism levels of N. barkeri population on artificial diets were evaluated. The nutrients information of the best artificial diet, target prey (Tetranychus urticae) and alternative prey (Aleuroglyphus ovatus) were measured and further the artificial diet was optimized. The age, stage, two-sex life table analysis was used to compare the development, survivals, and fecundities of N. barkeri fed on four artificial diets and two prey species (T. urticae and A. ovatus). When fed on four artificial diets, N. barkeri held a lower fecundity and intrinsic rate of increase than those fed on two prey species. Among the N. barkeri fed on artificial diets, fecundity was highest on AD3 (24.94 eggs) and lowest on AD2 (14.25 eggs). It indicated that AD3 had better potential for mass rearing of N. barkeri. Compared with rearing prey species, the predation ability of N. barkeri under artificial diet was decreased, and the cannibalism level in the population was higher after 24 h. The contents of main saccharides, amino acids and fatty acids in the T. urticae, A. ovatus, and artificial diet were determined. The total content of the three saccharides in the artificial diet (AD3) was 10.7 times and 20.8 times that of the T. urticae and A. ovatus, respectively. The total content of amino acids in T. urticae and A. ovatus were higher 9.1% and 19.3% than AD3, respectively. According to the measurement results, the AD3 was improved by separately supplement Corcyra cephalonica eggs (AD5) and amino acid mixture (AD6). After rearing AD5 and AD6, the developmental duration of nymph was longer. The oviposition duration, the intrinsic rate of increase and the net reproductive rate of N. barkeri reared on AD5 and AD6 were no significantly different with that on AD3. After supplement of the C. cephalonica eggs and amino acid mixture, the pre-ovipositional period of N. barkeri was shorter than that of AD3, and the fecundity increased after supplement of the C. cephalonica eggs. The results indicated the potential artificial diets for use in the mass rearing of N. barkeri.

Insect flight velocity sensing with a CW near-IR Scheimpflug lidar system

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Abstract: Flight velocity measurement plays an important role in insect research that can aid insect identification, facilitate studies and monitoring of insect movements, and enable the early alert on the invasion of agricultural pests and disease vectors. A NIR Scheimpflug lidar-based novel scheme for the 1-D flight velocity measurement of insects has been proposed. We implement this new technique and apply it to study insects at the Salter Research Farm, Robertson County, Texas. The resolution property in the direction perpendicular to the probing direction of the Scheimpflug lidar system is explored and reveals the capability of retrieving the velocity component normal to the probing direction of insects passing through the field of view of our system. During the field measurement, a shift in the wingbeat frequency distribution is observed, which indicates a change in the local species component on the farm. The velocity information further shows that this change could be attributed to a net directional movement of insects. With Hierarchical Clustering Algorithm, the net flux of insects with similar wingbeat power spectra can also be revealed.

From studies to applications: the development of invasion ecology and surveillance on economically important fruit flies in China

Authors: Li Zhihong, China Agricultural University, China

Abstract: Tephritids are regarded as economically important pests and spread widely in the world under the background of global change and international economic integration. According to current regulations, there are six genera and five species of Tephritidae listed as quarantine species in China, which gained more attentions on the studies and applications of prevention and control. This review focused on the development of studies and applications on invasion ecology and surveillance of economically important fruit flies in recent ten years in China. It reviewed the related studies of establishment probability, potential geographical distribution, potential economic loss, invasion tracing and temperature adaptation mechanism of Tephritids, such as Bactrocera dorsalis. Meanwhile, it analyzed the related applications of surveillance based on above studies in China, e.g., identification of areas, months, species and source of monitoring survey on economically important fruit flies. The perspectives and suggestions of further studies and applications of invasion ecology and phytosanitary measures on Tephritids were illustrated for reference.

A study of Halyomorpha halys populations in kiwi orchards using Remote Sensing and Geostatistics

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Abstract: Halyomorpha halys' invasion from Asia to the US and Europe caused serious damages to fruit and vegetables. In Greece, damages are mainly reported in kiwi orchards. The aim of this research is to study a) if the crops nearest to the kiwi orchards affect the H. halys population and b) if kiwi plant vigour has an impact on H. halys populations. Two kiwi orchards were selected and ten traps were installed from early June to late October in each orchard – two types of traps at every side and at the center. Afterwards, crops that were up to 500m far from the selected orchards were identified. Traps were examined weekly. Additionally, sentinel satellite images were analyzed using Geostatistics to calculate the vegetation index NDVI. Moreover, we recorded the terrain variability using RTK GNSS and the spatial variability of elevation presented in maps using Geostatistics. The results showed that the nearest crops to the kiwi orchards have an impact on the populations of H. halys. Furtehrmore, population of H. halys was higher at the areas with high NDVI values. Finally, H. halys showed a preference to develop in the highest altitudes within an orchard.

Molecular and epigenetic control of reproduction in response to social context in ants

Authors: Libbrecht Romain, Johannes Gutenberg University of Mainz, Germany

Abstract: Understanding the evolution of social life is one of the great challenges in evolutionary biology. Particular attention has been given to the extreme case of insect societies, and to the evolution of reproductive division of labor between fertile queens and sterile workers. The typical approach to investigate the mechanisms underlying the evolution of reproductive division of labor is to compare queens and workers in species with morphologically distinct castes, but the interpretation of such comparisons is limited by multiple confounding factors and the fact that castes are typically fixed and cannot be manipulated at the adult stage. In this talk, I will present two alternative study systems to investigate the evolution of reproductive division of labor in ants. These study systems are the phasic life cycle of the clonal raider ant Ooceraea biroi and the colony foundation process of the black garden ant Lasius niger. In both systems, reproductive physiology changes in response to the social environment, thus allowing for experimental manipulation of reproduction. I will elaborate on some of our recent and on-going work on how gene expression, epigenetic processes and hormones underlie variation in reproduction, and on their potential role in the evolution of reproductive division of labor in insect societies.

Cellular and molecular mechanisms of a unique parasitic behavioral manipulation

Authors: Libersat Frederic, Ben Gurion University of the negevity, Beer Sheva, Israel

Abstract: Neuro-parasitology is a field that explores how parasites control the nervous system of their host. The parasitoid jewel wasp Ampulex compressa stings cockroaches and injects venom directly into and around the central complex (CC), a central region in the insect brain. In order to provide a fresh food supply for its offspring, the wasp venom induces and long-lasting sedative condition in the cockroach, termed “hypokinesia”. Our aim is to investigate the cellular and molecular mechanisms underlying this unique behavioral manipulation.

In order to decipher the physiological mechanism of such manipulation, we have recorded spontaneous descending activity in stung and control cockroaches. The descending activity in stung animals was decreased compared to that of control. Using direct injections of procaine (a Na voltage dependent reversible blockers) or venom into the CC show similar results. In order to decipher the molecular mechanisms underlying the behavioral manipulation, we used affinity chromatography for identification of venom targets in the cockroach brain and Label Free Quantitative Mass Spectrometry (LFQMS) to identify changes in protein expression that occur in the stung cockroach brain. We found that the venom binds to synaptic proteins and numerous proteins are differentially expressed in the brain of stung cockroaches, many of which are involved in signal transduction pathways such as the Rho GTPase pathway implicated in synaptic plasticity.

Altogether, our data suggest that the jewel wasp exerts control over cockroach behavior through molecular cross-talk between venom components and molecular targets in the host brain, leading to broad-based alteration of synaptic efficacy in the CC. Such a decrease in synaptic drive to the CC results in a decrease in descending activity and a reduction in excitatory drive from the brain to the thoracic motor circuitries. This may account for the observed motor impairments induced by the venom to promote successful development of wasp progeny.

Parasitoid wasp venom manipulates host innate behavior via subtype-specific dopamine receptor activation

Authors: Libersat Frederic[2], Nordio Stefania[1] and Kaiser Maayan[1], [2]Ben Gurion University of the negevity, Beer Sheva, Israel, [1]Ben Gurion University

Abstract: The subjugation strategy employed by the Jewel wasp is unique in that it manipulates the behavior of its host, the American cockroach, rather than inducing outright paralysis. Upon envenomation directly into the central complex (CX), a sensory-motor center in the brain, the stung cockroach initially engages in intense grooming behavior, then falls into a lethargic “sleep-like” state referred to as “hypokinesia”. Behavioral changes evoked by the sting are due at least in part to presence of dopamine in the venom. The specific roles played by dopamine receptor subtypes in venom-induced behavioral manipulation by the jewel wasp remain largely unknown. In the present study, we used a pharmacological approach to investigate roles of D1-like and D2-like receptors in behaviors exhibited by stung cockroaches, focusing on grooming. Specifically, we assessed behavioral outcomes of focal CX injections of dopamine receptor agonists and antagonists. Both specific and non-specific compounds were used. Our results strongly implicate D1-like dopamine receptors in venom-induced grooming. Regarding induction of hypokinesia, our findings demonstrate that dopamine signaling is necessary for induction of long-lasting hypokinesia caused by brain envenomation.

Oxidative stress and ageing in feral honey bees

Authors: Li-Byarlay Hongmei[1], Ward Kilea and Cleare Xaryn, [1]Central State University

Abstract: Molecular damage caused by oxidative stress may lead to organismal aging and result in acute mortality to organisms. Thus, oxidative stress resistance and longevity are closely linked. Honey bees are the most important managed pollinator in agriculture, but the long-term survival of honey bees is seriously threatened. Feral honey bee colonies display persistence to Varroa mites. However, whether feral honey bees are stress-resistant or survive longer than managed bee populations is unknown. More work is needed to determine the impact of oxidative stress on honey bee health and survival. In this study, we used a paired colony design to determine the life span of worker bees from either a feral or a managed colony and their levels of oxidative stress. Each pair of colonies shared similar foraging resources. The results indicated that foragers in feral colonies had longer survival times and life spans than those in managed colonies.

In vivo antioxidant effect of reared edible cricket (Order: Orthoptera) peptides using a Caenorhabditis elegans model

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Abstract: Entomophagy has become relevant as it could potentially help reduce food insecurity, due to the highly nutritious and sustainable characteristics of reared edible insects. In addition to their nutritional content, research on the potential bioactive components of insect extracts has also gained interest. In this study, the antioxidant activity effect of simulated gastrointestinal digested (SGD) cricket (Gryllodes sigillatus) peptides was evaluated. Antioxidant activity was determined by 2,2′-azino-bis (3-ethylbenzothiazoline-6-sulphonic acid) (ABTS) radical scavenging activity, oxygen radical antioxidant capacity (ORAC), and using a caco-2 cellular antioxidant model. In vivo acute and chronic oxidative stress was determined using Caenorhabditis elegans as a model. Results showed that SGD peptides had greater ($p < 0.05$) antioxidant activity than the control. In the Caco-2 model, cells exposed to SGD peptides showed the same level of antioxidant activity as those exposed to ascorbic acid under oxidative stress ($p<0.05$). After exposure to cricket peptides (0.125 to 1.0 mg/mL), the lifespan of C. elegans was increased ($p<0.05$) under chronic and acute oxidative stress conditions. Under acute oxidative stress, mean survival time of control nematodes was 322 minutes, while the mean survival time in nematodes exposed to SGD-peptides was 537 minutes. Under chronic oxidative stress, the same trend was observed with mean survival time of nematodes exposed to SGD-peptides being significantly ($p<0.05$) longer than that of the control, 4.6 days and 3.5 days, respectively. RT-PCR studies revealed that the increased resistance to oxidative stress in C. elegans fed SGD-peptides could be due to the increased expression of the stress-related gene gst-4. These results indicate that C. elegans can effectively be used as an in vivo model to evaluate bioactive properties of cricket peptides, and edible cricket peptides have potential use as nutraceutical & pharmaceutical compounds to combat oxidative stress.

Human Impacts on the Polynesian Beetle Fauna: An Ongoing Apocalypse

Authors: Liebherr James[1] and Porch Nick[2], [1]Cornell University, United States, [2]Deakin University

Abstract: Polynesia is home to numerous diverse beetle lineages. We combine data from pre-colonization subfossil deposits with comprehensive field collecting of extant species to provide a deep temporal view of biodiversity loss in Polynesia. Man's earliest impacts on smaller islands resulted in mass extinctions. The Austral Islands, French Polynesia, hosted a diverse prehistoric radiation of 17 species of saproxylic Pycnomerus beetles (Zopheridae), though only four persist after human colonization. In Kauai, Hawaii, the predatory carabid beetle genus Blackburnia is represented by 34 species, 7 of which are known only from subfossils from lowland pre-Polynesian deposits. Today extant species are restricted to habitats above 800 m elevation. Finally, in Oahu, Hawaii, the Polynesian island with the longest and densest history of entomological exploration, 14 of 66 known native Carabidae have not been collected for over a Century. Loss of beetle diversity has been driven by habitat destruction associated first with agriculture, and now with urbanization, complemented by waves of invasive species. Thus forces reducing Polynesian beetle diversity are consistent with those hypothesized for other taxa across the World, though their effects are especially apparent in Polynesia due to the large numbers of endemic beetle species that have evolved on these small islands.

Comparing host associations of native and non-native Scolytines

Authors: Liebhold Andrew, USDA Forest Service Northern Research Station, Czech Republic

Abstract: The Scolytinae exhibit considerable variation in the specificity of host associations with some species associated with a single host tree species and others with hosts that span multiple plant families. Here we report on a comprehensive analysis of host associations, comparing native vs. non-native species, European vs. North American species and true bark beetles vs. ambrosia beetles. We fine that ambrosia beetles tend to be more polyphagous than bark beetles, non-native species tend to be ore polyphagous than native species and European and North American species are comparable in their host specificities. These results contribute to a more comprehensive understanding of non-native Scolytine species.

Taxonomic patterns of global insect invasions reflect historical pathways, socioeconomic drivers and insect invasiveness

Authors: Liebhold Andrew, USDA Forest Service Northern Research Station, Czech Republic

Abstract: Biological invasions are largely an unintended consequence of globalization. With increasing mobility, humans have accidentally transported organisms around the world, breaking the geographical boundaries that separated species ranges that persisted for millions of years of evolution. Among animals, insects are the most numerous group of species, with thousands of insect species having been established outside of their native ranges and many of these species causing immense impacts on agriculture, human health and conservation of native ecosystems. Here, we report on an analysis of historical insect invasions in 11 world regions. We use these data to compare frequencies of invasions among different insect orders and among different insect families. Certain groups, such as the Hemiptera, Formicidae and the Staphylinidae are generally over-represented in non-native insect assemblages, while other taxa are under-represented. These patterns generally reflect characteristics of these insects that cause them to enter important invasion pathways and biological characteristics that facilitate invasions. These results ultimately can be of use when conducting invasive pest risk analysis.

Research Actions for Conservation of an Endangered Species and a Korean Natural Monument, Callipogon relictus Semenov (Coleoptera: Cerambycidae: Prioninae) in South Korea

Authors: Lim Jongok[1], Lee Bong-Woo[1], Kim Cheol-Hak[2], Lee Seung-Gyu[1] and Oh Seunghwan[1], [1]Korea National Arboretum, Korea Forest Service, South Korea, [2]Osang K-insect Biological Resource Research Center, South Korea

Abstract: The relict longhorned beetle, Callipogon relictus Semenov (Coleoptera: Cerambycidae), is the unique species among the species of Callipogon which is distributed in the Palearctic region. The cerambycid species was designated as an endangered species and a Korean natural monument in South Korea and it has been protected by the Korean laws. The distribution records of Callipogon relictus in South Korea were from several northern regions of South Korea, however, the species has been just discovered from a Gwangneung forest where the Korea national arboretum located in. For conservation of C. relictus in S. Korea, we have studied the biological features and developed useful techniques for mass-rearing in short period with accumulation of survey data of inhabitation over last ten years in S. Korea. In this presentation, we introduce recent studies for conservation of C. relictus and the results in South Korea to discuss on further studies.

Negative effect of tau-fluvalinate on olfactory sensitivity in honey bees

Authors: Lim Sooho[1], Kim Dong-In[1], Wook Kwon Hyung[1], Ilyasov Rustem[1], Woo Sehoon[1] and Yunusbaev Ural[1], [1]Department of Life Sciences & Convergence Research Center for Insect Vectors, Incheon National University, South Korea

Abstract: tau–Fluvalinate (fluvalinate) is commonly used against Varroa mites, the major drivers of colony collapse disorder (CCD), in the apicultural industry. Although honey bees have tolerance and low toxicity to this miticide, little is known about the effects on sensory modulation in honey bees. Here, we demonstrated that abdominal contact of fluvalinate has adverse effects on mortality and olfactory sensitivity of Apis mellifera. First, we found that topical application of fluvalinate to honeybee abdomen elicited somewhat severe toxicity to honey bees. Then, electrophysiology showed that honey bees treated with sub-lethal doses of fluvalinate significantly decreased in olfactory responses. At the molecular level, there was no change in molecular expression patterns of cytochrome p450s monooxygenases (CYP9Q1-3), odorant receptor co-receptor (Orco) and tachykinin (TK) in antennae of treated bees. Rather, the expression level of short neuropeptide F (sNPF) which would be involved in olfactory sensitivity was increased after fluvalinate treatment. Insulin expression levels in the brain of honey bees suggested that it would be associated with the olfactory cascade pathways in antennae, indicating that olfactory deficits induced by abdominal contact of fluvalinate may stem from specific neuropeptide pathways rather than the direct effects of neurotoxins. The current study was the first attempt to demonstrate the effects of xenobiotic chemicals on olfactory modulation in honey bees.

Efficacy of Beauveria bassiana ARP14 against egg of Bemisia tabaci (Homoptera: Aleyrodidae)

Authors: Lim Un Taek[2], Eun Jang La[1] and Arefur Rahman Md.[1], [1]Andong National University, South Korea, [2]Andong National University, South Sudan, South Korea

Abstract: We compared efficacy of Beauveria bassiana strain (ARP14) with commercial one (GHA) against eggs of Bemisia tabaci (Gennadius), important pest of many crops worldwide. After dipping eggs of B. tabaci in a concentration of 1×108 conidia/mL of the entomopathogenic fungus, mycosis rate of the eggs were assessed and found low for both ARP14 (12.5%) and GHA (10.0%) without statistical significance. However, mortality of hatched 1st instar became higher for both ARP14 (65.6%) and B. bassiana GHA (80.0%) with statistical significance. The egg period was significantly shorter in ARP14 (7.1 d) than either GHA (7.4 d) or control (7.5 d) at 25°C with unknown reason. In conclusion, B. bassiana ARP14 can be developed as a new mycoinsecticide to control B. tabaci.

Enzymatic characterization and evolution of a unique lepidopteran GMC oxidoreductase that re-arranges the green leaf volatile profile of plants

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Abstract: Lepidopteran hexenal isomerases (Hi) which are part of the GMC oxidoreductase family were first identified in the oral secretions (OS) of the Manduca sexta. When caterpillar OS comes in contact with damaged leaf, Hi causes a re-arrangement of the plant-derived green leaf volatile Z-3-hexenal (Z3AL) to E-2-hexenal. This change in the volatile profile serves as host location cue for conspecific moths, as well as their natural enemies. Phylogenetic analysis of putative Hi homologs from 32 Lepidopteran species revealed the presence of several Hi candidates in the advanced Ditrysia clade. Putative Hi homologs were furthermore sporadically present in some superfamilies of Obtectomera but ubiquitously in superfamilies of Macroheterocera. This suggests that Hi arose from the mid-Cretaceous, and its occurrence might be associated with the expansion of angiosperms. We further synthesized recombinant protein of Hi from Chloridea virescens, Danaus plexippus and Bombyx mori, and confirmed Hi activity under both in vitro (with synthetic Z3AL) and in vivo (on host plants) conditions. Interestingly, these Hi homologs not only showed different tissue-specific expression profiles, but also distinct pH optima. In summary, our study demonstrates the divergent enzymatic properties between different lepidopteran Hi and gives first insides into the evolutionary history of Hi in Lepidoptera.

Chalcidoidea Phylogeny in the Era of Genomics (Hymenoptera)

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Abstract: Chalcidoidea (Hymenoptera) are a megadiverse superfamily of wasps that rank numerically among the largest groups of insects with an estimated 500,000 species. They are by far the most important group of natural enemies of insects in terrestrial ecosystems, and the majority of successful biological control projects have utilized these minute wasps for partial or complete control of insect pests. Currently, the superfamily is classified into 23 families and about 90 subfamilies. A recent temporal divergence study of Chalcidoidea suggested these wasps likely originated in late Jurassic, followed with rapid diversification between late Cretaceous and early Paleogene (75-53 mya). The rapid early radiation of Chalcidoidea has made it difficult to resolve its early evolutionary history using morphological and Sanger-sequencing data. In this globally collaborative project, we explore the application of phylogenomic approaches to resolve the backbone phylogeny of this megaradiation of wasps, utilizing the taxon-poor but gene-rich transcriptome data and the taxon-rich but gene-poor anchored enrichment data. The results provide valuable insights into the phylogenetics and character evolution across the superfamily. However, some of the backbone relationships on the Chalcidoidea phylogeny are still poorly supported even with the great wealth of genomic data. At the deeper nodes, the results uncover a wide spectrum of gene discordance in the transcriptomic markers and identified a strong signal of functional bias in genes supporting alternative phylogenies which is likely a signature of incomplete lineage sorting.

Roles of acetylcholinesterase genes in organophosphate and carbamate resistance in Leptinotarsa decemlineata

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Abstract: The evolution of insecticide resistance is a major challenge for pest control and can also have great impact on human health, the environment, and non-target species. Pests can become resistant to insecticides through both quantitative (e.g. altered gene expression) and qualitative (e.g. mutation in binding sites) mechanisms. Despite increasing knowledge on the biochemical basis of insecticide resistance, there is little knowledge as to whether geographic populations may differ in their response to insecticides. We tested whether two populations of the Colorado potato beetle, Leptinotarsa decemlineata (Vermont, USA and Belchow, Poland) differ qualitatively or quantitatively in the expression of acetylcholinesterase genes (AChE), Ldace1 and Ldace2, which is the major contributor of the AChE catalytic enzyme and are associated with resistance to two commonly used insecticides, organophosphates and carbamates. We found that native USA beetles were 107 and 20 fold more resistant to azinphos-methyl and carbaryl insecticides, respectively, than introduced Polish beetles. Although both populations possessed similar frequency in the resistance-associated mutation (i.e. S291G) in the Ldace2 gene, the Vermont population had two nonsynonymous mutations (G192S and F402Y) in the Ldace1 gene that were absent in the Belchow population. Moreover, the Vermont population showed higher expression for the Ldace1 gene, and the Vermont population was also less sensitive to AChE inhibition by azinphos methyl oxon than the Belchow population. These findings demonstrate that the insecticide resistance can involve many different mechanisms, as native population possesses both qualitative and quantitative changes in target site, which both confer resistance to two common insecticides when compared to the introduced population.

Glyphosate-based herbicide affects the oxidative status and microbial composition of the Colorado potato beetle indirectly via soil

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Abstract: We examined whether glyphosate, a commonly used herbicide, affects the survival, oxidative status and intestinal microbiota of herbivores feeding on non-target plants. For our experiment, the Colorado potato beetles (Leptinotarsa decemlineata) were reared on potato plants grown in pots containing soil treated with glyphosate-based herbicide (GBH) or untreated soil. Per the manufacturer's safety recommendations, the GBH soil treatments were done two weeks prior to the potato planting. Three weeks after potato planting, two-day-old larvae were introduced to the potato plants and then collected in two phases, as 4th instar larvae and as adults. We found that GBH treatment had no effects on survival of the larvae or the adults. The oxidative status was affected by the GBH treatment. In larvae, total glutathione (tGSH) concentration and the enzyme activities of catalase (CAT), superoxide dismutase (SOD) and glutathione-S-transferase (GST) were increased in GBH treated group, suggesting GBH-induced activation in antioxidant enzyme activities to defend the beetles against reactive oxygen species. In adults, GR and CAT activities and tGSH levels were affected by interactive effect of GBH treatment and body mass of the adult beetles. The adult beetles had a higher overall microbial diversity and richness compared to the larvae, but neither diversity nor richness were significantly affected by the GBH treatment. However, the microbial composition of the beetles was affected by the GBH treatment, and the difference was more pronounced in the adults than in the larvae. The GBH treatment increased the number of Agrobacterium in the larvae and the adults. This effect may be related to the tolerance of some Agrobacterium species to glyphosate or to glyphosate-mediated changes in potato plants. On the other hand, the reduction of Enterobacteriaceae, Rhodobacter, Rhizobium and Acidovorax in the adult beetles and Ochrobactrum in the larvae after GBH treatment suggests their sensitivity to glyphosate. These results demonstrate that glyphosate can affect the antioxidant defence and intestinal microbiota of herbivores feeding on non-target crop plants.

Commercialization of a Successful Monitoring System and Other Practical Applications of Attractants for Brown Marmorated Stink Bug (Halyomorpha halys) Management

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Abstract: Commercialization of the brown marmorated stink bug (BMSB) monitoring system involved USDA ARS, multiple universities and many elements of Trécé's chemistry laboratory, field research and development, engineering and manufacturing teams all working together towards a common goal. Legal agreements in some cases were used to provide flexibility to cooperate and communicate between government and industry entities. Video conference, email and other communication technology along with site visits were strategically used to speed the development process. Careful planning and execution by all cooperating entities resulted in a rapid pace of development, where some projects were repeated in the same season to expedite data collection. The BMSB monitoring system development was highly complex, but other commercial products were created or benefited from related developments in a relatively short period of time. The creation and development of a long-lasting, reliable monitoring system focused on multiple tiers of technology including the active ingredient chemistry, controlled-release formulations, adhesives suitable for adult and nymphal insect capture under all outdoor environmental extremes, trap design and limitation of capture of non-target insects.

The phenology of ambrosia beetles (Coleoptera: Scolytinae) and their clerid predators in a montane forest in Taiwan

Authors: Liu Lan-Yu, Department of Science Communication National Pingtung University Taiwan, Taiwan

Abstract: The author investigated the wood-boring beetle fauna in the Cilan montane cloud forest area in Northeast Taiwan from 1 Jan. to 31 Dec. 2019. The Cilan Mountain Cypress Forest is an area of steep peaks and deep valleys at an elevation of c. 1,200 m, and home to some of the rarest fauna and flora in Taiwan. An average rainfall of 5,000 mm per year has given rise to a year-round mist that shrouds the forest's peaks. In this study, 6 multiple funnel traps baited with ethanol or ethanol and pinene were installed from 1520m to 1780m above sea level. This is the first study on ambrosia beetles to be carried out in the Cilan montane forest in Taiwan.

The results of the whole year investigation show that ambrosia beetles, mainly belonging to the tribe Xyleborini (Anisandrus, Euwallacea, Xyleborinus, Xyleborus and Xylosandrus), and to the genus Scolytoplatypus dominated the scolytine fauna. The tribe Xyleborini emerged mainly in April, and genus Scolytoplatypus mainly between Jan. and April. Three clerid predators of ambrosia beetles were found in this study. Callimerus sp. mainly emerged from Feb. to Apr., Diplopherusa sp. mainly emerged from Apr. to May in large numbers, and Opilo sp. emerged mainly in May and in low numbers compared to the other two species.

The emergence of ambrosia beetles in Cilan forest is primarily related to temperature. Trap location affects the diversity of ambrosia beetles, but the addition of alpha- or beta-pinene to the ethyl alcohol bait had no distinct effect on the results.

Changing gut bacteria diversity using antibiotic suppressed the reproduction of Bactrocera dorsalis

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Abstract: The oriental fruit fly Bactrocera dorsalis (Hendel) is a destructive insect pest of a wide range of fruit crops. Because of the important part of gut bacteria in the development, reproduction and fitness of their host fruit fly, uncovering their function has become a worldwide question. Using antibiotics to remove gut bacteria is a common method to investigate gut bacteria function. In our previous study, the combination of three types of antibiotics (tetracycline, ampicillin and streptomycin) can significantly change the gut bacteria diversity of laboratory-reared Bactrocera dorsalis. However, the function of special gut bacteria is still not clear. In this study, we detected the infection of gut bacteria on the reproduction of B. dorsalis through feeding back experiment. The result showed that gut bacteria diversity changes using antibiotic prolonged the preoviposition period, suppressed the development of ovary and reduced the egg production significantly. RT-qPCR showed that the changes also resulted in different expression of the key genes in Insulin pathway (Akt, InR, IRS, FoxO), JH pathway (JHAMT, JHEH, Kr-h1) and 20E pathway (EcR, USP, E75). Feedback of one strain of bacteria named Enterobacter cloacae, which was isolated from the gut of B. dorsalis can eliminate these effects. This study forms a basis for deciphering the molecular mechanisms underlying the gut bacteria regulate reproduction via three important pathway in the oriental fruit fly. It also provides valuable resources for future studies on the correlation between insect and their gut bacteria.

Key words: Bactrocera dorsalis, gut symbionts, reproduction, Enterobacter cloacae, different expressed genes.

Effects of Viruses on Phytohormone Pathways and Plant-Insect Interaction

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Abstract: Co-infection of plants by both viruses and insects is common in nature. Yet the dynamics of the tripartite system, in particular the effects of viral infection on plant-insect interactions and the factors involved, remained little studied until very recently. In this article we review the progress in research on these aspects of the tripartite interactions, explore the questions associated with the investigation, and suggest direction for future research on this exiting and likely fruitful field. Virus-induced changes of the tripartite interaction are in many cases attributable to the modulation of phytohormone pathways by viruses. Infection of viruses can affect significantly the synthesis and function of the three well-known phytohormones, i.e., jasmonates, salicylic acid and ethylene as well as plant-insect interactions associated with these phytohormones. The virus-induced changes of the dynamics of these phytohormones and other aspects in the tripartite system are influenced by both intrinsic and external factors such as plant nutrition, secondary metabolites and natural enemies of the vector insects. The effects of viral infection on other phytohormones, such as auxin, gibberellins, cytokinins, brassinosteroids and abscisic acids are yet to be investigated.

Effects of temperature and host instar on competition of two whitefly parasitoids

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Abstract: For augmentation biological control, the choice of biological control agent is critical for scientists and growers. Eretmocerus hayati and Encarsia formosa are two species of important parasitoids of the whitefly Bemisia tabaci. In order to evaluate the parasitoids for more effectively usage, interspecific competition between the two species and effects of temperature and host instar were conducted in laboratory and plastic houses. The results showed that Er. hayati dominated in interspecific competition and could affect the outcome of En. formosa at 20°C, 27°C and 32°C. Parasitism rate per female of En. formosa was significantly reduced due to interspecific competition, whereas Er. hayati was not affected significantly. Both species of parasitoids showed preference to host instar. More offspring of Er. hayati were obtained from young nymphs of whitefly whereas En. formosa prefered to old nymphs of whitefly. However, the parasitoid Er. hayati is in a dominant position in competition regardless the host instar. The ability to discriminate and avoid hosts parasitized is a possible behavioral mechanism underlying.

The Unique Function of Buckwheat on Wireworm Control

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Abstract: Agriotes sputator is the principal wireworm species confronted by the agricultural industries in Prince Edward Island, Canada. Due to the lack of effective control methods and mounting population pressure, this pest has become a major concern not only in potato, but also many other crops.

Buckwheat (Fagopyrum esculentum) is usually cultivated as a cover crop to suppress or reduce weeds and improve soil condition. In our previous study, buckwheat gave significant potato tuber protection from wireworm damage. To clarify the potential mechanism, A series of bioassays were designed. The food choice test of wireworms with three commonly used rotation crops revealed a higher wireworm number with buckwheat plants compared to barley and red clover under both greenhouse and field conditions. Paired food choice test between two cover crops, buckwheat and clover, demonstrated a significantly higher larval number in buckwheat under greenhouse condition ($P<0.05$).

When neonate wireworm larvae were reared with either barley or buckwheat plants for 120 days, the body weight and head capsule of larvae fed on buckwheat were 60% and 30% less than the ones fed on barley. Compared to 44% larval survival rate on barley, only 15% neonate wireworms survived in buckwheat plants.

Under the laboratory condition with fresh carrot as a food source, medium sized wireworms spent three to seven weeks to fully develop and reach the next growth stage with the maximum percentage of increased head capsule size at 16.9 % after once molting. However, wireworm larvae produced as high as 37.9 % increased head capsule size by feeding on buckwheat root for 13 days. Feeding on buckwheat over 60 days resulted in a slow increased body weight but significantly greater increased size of the head capsule of medium sized wireworms compared to those reared on potato. Therefore, buckwheat does not repel wireworms, and the secondary metabolites in buckwheat roots impact the normal growth rate of wireworm larvae and eventually kill wireworms.

Systematics and evolutionary history of pleasing lacewings (Neuroptera: Dilaridae)

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Abstract: The family Dilaridae, commonly called pleasing lacewing, is a small group of Neuroptera, which contains approximately 100 species in four genera worldwide except Australian region. This family is group of distinctive lacewings, characterized by the sexually dimorphic antennae, the presence of three ocellus-like tubercles on the head, and the narrowly elongate female ovipositor. Recent phylogenomic studies recovered that Dilaridae is a transitional lineage between the lower neuropterans (Coniopterygidae + Osmyloidea) and the clade including all higher neuropteran superfamilies. The faunal diversity of Dilaridae, particularly from the Oriental region, has been considerably increased by recent extensive taxonomic revisions. Here we summarized the current knowledge and recent progress on phylogeny of Dilaridae. The global species diversity of extant Dilaridae is overviewed. The latest results from the phylogenetic analyses of Dilaridae at the genus as well as the species level based on morphological and molecular data are presented. With combination of recently found dilarid fossils and distribution information, the evolution of the antennal sexual dimorphism and the historical biogeography of Dilaridae are recovered under the present phylogenetic framework.

Identification and functional characterization of sex pheromone receptors in mirid bugs

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Abstract: The mechanism of olfactory recognition in insects is a hot issue in neurology and chemical ecology, and the functions of pheromone receptors attract more attentions because of their special importance. Mirid bugs are a group of the important pests and cause a great amount of production lost in the fields. Due to the wide application of sex pheromones in the control of insect pests, extensive studies were focus on the isolation and identification sex pheromones in mirid bugs and the component and biological activity of the sex pheromones has also been studied. However, few studies have been focused on the mechanisms of pheromone perceiving.

Apolygus lucorum, Adelphocoris lineolatus, and Adelphocoris suturalis are the three common and seriously harmful pests in China. All of these three miridae species used (E)-2-hexenyl butyrate (E2HB), hexyl butyrate (HB), and (E)-4-oxo-2-hexenal (4-OHE) as the main components of the sex pheromone, which makes them an ideal model for studying the sex pheromone recognition mechanism of the mirid bugs. In this study, we first identified the OR repertoires in three mirid bugs Apolygus lucorum, Adelphocoris lineolatus and Adelphocoris suturalis through antennal transcriptomic sequence and bioinformatics analysis. The expression of all the candidate AlucOR genes in male and female antennae were analyzed by semi-quantitative RT-PCR (RT-PCR). Four AlucORs, five AlinORs, and five AsutORs, which were clustered in two branches of the evolutionary tree, were predicted as candidate PRs by comparative analysis of expression patterns and sequence alignment. And full length ORF of the 14 PR genes were verified by rapid amplification of cDNA ends (RACE) and cloned. Finally, we functionally characterized the 14 PRs in vitro using the heterologous expressing in Xenopus oocytes with two-electrode voltage-clamp recordings, and found 13 PRs could be activated by E2HB or HB. This work could provide a basis on understanding the olfactory recognition molecular mechanism in mirid bugs and lay foundation for developing novel strategies for the pest control.

Population regulatory possibilities of Aedes egg hatch inhibition by larvae

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Abstract: The inhibition or Aedes eggs by larvae, presumably through grazing of stimulatory microbes from egg surfaces, merits further attention. Experimental evidence of this phenomenon at both the intra- and interspecific levels is reviewed here, along with simple models developed to explore the theoretical possibility of inhibition as a regulatory mechanism as well as a factor influencing species coexistence or extinction. Laboratory evidence for inhibition is shown for Ochlerotatus triseriatus, Aedes albopictus and Aedes aegypti. Field evidence has been shown for Ochlerotatus triseriatus. Preliminary results of population models indicate that this phenomenon can regulate populations even in the absence of food limitations or other density dependent factors, as long as some minimal egg mortality occurs between hatch stimuli.

Sensory adaptation and dynamic odor representation in the honey bee antennal lobes

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Abstract: Animals process and perceive environmental information in a flexible way. Some changes in perception are sustained and involve learning and memory processes while others occur quickly and are only transient. In this framework, sensory adaptation is defined as the phenomenon by which the sensitivity to a stimulus decreases after a sustained exposure to it. This phenomenon is characterized by a rapid loss of sensitivity and full recovery within few seconds after the stimulus disappears. Curiously, this phenomenon has been mostly studied by focusing on what the animal fails to perceive, but not on the consequences that it has on the perception of the stimuli for which the animal has not experienced adaptation. In this project we study the enriching effect that sensory adaptation has on the ability of animals to detect stimuli to which it has not been adapted and that would remain overshadowed by dominant stimuli under normal conditions. We use honey bees Apis mellífera that have a high capacity to learn and recognize odors. We perform behavior experiments to show that sensory adaptation reduces appetitive learning of adapted stimuli while it favors learning of minor components that would normally stay occluded. We studied this phenomenon at the level of sensory and projection neurons of the olfactory system. We determine that antennal lobe activation patterns that encode mixtures in the antennal lobe are drastically altered after sensory adaptation, in a way that favors the representation of stimuli that are present at sub-threshold concentrations. The results obtained so far emphasize that sensory adaptation is a fundamental mechanism to increase the sensitivity of the animal and not to reduce it.

Evolution of the genetic load in invasive insects: first insights from a genomic cross-species study

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Abstract: Biological invasions are a major component of global change. Yet it is still not understood why some introduced populations are invasive and others are not. Among the most interesting hypotheses is the purging of deleterious mutations during the introduction process. Deleterious mutations constitute what is called the genetic load because they are responsible for a decrease in the fitness of individuals by accumulating in the genome over time. After the introduction of a small number of individuals into a new area, high levels of inbreeding and genetic drift can have two major consequences: either the fixation or the purging of deleterious mutations. The assumption we make is that the populations that successfully become invasive are those that have purged part of their deleterious alleles. We currently work on a project that aims at testing the purge hypothesis on a large taxonomic scale – at least 10 invasive insect species. Using a pool-seq transcriptome-based exon capture protocol developed in our laboratory and suited to non-model species, we are quantifying and comparing the genetic load of native versus invasive populations. In this presentation, we will present a first round of results on two emblematic insect invasive species, the Asian ladybird Harmonia axyridis and the western corn rootworm Diabrotica virgifera virgifera.

My wave is THAT pushed: quantitative characterization of expansion dynamics with genetic and demographic data

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Abstract: Spatial expansions, like those of insect pests or their biological control agents, are characterized by strong variations in population density and composition that interact with evolutionary processes. The distribution of demographic, phenotypic and genetic diversity across time and space is thus a critical determinant of how populations are expected to evolve, sometimes dramatically, during expansion.

Propagation waves have been described as “pulled”, when expansion is driven by the reproduction and dispersal of few individuals on the edge of the propagation front, or “pushed”, when individuals from the core of the population are involved in its expansion. While pulled and pushed waves are likely to display contrasted eco-evolutionary dynamics, the definition currently available of the nature of a wave is based on specific mathematical properties of certain types of reaction-diffusion models, which strongly limits their use in practice and pleads for the definition of other, more practical, indicators.

Earlier results using numerical simulations revealed (i) that pure pulled waves tend to become pushed under stochastic conditions, and (ii) that depending on the demographic mechanism implied, pushed expansion dynamics deviated more or less severely from pulled expectations. Therefore, it appears that the distinction between pushed and pulled waves in empirical datasets is more likely a continuum than deriving from discrete categories.

In this work, we propose to define a “pushness index” to help characterizing more accurately the diversity of expansion patterns in nature. Using individual-based simulations and empirical data from laboratory expansions of parasitoid wasps of the genus Trichogramma, we investigate how expansions characterized by different underlying demographic mechanisms associated with pulled or pushed waves can be discriminated using quantitative metrics related to population and genetic dynamics in time and space.

Ecology of the chestnut gall wasp (Dryocosmus kuriphilus) in the western edge of sweet chestnut tree distribution in Europe

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Abstract: The Asian chestnut gall wasp, Dryocosmus kuriphilus Yasumatsu, 1951 (Hymenoptera: Cynipidae), is a parthenogenetic species original from China that rapidly invaded Europe since its detection in 2002. The wasps lay eggs in the buds of chestnut trees (Castanea spp.) inducing galls on leaves, stipule, flowers and shoots. The consequences are significant economic damage due to a reduction of nuts and wood production, as well as a progressive decrease in tree vigour, which can make the tree susceptible to other secondary pests. We report here the results of a 4-year study of this species conducted in Galicia (NW of Iberian Peninsula), one of the most important areas for chestnut production in southern Europe. The insect was detected in 2014 but was apparently present at least two years earlier. It has since spread rapidly throughout the territory. It mainly dispersed naturally, although some long-distance dispersal events influenced the rate of spread across the landscape. Population abundance varies throughout the territory, and we were able to establish hotspot and coldspot areas, mainly associated with maximum temperatures in the summer months. At a local scale, the trees attacked by D. kuriphilus and the number of galls on each tree were spatially clustered in the first years from the invasion. Tree height significantly predicted both variables, suggesting that gall wasps may use visual cues to locate suitable host trees, at least in the early stage of invasion. The species showed a rapid recruitment of native parasitoids: three years after detection we found 19 species of native parasitoids attacking D. kuriphilus in Galicia. Percent parasitism by native parasitoids decreased greatly with time since introduction. This was because galls became larger, more thickly walled, and with more individuals per gall as the abundance of D. kuriphilus increased. Per capita growth rate of D. kuriphilus was linearly density dependent with an apparent equilibrium of ≈ 5.2 galls/shoot. D. kuriphilus in plots with low abundance had higher population growth rates. At high abundance, the number of suitable buds for oviposition decreased because the crowns had thinned, and only current year buds were available. Population abundance was higher in low quality sites. Our studies revealed seven hybrid clones resistant to the pest as well as high variability in the susceptibility of another 24 hybrid chestnut clones. Susceptibility did not depend on insect selection since there was no differences in number of eggs per bud among resistant or susceptible genotypes, and neither on changes of plant secondary metabolites during gall developmental. An early hypersensitive response within attacked buds that received eggs seems to be the most effective defensive trait of chestnut trees against the gall wasp.

Impact of active human complement on trascriptome and microbiota of Ae. aegypti and Ae. albopictus

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Abstract: Our analysis shows that feeding Aedes mosquitoes induced significant changes in the expression of antimicrobial peptides in both Ae. aegypti and albopictus with significant differences in the expression of cecropins between the two species. Also, we observed an increase in Wolbachia replication in Ae. albopictus mosquitoes feed with normal human blood. Our studies suggest that activation of human complement in Aedes mosquito midguts may have a significant impact on the physiology and immune responses influencing the potential for transmission of arboviruses.

Spatial-temporal analyses of Glossina fuscipes fuscipes abundance in the West Nile region of Uganda

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Abstract: Concentrated screening, accessible treatment, and vector control have resulted in a dramatic decline in the number of reported Gambiense human African trypanosomiasis (g-HAT) cases within Northern Uganda over the last two decades (average 877.6 cases per year during 1997-2001; 3.6 cases per year, 2014-2018) (World Health Organisation, 2020). Tiny targets, small pieces of impregnated fabric, are used to control tsetse within Northern Uganda, and play a vital role in suppressing tsetse populations to insufficient numbers to sustain transmission. In addition to vector control, other factors may be influencing tsetse population dynamics within the area such as land use change, climate change and urbanisation. The aim of this work was to analyse the spatio-temporal distribution of tsetse within a geostatistical modelling framework, and subsequently to investigate the influence of these factors on tsetse dynamics.

Between 2010 and 2019, pre- and post-intervention monthly tsetse abundance data were obtained from monitoring sites located in seven districts within the West Nile region of Uganda. Abundance data was collected through longitudinal monitoring (301 sites), or by exploratory surveys consisting of between one and three sampling days (310 sites). Such data were used to inform a spatio-temporal model exploring factors influencing tsetse abundance across the West Nile region. Firstly, remotely sensed data were combined with pre-intervention data (collected in the absence of vector control) within a species distribution-modelling framework to produce annual surfaces detailing habitat suitability. The species distribution model was informed by covariates describing several vegetation indices and environmental conditions believed to influence the distribution of riverine tsetse (Glossina fuscipes fuscipes). Spatial-temporal trends in monthly abundance were then characterised through the construction of a geostatistical model incorporating covariates detailing intervention coverage and associated metrics, temporal trends and habitat suitability outputs. Surfaces predicting spatial variation in tsetse abundance across the region were produced. Utilising the described model the relative contribution of each factor on the observed decline in tsetse abundance was assessed.

The generated results identify areas of tsetse persistence over time, providing information on the relative abundance of tsetse at previously un-sampled locations. The outputs described have the potential to guide further monitoring and control efforts within the West Nile Region of Uganda.

World Health Organisation. 2020. Global Health Observatory (GHO) data: Human African trypanosomiasis. https://www.who.int/gho/neglected_diseases/human_african_trypanosomiasis/en/ Accessed 10th February 2020.

Every Generalist Requires a Special Risk Assessment

Authors: Loomans Antoon, independent, Netherlands

Abstract: In an Environmental Risk Analysis benefits and risks of biological control agents and other beneficial organisms are assessed using criteria based on ecological determinants like the potential and impact of establishment and dispersal, on known and new hosts (host range vs specificity) and recorded direct and indirect non-target effects. There is a wide variety of natural enemies used for biological control, each of which has its specific biological and ecological requirements. Establishing the potential of its potential host range in its new area is one of the most challenging issues to be assessed prior to its introduction and release. Classical Biological Control programs of pest species nowadays mainly focuses on natural enemies specific for the target pest. In the regulatory requirements for regulation and the registration of non-native Invertebrate Biological Control Agents, assessment of host specificity is one of the main criteria in evaluating the risks, thus often excluding generalist predators and parasitoids a priori from being licensed. Here we will present and discuss several examples of different taxa with a generalist host range, and show that each of them have specific requirements and as a result require a specific risk assessment on their own.

What do environmental risk assessments tell us about non-target effects of omnivorous predators?

Authors: Loomans Antoon, independent, Netherlands

Abstract: The release of biological control agents (BCA's) is an important means to control plant pests worldwide in a sustainable and economic way. Prior to introduction and release of a natural enemy as a biological control agent, an assessment is necessary of both efficacy on the target pest as well as safety for the environment. In an Environmental Risk Analysis (ERA) information on a specific BCA or other beneficial is analyzed whether it is 'safe' to release, or not. Information on taxonomic identity, impact on human and animal health as well as the ecological impact are essential requirements. Main criteria to assess the environmental impact are the potential and impact of establishment and dispersal, impact on known and new hosts or prey (host range vs specificity) and recorded and potential direct and indirect non-target effects.

There is a wide variety of natural enemies used for biocontrol, each of which has its own specific biological, ecological and climatic requirements. Classical Biological Control programs of pest species traditionally mainly focuses on natural enemies which are specific for the invasive target pest. In Augmentative Biological Control programs in greenhouses and crops, a shift has taken place over time from the inoculative and inundative releases of monophagous or oligophagous natural enemies (parasitoids, predators) to the release of polyphagous or generalist predators (mainly predatory mites and predatory bugs). Omnivorous predators feed on more than one host or target species, but also on plants or fruits during the same life stage to survive and reproduce. Mirid bugs are an excellent example of this guild of predators, with a wide array of feeding strategies amongst species, varying from obligate carnivory to facultative or obligate herbivory. Establishing the potential of the potential host range of such an omnivorous BCA in a new area is one of the most challenging issues to be assessed prior to its introduction and release. Here we will discuss several examples of different taxa with an omnivorous prey range, and show that each of these BCA's has specific requirements on their own and as a result in specific non-target effects.

Separated at induction? Experiments with host plant associations and taxonomic boundaries of Diplolepis in western North America

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Abstract: The genus Diplolepis induces galls on rose species throughout the Northern Hemisphere. Most named species are described from the United States, but recent molecular analyses suggest that many currently accepted species are synonyms. Four of these species occur in the Pacific Northwest of the United States and Canada, in two distinct groups. In the Diplolepis bassetti and D. polita group the wasps induce round, unilocular galls on Rosa woodsii and R. nutkana, respectively. D. bassetti galls are covered by long dense hairs, while those of D. polita are covered by abundant thin spines. The molecular data raise questions about whether there are in fact two distinct species, or if one species induces galls that vary with host plant. To test these hypotheses, wasps of D. bassetti and D. polita were caged on both host plants in 2019-2022, and resulting galls examined. In all cases galls were only induced on the expected host, suggesting that they are distinct species. The experiment was repeated in 2020 and 2021 with another "problem" group that shares host plants but gall different plant tissues. Results and limitations of these experiments will be presented in light of the current taxonomy, and known distribution and host plants.

Interpopulation variation and intrapopulation plasticity of the thermal reaction norms for development in insects by an example of the linden bug, Pyrrhocoris apterus

Authors: Lopatina Elena, Saint Petersburg State University, Russia

Abstract: The degree and limits of phenotypic plasticity in insect development should adaptively change under the influence of natural selection in accordance with local climate characteristics and other environmental factors. As a result, geographic, interpopulation, seasonal, and other forms of variability of temperature and photoperiodic developmental norms arise.

Seventeen populations of the linden bug were studied at five constant temperatures (from 20 to 28°C) in the range from 32° to 58° of North latitude. Assuming a linear relationship between developmental rate and temperature we have demonstrated that the thermal sensitivity of egg and larval development shows a tendency to increase from the South to the North. Clinal variability of the thermal reaction norms for development (TRND) is more pronounced in larvae where the developmental time increases at 20°C and decreases at 28°C from the South to the North. As a consequence, there is a marked increase in both temperature thresholds and thermal sensitivity coefficient of development in northern populations.

The linden bug has an imaginal diapause, and so the larvae have to finish their development before winter falls. We found seasonal changes in TRND of larvae. In five studied European populations, larval developmental rate becomes gradually less dependent on temperature and proceeds faster at relatively low temperatures (below 24°C) and longer at relatively high temperatures, when the day length is reduced. A gradual decrease in the temperature threshold and the coefficient of the thermal sensitivity of development takes place. This allows the bugs to successfully reach the wintering stage before the winter onset. A peculiar change in TRND under the influence of photoperiodic conditions is observed in the linden bug population from Tel Aviv (Israel, 32°N), which lives in an arid Mediterranean climate. Here, the acceleration of larval development is induced by long-day conditions (16 hours) in the entire range of selected temperatures (from 20 to 28°C). In this case, the temperature threshold is lower than that under short day conditions (10 hours), and the thermal sensitivity of larval development is similar in both photoperiodic regimes. In Tel Aviv, linden bugs of the first generation have to complete development in the spring and early summer before the onset of summer drought. The development of the second generation takes place in the autumn. Slower development under short day conditions leads to the emergence of larger individuals that are able to successfully tolerate the lack of food in the winter in Israel at fairly high daytime temperatures.

The existence of the latitudinal variability of the thermal reaction norms for development in the linden bug and the presence of geographic differences in their photoperiodic plasticity allows P. apterus to maintain bivoltinism up to the northern boundary of its distribution.

The work is supported by the grant of Russian Foundation for Basic Research (RFBR N 20-04-00185a).

Colour preference in western flower thrips varies intraspecifically

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Abstract: Discrepancies in literature regarding the response of the economically important pest western flower thrips (WFT) to different colours confounds extrapolation to the field to optimise traps for their management. To clarify whether differing experimental conditions of independent studies was a factor, or if intrinsic differences occur, we examined the colour responses of two WFT laboratory populations from Germany and The Netherlands that had independently shown different blue/yellow colour preference. To account for potential differences in host-rearing regime, both populations were established on bean for ~20 weeks, then on yellow chrysanthemum for 4–8 and 12–14 weeks. In blue/yellow LED lamp choice bioassays, country of origin, irrespective of rearing regime, remained a significant effect ($p<0.001$) with 65% of the Netherlands WFT landing on yellow compared to blue (35%), while 66% of the German WFT landed on blue compared to yellow (33%). There was also a significant host plant effect ($p<0.001$), with increased response to yellow, independent of country, after rearing on chrysanthemum for 12–14 weeks. Results suggest that original differing responses of WFT populations to colour is, in this case, a result of intrinsic differences and independent of experimental situation. Implications and underlying reasons for these results are discussed.

Mountain forest die-back and its impacts on terrestrial and aquatic insect diversity

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Abstract: Mountain forest ecosystems are under strong anthropogenic pressure. Increased mortality of key tree species due to rising global temperatures is a serious issue and is exacerbated through increased frequency of droughts and pathogen outbreaks, which results in drastic changes in forest structure and composition. Malaise trap sampling, to assess arthropod biodiversity, is gaining momentum as the method of choice for routine biomonitoring and the increased urgency induced by governments and the general public generates a favourable research environment. As passive devices malaise traps are perfectly suited for long-term, large-scale, nation-wide insect biomonitoring; however, morphological identification of the large numbers of collected insects is not feasible. We developed and applied DNA metabarcoding methods in an effort to identify insect taxa within Malaise trap samples.

This study was conducted in collaboration with the Bavarian Forest National Park, which has ample experience and a long tradition of research on mountain forests, in particular on Norway spruce (Picea abies), as well as an ongoing insect monitoring program.

From May to October 2017, we collected insects using malaise traps on 10 forest plots within each of three different forest habitats (intact, naturally disturbed, salvage-logged) for a total of 240 samples. Malaise traps were emptied every 2 weeks. We also collected kick-net samples in May 2018 from 10 streams within each of the same 3 habitat classifications to complement the terrestrial samples. After minimal handling, DNA was extracted from bulk subsamples and DNA metabarcodes were generated using Leray-Geller primers (313 bp mitochondrial COI) and Illumina MiSeq sequencing. PCR replicates, twin-tagging, a mock community and negative controls were used to ensure quality for subsequent sequencing and bioinformatics. Terrestrial samples were filtered using the DAMe pipeline with modifications, and a custom R script was employed to obtain OTU assignments from the BOLD database.

A total of 63% of ~4000 OTUs could be identified to species with a confidence of > 97%. Species richness differed only slightly between habitats but species composition was significantly different between habitats, showing high temporal and moderate spatial turnover. Plots within the intact forest communities had the fewest shared species compared to disturbed and salvage-logged forests. We expect the aquatic invertebrates to also respond to the effects of climate change on forests, although it is difficult to predict the patterns. Stream invertebrates are more dependent on abiotic factors such as sedimentation and direct solar irradiation leading to potentially different responses. The methods developed and knowledge gained is intended to help practitioners and policy-makers improve current biomonitoring programs for both terrestrial and aquatic communities facing alterations due to climate change.

How new knowledge on the pathology of baculoviruses modify their use as biological control agents

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Abstract: Baculoviruses are known to regulate many insect populations in nature. They are host-specific and usually restricted to a single or a few closely related insect species, and it has been shown that they have no, or negligible, effects on non-target organisms (beneficial insects, plants and vertebrates). Accordingly, baculovirus-based pesticides are one of the safest existing pesticides. They can be used in integrated pest management strategies and contribute reducing the use of synthetic chemical insecticides and the risks associated. To date, they have been used for 30 years with success and with some issues; most of them due to the lack of knowledge on the relationships between baculoviruses and hosts. The new researches on baculovirus infections in insects and the problems encountered in field treatment have brought new hints to increase their effectiveness as biocontrol agent (resistances, directed evolution, better comprehension, gene regulation, IPM utilization…). This paper is a review of what is currently known about baculovirus pathology and how it influences its utilization as a biological control agent.

Tips and Tricks for Developing Genomic Tools for Hemipterans

Authors: Lorenzen Marce[1], Whitfield Anna[1], Rotenberg Dorith[1], Grubbs Nathaniel[1], Huot Ordom[1] and Klobasa William[1], [1]North Carolina State University, United States

Abstract: Despite the power of CRISPR/Cas9-based genome editing, published reports of confirmed genome editing in hemipteran species are rare. Here we add a new hemipteran species to the list, the corn planthopper, Peregrinus maidis. While we had an excellent "guidebook" to follow – CRISPR/Cas9-based genome editing of the brown planthopper, Nilaparvata lugens – the process of deploying this technology in a new planthopper species was far from easy. Therefore to aid others working with hemipteran species, we plan to offer a number of tips and tricks we wish we had known. We will start from the first step, that of developing genomic and transcriptomic resources for P. maidis. The next steps involved developing protocols for harvesting and microinjecting precellular embryos, which are critical for Cas9-based genome editing, since DNA and proteins cannot easily cross cell membranes. The later steps cover Cas9-based genome editing itself, including selection of target genes. For example, drawing on the work performed in N. lugens, we initially targeted the pivotal eye-color gene, white (w), which results in white eyes when disrupted in the brown planthopper. However, while Cas9-mediated knockout of w was successful in generating P. maidis embryos that lacked eye-spot pigmentation, only embryos that still possessed eye-spot pigmentation hatched. Since this suggests that w may play a vital role in P. maidis development, we tested another eye-color gene, cinnabar (cn). Unlike w, loss-of-function mutations in cn had no apparent impact on development, allowing us to establish a red-eyed P. maidis colony. Our current work focuses on a more difficult challenge, that of editing the genome of the bird cherry-oat aphid, Rhopalosiphum padi, during clonal reproduction. Importantly, these are merely the first steps towards a much boarder goal: bringing game-changing genomic tools to bear on understanding and controlling these important agricultural pests.

Male sexual communication in a vector of Chagas disease requires robust expression of the ionotropic co-receptor IR8a

Authors: Lorenzo Marcelo[2], Barcelos Pontes Gina[3] and Manuel Latorre Estivalis Jose[1], [1]CREG-CONICET, UNLP, Argentina, [2]CVIP, IRR-FIOCRUZ, Brazil, [3]FCEyN-UBA, Argentina

Abstract: The ionotropic receptor co-receptor IR8a has been reported to have multiple roles in arthropod chemosensory processes. This co-receptor seems critical for both mosquito host seeking, while it has been reported to have significantly higher expression in the antennae of a male copepod. We recently reported increased expression of IR8a in the antennae of male Rhodnius prolixus, a main vector of Chagas disease. In this study, we will present results showing that lack of robust expression of RproIR8a induces limited male performance in the mating context of the latter species. The RNAi technique was used to significantly knock-down the expression of RproIR8a. Insects having been exposed to knock-down of this genes were used for two behavioral experiments to test male sexual performance. In a first experiment, RproIR8a knocked-down males failed to leave shelters in the presence of females in the arena, when compared to mock (non-specific dsRNA injected) or intact males. In the same experiment, a lower proportion of knocked-down males approached females when compared to both control conditions. In a second experiment, a significantly lower proportion of RproIR8a knocked-down males mated up to 20 minutes when compared to males exposed to the two control conditions. To our knowledge, our report is the first to incriminate an IR co-receptor in the sexual behavior of an insect. Further experiments are necessary to establish details about sensory processes underlying these negative effects on male sexual performance.

Global decline in ladybird diversity: Causes and consequences

Authors: Losey John E.[1], Haelewaters Danny[2] and Gill Harsimran E.[1], [1]Cornell University, [2]Ghent University, Czech Republic

Abstract: The last several decades have seen a major shift in the global complex of ladybird beetles (Coccinellidae) from a diverse assemblage of "native" species to one of reduced diversity and dominated by a few cosmopolitan species, especially Harmonia axyridis. The extremely rapid decline and current rarity of several native species presents challenges for determining species distribution and collecting specimens to initiate laboratory colonies to allow further testing. These challenges have been addressed through several citizen-science projects across the world that educate non-specialists and recruit them to become ladybird beetle "spotters". Combining these submitted observations with directed experiments using captive populations, and comparing to published studies we have begun to test the potential role of introduced coccinellids in the decline of native species. All results point to increasing domination of H. axyridis and corresponding loss of coccinellid diversity at a global level. Modelling these trends will aid in predicting the ability of the coccinellid complex to aid in pest suppression in the future and facilitate the development of international strategies to restore and maintain coccinellid diversity.

Forecasting biological control efficiency of grapevine pest under climate change by using fine-grain climatic modelling and a multi-trait approach

Authors: Louâpre Philippe[2], Iltis Corentin[3], Thiéry Denis[1] and Moreau Jérôme[2], [1]INRA - UMR Health and Agroecology of vineyards, France, [2]University of Burgundy UMR CNRS 6282 Biogéosciences, France, [3]University of Burgundy, France

Abstract: Because of their key position in trophic webs, the ability of insects – as hosts or natural enemies – to respond to climate change may determine the evolution of trophic system's structure and dynamic. For instance, the way phytophagous insects modify their physiology and their behavior with raising temperature may force natural enemies to evolve in order to maintain in natural or agricultural systems.

Based on in situ climatic data and projections from climate models, we tracked the variation in individual performance of a major grapevine pest, the European grapevine moth (Lobesia botrana), and the associated consequences for interactions involving this phytophagous insect and adjacent trophic levels, more specifically parasitoids. The experiments to be presented here combined both an increase in mean temperature, and an alteration of daily thermal range, as two local facets of climate change captured by climate models.

Results highlight an impact of temperatures on defensive traits of the grapevine moth (at egg and larval stages) and adult reproductive success, with repercussions for the interaction between this pest and their associated larval and egg parasitoids. Furthermore, our results reveal an important variability of thermal responses occurring among several traits. The ability of the grapevine moth to deal with pressures exerted by natural enemies for the coming century should be constrained by several trade-offs between immune function, defensive behaviors, and reproduction. Hence, predicting life history trait evolution in host-parasitoids interactions under climate change requires adopting an integrative perspective of the biology of the focal species (here the host) while considering the complexity of changes occurring in insect direct thermal environment.

#SciComm at the interface of disciplines

Authors: Lovett Brian, University of Maryland, Department of Entomology, United States

Abstract: Interdisciplinary science is best positioned to address challenges facing the modern world, and innovative technology, tools, and apps facilitate international collaborations across disciplines, allowing researchers to answer increasingly complex questions. Researchers working at the interface of multiple disciplines face unique challenges when communicating their results. For example, mycologists who study fungal groups that are pathogenic or (ecto-) parasitic on insects must learn the terminology for each discipline relevant to their work, which can present barriers for communicating with audiences that are familiar with field-specific jargon. Though this may be prohibitive initially, this issue can prime interdisciplinary scientists to be effective communicators. Communicating science at the interface of disciplines requires scientists to constantly assess who their audience is, what they already know, and what they value. Additionally, it encourages scientists to move away from using jargon. This increased audience awareness is a gateway for effective science communication, as understanding your audience enables a tailored, high-impact message. Bridging the gap between disciplines at a professional level effectively prepares interdisciplinary scientists for bridging communication gaps with the public. This is a profound benefit to practicing interdisciplinary science, which should be considered when evaluating and training scientists as effective communicators in academia and outside. Here we discuss some of the challenges related to interdisciplinary research from personal experience, present suggestions for improved communication, and make a case for tying the skill of interdisciplinary science communication to the academic hiring process and (tenure-track) promotions.

Using public education to reduce household insecticide use

Authors: Lowe Lizzy, Macquarie University, Australia

Abstract: Insecticide use in urban areas has a detrimental impact on both public and environmental health. Overuse of chemical pest control products by residents is common, with people often applying pesticides even when there is no threat to health or property. The problem of excessive insecticide use is driven by attitudes and management practices, therefore it requires an approach that integrates the social and ecological sciences. To understand household pest control practices, I conducted an online survey asking people about their attitudes towards insects, why they do/don't use insecticides and which products they use.

My survey received 1878 responses, mostly from the Sydney area. We found that 83% of respondents use insecticides of one kind or another, the most popular of which were broad spectrum insect sprays and cockroach baits. Attitudes towards insects were more moderate than expected, with most people choosing to ignore or conserve insects (with the exception of mosquitoes and termites), especially in their gardens. Promisingly, of those who use sprays, the majority (68%) of people prefer to use a small amount over a restricted area, rather than small or large amounts over a large area.

I am using this new understanding of public attitudes to develop targeted community education materials and provide guidance to local governments to help reduce insecticide use. Examples of public education initiatives include: public talks, school yard biodiversity surveys, pamphlets distributed by local councils, and pesticide free pledges for local community gardens.

Does infection of endosymbiotic bacteria Wolbachia cause the high female-biased population of coffee berry borer Hypothenemus hampei?

Authors: Lu Hsiao-Ling, Department of Biotechnology, National Formosa University, Taiwan

Abstract: Coffee berry borer (CBB) is an important economic pest, which was invaded Taiwan in 2007 and caused injury. Previous studies on CBB have shown that they coexist with endosymbiotic bacteria Wolbachia and display a characteristic of a female-biased sex ratio in the population. Due to its encrypted life cycle, female-biased population, and a handful of basic biological information, current strategies cannot suppress pest population efficiently. We aim to promote CBB as a model for studying the mechanisms of insect sex determination, symbiosis, embryonic development and to develop pest-control strategies for those pests that spend most of their life cycle inside of plant host. To explore whether the female-biased population is caused by Wolbachia and the mechanism of sex determination for producing more female offspring, we adopted a polymerase chain reaction protocol to detect the maternally inherited cytoplasmic proteobacteria Wolbachia in total genomic DNA from CBB collected from 42 sample sites in southern and central Taiwan. Our preliminary results show that only one sample yields positive detection. The low Wolbachia infection rate of coffee berry borer highlights that the female-biased sex ratio may be regulated by other mechanisms.

Current situation and trend for red imported fire ant in mainland China

Authors: Lu Yongyue, Red Imported Fire Ant Research Center, South China Agricultural University, China

Abstract: Red imported fire ant Solenopsis invicta Buren is one of the 100 most threatening alien species in the world. Originally distributed in parts of South America, it has invaded 24 other countries and regions now. Because of its ferocious habits, rapid reproduction and strong competitiveness, it is easy to outbreaks and cause disaster in a short period of time after the invasion, and will endanger agriculture and forestry, human health, biodiversity and public safety. The fire ant was found in Taoyuan, Taiwan in Sept., 2003, and Guangdong, mainland China on Sept., 23, 2004. As a new invasive species in China, although it was paid serious attention by the governments, institutions, the public and scientists, but the fire ant still has kept spreading fast after its invasion.

In order to delay its expansion and control its infestation, many Action Plans, and science and technology programs on the fire ant had been carried out and completed in China. The National Fire Ant Detection and Management Union, and Advisory Committee were found in 2005. Red Imported Fire Ant Research Center, South China Agricultural University was built up in July, 2005. And then, work plans, technical plans for quarantine and extermination, and technical training plans at the national and provincial levels were presented, and implemented in the infected areas with the fire ants. National and provincial emergency management plans for plant quarantine pests was proposed and implemented firstly in mainland China. Standard framework and procedure for the fire ant management was also put forward, and 6 national, industrial and local standards were promulgated before 2009. Since finding the fire ant invasion, more than 4 million USD was invested in R&D, and more than 150 million USD in recent 5 years were used in the fire ant management in mainland China. The infestation degree of the fire ant at most of the infected area decreased below the middle level, and the fire ants had been eradicated successfully at 9 independent infected areas after the high intensity measures had been adopted.

According to its spreading speed with 27 county-level regions per year in the past 15 years, it was predicted that more than 400 county-level regions would be infected by the fire ant in the late 2019. There were already 15 provincial regions infested by the pest, including Hongkong, Macau, Taiwan, Guangdong, Guangxi, Hainan, Fujian, Zhejiang, Jiangxi, Hunan, Hubei, Guizhou, Chongqing, Sichuan, and Yunnan. The general trend was that the ant was expanding northward, and invading the Yangtze River Basin constantly. It was not ruled out that there may be sporadic invasion and occurrence in North China, Northeast China and Northwest China because of the extensive greenhouses in the future.

Bacteriocyte function and inheritance in the bacterial symbiosis of whiteflies

Authors: Luan Junbo[2] and Douglas Angela[1], [1]Cornell University, United States, [2]Shenyang Agricultural University, China

Abstract: Various insects require intracellular bacteria that are restricted to specialized cells (bacteriocytes) and are transmitted vertically via the female ovary. It is of great interest to investigate the function and inheritance of such novel host cells. We discovered that multiple horizontally acquired genes with bacteria origin are enriched in the bacteriocytes of the whitefly Bemisia tabaci. Each horizontally acquired gene can function with other genes in the pathway coded by the symbiont, while facilitating the decay of the symbiont gene coding the same reaction. We found that developmentally orchestrated remodelling of gene expression and correlated changes in cell behaviour underpin the capacity of bacteriocytes to mediate the vertical transmission and persistence of the symbiotic bacteria on which the insect host depends. We further demonstrated in the whitefly B. tabaci MEAM1 species, transmission is mediated by somatic inheritance of bacteriocytes, with a single bacteriocyte transferred to each oocyte and persisting through embryogenesis to the next generation. Then we investigate the mode of bacteriocyte transmission in two whitefly species, B. tabaci MED, the sister species of MEAM1, and the phylogenetically distant species Trialeurodes vaporariorum. We demonstrated that B. tabaci MED bacteriocytes are genetically different from other somatic cells and persist through embryogenesis, as for MEAM1, but T. vaporariorum bacteriocytes are genetically identical to other somatic cells of the insect, likely mediated by the degradation of maternal bacteriocytes in the embryo. These two alternative modes of transmission provide a first demonstration among insect symbioses that the cellular processes underlying vertical transmission of bacterial symbionts can diversify among related host species associated with a single lineage of symbiotic bacteria.

Pavement ants to population genomics: using citizen science to benefit invasion science

Authors: Lucky Andrea[4], Hulcr Jiri[2], Payton Adam[3], Storer Caroline[3], Dunn Rob[1], McDaniel Stuart[3], Vitone Tyler[3] and Zhang Yuanmeng[3], [1]North Carolina State University, United States, [2]School of Forest, Fisheries, and Geomatics Sciences, University of Florida, United States, [3]University of Florida, United States, [4]University of Florida, United States

Abstract: Clarifying the population structure and introduction history of non-native species is essential to preventing and mitigating effects of invasion, yet the invasion history of many long-established non-native species remain poorly understood. We characterized the population structure of one of the most commonly encountered urban ants in North America using public participant-collected specimens from the School of Ants citizen science project, in combination with double-digest restriction-site associated DNA sequencing (ddRADseq). Based on this genomic approach we confirm the identity of populations ranging across the continent as Tetramorium immigrans Santschi, and report low genetic diversity across its range, suggesting that this entire population resulted from the establishment of one single, or few closely related ant colonies, approximately two hundred years ago. The absence of strong population structure suggests that this ant's spread across North America has been repeatedly aided by human-assisted dispersal. We find no evidence of inbreeding in T. immigrans; this contrasts with the inbreeding and unicoloniality of many other invasive ants. These results demonstrate how collections-based public participatory science and emerging high-throughput sequencing techniques each have the potential to vastly improve the amount of data available to researchers; together, these techniques can be deployed to address ecological and evolutionary questions in non-model organisms, including invasion biology. We suggest that this model is particularly well suited for research on common taxa that are ecologically important but poorly understood.

Effect of Genetically modified Corn on non-target arthropods in Mexico

Authors: Luis A. Aguirre[1], Hernández-Juárez Agustín[1], Cerna Ernesto[1], Ochoa Yisa M.[1], Flores Mariano[1], Frias Gustavo[1] and Sánchez Victor M.[1], [1]Universidad Autonoma Agraria Antonio Narro

Abstract: Approval of genetically modified corn (GM) under controlled conditions in Mexico, allowed to evaluate corn hybrids AgrisureTM 3000 GT, Agrisure® VipteraTM 3110 and Agrisure® VipteraTM 3111 events, with several genes coding Cry1Ab, Vip3Aa20 and mCry3A proteins of Bacillus thuringiensis (Bt), in Sinaloa, Mexico Effect over non-target arthropods was evaluated determined by community attributes: number of families, arthropods abundance, diversity, richness, and population uniformity. A Kruskal-Wallis and U Mann Whitney test were used to estimate abundance to detect differences between populations of GM and conventional corn. Phytophagous and predators associated with maize were found more abundant in the GM events, whereas parasitoids and saprophagous were evenly distributed among hybrids, where the statistical analysis showed no significant differences between the GM and their respective conventional hybrids. Management of corn pests with GM hybrids is a control strategy to be incorporated into an integrated pest management program, increasing possibility to obtain better grain quality and yield. No adverse effects on abundance of non-target arthropods associated with corn was found; providing better opportunity to use this technology, which will reduce the use of chemical insecticides. Therefore, this technology can help preserve agroecosystem biodiversity in relation to other pest management options

Microbial symbioses as a critical aspect of insect community ecology

Authors: Lukasik Piotr[1], Kolasa Michal[1], Nowak Karol[1], Buczek Mateusz[1], Prus Monika[1], [1]Jagiellonian University, Poland

Abstract: Symbiotic microorganisms have played crucial roles in the ecology and evolution of insects. They have enabled major ecological transitions, and still influence their hosts' biology in multiple ways, often highly significant in heterogeneous and changing environments. With their ability to affect insect traits such as performance on different diets and susceptibility to natural enemies or abiotic stressors, and move within and across host populations or species, microbial symbionts can be viewed as an enormous genetic reservoir for their host's rapid adaptation to environmental challenges. However, our understanding of microbial diversity, distribution, and roles in natural populations and communities of insects has been limited.

Recent developments in high-throughput sequencing and bioinformatics have allowed studies of microbial associations across very large numbers of samples. My research group has devoted substantial efforts to the implementation and optimization of cost-effective and scalable approaches for quantitative amplification of host and microbial marker genes. We have successfully applied them to over ten thousand diverse wild insects. In this presentation, I will outline our methods and explain what we have learnt from looking at community-level host-microbiota datasets. I will also talk about the challenges, limitations, and possible applications of such approaches.

Not just nitrogen: Ancient, waste-recycling turtle ant symbionts encode complex carbohydrate catabolism

Authors: Lukasik Piotr[3], Russell Jacob[4], Bechade Benoit[2], Cabuslay Christian[2], Sanders Jon[1] and Hu Yi[2], [3]Drexel University, United States, Poland, [4]Drexel University, United States, [2]Drexel University, United States, [1]Cornell University, United States

Abstract: The work combines experimental and genomic inferences. We show directly that symbiont-recycled waste nitrogen is acquired by ants in large capacity. And we demonstrate the genetic mechanisms by which this occurs, and the symbionts responsible. We also show that ancient symbionts have retained capacities to break down plant cell wall biomass, suggesting an unforeseen capacity reminiscent of that seen for termite gut communities.

The digestive systems of many ants are sparsely colonized by microbial symbionts. But ants from several lineages with nitrogen-poor diets provide strong exceptions, harboring large masses of gut bacteria, which they transmit through trophallaxis. Turtle ants of the genus Cephalotes provide an intriguing example, engaging in ancient interactions with a diverse suite of specialized symbionts, which populate the midgut and ileum of adult workers. Using stable isotope labeling, and antibiotic manipulation, we show that gut bacteria recycle nitrogen-waste in adult turtle ants, and host ants acquire this recycled nitrogen in large quantities. Genomic analyses reveal specialized recycling roles for a subset of the bacteria, and that the majority can assimilate ammonia and synthesize amino acids. Further assessment of symbiont genomes reveal an unexpected feature - several specialized bacteria encode enzymes for the degradation of plant cell walls, including cellulases and xylanases. These enzymes are also encoded by the less specialized gut residents found in turtle ant larvae. We hypothesize that these conserved interactions function as multi-faceted, nutritional and digestive mutualisms, setting Cephalotes apart from most other ants. We also conclude that the use of nitrogen-limited diets have been facilitated by convergent acquisition of unrelated waste-recycling symbionts, but that unrelated herbivores derive idiosynchratic benefits from their unique symbioses.

DNA metabarcoding reveals host-specific communities of arthropods residing in fungal fruit bodies

Authors: Lunde Lisa, Norwegian University of Life Sciences (NMBU), Ås, Norway

Abstract: Many arthropods spend their immature life inside fruit bodies of wood-decay fungi. There is a succession of arthropod species within the fruit body as it ages, but earlier research has focused more on the fauna inside dead, rather than living, fruit bodies. Further, how fungal traits, like fruit body persistency and size, affect arthropod communities is poorly explored. Using DNA metabarcoding, we characterised the arthropod communities in living fruit bodies of eleven wood-decay fungi from boreal forests and investigated how they were affected by different fungal traits. Arthropod diversity was higher in fruit bodies with a larger surface area-to-volume ratio, suggesting that colonisation is crucial to maintain arthropod populations. Diversity was not higher in perennial fruit bodies, most likely because these fungi invest in defences against arthropods. Arthropod community composition was structured by fruit body size, thickness, surface area, morphology and toughness. Notably, we identified a community gradient where soft and annual fruit bodies harboured more dipterans, while tougher and perennial fruit bodies had more oribatid mites and beetles. Ultimately, close to 75% of the arthropods were specific to one or two fungal hosts. Our study has revealed surprisingly diverse and host-specific arthropod communities within living fungal fruit bodies.

Undersowing clovers in oats supports pollinators but does not benefit biological pest control

Authors: Lundin Ola[2], Boetzl Fabian[1], Douhan Sundahl Anna[1], Friberg Hanna[1], Viketoft Maria[1], Bergkvist Göran[1], [1]Swedish University of Agricultural Sciences, [2]Swedish University of Agricultural Sciences, Department of Ecology, Sweden

Abstract: A promising way of achieving more sustainable agricultural production is by replacing external inputs such as fertilisers and pesticides with yield-supporting ecosystem services generated by beneficial organisms within the agroecosystem. Increasing plant diversity within the field by intercropping with legumes has potential to achieve this but the effects on biodiversity and ecosystem services are so far not sufficiently understood. Using a design with paired plots in commercially cropped fields, we studied the effects of intercropping oats with a mixture of three annual undersown clovers on a total of 16 below-and above-ground ecosystem service indicators that included pollinator densities, insect pest damage, activity densities of natural enemies and predation rates. Intercropping promoted pollinators but had no effect on pest damage, predation rates, carabids or rove beetles, and a slightly negative effect on spiders. Additional benefits of intercropping included suppression of arable weeds and root-feeding nematodes, and a tendency of increased soil mineral nitrogen. Oat yield levels were not affected by intercropping, whereas oat yield nitrogen content unexpectedly decreased by ca. 4%. Undersowing annual clovers is a simple method to support pollinators without reducing cereal crop yields or taking land out of arable production. Intercropped plant mixtures should, however, be optimised to benefit natural enemies and biological pest control in order to support a higher level of overall cropping system multi-functionality.

Microplitis bicoloratus bracovirus modulates innate immune suppression through the eIF4E-eIF4A axis in the insect Spodoptera litura

Authors: Luo Kaijun, School of life Sciences,Yunnan University, China

Abstract: Eukaryotic initiation factor 4E (eIF4E) is regulated during the innate immune response. However, its translational regulation under innate immune suppression remains largely unexplored. Microplitis bicoloratus bracovirus (MbBV), a symbiotic virus harbored by the parasitoid wasp, Microplitis bicoloratus, suppresses innate immunity in parasitized Spodoptera litura. Here, we generated eIF4E dsRNA and used it to silence the eIF4E gene of S. litura, resulting in a hallmark immunosuppressive phenotype characterized by increased apoptosis of hemocytes and retardation of head capsule width development. In response to natural parasitism, loss of eIF4E function was associated with similar immunosuppression, and we detected no significant differences between the response to parasitism and treatment with eIF4E RNAi. Under MbBV infection, eIF4E overexpression significantly suppressed MbBV-induced increase in apoptosis and suppressed apoptosis to the same extent as co-expression of both eIF4E and eIF4A. There were no significant differences between MbBV-infected and uninfected larvae in which eIF4E was overexpressed. More importantly, in the eIF4E RNAi strain, eIF4A RNAi did not increase apoptosis. Collectively, our results indicate that eIF4E plays a nodal role in the MbBV-suppressed innate immune response via the eIF4E-eIF4A axis.

Plant–Pathogen Interactions under Herbivore Influence: Applying Evidence from the Coexistence of Wheat Spikes Colonizers

Authors: Luo Kun, Shaanxi Key Laboratory of Chinese Jujube, Yanan University, China

Abstract: The English grain aphid Sitobion avenae Fabricius (Hemiptera: Aphididae) and the fungus Fusarium graminearum Schwabe (Hypocreales: Nectriaceae) are two economically important pests residing on wheat spikes, a ‘synergistic’ relationship between the coexistence of S. avenae and F. graminearum on wheat spikes resulting in devastating damage to grain yield and quality was detected. However, the biological and ecological reasons why herbivore pre-exposure positively influence the plant–pathogen interactions have been understudied. In recent decades, extensive studies typically focused on unravelling more detail on the relationship between wheat–aphids and wheat–pathogens, which have greatly contributed to our understanding of this tripartite interactions at ecology level. Here we synthesize recent advances related to the tripartite interaction S. avenae–cereal–F. graminearum from the aspects of environmental nutrients and hormonal signals. We propose that the aphid honeydew excreted by S. avenae and their endosymbionts provide ready-to-use nutrients accelerating infection by the pathogen F. graminearum. Furthermore, F. graminearum infection is associated with accumulation of the growth phytohormone auxin, possibly interfering with hormone-dependent defense responses and stimulating the infected plants to release more nutrients. The findings highlights the relevance of herbivore S. avenae pre-exposure to trigger the accumulation of mycotoxins production, which stimulates the infection process of F. graminearum and epidemic of Fusarium head blight in natural ecosystems.

Chemical defense responses of Douglas fir seedlings to bark beetle associated blue stain fungi

Authors: Lusebrink Inka, Georg-August-University, Göttingen, Germany

Abstract: Douglas-fir is considered as a great hope for European forests in the face of climate change, however it is non-native. ... In Central Europe a few native bark beetles are pests in Douglas fir, including the fir bark beetle (Pityophthorus pityographus), the six-toothed spruce bark beetle (Pityogenes chalcographus), the larch bark beetle (Ips cembrae) and the European spruce bark beetle (Ips typographus). However, they have not caused major damage so far, but it is likely that the adaptation process of native bark beetles to Douglas-fir will continue and that increasingly successful attacks will occur on Douglas-fir in the future. Most bark beetles carry blue stain fungi that are considered critical to overcome tree defenses and to cause host tree mortality, additionally they lead to a reduction in the value of timber. In order to assess if the blue stain fungi associated with the above-mentioned bark beetles (1) are able to establish in or kill Douglas fir; and (2) induce different chemical defense responses, a seedling experiment was conducted. ... full abstract see attachment

Ultra-low fruit fly populations in mosaic landscapes: behavior, development, establishment and detection.

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Abstract: Periodic detections of medfly in areas recognized as fly-free raises a lot of theoretical and regulatory controversy. The latter can be largely reduced to the question: “how long can local populations survive in the cryptic ultra-low-density phase and remain undetected by the surveillance network”.

To answer this question in the absence of empirical options, a series of stochastic simulations were carried out, emulating the behavior, development and fate of individual members of the residual / initial medfly populations. For this purpose, the PESTonFARM model was used, parameterized according to current knowledge about medfly biology and its behavior in the field conditions. The simulations were carried out for a specific area where medfly was recently detected, taking into account the key features of local topography, historical weather patterns and a surveillance system.

The projections generated by the model support the hypothesis about the possibility of the prolonged existence of cryptic populations fluctuating at very low densities, which may slip out of the surveillance grids and remain undetected for longer periods of time. Analysis of various scenarios emulated by the model has revealed a number of specific environmental factors that, acting simultaneously, are able to maintain fly populations at low densities. The application of the model also allowed estimating the chances of detection for various scenarios of terrain topography, host and weather patterns.

The theoretical and practical implications of the proposed approach and methodology, its key merits and limitations, were also discussed.

Methods for studying insects on carcasses for the use of data in determining postmortem interval. Cases from practice.

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Abstract: Carrion insects have recently been often used in criminal investigation. From large species of them, information on the biological characteristics of Diptera and Coleoptera is used. These insects, with good access to the corpse, in very quickly of time colonize it and lay eggs or give birth to larvae, and give high accuracy in establishing the postmortem interval (PMI). During experiments of the decomposition of pig carrion (Sus scrofa domesticus), the species spectrum and analyzed the chronological succession colonized a corpse by insects. During studies four stages of decomposition of carcasses was recognized. In Russia, the practice of using knowledge of invertebrate fauna to solve in establishing the postmortem interval (PMI) under unclear circumstances are increasingly being introduced. Most often Diptera use from the families blowflies (Calliphora vicina, Protophormia terraenovae, Cynomyia mortuorum), flesh flies (Sarcophaga) and houseflies (Hydrotaea dentipes). In cases where large species of necrophilic beetles, such as carrion beetles of the genus Necrodes, it accelerates tissue decay. This is facilitated by severe damage to the skin and deep internal holes caused by beetles. A complication for diagnosis can be caused by the presence of ants or the presence of corpse near an anthill.

Influence of lipopolysaccharide from bacteria on the expression of BmToll9-2 gene in larval silkworm

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Abstract: Toll-like receptors in Toll signaling pathway in insects play an important role in activating the innate immune response to invading pathogenic microorganisms. This study aims to explore the influence of lipopolysaccharide (LPS) on the expression of the Toll-like receptor gene BmToll9-2 in larvae of the silkworm, Bombyx mori. LPS and Escherichia coli were respectively injected into the body cavity of the 5th instar larvae to induce their immune response, and the expression levels of BmToll9-2 after injection were detected by real-time quantitative PCR. The real-time quantitative PCR results showed that injection of LPS could induce the expression of BmToll9-2 in the midgut of the 5th instar larvae. Injection of E. coli could also induce the expression of BmToll9-2 in the midgut of the 5th instar larvae. Expression of BmToll9-2 in B. mori larvae is up-regulated after injection of LPS and E. coli, suggesting that BmToll9-2 receptor may be involved in the recognition process of Toll-like receptors to LPS and E. coli in insects.

Phylogenomic species delimitation of the twisted winged parasite genus Stylops (Strepsiptera)

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Abstract: The advancements both in sequencing technologies and in statistical models used to analyse genomic datasets have provided new tools to resolve taxonomical controversies in many historically problematic groups. Stylops is the most species rich genus of the insect order twisted winged parasites (Strepsiptera) and has been the subject of alternating species concepts based on their host specialization, with vast implications for species diversity estimates. The concept of a single supergeneralist species in Europe (Stylops melittae Kirby, 1802), has been challenged by studies based on single molecular markers. In our study, we aim to resolve the controversies around the species delimitation of Stylops with adequate molecular data and species delimitation analyses. We generate whole-genome sequence data for over 200 samples, with a focus on European taxa, representing a large selection of the candidate species presented in a recent preliminary world checklist of Stylops. These include both freshly collected material and museum samples from 94 different host species. We use BPP which allows analysing multi-locus genomic sequence data under the multispecies coalescent model, to test the species limits. Here we present preliminary results of the phylogenomic species delimitation analyses and discuss their implications for the taxonomy and diversity of Stylops.

Relationship between the thermal tolerance of cereal aphids and their bacterial symbionts

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Abstract: High temperature events influence the demographic parameters and population performances of insects such as aphids. This could be due to the complete or partial disturbance of their gut-associated symbionts during the physiological acclimation of host insect species to extreme high temperature events. This study aimed to determine if there was any effect of heat acclimation and chronic heat exposures on the density and community structure of symbiotic bacteria of cereal aphids Rhopalosiphum padi (L.) and Sitobion avenae (F.). Aphid clones were randomly collected from the wheat fields and were reared in the laboratory at 20±1 °C and 50-65 % RH with 16L:8D h photoperiod. Thermal tolerance indices (chronic, basal and acclimated CTmax) were determined for five-day old female aphids from parental, F1, F2 and F3 generations. Quantification of total (16S) and aphid-specific bacterial symbiont gene copy numbers was done by real-time q-PCR. Results revealed that thermal thresholds (both basal and acclimated) gradually increased from parental to F3 generation. On average, thermal threshold values of R. padi were 1.0°C higher than those of S. avenae. Although average total bacterial (16S) density was found higher in S. avenae than R. padi, average density of symbiont genes per aphid was almost similar for both aphid species. Temperature-tolerant aphid individuals harboured significantly higher symbiont genes than susceptible ones for both species. Moreover, thermal tolerance indices of both aphid species were found significantly correlated with gene densities of total symbionts (16S), Buchnera aphidicola, Serratia symbiotica, Hamiltonella defensa, Regiella insecticola and Spiroplasma spp, suggesting their role in thermal tolerance of host aphids.

Night warming on predator–prey interactions: Implications for biological control

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Abstract: Most previous research concerning climate warming on interspecific interactions mainly focus on changes in temperature means, with a rise in both daytime and nighttime temperatures or a rise just in daytime temperatures. However, it has been found that the rise of global mean surface air temperatures has resulted from daily minimum temperatures increasing at a faster rate than daily maximum temperatures. Importantly, daytime and nighttime warming may lead to different thermal effects on organisms, indicating that night warming may have different effects on species and interspecific interactions from that of daytime warming. Thus, although many studies have reported the ecological consequences of warming in mean temperatures, nighttime warming are often omitted. Here we used the lady beetle Propylaea japonica and the English grain aphid Sitobion avenae as a predator–prey model system to study the effect of night warming on interspecific interactions. We examined how night warming would affect the demographic parameters, stage structure and population growth of the lady beetle. We also compared the different effects of night warming and mean temperature increase.

Compared with mean temperature increase, nighttime warming accelerated the growth rate of the lady beetle while reduced the reproduction, but had no significant effect on life span. The lifetime predation and energy efficiency of the lady beetle decreased with temperature under constant conditions while changed little with temperature under night warming, which indicated that the energy efficiency of the lady beetle was stable under realistic nighttime warming. Both nighttime warming and mean temperature increase altered population structure of the lady beetle, with the proportion of adults increased with temperature whereas the proportion of larvae decreased with temperature. The proportion of adults was higher than that of constant temperature warming. Importantly, the population growth rate of the lady beetle decreased with temperature under mean temperature increase while increased with nighttime warming, which indicated an opposite result of warming effect on predator–prey interspecific interactions between nighttime warming and mean temperature increase. These results and conclusions have important significance for the study of warming effects on insects and interspecific interactions. Our study thus has potential implications for biological control in the context of ongoing climate change.

Thermoregulation-mediated predator-prey interaction under climate warming

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Abstract: Previous studies concerning climate warming on insects mainly focus on the direct effects of temperature increase. However, the indirect effects through interspecific interactions are often overlooked. Behavioral thermoregulation is an important strategy to cope with climate warming in insects. Therefore, under climate change, the changes in interspecific interactions may be indirectly caused by insect thermoregulation behavior due to the differences in thermal tolerance between species. Small insects like sap-sucking aphids can avoid thermal extremes such as heat stress either by walking away or dropping-off form their host plant to seek for cooler places. Here, by using the English grain aphid Sitobion avenae and the lady beetle Propylaea japonica as a model predator-prey model, we aimed at revealing the interspecific interaction between the aphid and its natural enemy mediated by the thermoregulatory behavior of the aphid under climate warming. We tested the hypothesis that the fitness related life history traits of the lady beetles can be altered by the thermoregulatory behavior of the aphids. Our results showed that behavioral thermoregulation can increase aphid survival under warming while lead to changes in body size, development and reproduction. Such changes in fitness related parameters of the aphid altered the life history traits of the lady beetle and thus support our hypothesis. Therefore, the effects of climate warming on species mediated by thermoregulation behavior highlight the indirect effects of climate change on trophic cascades. Insect behavioral thermoregulation should be taken into account when predicting the changes in interspecific interactions as well as biological control and ecosystem functioning under climate change.

Thermal resilience of Prostephanus truncatus (Horn): Can we derive optimum temperature-time combinations for commodity treatment?

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Abstract: Prostephanus truncatus (Horn) (Coleoptera: Bostrichidae), is a wood-boring, destructive quarantine insect pest of stored cereal grains and tuber crops. Current disinfestation methods against this pest mainly include fumigants, whose usage in some countries has been contested and discontinued owing to increasing pesticide resistance, public health risks and environmental hazards. Grain temperature treatments thus, offer a sustainable non-chemical and near universally acceptable form of disinfestation for international commodity movement. Currently, blanket temperature treatments are applied regardless of as-yet-unknown P. truncatus developmental stage thermal mortality thresholds that simultaneously optimise grain quality. Here, we used established static and dynamic protocols to determine the low and high thermal profile of P. truncatus larvae and adults measured as critical thermal minima (CTmin), lower lethal temperatures (LLT0), chill coma recovery time (CCRT), supercooling points (SCPs), critical thermal maxima (CTmax), upper lethal temperatures (ULT0) and heat knock-down time (HKDT). We tested the adult ULT-time matrices on maize and sorghum grain quality (germination %) to determine the most effective temperature-time combination retaining optimum grain germination quality. Our results showed adults had higher basal heat (CTmax and HKDT), cold (CTmin, CCRT and SCP) and potential thermal plasticity than larvae ($P < 0.05$). The LLTs and ULTs ranged -1 to -15°C and 41 to 49°C respectively. Using LLT0 and ULT0, our results showed that for heat treatment, moderate temperature × long duration matrix; i.e. either 45.5°C × 4 h or 47°C x 2h were more efficacious while retaining commodity quality. Similarly, for cold treatment; -9°C × 4 h, -11°C × 2 h, -13°C × 1 h and -15°C × 0.5 h were effective for complete mortality. These temperature-time combinations may be a sustainable alternative to fumigants in phytosanitary grain disinfestation against P. truncatus or related pests. Such pest- and commodity- specific thermal profiling is critical for development of effective standardised grain disinfestation protocols.

It’s raining species: Rainwash eDNA metabarcoding as a minimally invasive method to assess tree canopy invertebrate diversity

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Abstract: Forest canopies are highly diverse ecosystems, but despite decades of intense research, substantial knowledge gaps of their biodiversity remain. The limited accessibility of these ecosystems is a fundamental challenge. Here, time- and cost-efficient, ideally minimally invasive yet comprehensive applications are required to help close this knowledge gap. A solution could be provided by metabarcoding of environmental DNA (eDNA). This minimally invasive method has been proven as efficient monitoring tool in various ecosystems, yet its potential for canopy monitoring remains unexplored. Thus, we conducted metabarcoding on eDNA collected from rainwater that fell through tree canopies to explore its monitoring potential. We placed four 1 m² rain samplers beneath the canopies of four different tree taxa prior to a major rain event, filtered eDNA from the collected rainwater, and performed eDNA metabarcoding to profile the invertebrate community. We detected 50 invertebrate species by eDNA metabarcoding, of which 43 were representing true canopy biodiversity signals. Furthermore, we observed clear species occurrence patterns corresponding to the four tree taxa, suggesting that ecological patterns can be assessed using the method. In conclusion, our study provides a proof of concept that rainwash eDNA metabarcoding offers a minimally invasive and comprehensive method for tree canopy diversity monitoring.

Dissecting physiological cause and effect at the limits of insect thermal performance

Authors: MacMillan Heath, Carleton University, Canada

Abstract: The limits of environmental stress are increasingly appreciated as important predictors and determinants of insect biogeography. Unfortunately, complexity and variation at multiple levels of biological organization create a formidable barrier to determining what physiological and molecular mechanisms set the limits of environmental stress tolerance. Progress in our understanding of these limits (and thus our ability to make sound predictions) will require systematic approaches that embrace this complexity and allow us to separate the causes of failure from the physiological consequences that can quickly follow. In this talk, I will give an overview of the ionoregulatory collapse model of insect chill susceptibility. Using this model as an example, I will attempt to convince you that integrative models that explain cause and effect links among multiple organ systems will allow us to quickly arrive at a holistic understanding of the many and varied challenges facing animals under environmental stress.

Consistency in provision of nutrients in dung beetles: Seasonal changes in nutrient levels.

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Abstract: The nutrient content of animal dung is important for the growth, development and activity of dung beetles. The dung itself is a metabolic end product. It is made up of partially digested, undigested and undecomposed food particles such as plant cell walls, bacteria, fungi and gut epithelial cells. This leads to dung having a high carbohydrate content and very little protein. The nitrogen source is important for growth and reproduction. Protein, measured as nitrogen, changes with the seasons because of forage, temperature and moisture content fluctuations, and can affect factors such as dung beetle activity and egg production.

In this experiment we investigated how dung beetles manipulate nitrogen in the dung when feeding and nesting, and also how they respond to changes in dung nutrients across the seasons when nesting and feeding. The maternal gift from the brood balls of Euoniticellus intermedius and the foregut contents of Kheper nigroaeneus and Scarabaeus goryi (all Coleoptera: Scarabaeinea) were compared monthly with that of the raw dung. The maternal gift is a maternal addition to the broodball.

Relative to raw dung the nitrogen content of the foregut and maternal gift increased, and carbon content remained the same, while the C:N ratio decreased during ingestion. In contrast the nitrogen and carbon content, and the C:N ratio of the raw dung changed with the seasons throughout the year. The nitrogen content of the maternal gift and the foregut content of each species increased throughout the seasons by a percentage, while the carbon content changed little compared to the raw dung. Furthermore, the C:N ratio of the raw dung corresponded with the nitrogen and carbon content throughout the seasons while that of the foregut and maternal gift remained the same. Dung beetle nutrient provision appears not to be driven by nitrogen alone but both the carbon and nitrogen content. Despite seasonal changes in C:N ratios of the raw dung (driven presumably by changes in herbivore forage quality), selective feeding by adult dung beetles enables them to maintain a sufficiently nutritious intake and provide a nutritious maternal gift, “starter” diet for the newly hatched larva.

Edible Insects and the Collection of the Natural History Museum Bulawayo (NHMB), Zimbabwe

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Abstract: A report on research attempting fully to document available data and specimens of edible insects in the natural history museum of Zimbabwe and to raise awareness on the role of museum collections in taxonomy and monitoring of species distributions. The project also highlights the museum's role in gathering information on indigenous knowledge systems that have sustained the practice of Entomophagy and disseminating knowledge to relevant stakeholders. The Zimbabwean story tell of entomophagy as a fairly commonly accepted practice in the country. We wish to contribute to consolidating answers on how much knowledge of the practice still exists, what the extent of entomophagy is as well as the number of species still known and available in Zimbabwe, and to give an account of efforts made thus far in testing farming methods for these insects in the country. Micro-livestock have been proven to offer more nutrition per gram compared to the conventional livestock, with the added advantage of ease of rearing. Exploring already existing information will count towards making strides to deliberately rear insects to improve livelihoods and show museums as central to gathering and disseminating information on edible insects.

The three insulin receptors of cockroaches

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Abstract: The insulin receptor pathway, remarkably conserved throughout Metazoan evolution, regulates such important processes as cell growth and proliferation, sugar levels, longevity, stress resistance, and reproduction. Insects generally have two insulin receptors (InR) as a result of an ancestral gene duplication. However, in the lineage that gave rise to the Polyneoptera branch that includes stick insects, termites, and cockroaches some 250 million years ago, a further duplication occurred that increased InR number to three. There are three outcomes in the evolution of duplicated genes. One is that one copy is functionally redundant (nonfunctionalization). Another is that one copy acquires a novel function, while the other retains the original one (neofunctionalization). A third possibility is that both copies may become partially compromised to the point at which their total capacity is reduced to the level of the single-copy ancestral gene (subfunctionalization). Using the cockroach Blattella germanica as a model, we are seeking to determine the function of its three InRs, and the evolutionary fate of the new duplication. Until now, the results show that InR2 is the most abundantly expressed gene in all tissues examined, and its depletion produces the most dramatic effects in relation to the female reproductive processes.

The life-table parameters of Perilla Seed bugs (Nysius Spp.) (Heteroptera: Lygaeidae: Orsillinae) in different radiofrequency fields

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Abstract: The genus Nysius is polyphagous pests, and it can cause a serious damage to seeds, foliage and flowers of various plants. In this study, we investigated the oviposition preference, development, and adult performances of Nysius plebeius and Nysius hidakai at five Radiofrequencies of 0 (control), 5, 10, 20, and 30 kHz on perilla seeds. In addition, the effects were also studied in four generations (Parent, F1-, F2-, and F3-generation) of each species. The results showed that radiofrequency application had significant effects on the life-table parameters of Nysius species. Radiofrequency exposures on species not only affected developmental period, adult weight and longevity, but also negatively affected the fecundity of subsequent generations. The total developmental period from egg to adult emergence was longer and adult longevity was shorter in the radiofrequency treatments than in the untreated control. Reduced the radiofrequency level further affected the life-parameters of Nysius species. The lowest rate of adult emergence and the shortest adult longevity both occurred at 5 kHz. The outcomes of this study are discussed in terms of targeting susceptibilities to radiofrequency as an alternative to chemical treatments.

Revising the phylogenetic position of the genera Ablattaria, Phosphuga and Silpha

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Abstract: The phylogenetic position of the genera Ablattaria Reitter, 1884, Phosphuga Leach, 1817 and Silpha Linnaeus, 1758 of the subfamily Silphinae (Coleoptera: Silphidae) is unclear and variable in different classifications. The genus Ablattaria is either classified as a sister lineage to Phosphuga and Silpha, or all three taxa are treated as subgenera of broadly defined Silpha. The genus Ablattaria contains four extant species, the genus Phosphuga two species and the genus Silpha has 22 species (with 18 species in the Palaearctic region). The genera have diverse food strategies. The genera Ablattaria and Phosphuga are specialized gastropod predators, and the species belonging to the genus Silpha are either necrophagous, scavengers or predaceous. The centre of the distribution of all genera is through Palaearctic Region, Trans-Palaearctic in Phosphuga and Silpha (with highest diversity and high endemism of the later in Nepal and China) and Western Palaearctic in Ablattaria. The relationship of the three genera was carried on collected specimens belonging to six species (P. atrata Linnaeus 1758, S. carinata Herbst 1783, A. laevigata Fabricius 1775, S. obscura Linnaeus 1758, S. olivieri Bedel 1887 and S. tristis Illiger 1798) stored in 96% ethanol in -25 °C and additional sequences available from NCBI. Three genes (two mitochondrial – 16S and COI and one nuclear – 28S) were used to uncover the phylogenetic relationship of the genera within the crown lineage of the subfamily Silphinae.

Semiochemical-based management of stored product insects: Mating disruption and mating delays

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Abstract: Current research have focused on non-chemical alternatives for the control of stored product insects with the ban of methyl bromide and the many problems associated with the use of other synthetic chemicals. Mating disruption either using synthetic sex pheromones in storage environments along with laboratory manipulated mating delays are some of the techniques investigated in this study. The effect of age at mating on the reproductive rate and longevity of the cigarette beetle, Lasioderma serricorne (Coleoptera: Anobiidae) was determined. The mating approach was disrupted by delaying the insects from mating for different time periods in days. Same age virgin male and female cigarette beetles were paired to mate soon after emergence (0 day old), or delayed from mating for 1–14 days. In another experiment, we maintained the age of the male at 0 day old and varied the age of the female from 0¬–14 days old and vice versa. Insects were observed daily for longevity and F1 progeny was recorded 7–10 weeks after set up. Progeny production generally decreased with age of adults at mating. Average developmental time, adult body size and adult dry weight for F1 and F2 generations were estimated. The number of F1 progeny produced by same age adults varied from 59 per female to 10 per female. Similarly the number of progeny decreased the longer one of the sex was delayed from mating. Findings from this study may provide biological insights on mating disruption techniques and how it may be effective in keeping populations of L. serricorne below levels that would warrant a control action.

BMSB management strategies on tree fruits in Italy

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Abstract: The brown marmorated stink bug (BMSB) is an invasive hitchhiker and a plant pest, which primarily threatens fruit and vegetable crops. Since its first discovery in Italy in 2012, it has rapidly spread throughout the country and in Europe. Recognized as a key pest of orchards since 2015, a dramatic situation occurred in 2019, when fruit production losses in northern Italy were estimated at € 588 million. Biological parameters obtained in an outdoor life table study showed it has two generations/year and high reproduction rates for both generations. Field and laboratory investigations indicate that the potential for biocontrol by native antagonists is currently quite limited. The establishment of BMSB has brought about a radical transformation of the management of the orchards, causing an impressive reversal of the trend towards sustainability. Currently BMSB control is mainly based on broad-spectrum insecticides and the maximum number of treatments allowed has doubled since 2014, resulting in disruption of existing Integrated Pest Management (IPM) programs, with an increasing negative environmental impact. The management of BMSB is particularly challenging, and chemical control has proved ineffective due to the general robustness, as well as to the high polyphagy combined with the high mobility of all instars, which result in continuous movements of insects between different host plants. More sustainable approaches to manage BMSB in fruit orchards include the use of exclusion netting systems and behaviour-based strategies such as “attract and kill” and IPM-Crop Perimeter Restructuring (IPM-CPR). However, none of these strategies proved to be both fully successful and easily applicable in different contexts.

Long-term and more sustainable management strategies include inundative and classical biological control with native and exotic antagonists, respectively. However, in European countries the use of exotic biocontrol agents is restricted by the ‘Habitats directive’. Although Anastatus bifasciatus (Hymenoptera, Eupelmidae) is the most successful native species in parasitizing BMSB eggs, augmentative field releases with this species did not lead to an effective reduction of the BMSB population.

Field surveys on naturally laid BMSB egg masses revealed a widespread presence of adventive populations of the non-native parasitoids Trissolcus japonicus and T. mitsukurii (Hymenoptera, Scelionidae) in northern Italy, Switzerland and Slovenia in 2018-2020. In 2020, in Italy, following the high negative economic impact caused by BMSB on fruit production, a decree of the Italian Ministry of Environment and of Land and Sea Protection finally authorized the use T. japonicus for the BMSB biocontrol, leading to one of the largest biological control projects ever attempted in Italy and Europe.

Reduction of unpleasant odours from HO.RE.CA. leftovers used for black soldier fly rearing

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Abstract: The larvae of the black soldier fly Hermetia illucens (Diptera, Stratiomyidae) can be reared on a wide variety of organic substrates, such as HO.RE.CA. (Hotel-Restaurant-Catering) leftovers that include heterogeneous foods: pasta, pizza, bread, rice, meat and fish scrapes, vegetables, fruits, eggshells, bivalve shells, oily condiments, spices, etc. However, during the rearing process, strong and unpleasant smells are released from the growth substrate. The present study aims at improving this undesirable aspect through the addition of materials with adsorbent properties to the feeding substrate. Finely ground grape stalks (212-500 µm), coarsely ground grape stalks (500-850 µm), activated charcoal, and zeolitite were selected for the investigation, due to their adsorbent properties.

The rearing methodology consisted in providing 300 g of HO.RE.CA. substrate to 100 young larvae and the addition of the specific adsorbent material (6% w/w). To evaluate the volatiles released by the system (consisting of: substrate, larvae and their excretion products, outcome from microbial metabolism, and adsorbent material), sampling was performed at 2, 5, 7, 9, 12, 14, 16, 19 days after larvae inoculation. The volatiles were determined using through solid phase microextraction (SPME) of head space over substrate aliquots using 27 cm3 vials, sealed with a rubber septum and a metal ring. The samples were oven conditioned at 35 °C (15 min), after which the needle of the SPME holder was introduced through the septum and the fibre exposed for 15 min.

A gas chromatograph (GC) coupled with a mass spectrometer (MS), equipped with a carbowax-like column, was used to carry out a semi-quantitative analysis of volatiles. Peak identification was performed by comparing mass spectra with those of pure reference standards and those present in software libraries (Nist 14 and Wiley).

The volatile compounds were grouped into four categories: malodorous volatile compounds (short and medium chain fatty acids, phenolic substances, and thioethers), low boiling liquids (solvents), aromatic compounds already present in HO.RE.CA. leftovers, and products deriving from various fermentation processes.

All the adsorbent materials tested showed similar aptitude to retain many of the volatile compounds responsible for unpleasant smells. Furthermore, no inhibitory effects on the larval growth were detected by adding any of the adsorbent materials, although finely ground grape stalks ensured a higher larval growth compared to the other substrates. However, this material needs to be dried, grinded, and sieved, thus worsening the life cycle assessment of the process. The actual possibility of employment therefore remains to be assessed.

Results incorporated in this publication originate from the SCALIBUR project, which received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 817788.

Evaluation of different feeding strategies of Black Soldier Fly larvae for scale-up purposes

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Abstract: The black soldier fly Hermetia illucens (L.) constitutes a particular interest for the feed, food or industry sector. Its larvae have the capacity to convert quickly and efficiently large quantities of organic waste into a protein biomass rich in fats.

This work represents a part of a European project (SCALIBUR) wherein the purpose is to obtain high quality bio-products from black soldier fly larvae (BSFL) reared on organic urban waste, in particular HO.RE.CA. (hotel-restaurant-catering) leftovers, which include: pasta, pizza, bread, rice, meat and fish scrapes, vegetables, fruits, eggshell, bivalve shells, oily condiments, spices, salt, etc. The aim of this study was to assess the best feeding strategy using HO.RE.CA. leftovers as substrate for BSFL in order to obtain heavier larvae, suitable for a scale-up perspective. Moreover, we aimed at establishing correlations between the main nutrimental components within HO.RE.CA. fresh substrates, the chemical composition of mature larvae and the content of residual substrate (frass), in comparisons with the control substrate (Gainesville housefly diet).

Three replicates were performed for each rearing strategy for both type of substrates. Therefore, for each container, 300 g of feeding substrate were provided to 100 young larvae as follows: i) all at once at the beginning of experiment, considered as day 0; ii) in two tranches, half on day 0 and half on day 3; iii) four equal tranches in day 0, 2, 4, and 6. Experiments were performed in a climatic chamber at 27.0 ± 0.5 °C and 70 ± 10% HR. Daily for 12 days, a sample of 15 larvae was collected from each container, weighed and reintroduced into the specific rearing container.

The samples of initial and residual feeding substrate were subjected to the following analytical determinations: i) ash content; ii) crude protein content (Kjeldahl); and iii) lipid content (Soxhlet), after being oven dried at 60 °C and then grinded and homogenized. The content of ashes, proteins, and lipids of mature larvae was also evaluated.

Results indicate that feeding strategy did not significantly affect larvae fed on HO.RE.CA., whereas using the control diet, the heaviest larvae were obtained by administering the substrate in four tranches. Moreover, regardless of the feeding strategy applied, the trend for larval growth followed different patterns for the two tested diets. Larvae fed on HO.RE.CA. leftovers showed a high growth between days 7-10, while larvae fed on control diet had a constant growth all over the period. Detailed results will show the chemical composition of the larvae and related substrates. The results allowed the identification of the optimal conditions for BSF larvae rearing on HO.RE.CA. leftovers.

Results incorporated in this publication originate from the SCALIBUR project, which received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 817788.

Augmentative releases of the native egg parasitoid Anastatus bifasciatus for the control of the invasive Halyomorpha halys in northern Italy

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Abstract: The invasive Brown Marmorated Stink Bug (BMSB) Halyomorpha halys (Heteroptera, Pentatomidae) is currently the most serious pest of fruit crops in northern Italy, where it caused €588 million damage in 2019. Management of BMSB is very challenging, due to its mobility and very high polyphagy. To face this threat, farmers doubled the number of treatments with broad-spectrum insecticides, seriously disrupting previous IPM programs. Biological control is the most sustainable alternative to manage invasive pests; however, legal restrictions prevented the use of exotic biocontrol agents in Italy until 2019. The generalist Anastatus bifasciatus (Hymenoptera: Eupelmidae) is the predominant species of native egg parasitoids attacking BMSB in Europe, and it is able to successfully develop on viable BMSB eggs. In order to verify the potential of this parasitoid as a biocontrol agent for augmentative releases, a first field trial was carried out at the end of July 2018, releasing 600 A. bifasciatus females at once in 0.5 ha organic pear orchard in Emilia-Romagna. Results showed an average parasitization of 16% on frozen BMSB eggs and up to 48.5% on naturally laid eggs (Stahl et al. 2019). In 2019, further trials were performed in the same region releasing the parasitoids in woody areas near IPM fruit orchards and verifying parasitization on both, fresh and frozen sentinel egg masses. Releases were performed once a week at the beginning of the BMSB oviposition period(from mid-June to early July) reaching a density of 1 female per m2. In trial 'A' (in Modena province), a total 20,000 A. bifasciatus females were released in a wooded area of 2 ha adjacent to an IPM pear orchard. In trial 'B' (in Ravenna province), 1,300 A. bifasciatus females were released in a wooden area of 0.13 ha surrounded by tree fruit crops, including an IPM pear orchard. Both trials included a control area in which no parasitoid release was performed.

In trial "A", where 11,312 eggs were exposed, average parasitism was 6% on naturally laid eggs (obtained in sleeve cages) and 1.5% on frozen sentinel eggs, with no differences between control and release areas. In trial 'B', where 7,712 sentinel eggs were exposed, in the release area average parasitism was 1.4% on the fresh egg masses (laid on Vicia faba potted seedlings) and 0% on frozen eggs; in the control area parasitism was 1.1% on fresh eggs and 2.0% on frozen ones.

Results from 2019 indicated that mass releases of A. bifasciatus were not efficient for biocontrol of BMSB under the current test conditions.

Cooperative or not? Big groups of foundresses in a quasisocial parasitoid

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Abstract: In the parasitoid genus Sclerodermus, multiple foundresses communally produce and care for broods. When hosts are large, group members have greater reproductive success than when attempting to reproduce alone. Prior studies evaluated groups of ≤10 foundresses but the natural range of group sizes is undocumented. We create groups of up to 55 foundresses and explore the consequences for the success and timing of cooperative brooding and on brood sex ratios. As group size increases, brood failures increase and per capita success decreases. Most broods fail at the early developmental stages. Foundresses competition for oviposition sites is likely as is determined by reproductive dominance and ovicide. While most foundresses likely produce some progeny, many foundresses do not produce any adult sons. Sex ratios are very biased: 10% of offspring are males. Based on this result, and a recent finding that larger and earlier-arriving females within smaller foundress groups produce most male offspring, we suggest that Sclerodermus brood sex ratios are the result of a combination of local mate competition and the dominance (via suppression or infanticide) of male production by some foundresses within what initially appeared to be cooperatively reproducing groups.

Insect-plant-soil microbial tug of war: which is the major force structuring insect- and plant-associated microbiomes?

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Abstract: Insect herbivores are a driving force in shaping plant communities and their relationship with the surrounding environment. Microorganisms are key partners of both insects and plants, influencing their development and physiology, and can modulate the outcome of plant-herbivore interactions. In this plant-microbe-insect system, a question is still open: which is the major force structuring insect- and plant-associated microbial communities? Answering this question will increase our ability to predict the effects of the environment on plant and insect microbiomes and, in turn, their influence on plant-insect relationship. Here, we tested whether soil microbiome, plant species and herbivory are able to influence insect- and plant-associated microbiomes. Using a microcosm setup, we manipulated the herbivore, plant species and soil microbial diversity, and we characterized the microbiota at different compartments: rhizosphere, roots, leaves and herbivore. We showed that herbivores drive a top-down effect shaping the microbiota of leaves, roots and rhizosphere. Furthermore soil microbiome and plant species drive a bottom-up effect that influences the microbial communities at rhizosphere, roots, leaves and, eventually, the microbiota of the herbivore. The soil-drive effect not only influenced insect microbiota, but also the insect fitness.

Effects of genetic diversity, inbreeding and outbreeding investigated in six reared biocontrol agents

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Abstract: Genetics are expected to impact phenotypic traits of biocontrol agents, and as a consequence our capacity to produce them or use them in the field. Here, we report the results of studies that investigated the effects of population characteristics (genetic diversity) or genetic processes (inbreeding, outbreeding) on phenotypic traits or population establishment in six biocontrol agents (Allotropa burrelli, Chrysoperla comanche, Cryptolaemus montrouzieri, Macrolophus pygmaeus, Psyttalia lounsburyi, Trichogramma brassicae). Sensitivity to inbreeding was studied in A. burrelli, M. pygmaeus, C. nr comanche and C. montrouzieri by comparing phenotypic traits between individuals coming from sibling crossings (inbred) or non-sibling crossings (outbred). Inbred C. montrouzieri males displayed a 7% reduced longevity. Prey consumption of C. inbred nr comanche larvae was 39% higher. Outbred M. pygmaeus individuals displayed 30% higher reproduction success. Impacts of outbreeding (intraspecific hybridization) were investigated in C. nr comanche and M. pygmaeus. Field populations were sampled and crossing experiments were carried out, with crossings within or between populations. In Chrysoperla sp., the occurrence of cryptic taxa within populations prevented from producing enough biological material to perform the experiments. In M. pygmaeus, genotyping-by-sequencing data revealed three genetic clusters mixed in the field-sampled populations. Between genetic clusters, partial reproductive isolation was observed. Within genetic clusters, female heterozygosity rates were positively correlated to the number of offspring produced. Impacts of initial genetic diversity on population establishment in controlled conditions were studied in P. lounsburyi and A. burrelli. For P. lounsburyi, population samples were imported from South-Africa and Kenya, introduced in the laboratory and monitored over several generations. A positive relationship between the population initial microsatellite allelic richness and the time before population extinction was observed. An impact of the initial Wolbachia infection status in the populations was also detected. For A. burrelli, populations were created and introduced in laboratory conditions. Extinction rates and population densities over three generations were monitored and compared between two treatments: (i) populations created from a unique isogenic line vs (ii) populations created from a mix of five isogenic lines. Although differences were observed among isogenic lines, the average growth rate of all populations started from one line was not different to that of populations started from a mix of lines. These results motivated the start of public-private projects on the management of biocontrol agent genetics. Among them, one demonstrated that isogenic lines of Trichogramma brassicae can be efficiently produced and enable higher biocontrol efficacy than previously commercially available populations.

Bio-ecology and Over Seasoning Strategy/Alternate Host Plants of the Cotton Stainer bug, Dysdercus volkeri F. [Heteroptera: Pyrrhocoridae] on Cotton in North-Eastern Nigeria

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Abstract: Field trials and survey were conducted in two cropping seasons and two locations at the Teaching and Research Farm of the Department of Crop Protection, Modibbo Adama University of Technology Yola and at the College Farm of Government Girls Secondary School Kaltungo, in Adamawa and Gombe states in 2017 and 2018 respectively. The study was carried out to determine the bio-ecology and over seasoning strategy/alternate host plants of the cotton stainer bug, Dysdercus volkeri F. (Heteroptera: Pyrrhocoridae) on cotton in the Eastern cotton of Nigeria. The week that haboured the highest population of D. volkeri in a combined analysis was at 18WAS with a number of 66.30 in 2017 and at 16WAS with 20.70 in 2018 per 10 cotton plants sampled population. The least population in both locations was recorded at 12WAS had 27.70 and 2.83 in 2017 and 2018 per 10 cotton plants respectively. Boll maturation stage supported the highest population of D. volkeri at Yola and Kaltungo in 2017 and 2018 cropping season with 89.23and the least at the beginning of boll formation with 48.34/10plants. During the survey while the cotton plants were sprayed, some crop plants and weeds were observed with high relative number of D. volkeri as an alternate host plants. This include: roselle, Hibiscus sabdariffa L.; kenaf, Hibiscus cannabinus L.; okra, Abelmoschus esculentus; rice, Oryza sativum; maize, Zea mays; pig weed, Commelina compresus; Detarium microcarpum; Jew telteria, Corchorus oliotorius Linn. and on dried leaves of groundnut, Arachis hypogeae L. as well as on the debris after harvesting cotton which encouraged the survival and spread of D. volkeri to the next cropping season. This results will give farmers an idea of some of the plants that should not be inter cropped with cotton or Malvaceae because it will increase the incidence of the pest on the cotton farms. This is a key factor that will lead towards developing an Integrated Pest Management of cotton.

Efficacy of biopesticides against cotton pests under field conditions in South Africa

Authors: Malinga Lawrence, South Africa

Abstract: Cotton is a major fibre crop grown in South Africa; and is subjected to pest attacks, which reduce its yield and profitability for farmers. Field trials were conducted in 2017 and 2018 to evaluate three biopesticides, namely, Eco-Bb®, Bb endophyte, and Metarhizium rileyi in comparison with the insecticides Chlorpyrifos® 480 EC, Karate® EC, and Bandit® 350 SC. The objective was to determine their efficacy against sucking pests, leafhoppers Jacobiella facialis, aphids Aphis gossypii, thrips Thrips tabaci, whiteflies Bemisia tabaci, red spider mite Tetranychus urticae, and cotton stainers Dysdercus spp. Karate® significantly reduced the leafhopper population and outperformed all the other treatments. Eco-Bb® and Bb endophyte did not control the aphids in 2017. However, in 2018 the best aphid control resulted from the biopesticides used. In 2017 plots treated with Eco-Bb® had the lowest number of thrips, while in 2018 plots treated with Bandit® had the least thrips, followed by treatments with M. rileyi and Karate®. There were no significant differences in the populations of whiteflies, however, insecticides were more effective than the biopesticides. All the treatments, except for Bandit®, significantly reduced the number of spider mites compared in 2017. Applications of Eco-Bb® and Bb endophyte significantly reduced spider mites in 2017, while in 2018 plots treated with Karate®, followed by M. rileyi, resulted in the lowest number of spider mites. Application of Bb endophyte, Chlorpyrifos®, and Karate® resulted in the lowest number of cotton stainers. The highest mean cottonseed yields of 6 395 kg/ ha, 6 295 kg/ha, and 6 141 kg/ha were recorded in plots sprayed with Bandit®, Bb endophyte, and Eco-Bb®, respectively. Biopesticides and chemical insecticides can be combined or alternated for future IPM programmes to control cotton pests.

Global biogeography of non-native Lepidoptera

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Abstract: Lepidoptera is a highly diverse, predominantly herbivorous insect order, with species transported to outside their native range largely facilitated by the global trade of plants and plant-based goods. Analogous to island disharmony, we examine invasion disharmony, where species filtering during invasions increases systematic compositional differences between native and non-native species assemblages, and test whether some families are more successful at establishing in non-native regions than others. We compared numbers of non-native Lepidoptera species with the land area of 11 regions worldwide. Differences among native and non-native assemblages in the distribution of species among families were investigated using ordination analysis. We tested whether invasion disharmony is explained by propagule pressure (proxied by species richness in border interceptions) and if families were associated with specific trade commodities. Much of the variation in species numbers in the native, and less so in the non-native assemblages could be attributed to land area. Although native assemblages were similar among nearby regions, non-native assemblages were not, suggesting geography had little effect on invasion disharmony. Macromoth families were generally under-represented in establishments, whereas several micromoth families were under-represented in interceptions. Invasion disharmony in Lepidoptera appears to be driven by processes unrelated to the success of native assemblages.

Early sex, short lives: effects of nutrition and selection for age of female reproduction on oxidative damage, antioxidant protection and nutrient reserves in a tephritid fruit fly

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Abstract: Life-history traits, such as lifespan or reproductive effort, are tightly correlated with the amount and blend of ingested macronutrients. In herbivorous insects, high protein to carbohydrate ratios (P:C) consistently decrease life expectancy, whereas such ratios promote female egg-laying. The physiological mechanisms behind shortened lifespan due to macronutrient intake are yet to be elucidated. The Free Radical Theory of Ageing (FRTA) was one of the most popular theories attempting to explain ageing mechanisms. The keystone of the FRTA is the equilibrium between reactive oxygen species (ROS) and antioxidant protection: if ROS exceed antioxidant protection it induces oxidative damage to cellular components, which ultimately leads to death. Although the FRTA is controversial and now considered simplistic, evolutionary biologists have shown interest in the relationship between ROS and antioxidant protection to explain trade-offs such as that between lifespan and reproduction. Because this trade-off is diet mediated, and there is evidence that oxidative damage and antioxidant protection change with dietary manipulation, all may be interconnected. In this study, we tested how dietary manipulation modulates oxidative stress balance, and whether this relationship is conserved across selection lines of the marula fly, Ceratitis cosyra (Diptera: Tephritidae) that differ in lifespan and reproductive traits. In addition, nutrient storage by flies was also assessed because it is linked with survival and reproductive performance. Flies selected for early reproduction and shorter lifespan had more oxidative damage than laboratory adapted (i.e. control flies), but also had more total antioxidant capacity than wild flies. Lipid storage, which is associated with longer lifespan, was lower in flies selected for early age of female egg-laying and similar between laboratory adapted and wild flies. Flies fed the diet promoting female fecundity suffered more oxidative damage to protein than flies fed the worst diet for lifespan, or the best diet for lifespan. Total antioxidant capacity matched the change in oxidative damage due to diet and was lowest in flies fed the diet promoting lifespan. In brief, selection for early age of reproduction increased oxidative damage and antioxidant protection, but decreased lipid reserves. Dietary related increases in oxidative damage and antioxidant protection depended on the reproductive outputs associated with the diet fed to the flies.

Wolbachia prevalence in Russian populations of Loxostege sticticalis (Pyraloidea: Crambidae)

Authors: Malysh Julia[1], Malysh Svetlana[1], Kononchuk Anastasia[1], Kireeva Daria[1] and Tokarev Yury[1], [1]All-Russian Institute of Plant Protection, Russia

Abstract: Beet webworm Loxostege sticticalis L. is a notorious pest of numerous crops of European and Asian parts of Russia, as well as Northern China. L. sticticalis L. has an eruptive type of population dynamics and high migratory activity. The outbreaks are therefore difficult to predict, and the pest belongs to the category of highly dangerous pests. However, during periods of depressions this insect is not observed within the most of its range and is very susceptible to infection by pathogens, including various species of microsporidia, some of which are not specific parasites of the order Lepidoptera. Screening of insect populations for naturally occurring parasites and pathogens is inevitable for understanding the dynamics of pest populations. In particular, obligate intracellular parasites, such as Microsporidia, play an essential role in L. sticticalis density dynamics. Withal, other intracellular symbionts in populations of L. sticticalis have not been reported yet.

Bacteria of the Wolbachia genus are widespread endocytobionts of arthropods. In certain species of Lepidoptera, Wolbachia may contribute to population biology of the hosts, as it regulates reproductive processes (including sex determination) and influence host vitality and fertility in direct or indirect ways. The knowledge of Wolbachia distribution in populations of insect pests is therefore of great interest. Here, we report the first results of screening Wolbachia infection in L. sticticalis populations.

PCR with primers specific for wsp gene fragment of Wolbachia yielded amplicons with the expected size of ~600 bp in 23 % of analyzed samples. In a single sample set collected in 2005 from Rostov Region, Wolbachia infection was detected at the prevalence rate of 8.3 %. Larvae collected in Saratov Region were Wolbachia free in 2006, but about 47 % were Wolbachia-positive in 2013. In the Asian part of Russia Wolbachia prevalence ranged from 16.7 to 40 %.

Prevalence rates of Wolbachia in insect hosts may significantly vary over time and space. For example, in pyraloid moths of the genus Ostrinia, Wolbachia was found in all examined populations in the European part of Russia, and the prevalence rates were dependent upon the species and the forage plant. We found only one strain of Wolbachia for Ostrinia and several strains for L. sticticalis. Some strains of Wolbachia from L. sticticalis are most similar to the strains from different species of Ostrinia, and others are similar to Wolbachia from beetles. Long-distance migrations are likely to provide symbiont exchange between local populations of beet webworm, and various ecological factors may also affect the diversity and dynamics of Wolbachia infection.

Sticky LED trap for pest monitoring: the European corn borer, Ostrinia nubilalis hbn. (Lepidoptera: Crambidae) as an example

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Abstract: Phytosanitary monitoring is one of the most important elements of integrated pest management (IPM). In recent years, LEDs have begun to be widely used in lighting technology, which are characterized by high efficiency, small size and long life (Schubert, 2006). Although the possibilities of using LEDs in IPM have been actively discussed for several years (e.g. Shimoda, Honda, 2013), there are few examples of their practical use in pest phytosanitary monitoring. Despite the obvious advantages of pheromone traps used for the European corn borer (ECB), Ostrinia nubilalis (Hbn.) monitoring, more and more data are accumulating that testify to certain problems that arise when using them (Cizej, Persolja, 2013; Frolov, Ryabchinskaya, 2018; Frolov, Grushevaya, 2018, etc.). Original sticky LED trap with an electronic control unit developed in the VIZR Agricultural Entomology Lab. (Miltsyn et al., 2019) was used in trials for monitoring of the ECB carried out in 2019 on maize sowings in three geographical points located at the Krasnodar Territory, namely vil. Botanika (Gulkevichi Region), vil. Kurchanskaya (Temryuk Region) and huthor Slobodka (Slaviansk Region). Pheromone traps manufactured by JSC “Shchelkovo Agrokhim” were used as standard. The number of the moths caught per one LED trap exceeded 3.7 to 12.1 times the number caught by set of three pheromone traps supplied with Z (97% of Z11-: 3% of E11-14:OAc), E (1% of Z11-: 99% of E11-14:OAc) and ZE (35% of Z11-: 65% of E11-14:OAc) pheromones of the ECB races. Unlike pheromone traps catching only males, LED traps attracted also females: their percentage ranged from 7 (Kurchanskaya) up to 49% (vil. Botanika) of the total number of moths caught. Trials in the vil. Botanika showed that though LED and pheromone traps registered the beginning of the ECB flight in the same date, the peak of moth catching by LED traps was strongly displaced by the beginning of flying period, for a week preceding the beginning of oviposition by females. The peak of male capture by pheromone traps was noted a week later after achievement of a maximum of egg-laying activity by females. Provided that LED traps installed inside the maize planting, they caught a small number of entomophages. In 2020 we are going to conduct extensive trials of LED traps for monitoring the pest in various ecological zones of the country. The research is supported by RFBR No 19-016-00128.

Overview of vibratory communication applications for pest management

Authors: Mankin Richard, USDA Agricultural Research Service, United States

Abstract: Detection of mechanical vibrations is one of the oldest, most widely used of the insect senses, and more insects employ vibrational communication for courtship and for predator avoidance or prey detection more than they employ acoustic, chemosensory, or visual communication. We consider several examples in Hemiptera, Coleoptera, Lepidoptera, Termitidae, and Hymenoptera where detection of pest insects or disruption of courtship has been used for pest management applications.

Acoustic Detection of Hidden Invasive Pests: Progress on Development of Inexpensive, User-friendly Detection Systems

Authors: Mankin Richard[2] and Rohde Barukh[1], [1]University of Florida, United States, [2]USDA Agricultural Research Service, United States

Abstract: Early, rapid detection methods are important to amplify the effectiveness of management programs against invasive species attacking food crops, ornamental crops, and forests. Hidden infestations of pest insects in stored products, trees, and soil are particularly difficult to detect. Red palm weevils, for example, spend most of their lives inside the trunks or crowns of palm trees and typically cause extensive harm to trees before they are discovered; consequently, infested trees often are transported to uninfested areas. Acoustic detection is a useful method for early detection of red palm weevil infestations and has also been applied against stored product and soil dwelling insect pests. The cost and user-friendliness of acoustic insect detection systems has limited its usage, but new detection systems and interfaces are being developed. Here we present an overview of some of new systems under development that may come into more general use for early detection of invasive insects over the next decade.

Over and over (again): Repeated evolution of co-obligate symbioses across aphids

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Abstract: Aphids are a large group of animals comprising 4,000+ currently described species. This group of sap-sucking insects depend on the Gammaproteobacteria Buchnera aphidicola for the provision of essential amino acids and some B vitamins. However, recent evidence has demonstrated that in some cases, the typical aphid-Buchnera association has evolved to incorporate yet another obligate symbiotic partner. These new associates complement their Buchnera partner, which have lost the capacity to synthesise compounds essential for their nutritional complementation role. These multi-partner associations occur not only in aphids, but also in several other insect taxa. However, we still know little about the way these associations evolve and which role, if any, they might play in the adaptation of their hosts. Through the use of high throughput NGS, we have explored the existence and nutritional roles of such multi-partner associations across aphids. We have explored tissue tropism in selected species and revealed repeated patterns of symbiont localisation across species. In addition, these explorations have revealed that these associations are more common than previously thought, and that, based on a newly resolved phylogeny for Aphidinae based on Buchnera sequences, they have evolved not once, but multiple times throughout the evolutionary history of their aphid hosts.

Molecular Study on field evolved Resistance of Red Palm Weevil (Rhynchophorus ferruginous) and Its Management through RNAi

Authors: Manzoor Mujahid, Institute of Agricultural Sciences, University of the Punjab, Lahore, Pakistan, Pakistan

Abstract: Molecular and proteomic study was conducted on field evolved resistance of Red Palm Weevil (Rhynchophorus ferruginous) against Parathyroid group of insecticide (Cypermethrin). Cytochrome P450 genes have been associated with insecticides resistance. Field collected population of R. ferruginous from different provinces of Pakistan was investigated for insecticides resistance development against P450 gene. Insect bioassay indicated highly significant level of LC50 values among laboratory reared and field collected population against Cypermethrin. The laboratory reared resistant population, Sindh and South Punjab collected population showed high LC50 values as compared to susceptible, Baluchistan and KPK population. The expression of P450 gene through PCR showed enhanced level of P450 gene in different Instars as well as collected population. The dsRNA specific for CYP450 gene was designed and

targeted through dsRNA in thoracic region of R. ferruginous through micro-injection. Gene expression and proteomic study confirmed the down regulation of P450 gene and associated protein in dsRNA treated

population. The application of ds RNA specific for CYP450 also reduced insecticide resistance in R. ferruginous. The developmental parameters were highly affected in RPW treated with dsRNA as compared to control samples treated with water or dsGFP. These results support the RNAi application as a suitable tool for the management of insecticide resistance and control of R. ferruginous.

Intensity Prediction for Aerial Animal Migration Based on Weather Radar Network

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Abstract: Weather radar networks now enter an exciting stage for monitoring large-scale aerial animal migration with rapid developments of bio-echo extraction, biomass quantification, scientific researches, etc. For migration intensity prediction problem, we propose a novel method for weather radar network by taking spatial and temporal correlations of migration intensity into account. The weather radar network is modeled as a graph, and the graph convolution is applied to utilize the spatial correlation among different radars. Then recurrent neural network extracts the temporal correlation along the time axis and predicts the bio-echo. Our method is evaluated by the dataset collected from 40 weather radars in China, and achieves the coefficient of determination with 0.77.

Generic approach for the development of genetic sexing strains of the codling moth for SIT applications

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Abstract: Sterile Insect Technique (SIT) has become an important component of area-wide integrated programs to control several major lepidopteran pests, including codling moth (Cydia pomonella). One of the most successful SIT applications is the Okanagan-Kootenay Sterile Insect Release (OKSIR) program to suppress codling moth populations in the Okanagan Valley, British Columbia, Canada. Currently, this program, like other lepidopteran pest control programs using SIT, relies on bisexual releases. Male-only releases could significantly reduce costs and increase efficiency of SIT. However, a suitable genetic sexing system for producing male-only offspring is not yet available for any lepidopteran pest. We develop generic strategies for the construction of genetic sexing strains in codling moth using two approaches: (1) inserting a dominant conditional lethal mutation into the female-specific W sex chromosome using the CRISPR/Cas9 method to abort the development of female embryos, and (2) identifying genes involved in sex determination with the aim to find new possibilities for genetic sexing. Here we present the results obtained so far and our progress in achieving the objectives in both approaches.

Large scale drivers of bark beetle population outbreaks across Europe

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Abstract: Bark beetles are among the most destructive biotic agents affecting forests globally and population dynamics of several species are expected to be boosted by climate change. Given the potential interactions of bark beetle outbreaks with multiple biotic and abiotic disturbances, and the potentially strong impact of changing disturbance regimes on forest resources, investigating climatic drivers of destructive bark beetle outbreaks is becoming of paramount importance. Here, we analysed 17 time-series of the amount of forest damaged by the European spruce bark beetle (Ips typographus L.) collected across Europe in the last three decades. We aimed to quantify the relative importance of key climate drivers in driving population outbreak dynamics testing whether abiotic disturbance such as wind or snow storms synergistically enhanced outbreak propensity when coupled with drought and temperature warming. We found that regional outbreaks shared the same drivers, including increasing summer rainfall deficit and warm temperatures. Large availability of storm-felled trees in the previous year increased spruce bark beetle damage, likely by providing an alternative source of suitable breeding material. We did not find any positive synergy among outbreak drivers. On the contrary, the occurrence of large storms cancelled the effect of warming temperatures and rainfall deficit, suggesting that the large surplus of breeding material likely boosted bark beetle population size above the density threshold required to colonize and kill healthy trees irrespective of the climatic conditions. Across Europe, we found a strong direct negative density dependence that lead the population to decline after demographic outbreaks. The generality in the effects of the abiotic drivers observed across different geographical areas suggests that the large-scale drivers can be used as early warning indicators of increasing local outbreak probability. In conclusion, European spruce forests are expected to become increasingly susceptible to bark beetle outbreaks under global change with important economic and ecological consequences for forest ecosystems. However, in most of the situations the negative density feedback seems to be a natural regulating mechanism that impedes a long-term propagation of the outbreaks.

Edge lineages in Orthoptera (Xyronotidae and Tanaoceridae): current status and challenges

Authors: Marino-Perez Ricardo, University of Michigan, United States

Abstract: Family Xyronotidae consists of four species, they are unique and relict lineage (its closer relative is endemic to Southeast Asia) found in cloud forest in the states of Veracruz, Oaxaca and Chiapas, Mexico.

Family Tanaoceridae consists of three species, they are unusual and relict lineage with a very restricted distribution in desert habitats in southwestern USA (California and Nevada) and northern Mexico (Baja California). They are small, wingless and are unique in all grasshoppers in having long and filiform antennae (longer than the entire body itself).

Both families are relict lineages, evolutionary distinct from their closest relatives, possess unique stridulatory structures and have very narrow distributions threatened by land conversion. Both taxa are priorities (targets) of the Grasshopper Specialist Group and here we discuss new and valuable information from recent expeditions sponsored by a SSC EDGE Internal Grant. Now, we will be able to provide precise IUCN assessments that will help stakeholders to take decisions to protect their habitats. People from Mexico and USA will be benefit as well as humanity in general because two EDGE lineages will be better understood.

Lathiceridae, Lithidiidae and Schizodactylidae in Southern Africa: current status and challenges

Authors: Marino-Perez Ricardo, University of Michigan, United States

Abstract: We present the status of these three enigmatic groups from literature and recent field trips to arid regions in South Africa and Namibia.

Trade in ornamental plants - Which associated species may become significant pests of Nordic coniferous forests?

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Abstract: In a recently published study we screened plant pests potentially associated with the trade of ornamental plants to identify pests that could pose a high risk to the coniferous forests of Finland, Sweden and Norway. Specifically, our aim was to find pests that potentially could fulfil the criteria to become regulated as quarantine pests. We used an approach developed by EPPO for commodity studies, which includes several steps of screening. From an initial list of 1062 pests, 65 pests were identified and ranked using the FinnPRIO pest risk ranking model and the hypervolume approach, which resulted in a top list of 14 pests namely Chionaspis pinifoliae, Coleosporium asterum s.l., Cytospora kunzei, Dactylonectria macrodidyma, Gnathotrichus retusus, Heterobasidion irregulare, Lambdina fiscellaria, Orgyia leucostigma, Orthotomicus erosus, Pseudocoremia suavis, Tetropium gracilicorne, Toumeyella parvicornis, Truncatella hartigii and Xylosandrus germanus. In the next step we, jointly with EPPO, conducted full pest risk assessments according to the International Standards for Phytosanitary Measures for two of the pests in the top list, namely white-marked tussock moth (Orgyia leucostigma) and pine needle scale (Chionaspis pinifoliae). The results of these assessments provide support for decisions within the EPPO-region on whether the assessed pests should be regulated as quarantine pests.

Host plant condition determines the abundance and composition of herbivorous insect communities on urban maple trees (Acer spp.)

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Abstract: Maple species (Acer spp.) are among the most common urban trees throughout North America and Europe. Sycamore (Acer pseudoplatanus), Norway (A. platanoides) and field (A. campestre) maple are native to Central Europe and commonly planted in urban areas. On the one hand, all the three maple species support large diversity of herbivorous insect species with different degrees of host plant specialization. On the other hand, the ecological requirements of the three maple species are different, and therefore they tolerate urban stress to varying degrees. In this study, we examined how these two factors (host plant identity and condition) affect the abundance of insect pests and composition of herbivorous insect community in the canopy of maple trees, and how the studied maple species support urban biodiversity.

The study was carried out in the city of Budapest, Hungary. We selected four study sites in urban environment (Arboretum of Buda, Gellért Hill, streets around the Buda Campus of Hungarian University of Agriculture and Life Sciences, and Alkotás street), each with sycamore, Norway, and field maple trees of roughly the same age and in close proximity to each other. Insects were collected from the canopy of the trees by the beating method for two years. We also examined the stress level [expressed as peroxidase (POD) enzyme activity], and physiological condition (expressed as degree of leaf necrosis and leaf fall) of the maple trees, and their relationship to herbivore abundance. We found that in urban environment field maple trees were in the best and Norway maple trees in the worst condition. The abundance of the herbivorous insect community was similar in the canopy of field maple and sycamore and was significantly lower in the canopy of Norway maple. Most herbivorous insect species were associated with field maple, sycamore had the highest aphid densities, while Norway maple not only had the lowest abundance but also the harboured the least specific herbivorous insect community. The super-abundant planthopper species, Metcalfa pruinosa positively affected the POD activity of trees, but did not influence their condition. On the contrary, M. pruinosa abundance was driven by tree condition, with higher numbers on healthier trees.

Our findings suggest that the abundance of phytophagous insects in the canopy of maple trees is highly determined by tree condition, and in this study field maple had the highest and Norway maple the lowest tolerance for urban stress.

This research was supported by the NKFIH (K-129311).

RNAi studies with stink bugs: from basic science to agricultural losses

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Abstract: Brazil is the second largest producer of soybean, Glycine max (L.) in the world. However, $ 6 billion is lost each year due to the action of pests. From this amount, about one third is caused by true bugs, and Euschistus heros (F.) (Hemiptera: Pentatomidae) plays a central role in this financial impact. Traditional methods based on pesticides generate annual expenses of R $ 8.5 billion and still E. heros is one of the main causes of agricultural losses in soybean. In addition, constant applications of pesticides can cause environmental contaminations and the emergence of pest resistance to insecticides. RNAi technique is one of the best molecular tools to reduce the function of genes in eucaryotes. The beetle Tribolium castaneum (L.) has been deeply studied using RNAi to understand its embryology, metamorphosis, behavior, etc. In model organisms such as this beetle and nematode, RNAi has proven to be highly efficient and specific to knock down virtually any gene. By choosing a gene with essential function for the organism, RNAi can be used to induce mortality of the target organism and has become a valuable alternative for agricultural pest control. The present work identifies silencing molecules capable of inducing mortality in E. heros, by targeting genes essential for the insect survival. The tests were carried out by means of microinjections in the ventral region of the animal, using different concentrations and combinations of target genes. Insect mortality was checked every 24 hours and the level of gene expression was evaluated by qPCR 12 and 24 hours after microinjections. We showed that mortality rates of up to 78% can be obtained 72 hours after injections and the effect was dose-dependent. Also, combining silencing molecules resulted in an increment of the mortality rate to about 85% after three days. These mortality rates happen concomitantly to reductions of expression of the target genes of about 86%, for the individual assays, and up to 98% when silencing molecules are combined. These results highlight the high efficiency of the RNAi technique by means of a gene pool in the control of this major pest of soybean in a sustainable, specific, and innovative way.

History, Status and Future of Bioprotection (Biocontrol)

Authors: Marrone Pamela, Marrone Bio Innovations, United States

Abstract: There is a long history of using microorganisms, pant extracts, biochemicals and other natural substances as the basis for creating new pesticides, but there is still a relatively low percentage of naturally-derived pesticides relative to the percentage of pharmaceuticals derived from natural sources (>50% vs 11% for pesticides). Biologicals for pest management, called biopesticides, biocontrol or bioprotection have been around for seventy years, starting with there bioinsecticide from Bacillus thuringiensis (Bt). They are now experiencing rapid growth as the products have better efficacy, are more science-based and there are more restrictions on synthetic chemical pesticides driven by consumers' requirements for sustainability and transparency of our food supply. Still, biopesticides are still a small percentage (approximately US $3-4 billion) of the US $60 billion chemical pesticide market. Growth of biopesticides is projected to outpace that of chemical pesticides, with compounded annual growth rates of between 15-20%. When integrated into crop production and pest management programs, biopesticides can offer the potential for higher crop yields and quality than chemical-only programs. Added benefits include reduction or elimination of chemical residues, therefore easing export, delay in the development of resistance by pests and pathogens to chemicals, shorter field re-entry, biodegradability lower carbon footprint, and low risk to non-target organisms, including pollinators. Challenges to the adoption of biopesticides include lack of awareness and education in how to deploy their unique modes of action in integrated programs, testing products alone versus in integrated programs, and lingering perceptions of cost and efficacy.

Towards a macroecology of "the little things that run the world"

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Abstract: A key aim of macroecology is to quantify and predict how Earth's great abiotic drivers--temperature, precipitation, and biogeochemistry--govern how ecological communities of individuals and species vary from place to place. Community data at continental extents are sparse and restricted to a few taxa. They vastly underrepresent the terrestrial arthropods--perhaps the most diverse and abundant animal group--in part due to the immense effort required to count, size, and identify ground-dwelling arthropod taxa. Here we present a project that aims to address this gap by the analysis of samples from the NEON pitfall network (arrays of traps, sunk in the soil, that capture and store biweekly samples of arthropods in ethanol). We are developing two complementary methods to do so. First, we are developing an environmental barcoding pipeline to identify pitfall taxa from extracts of ethanol. Secondly, we are developing an image analysis pipeline that uses machine learning to count, size, and classify arthropods in a sample. Pitfall samples containing key orders of Earth's arthropods will be analyzed from NEON's 47 sites throughout the United States. Here we present our current work on the image analysis pipeline, including a framework and working machine learning models for insect identification. This project represents an opportunity to collect standardized field data from entire communities of ground dwelling arthropods, and to test macroecological theory at continental scale.

Overcoming the barriers: the case study of Bagrada stinkbug and its egg parasitoid for biocontrol purposes

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Abstract: For any egg parasitoid that aims to find host eggs in the environment, synchronized climatic suitability, foraging time allocation, and egg availability are the main issues for achieving success. These three components can be considered as barriers that only coevolved parasitoids can overcome. Among invasive stinkbugs in North America, Bagrada hilaris Burmeister (Hem.: Pentatomidae) possesses specific biological and behavioral traits, including high thermal development requirements, strong population variations in the field, and a unique oviposition behavior among the Pentatomidae. The objectives of the current study were to evaluate the capacity of a Pakistanis' biocontrol parasitoid candidate, Gryon gonikopalense Sharma (Hym.: Scelionidae), to cope with the different above mentioned bagrada behavioral and biological parameters. Originating from Asia and Africa, B. hilaris was first reported to be invasive in California in 2008. Since this time, this severe invasive pest of crucifer crops has expanded its range into several southern U.S. states and South America. Within the context of a biocontrol program, we examined the life history traits of G. gonikopalense, with focus on its suitability as a potential candidate for a field-based B. hilaris biological control. The first barrier to overcome for G. gonikopalense was for it to develop, reproduce and survive within the same climatic range as B. hilaris, or even beyond. Laboratory studies showed G. gonikopalense's ability to complete its life cycle between 15 and 35°C, which is perfectly consistent with bagrada thermal development requirements. The second barrier was to ascertain that G. gonikopalense was able to live long enough for successful parasitization of B. hilaris after an extended period of host deprivation. Our results showed that G. gonikopalense could easily live more than 2 months and still be able to parasitize B. hilaris eggs. These data indicate that adult parasitoids could survive when host populations decrease in the field (winter and summer periods in California's coastal regions) and still be able to parasitize eggs once bagrada start to build up field populations (late winter and autumn periods in California). Finally, we tested the response of G. gonikopalense to the unique bagrada oviposition behavior, as females lay eggs individually and naturally bury them in the soil. This oviposition strategy theoretically limits access to natural enemies. After showing that more than 80% of B. hilaris were buried in the soil, with either broccoli or mustard host plants, we exposed G. gonikopalense females to naturally buried eggs in a quarantine laboratory. Results showed up to 90% successful parasitism of buried eggs. Collectively, these results on the biology and behavior of G. gonikopalense supported a strong co-evolution and synchronization with B. hilaris, and are therefore promising for its use within the framework of an importation biocontrol program in California, and beyond.

On size, time and hormones: Control of postembryonic development by the metamorphic gene network

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Abstract: Stage identity and progression in hemimetabolous and holometabolous insects is controlled by the regulatory activity of the temporal identity factors Krüppel-homolog 1 (Kr-h1), Ecdysone inducible protein 93F (E93), and Broad-complex (Br-C; also known as broad), which conform what we have called as the "Metamorphic Gene Network" (MGN). The sequential expression of these three factors during development is controlled by the interplay between ecdysteroids -20-hydroxyecdysone (20E) being the most active form- and juvenile hormones (JH), produced by the prothoracic glands and the corpora allata glands, respectively. Whereas the anti-metamorphic component of the MGN is exerted by Kr-h1, E93 acts as the metamorphosis-triggering factor as well as the adult specifier, and Br-C functions as the pupal specifier in holometabolous insects. However, the occurrence of important changes in the MGN functioning in the highly derived D. melanogaster reveals the degree of plasticity that the MGN can provide to the developmental program. Here, we present our new data on the regulation and function of these key temporal identity genes during the metamorphosis of D. melanogaster, thus contributing to a better understanding of the molecular basis of insect development and the evolution of insect metamorphosis.

Genotype influence in potato aphid (Macrosiphum euphorbiae) response to an aphid parasitoid

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Abstract: The potato aphid (Macrosiphum euphorbiae) is an economically important pest of strawberry crops. The withdrawal of insecticides and incompatibility of others to pollinators and biological controls of pests found within strawberry crops has increased reliance on aphid parasitoids and predators for the management of this pest. However, the recent description of innate resistance to a parasitic wasp (Aphidius ervi) in some populations of M. euphorbiae feeding on potato could reduce the effectiveness of biological control programmes used for this pest in strawberry crops. As it is not yet known if the parasitoid-resistant genotype of M. euphorbiae also infests strawberry crops, experiments have been developed to identify the different genotypes of potato aphid present in strawberry crops. This work uses aphids sampled from different geographical locations in the UK and microsatellite information is used to genotype these aphid populations. The susceptibility of these populations to A. ervi is then recorded using laboratory bioassays. Together this information informs on the likely effectiveness of biological control programmes based on releases of A. ervi for control of potato aphids in strawberry crops.

Health status of Eucalyptus nurseries in Uruguay

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Abstract: Nurseries are the source of seedlings and clones for the growing Eucalyptus- based pulp and timber industry in Uruguay. Annual production reaches 100 million Eucalyptus plants and it is conducted by 30 nurseries, although three of them account for more than 70% of the plant production. In the nursery, plants may exhibit health issues derived from the particular environment provided by the greenhouses, which differ from the conditions they will experience later in the plantation. The optimal temperature range, water supply, and light that benefit plant growth also promote the occurrence of several organisms that inflict damage to the plants and poses health risks to the future plantations. Herbivorous arthropods also benefit from a constant supply of fresh plant tissue, which may lead to outbreaks in certain moments of the year. Apart from this health issues directly derived from the conditions of the nurseries, several eucalypt pests can start multiplying inside the nursery and from there they can disperse into the plantations, such as the blue gum chalcid or different species of psyllids.

We started a seasonal survey on eucalypt nurseries in Uruguay aimed at assessing the main sanitary problems affecting plants in the early stages of development. Eleven nurseries were selected, accounting for the variation in size, production and geographical situation. All of them were visited each three months for two years. Plants were assessed for disease or insect attack randomly along transects inside greenhouses. Insect and plants exhibiting disease symptoms were collected for diagnosis in the laboratory. A set of five yellow and five blue sticky traps was hung in the rearing and in the hardening sector for 15 day on each visit. Additional insect collection was made by sweep net sampling. Collected insects were preserved dried or in 70% ethanol solution. Voucher specimens were additionally preserved in absolute ethanol for further DNA analysis. All specimens were identified to species level.

We share results from the first sampling year. Mites were the most frequent problem related to arthropods in the clonal gardens, followed by the greenhouse whitefly and caterpillars from several species. Although diseases were more frequent than insect-related issues in the rearing and hardening areas, we found several species of psyllids, aphids, and lepidopterans attacking plants; the attacks showed seasonal and geographical variability. The incidence of the blue gum chalcid or psyllids inside the nurseries was lower than expected. Several dipteran species occurred in the greenhouses; we are currently assessing the role of the different species of flies in the dispersion of pathogens within greenhouses. Beneficial insect fauna was also recorded in the different nursery sectors.

These preliminary results allow us to sectorise and prioritise health problems in eucalypt nurseries, as well as to improve current pest management strategies or to tailor new ones.

Root mutualistic microbes drive plant-insect interactions at multiple trophic levels

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Abstract: Trichoderma and arbuscular mycorrhizal (AM) fungi are widespread soil inhabitants that establish symbiotic interactions with the vast majority of terrestrial plants conferring positive effects on growth and fitness. Several studies indicate that they can affect plant-insect interactions, still the mechanisms involved remain obscure. In our lab, we used a systems biology approach, integrating transcriptomics and metabolomics data with performance and behavioral studies, and functional analyses, to identify novel key molecular traits driving the impact of Trichoderma and AM fungi on the interaction of tomato plants with the insect herbivores Manduca sexta and Spodoptera exigua. Bioinformatic analyses with the integrated data sets highlighted the differential regulation of networks of components related to antiherbivory responses triggered by the mutualistic fungi. Accordingly, root inoculation with the microbial symbionts strongly altered the dynamics of the plant-herbivore interaction by negatively affecting the insect performance. Moreover, the fungal symbionts increased the performance and host preference by the parasitic wasp Cotesia congregata, by affecting the blend of volatiles released by the plants, indicating that the effect of root symbionts on herbivores escalates up to further trophic levels.

Bird-biting Culicoides: host location, feeding patterns and avian blood parasite transmission

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Abstract: Biting midges of the genus Culicoides are one of the most important insect vectors involved in the transmission of a number of pathogens affecting humans, livestock and wildlife. Nowadays, most studies have been focused on the role of Culicoides species for the transmission of pathogens affecting livestock such as bluetongue virus, while their role in the transmission of parasites affecting wildlife have been comparatively poorly studied. In this talk, we present results from our field studies on the feeding patterns and host location of Culicoides species in southern Europe. In addition, we identify the role of bird-biting species including Culicoides circumscriptus and C. paolae for the transmission of blood parasites affecting wild birds, as is the case of avian malaria-like parasites of the genus Haemoproteus.

Controlling silverleaf whitefly (Bemisia tabaci) using kaolin: an integrated IPM approach

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Abstract: The silverleaf whitefly, Bemisia tabaci (Gennadius), has become a major pest in Florida, causing serious losses to many specialty crops including tomatoes and cucurbits. These whiteflies damage plants directly by phloem-feeding on crop foliage but also indirectly by transmitting at least 50 types of geminiviruses. Despite intensive control efforts, whiteflies remain a difficult pest to manage due to their wide host range and ability to easily switch feeding between vegetable hosts and surrounding weed hosts. In order to develop more economic management strategies, kaolin clay was tested as a whitefly repellent in association with limonene, a natural plant-based repellent. Both nymph and adult populations were surveyed in both a tomato and watermelon field trials conducted during the fall 2019 season in Quincy and Live Oak, Florida, respectively. The field trials were arranged using a randomized block design which included a limonene only treatment, kaolin only treatment, mixed limonene/kaolin treatment, and a control. It was found that tomatoes and watermelon treated with a kaolin/limonene mixture had a three to four-fold reduction in B. tabaci adult populations compared to controls and a two to three-fold reduction compared to both kaolin and limonene only treatments. Total quality weight of tomatoes harvested from kaolin/limonene treatments was also higher by two-fold compared to controls. Whitefly repellency to kaolin depends on its varying synergistic effects with additional repellents and demonstrates the potential for use in an integrated IPM strategy by lowering both the amount of conventional insecticides used and frequency of spraying for effective whitefly control.

Use of semiochemical and visual cues to control ambrosia beetles and laurel wilt spread.

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Abstract: Laurel wilt disease is a devastating vascular disease of plants within the family Lauraceae that includes redbay (Persea borbonia) and avocado (Persea americana). The redbay ambrosia beetle, Xyleborus glabratus is the vector of the pathogenic fungus Raffaelea lauricola that causes laurel wilt. Currently, the vector and the disease are spreading rapidly westward throughout the southeastern United States. Laurel wilt has killed over 1 million trees throughout the region and has caused significant loss to avocado production in southern Florida. If X. glabratus is the main vector of the laurel wilt pathogen in redbay, X. glabratus is rarely found in Florida avocado groves with Laurel wilt. Multiple exotic and native ambrosia beetle species found in Florida avocado groves have been found carrying R. lauricola and some species shown to be capable of transmitting the disease to avocado.

We first tested verbenone as a potential repellent for Xyleborus glabratus and ambrosia beetles found in avocado groves. The results of the field trials on avocado and redbay demonstrated that trunk application of verbenone reduces landing rates of ambrosia beetles. Subsequently, our team developed a trap using visual and odor to capture ambrosia beetles. Our trap associates visual and odor cues used by ambrosia beetles to locate their host. Ambrosia beetles use both host volatiles and bark reflectance characteristics to discriminate against non-host trees. Visual cues used in our trap are based on previous study demonstrating that ambrosia beetles are attracted toward the silhouette of trees. The trap was tested with three different colors and two odor sources. Our trap has been tested successfully in forest and avocado groves in north and south Florida, respectively. Visual traps and verbonene lures have been combined in a push-pull system in forest that significantly reduced the number of ambrosia beetles landing on redbay. Using a combination of visual and odor cues may allow for a better control of Laurel wilt and its vector.

Specificity of Pathogen-Induced Plant Volatiles from Two Viruses to Vectoring and Non-vectoring species of Flower Thrips

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Abstract: Insect-vectored plant pathogens are known to alter host-plant quality and associated cues, which subsequently affect the frequency of interactions with the vector and can influence pathogen transmission. Following infection, pathogen-induced changes in the host plant may result in direct effects on the vector such as increased survivability, fecundity, and altering feeding behaviors or indirect effects through host-mediated cues including plant nutrients, changes in plant morphology, and release of pathogen-induced plant volatiles (PIPVs). It is unknown if these PIPVs deliver information highly specific to the vector and have evolved as a result of host manipulation, or if they are a more generalist indicator of plant status. We investigated the response of two thrips species, the western flower thrips, Frankliniella occidentalis Pergande, the vector of the tospovirus tomato spotted wilt virus (TSWV) and a non-vectoring species, the eastern flower thrips, F. tritici Fitch. Both species compete within the same flower in tomatoes and may respond differently to PIPVs. Additionally, both species were exposed to PIPVs of the Begomovirus tomato yellow leaf curl virus (TYLCV) transmitted by the sweet potato whitefly, Bemisia tabaci Gennadius, to determine how specific these responses may be. Frankliniella tritici did not respond to pathogen-induced volatiles. F. occidentalis; however, was attracted to both TSWV and TYLCV-infected plants. Volatiles from TSWV- and TYLCV-infected plants were collected, and plant volatiles were identified using GC-MS. Principal component analysis of the volatiles showed a clear differentiation between the volatiles of the uninfected and infected tomatoes. There was, however, no differentiation in volatiles between the two virus-infected tomatoes, suggesting that PIPVs from both viruses elicit a generalist response in F. occidentalis absent in the non-vectoring species and are likely not the result of host manipulation.

Leaf-mining moths (Lepidoptera: Gracillariidae) as important invasive pests of deciduous trees in urban and suburban areas in Russia

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Abstract: Gracillariidae might be considered as unique example of a case when several species from one family simultaneously and during a relatively short period (late 20th and early 21st centuries) increased their invasiveness.
In Russia, the following species expanded their ranges and became pests: Parectopa robiniella (Clemens, 1863), Macrosaccus robiniella (Clemens, 1859), Caloptilia roscipennella (Hubner, 1796), Cameraria ohridella (Deshka et Dimic, 1986), Phyllonorycter issikii (Kumata, 1963), Phyllocnistis citrella (Stainton, 1856), and Acrocercops brongniardella (F., 1798). Secondary ranges of P. robiniella, M. robiniella, C. roscipennella, and Ph. citrella are relatively small in Russia because these species feed on thermophilic tree species common only in southern Russia: P. robiniella, M. robiniella develop on Robinia pseudoacacia L., C. roscipennella – on Juglans regia L., and Ph. citrella – on citrus.
Phyllonorycter issikii and C. ohridella quickly formed wide secondary ranges in Russia. Phyllonorycter issikii is currently distributed over almost the entire range of lime Tilia spp. in Russia. In St. Petersburg and Leningrad Region (the northern border of the lime range), it was noted for the first time in 2000. A slight increase in population density of this species was observed in 2002, 2008, and 2013 and 2018. Tilia × europaea L. and T. cordata Mill. are the most severely damaged hosts of this species in the region. In Russia, C. ohridella, an invasive pest of Aesculus hippocastanum L., was first recorded in 2013 in St. Petersburg. Already in 2014, damage caused by this pest became noticeable in St. Petersburg. Its secondary range is rapidly expanding east- and northward. In 2019, the species was recorded in Vyborg (north of the Karelian Isthmus) and, apparently, reached the range limit of A. hippocastanum.
Acrocercops brongniardella was first recorded in St. Petersburg and its environs in 2018. In 2019, single mines of this species on the leaves of Quercus robur L. were found in all parts of the city and its environs. It should be noted that the northern limit of the oak range lies in St. Petersburg.
Phyllonorycter populifoliella (Treitschke, 1833) (Lepidoptera: Gracillariidae), started to appear on poplars in St. Petersburg only in the second half of 20th century. First large-scale breeding outbreak of this species began in 1991, and the second in 2017.
The successful development of the third generation of C. ohridella and the second of Ph. populifoliella was recorder for the first time in 2021 due to extremely high temperatures in June and July.
Thus, at the beginning of the 20th century at least six species of Gracillariidae became significant invasive species in Russia. The invasive ranges of three species (P. issikii, C. ohridella, and A. brongniardella) have reached the northern range limits of their host plants.
The research was funded by the Russian Science Foundation, project № 21-16-00065

Bioefficacy of powder and ash of Carica papaya seed against Sitophilus zeamais

Authors: Mary Atere Bukola[1] and Ejemen Idoko Joy[1], [1]Department of Crop, Soil and Pest Management, Federal University of Technology Akure, Nigeria

Abstract: The study investigates the efficacy of powder and ash of Carica papaya seed on Sitophilus zeamais regarding mortality, adult emergence, seed weight loss, weevil perofration index and seed viability. C. papaya seeds were air-dried and ground to obtain the powder. Pulverized C. papaya seeds were heated in a muffle furnace and maintained at 5500C for four hours to obtain the ash. Doses of the powder and ash were applied solely at 0.2, 0.4, 0.6, 0.8 and 1.0g rates per 20g of maize grains and the untreated grains served as the control. Each experiment was replicated thrice. Insect mortality increased at higher concentrations of the powder. C. papaya seed ash and powder at 1g application rate were most effective at controlling S. zeamais evoking 56.7% and 66.7% mortality respectively after 96hrs of exposure and significantly reduced the number of emerged weevils in stored maize grain. The Weevil Perforation Index of maize grains treated with C. papaya seed ash ranges between 6.9 and 29.8 when compared to the control experiment. The effectiveness of the powder and ash of C. papaya seed in reducing damage caused by S. zeamais infestation during storage was proved in this work. Therefore powder and ash of C. papaya seed could be used as a substitute to synthetic insecticides.

Mosquito-borne arbovirus survey at hospitals and livestock markets: Concurrent detection of sindbis virus and insect-specific flaviviruses in culicine mosquitoes

Authors: Masiga Daniel[1], Chiuya Tatenda[2], Bastos Armanda[3], Fevre Eric[2], Villinger Jandouwe[1], [1]International Centre of Insect Ecology and Physiology (ICIPE), Kenya, [2]International livestock Research Institute (ILRI), Kenya, [3]University of Pretoria, South Africa

Abstract: Aedes aegypti and Culex pipiens complex mosquitoes are prolific vectors of the major arboviruses presenting a global threat to human and animal health. Due to increased globalisation and travel these viruses have been able to propagate across country borders causing epidemics. Vector control is therefore an important in mitigating the effects of arboviral diseases and recently research focus has been on the use of insect-specific flavivirus (ISFs) that naturally infect Aedes and Culex mosquitoes as potential regulators against infection with pathogenic arboviruses. Surveillance efforts for arboviruses in Kenya have been mainly concentrated in the endemic coastal regions with minimal efforts in other regions such as western Kenya which borders Uganda where high arboviral activity has been documented. In this study we trapped mosquitoes using CDC light and BG sentinel traps in the long and short rainy season in 2018 and 2019 at two livestock markets and six hospitals in western Kenya. We assessed how man-made habitats may impact the mosquito diversity, abundance and at hospital, how in-patients can be exposed to nosocomial arboviral infections. Mosquitoes were screened for pathogenic arboviruses, ISFs and their blood-meal sources determined by reverse transcriptase PCR coupled with high resolution melting analysis. A total of 6848 mosquitoes were collected of which 89% were trapped during the long rainy season with Aedes aegypti (59%) and Culex pipiens (40%) being the most abundant. The majority of the blood-fed mosquitoes were Culex pipiens that took blood meals from humans, chicken and one from a sparrow (Passer sp.). A single Culex poicilipes pool was positive for sindbis virus while 30 pools were positive for Cell fusing agent virus (CFAV), 11 for Aedes flavivirus (AeFV), and eight for Culex flavivirus (CxFV). The overall infection rate of mosquitoes by ISF was 12.66 (8.74-17.82) for CFAV infection and 4.27 (2.26-7.39) for AeFV in Ae. aegypti. Our findings highlight the presence of sindbis virus which causes febrile illness, myalgia and arthralgia which can complicate the diagnosis and prognosis of already immunocompromised patients. The comparatively high infection rates by ISF may explain why there has not been a lot of outbreaks reported in the region given their transmission blocking potential.

Evaluating the transferability of Glossina pallidipes occurrence and abundance models from an intensively sampled livestock-wildlife interface area in Kenya to less sampled areas in the country

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Abstract: Remote sensing of the environment provides the potential to transfer models to areas that are lacking ground sampling data, thus allowing surveillance over large areas. Successful transfer of Species Distribution Model has been reported in relation to the spread of invasive weed species, distribution of different butterfly species among others. However, sampling biases, dissimilarities in environmental conditions between the reference and target areas, species behaviors and biotic interactions are among the major challenges affecting the transfer of species distribution and abundance models. Also, the issue of spatial and temporal scale in terms of the data used to develop the model and the areas they are to be transferred to need to be addressed while performing the transfers. Additionally, to have confidence in the application of a model in other areas, we nonetheless require validation of its performance using ground data in those target areas. For the case of the different species of tsetse flies, the transfer of their occurrence and abundance model has not been attempted before. While occurrence models have been widely applied in areas where presence or absence tsetse fly data is available, abundance models are very limited. Since there are limited funds that allow the actual surveillance of tsetse flies in all the areas they occur, contriving methods that can allow their monitoring on a large scale while maintaining the data quality is paramount. Therefore, this study will focus on answering if;
1) the tsetse fly occurrence and abundance models from an intensely sampled area accurately predict and explain 80% of the variation in tsetse fly distribution and numbers in less sampled areas? 2) how precise and reliable are the resulting transferred occurrence and abundance models in these less sampled areas? The research hypothesizes that application of the occurrence and abundance tsetse flies (Glossina pallidipes) models from Shimba Hills to an area that has similar (Bray-Curtis < 0.4) environmental conditions will result in comparable Kappa accuracies and Root Mean Square Errors (RMSE), while a dissimilar area will have lower Kappa accuracies and higher RMSE. The study design will apply the resulting seasonal formulae of the occurrence and abundance models developed in Shimba Hills, a study site that has been intensely monitored between 2017 and 2019 by the International Centre of Insect Physiology and Ecology (ICIPE), to the rest of Kwale county, Arabuko Sokoke Forest Reserve and Ruma National Park. Ground validation data set will be collected for two months for accuracy assessment and model sensitivity analysis.

Integrative taxonomy of African stingless bees: Using Nest architecture, Morphology, Genetics and Chemistry

Authors: Masiga Daniel[3], Ndungu Nelly[1], Yusuf Abdullahi[4], Pirk Christian[4], Nkoba Kiatoko[2], [3]International Centre of Insect Ecology and Physiology (ICIPE), Kenya, [1]International Centre for Insect Physiology and Ecology (ICIPE), Kenya, [4]University of Pretoria, South Africa, [2]International Centre for Insect Physiology and Ecology, icipe, Kenya

Abstract: Stingless bees are important pollinators contributing significantly to biodiversity and food security. Stingless bees produce honey that has high medicinal value that fetches higher prices compared to the honey produced by honey bees (Apis mellifera). However, identification and classification of Afrotropical stingless bees, which is key and important for their domestication, still remains ambiguous and solely reliant on the use of morphological features. Colonies of the three Hypotrigona species from Kakamega forest and Mwingi, Kenya were nested at meliponary on the campus of icipe in Nairobi, Kenya. Nest sites and nest architecture were recorded. It was found that nest sites are specific with Hypotrigona gribodoi nesting mostly in crevices of mud walls in homesteads, while H. ruspolii and H. araujoi nest in specific indigenous tree species found in Kakamega forest. Using veins on the right forewing and hind leg for morphometrics analysis, H. gribodoi and H. ruspolii were separated from H. araujoi. On the other hand, using mitochondrial DNA, COI gene, the three Hypotrigona species were clearly separated. A lower genetic distance exists between H. araujoi and H. gribodoi from Kakamega (1.4%) than between H. gribodoi collected from Kakamega and H. gribodoi from Mwingi (4.3%). Lastly, using gas chromatography and mass spectrometry, workers were successfully grouped into their respective species and colonies. In conclusion, integrative taxonomy tools applied in this study provides a valuable alternative to identify African stingless bee species. In addition, this study indicates the need for a thorough revision of Hypotrigona species.

Improving access to biological control genetic resources

Authors: Mason Peter[1] and Silvestri Luciana[2], [1]Agriculture and Agri-Food Canada, Canada, [2]National Council for Scientific and Technical Research, Argentina

Abstract: The third objective of the Convention on Biological Diversity (CBD), adopted in 1992 seeks the fair and equitable distribution of the benefits derived from the utilization of genetic resources (GR). The access and benefit-sharing (ABS) regime aims to contribute to the conservation of biological diversity and to bridge the biotechnological gap between developed countries and developing countries, amongst other objectives. Since 1992, several countries have adopted national ABS regimes. Some of them turned out to be highly restrictive; as a result, they even limited access to GR for purely scientific research purpose. Such was the case of the Philippines. This drawback, added to the lack of enforcement of compliance measures in user countries brought about the need to negotiate a new ABS international regime. The Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization (NP), adopted in 2010, further develops the third objective of the CBD. Particularly, the NP establishes that Parties shall create conditions that promote research that contributes to the conservation and sustainable use of biological diversity, including through simplified measures on access for non-commercial research purposes (article 8.a). Since 2010, several countries have updated or even developed national ABS regimes in accordance to the NP. Biological control (BC) is by definition a not for commercial purposes research activity. Based on previous experiences, researchers and practitioners working in the field of BC warn that new national ABS regimes might hinder effective and efficient access to GR. Considering that the symposium will discuss whether national post-Nagoya ABS regimes satisfy Nagoya's requirements; particularly article 8.a, the approaches ABS legal frameworks have taken in relation non-commercial research, and the impacts they are likely to have on activities related to BC. This presentation focuses on the cases of Argentina and Brazil, two important suppliers of BC agents, which had highly restrictive regulations for access to their GR, and which have adopted new legislation to better enable access to GR for scientific research including BC.

Mosquito Monitoring Smart Trap European (Species, Genus and Age) Brazil and Global - field tests and results

Authors: Maspero Renato[2], Njaime Fabio Castelo[1], [1]Ministry of Health, General Coordination of Arbovirus Control, GDF, BR, [2]Technical Consultant - Ministry of Health, General Coordination of Arbovirus

Abstract: Process automation, generate surveillance data in real time, reduction of logistics costs, human resources, time optimization and correct prioritization of hot spots.

The VECTRACK project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 853758.

IoT sensor with Infra-Red optoelectronics that can generate spectral data related to the morphology and kinematics of the insects:

- Savings of 80% in field operations costs
- Remote and automatic classification of mosquitoes: species, sex and age.
- Provides real time information: each capture is tagged with time, coordinates, temperature and humidity.
- Machine Learning cloud server with API to share data with other platforms: Mosquito Alert and VECMAP
- Supported on standards based IoT framework: OGC-SWE, IEE1451
- Sensor capable of capturing data in adult traps with suction fans: mosquitoes detected in <50ms, in an air-flow of 3m/s

Lab results so far - Data analysis using machine learning techniques allow us to separate the different variables tested (species, sex and age) with a range accuracy from 61,3% to 99% .

Earth observation service for preventive control of insect disease vectors.

Assessing the effects of plant and pollinator traits, phylogenies and spatio-temporal distributions on the architecture of plant-pollinator networks

Authors: Massol Francois[2], Berquer Adrien[1], De Manincor Natasha[3] and Joffard Nina[4], [1]CNRS, UMR 7372 CEBC, France, [2]CNRS, UMR 9017 - CIIL, France, [3]University of California, Riverside, United States, [4]Uppsala University, Sweden

Abstract: Pollination is a critical ecosystem service affecting both biodiversity and agriculture through the control of breeding of many angiosperms. Therefore, it is an important concern for society and research. However, plant-pollinator networks are mostly studied from a descriptive point of view - despite considerable theoretical advances, existing methods mostly deal with summary statistics of networks, from connectance and modularity to motif and position counts. Assessing the effects of driving factors, such as insect and plant traits, phylogenies, or habitat preferences, on the structure of networks is still in its infancy. In this presentation, I propose to apply a novel method to assess the determinants of plant-pollinator interactions based on a decomposition of network matrix representations. The method is then applied to two datasets: (i) the network linking all Euro-Mediterranean orchids to their pollinators and (ii) six hoverfly-plant visitation networks sampled in French calcareous grasslands. Results obtained with these analyses pinpoint the leading roles of spatio-temporal variation of species occurrences (phenology and geography) in the determination of plant-pollinator networks. These examples illustrate how our understanding of plant-pollinator interactions might benefit from such large-scale statistical analyses and emphasize a need for more entomological studies aimed at assessing insect species traits and spatio-temporal distribution in order to understand the drivers of pollination.

Hoverflies use a time-compensated sun compass to orientate during autumn migration

Authors: Massy Richard, University of Exeter, United Kingdom

Abstract: The sun is the most reliable celestial cue for orientation available to daytime migrants. It is widely assumed that diurnal migratory insects utilise a ‘time-compensated sun compass’ to adjust for the changing position of the sun throughout the day, as demonstrated in some butterfly species. The mechanisms used by other groups of diurnal insect migrants remain to be elucidated. Migratory species of hoverflies (Diptera: Syrphidae) are one of the most abundant and beneficial groups of diurnal migrants, providing multiple ecosystem services and undergoing directed seasonal movements throughout much of the temperate zone. To identify the hoverfly navigational strategy, a flight simulator was used to measure orientation responses of the hoverflies Scaeva pyrastri and S. selenitica to celestial cues during their autumn migration. Hoverflies oriented southwards when they could see the sun, and shifted this orientation westward following a 6-hour advance of their circadian clocks. Our results demonstrate the use of a time-compensated sun compass as the primary navigational mechanism, consistent with field observations that hoverfly migration occurs predominately under clear and sunny conditions.

Distribution and status of important longhorned beetles (Coleoptera: Cerambycidae) of Croatia

Authors: Masten Milek Tatjana[1], Pintar Maja[2] and Šimala Mladen[2], [1]“Zeleni prsten” Public Institution of Zagreb County, Samobor, Croatia, Croatia, [2]Centre for plant protection - HAPIH, Zagreb, Croatia

Abstract: Family Cerambycidae (longhorn beetles) is one of the economically most important wood boring insect. On the other hand, some species from this family have been under strict legal protection in most European countries. Its high conserva¬tion status results from the global shrinking of its range and resulted in its placement on the IUCN world’s list of endangered species, with VU category.

In recent years, some alien species of longhorn beetles have arrived and spread rapidly through Europe. The most important are Anoplophora chinensis Forster, 1971 and A. glabripennis Motschulsky, 1853. Adult beetles feed on the leaves, bark of twigs and petioles of these hosts, and females chew pits into the bark where they lay their eggs. Larvae burrow into the sap and heartwood, forming galleries. Damage by the larvae can result in crown dieback and early senescence, and eventually the death of the tree. A. chinensis was registered for the first time in Croatia in 2007. Since 2008. Croatia is performing surveys of this quarantine pest. Till today, species have spread on 5 locations on the Croatian coast (Turanj, Sv. Filip and Jakov, Biograd, Cavtat and Vrana) and it is present on one location in the continental part of Croatia in Zagreb county (Rugvica). The important thing is that A. chinensis isn’t yet registered in forests. It is present in nurseries, parks and gardens.

The genus Monochamus Megerle, 1821 comprises of beetles that may become pests of economic importance in conifer stands in the Nearctic and Palearctic Regions. Besides direct damages due to the larval tunneling habits, they have also been recognized as main vectors of the phytoparasitic nematode Bursaphelenchus xylophilus (Steiner & Buhrer, 1934). So far, five European species of genus Monochamus are known. In Croatia two of them are registered; M. galloprovincialis (Olivier, 1795) and M. sutor (Linneus 1758).

Rosalia alpina (Linnaeus, 1758) and Cerambyx cerdo Linnaeus, 1758 are present in Croatia. These are threatened species which have been under strict legal protection and their status is “vulnerable” (VU). Species Morimus asper funereus Mulsant, 1862 are registered in Croatia as well, and even it is not under strict legal protection, it has VU status. All three species are saproxylic beetles, and widespread all over the country. Unlike R. alpine and M. asper funereus which are inhabiting dead woods and are of no economic importance, C. cerdo is primarily inhabiting healthy trees. Due to the damage C. cerdo causes to trees, especially oak communities, this species is considered as a serious pest in forests and orchards. Adults feed on the liquid that appears on the trees during mechanical injuries, as well as on ripe fruits rich with sugar. Larvae of C. cerdo also feed on the sap and heartwood, forming galleries. In some countries of Europe C. cerdo is near extinction, but in Croatia, it is still a quite common species.

Effects of an emergency sewage discharge into a large European river on the structure of Chironomidae larvae

Authors: Matela Mikołaj[1], Obolewski Krystian[1] and Mrozińska Natalia[1], [1]Kazimierz Wielki University, Poland

Abstract: The study was performed on the Vistula River in the urban area (Warsaw city) from December 2019 to May 2021. This period included analysis of the effects of the two failures of wastewater treatment plant (August 2019 and 2020). More than 10 mln m^3 of wastewater entered the lotic ecosystem during the accidents. Insect larvae of the family Chironomidae were selected for monitoring the effects of the accidents. Four study areas were established, including upstream of the urban area (reference point) and others corresponding to the impact of the sewage discharge at distances of 0.5, 2.5 and 4.5 km from the sewage discharge collector. Taxonomic studies identified the presence of 24 taxa of chironomid larvae, with total density was 3,347 individuals m^{-2}. Chironomus plumosus, Cryptochironomus borysthenicus and Polypedilum deletum formed the dominant group. They were accompanied by Cryptochironomus zabolotzkii and Paratendipes intermedius as subdominants. The highest density of larvae recorded during the whole study period was at the site nearest to the collector and the lowest at the distance of 2.5 km from it. However, there is a noticeable increase in the value of the Shannon index with the further distance from the place of sewage discharge into the river.

Chromosome-scale genome assemblies of aphids reveal long-term conservation of the X chromosome and extensively rearranged autosomes

Authors: Mathers Thomas[4], van Oosterhout Cock[5], Swarbreck David[2], Wouters Roland[3], Mugford Sam[1] and Hogenhout Saskia[3], [1]Department of Crop Genetics, John Innes Centre, Norwich Research Park, Norwich, United Kingdom, [2]Earlham Institute, United Kingdom, [3]John Innes Centre, United Kingdom, [4]John Innes Centre, United Kingdom, [5]University of East Anglia, United Kingdom

Abstract: Chromosomal rearrangement plays an important role in evolution. However, our understanding of chromosome dynamics at a sequence-level has been restricted to a relatively small number of model systems where multiple chromosome-scale genome assemblies have been generated. In insects, comparative genomics of Diptera and Lepidoptera has revealed high levels of chromosome conservation within these orders. However, across insects as a whole, chromosome number is highly variable, suggesting a more dynamic situation. In this talk I describe recent work investigating chromosome evolution across aphids, a fascinating group of sap-sucking plant pests belonging to the insect order Hemiptera. By comparing newly generated and published chromosome-scale assemblies of aphids and other Hemiptera we find that the aphid sex chromosome (X) has a highly conserved gene content, with negligible translocations having occurred over 60 million years of evolution. In contrast, aphid autosomes have been highly rearranged during this time, showing evidence of extensive translocations, fusions and fissions. The stability of X chromosome gene content contrasts with a dynamic evolutionary substrate – X linked genes are fast evolving, and the X chromosome is significantly more repetitive than the autosomes. I will discuss these findings in the context of aphid sex chromosome evolution and sex determination.

Exploring Genetic Determinants of Variation in Arboviral Competence in an Aedes aegypti population from Florida, USA

Authors: Mathias Derrick[1], Bozic Jovana[1], Stenn Tanise[1] and Wang Xiaodi[1], [1]Florida Medical Entomology Laboratory, Institute of Food and Agricultural Sciences, University of Florida, United States

Abstract: Since 2009 at least three Aedes aegypti-transmitted arboviruses non-endemic to the United States (chikungunya, dengue, and Zika viruses) have emerged or re-emerged in the state of Florida, illustrating their threat to public health. These emergence events have mostly remained localized, with the number of autochthonous cases reported per event ranging from 1 (dengue virus in 2015, 2018) to more than 200 (Zika virus in 2016). In Florida, local transmission of dengue virus (DENV) in particular has become more commonplace, as autochthonous cases were reported in 10 of 11 years from 2009 – 2019 with a maximum of 65 cases in 2010. A key factor governing the spread of emergent arboviruses is the vector competence (VC) of local mosquito populations. Conceptually, VC is defined as the ability of an arthropod to harbor a pathogen and transmit it horizontally to new hosts, and in mosquitoes VC can be estimated empirically as the proportion of females that produce virus in saliva following oral exposure in a bloodmeal and the extrinsic incubation period (EIP). During the EIP, arboviruses must negotiate physiological tissue barriers within the mosquito that include the apical and basal surfaces of midgut and salivary-gland epithelia. Data from the literature and reported here indicate that VC for a given arbovirus tends to vary within mosquito populations and that geographic origin of both the vector and virus strongly influences VC, demonstrating the importance of mosquito and virus genetics on VC phenotype. Although physiologically we have a basic understanding of the molecular pathways in mosquitoes (e.g., RNA interference, innate immunity, apoptosis, autophagy) that influence viral infection dynamics, what is less clear is how genetic variation in these pathways vary within natural populations and how such variation impacts VC. Data will be presented on variation in vector competence for dengue and Zika viruses in a population of Ae. aegypti from Florida, as well as efforts underway to characterize molecular-genetic variation segregating within this population and to investigate associations between mosquito genotype and VC phenotype.

De novo genome assembly combined with long-read RNA-seq reveal insights into early embryo development of an important agricultural insect

Authors: Mathiopoulos Kostas, Dept. of Biochemistry & Biotechnology, University of Thessaly, Greece

Abstract: Background
The olive fruit fly (Bactrocera oleae) is the most important pest of cultivated olive trees but poorly characterized at a genomics level.

Results
We assembled the 480 Mb B. oleae genome using short-, mate-pair-, long-, and linked-read sequencing technologies to generate a genome assembly (Genbank accession GCA_001188975.3) with a scaffold N50 of 4.69 Mb and L50 of 30 scaffolds. Using the chromosome quotient method enabled identification of Y-chromosome scaffolds which were extensively validated by PCR. Oxford Nanopore long-read RNA-seq of B. oleae embryos collected at hourly intervals for the first 6 hours of development yielded a median of 4.5 million total reads per timepoint. Through our custom pipeline, we generated a de novo long-read transcriptome assembly of the olive fly and identified 1768 novel genes and a total of 79,810 transcripts. We noticed sex specific isoforms some of which were found in genes related to sex development. Using internal ERCC RNA standards, we obtained absolute gene expression quantification and we were able to define a set of developmental stage-specific transcripts. On a global scale, the first six hours of embryo development were characterized by dramatic transcriptome changes with the total mRNA content per embryo dropping by half from the first hour to the second hour of embryo development.

Conclusions
These data provide the first insight into the transcriptome landscape of the developing olive fly embryos and provides avenues that can be used to identify new targets which can help suppress fly population in the field and prevent crop damage.

Role of Endophytes on Insect Induced Responses in Brassica juncea

Authors: Mathur Vartika[1] and Sharma Garima[2], [1]Department of Zoology, Sri Venkateswara College, University of Delhi, India, [2]Sri Venkateswara College, University of Delhi, India

Abstract: Endophytes are the most diverse and abundant colonizers of plants and share an intimate metabolic interaction with the host plant. In exchange of carbon and nitrogen resources, they contribute to the secondary metabolic profile of their host and play a crucial role in plant fitness and defence. However, the role of endophyte association in conferring resistance to the host upon insect attack is still unclear. Therefore, we studied early responses (superoxide dismutase, SOD; peroxidase, POD and protease inhibitor, PI) of Brassica juncea, with and without endophytes, against the damage by a generalist insect Spodoptera litura.
Plants with endophytes showed significantly elevated POD and PI after 24h of insect damage, compared to plants without endophytes. Although increased PI content upon insect damage was also observed in plants without endophytes, this change was considerably lesser compared to plants with endophytes. Furthermore, SOD increased upon insect damage irrespective of endophyte presence. These changes indicate an overall suppression in the early responses upon insect damage in plants without endophytes, suggesting their significance in insect resistance. Thus, the intimate association between endophytes and the host plant have the potential to offer an exclusive breakthrough for application in plant protection and biological control.

The use of whole-genome sequencing data to bridge macro- and micro-evolution in butterflies

Authors: Matos Maraví Pável[2] and Ribeiro Pedro[1], [1]Biology Centre CAS, [2]Biology Centre CAS, Czech Republic

Abstract: Short read whole genome re-sequencing (WGS) is a cost-effective approach to obtain genome wide nucleotide polymorphisms to study processes at the species and population levels. Although there is a growing number of high-quality reference genomes across butterfly families which can be used for read mapping, the characterization of genomic variation still relies on de novo contig assemblies for most lineages. We show that phylogenomic markers can be more efficiently mined from de novo assemblies that were generated using multi-kmer approaches and having at least 5X sequence coverage. We were able to produce more complete and informative alignments by merging data coming from low coverage WGS and sequence target capture, to produce a robust tribal-level phylogeny of the butterfly subfamily Eudaminae (Hesperiidae). Further, using gene tree-based methods, we estimated large-scale introgression events in Eudaminae clades where substantial phenotypic convergence has been estimated, which might indicate a possible correlation. Ongoing efforts are being made to characterize highly divergent genomic regions that potentially explain the genetic differentiation of phenotypically similar co-occurring sister species in the Neotropical genera Cecropterus and Spicauda (Eudaminae). Altogether, WGS is an efficient approach to understand the assembly of butterfly species and genetic diversity across evolutionary scales.

The challenge of managing an alien invasive forest insect pest-a successful case of classical biological control with introduced parasitoid Torymus sinensis

Authors: Matošević Dinka, Croatian Forest Research Institute, Croatia

Abstract: Dryocosmus kuriphilus (Hymenoptera, Cynipidae) is considered as one of the major pests of sweet chestnut (Castanea) worldwide and the only effective method of controlling the populations and damages of this invasive forest pest is biological control with introduced parasitoid Torymus sinensis. T. sinensis is a univoltine, host specific parasitoid, phenologically synchronized and morphologically adapted to D. kuriphilus. T. sinensis has good dispersal ability, builds up populations quickly and effectively controls the pest already few years after release. Ten years after first releases and natural dispersal in Croatia, we have evaluated the impact of this classical biocontrol agent on invasive population of D. kuriphilus. T. sinensis has shown traits of very effective biocontrol agent: the methods for raising and release are not difficult to apply, it disperses very quickly when released, it lowers the population of its host for more than 90% in only few years, suffers no bottleneck -induced founder effect phenomenon and leads to recovery of chestnut yield in natural sweet chestnut forests. This is first example of successful application of classical biocontrol agent in forests in Croatia, Slovenia and Hungary.

Increased voltinism and outbreak level of bark beetle Orthotomicus erosus populations in Mediterranean part of Croatia-high potential of a forest pest in changed ambient conditions

Authors: Matošević Dinka[1] and Pernek Milan[2], [1]Croatian Forest Research Institute, Croatia, [2]Department for forest protection Croatian Forest Research Institute, Croatia

Abstract: Bark beetles are important forest pests which have already been researched and discussed in relation to climate change, indicating that the predicted increase in temperature would lead to higher survival rates and faster development, thus directly influencing their population dynamics. Bark beetle Orthotomicus erosus is widely distributed across the Mediterranean and southern Europe, Asia and North Africa. It is considered as secondary pest found on recently dead or felled trees, but can also attack weakened living trees. In high population levels this species can attack healthy trees and cause their dieback. Severe outbreaks occur after dry periods, or after fire in adjoining stands in warmer parts of the Mediterranean region. Several locations in the Mediterranean part of Croatia (Marjan Forest Park in Split, islands of Lokrum and Korcula) had reported dieback of Aleppo pine from the year 2016. Visual examination of trunks, branches and bark showed symptoms of bark beetle infestation, and on-site examination of the observed adults and morphological identification pointed out to O. erosus. Population monitoring with pheromone traps in the years 2017, 2018 and 2019 showed 6 to 7 generations per year which has never been recorded in Croatia or in any other European country. O. erosus is native to Croatia and so far it has been considered only as a minor pest whose outbreaks have never been recorded. Drought intensity and frequency and aridification trends in the research area (Dalmatia, Croatia) cause cumulative stress to trees and have increased O. erosus occurrence. O. erosus has shown increased voltinism, better overwintering performance and earlier spring flights. Our first results confirm this epidemic stage of O. erosus with high abundances in Dalmatia. The population level and pest status of this bark beetle has been seriously altered probably due to climate change. High dispersal abilities of O. erosus through active flight and easy transportation with infested material (logs and branches with bark), O. erosus has the potential to become an important forest pest in Croatia and in other European Mediterranean countries.

Insecticides okaramines work as defense weapons for plants in nature

Authors: Matsuda Kazuhiko, Kindai University, Japan

Abstract: Indole alkaloids okaramines were discovered as insecticidal substances from fermentation products of fungus Penicillium simplicissimum in soy pulp okara. Testing the compounds on the silkworm larval neurons using patch-clamp electrophysiology led to a finding that okaramines selectively activate ligand-gated chloride channels. Hence, actions of okaramines were investigated on ?-aminobutyric acid receptors and glutamate-gated chloride (GluCls) channels expressed in Xenopus laevis oocytes. As a result, okaramines selectively activated GluCls expressed only in invertebrate nervous systems. Following the discovery of okaramines, many other insect-active compounds were isolated from fungal products in okara. They also modulated insect ion channels with high selectivity. It was therefore predicted that plants secret chemical signals that induce microorganisms to produce defense weapons for plants in the rhizosphere.

Understanding target site of actions of neonicotinoids for safer and environmentally benign crop protection

Authors: Matsuda Kazuhiko[1], Ihara Makoto[1], [1]Kindai University, Japan

Abstract: Neonicotinoids modulate insect nicotinic acetylcholine receptors to exhibit insecticidal actions. Neonicotinoids show high systemicity in plants, which enables seed treatment, and now make up >25% of insecticide sales in the world. However, recent studies suggest a potential risk of neonicotinoids to pollinator, notably to bees, and thus it is critical to understand neonicotinoid actions in detail. We have studied mechanisms of selectivity to insects as well as of diverse actions of neonicotinoids and found that 1) both a and non-a subunit possess structural features favorable for interacting with neonicotinoids; 2) Vertebrate a subunits possess glutamate residue in loop C, which plays a gate keeper role for repelling neonicotinoids; 3) Insect non-a subunits possess basic residues in loop D, which interact electrostatically with the nitro or cyano group of neonicotinoids to enhance the affinity. Further, we have recently found that basic residues in loops G and E may also contribute to the binding of neonicotinoids. With all these results, we discuss the future perspective of neonicotinoids.

Selectivity of okaramines, indole alkaloid insecticides targeting glutamate-gated chloride channels

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Abstract: Indole alkaloids okaramines were found as insecticidal compounds against the silkworm larvae (Bombyx mori) from the fermentation products of Penicillium simplicissimum in soy pulps 'okara'. They exhibit rapid toxicity when applied not only by injection, but also by oral administration. We investigated the target of okaramines using patch clamp electrophysiology to show that they selectively activated glutamate gated chloride channels (GluCls). Since it was unclear whether they modulate the other ligand-gated chloride channels, we tested okaramine B, the most potent okaramine, on Bombyx RDL ?-aminobutyric acid (GABA) receptor as well as human a1ß2?2 GABAR and a1ß glycine receptor expressed in Xenopus laevis oocytes. Okaramine B was ineffective on these chloride channels, suggesting high selectivity to GluCls. We also tested okaramine B on GluCls from other insect species than the silkworm larvae and found that it also modulated GluCls with different affinity and efficacy.

Modulation of neonicotinoids of recombinant nicotinic acetylcholine receptors containing a pollinator a subunit

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Abstract: So far neonicotinoids have been used for crop protection relying on their high plant systemicity as well as on pest control efficacy. Meanwhile, there is evidence that some neonicotinoids may cause the decline of bees. Hence it is urgent to understand how neonicotinoids act on their targets, nicotinic acetylcholine receptors (nAChRs) in pollinators. While the difficulty of their functional expression has impeded the study of neonicotinoids, robust nAChRs formed by insect a subunits and vertebrate non-a subunits in cell lines and Xenopus laevis oocytes have been employed to understand the mode of action and selectivity of neonicotoids. Thus, we attempted to co-express a pollinator a subunits with chicken ß2 subunit, resulting in robust nAChRs. The recombinant nAChRs can be used to evaluate the mode of actions, not only of neonicotinoids, but also of pest-selective ligands underlying plant-microbe-insect interactions.

Role for serine221 in loop C in determining neonicotinoid actions on Drosophila Da1/chicken ß2 hybrid nicotinic acetylcholine receptors

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Abstract: Neonicotinoids selectively modulate insect nicotinic acetylcholine receptors (insect nAChRs). Studies have shown that serine with ability to form a hydrogen bond in loop C of some insect nAChR a subunits may contribute to enhancing the neonicotinoid actions. However, there is no clear evidence what loop C properties underpin the target site actions of neonicotinoids. Thus, we have investigated the effects of S221A and S221Q mutations in loop C of the Drosophila melanogaster Da1 subunit on the agonist activity of imidacloprid and thiacloprid for Da1/chicken ß2 nAChRs expressed in Xenopus laevis oocytes. The S221A mutation hardly affected either the affinity or efficacy for ACh and imidacloprid, whereas it slightly reduced the efficacy for thiacloprid on the nAChRs with a higher composition ratio of ß2 to Da1 subunits. The S221Q mutation markedly reduced their efficacy of the neonicotinoids for the nAChRs with a higher composition of the ß2 subunit lacking basic residues critical for binding neonicotinoids. Hence, we council caution of enhanced neonicotinoid resistance in pests by a mutation of the serine when it occurs in the R81T resistant populations lacking the basic residue in loop D and demonstrate needs of new chemical leads which may be found from chemical signals controlling insect behaviors.

Molecular basis of pyrethrum repellency in Aedes aegypti

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Abstract: Pyrethrins I and II, the principal components of pyrethrum, and pyrethroids target voltage-gated sodium channels for insecticidal action. However, the molecular basis of pyrethrum/pyrethroid repellency remains enigmatic. Here we discovered that pyrethrum elicited repellency through a multi-target mechanism in Aedes aegypti. Here we discovered that pyrethrum elicited repellency through a multi-target mechanism in Aedes aegypti. Pyrethrins I and II activated a specific type (sst-1A) of olfactory receptor neurons (ORNs) and elicited odorant receptor (Or)-mediated repellency. We also discovered that sesquiterpene (E)-ß-farnesene (EBF), a minor component of pyrethrum extracts, can elicit repellency by activating a specific Or expressed in another type (sbt-1A) of ORNs. Furthermore, two mutations in sodium channels that attenuate the potency of pyrethrins on sodium channels also reduced pyrethrum repellency. Collectively, our results suggest a synergistic Or- and sodium channel-mediated repellent action by multiple components in pyrethrum extracts. Discovery of this multi-target mechanism provides a conceptual framework for development of a new generation of broad-spectrum and durable insect repellents.

Silkworms suppress the release of green leaf volatiles by mulberry leaves with an enzyme from their spinnerets

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Abstract: In response to herbivory, plants emit a blend of volatile organic compounds that includes green leaf volatiles (GLVs) among others. GLVs are known to attract natural enemies of herbivores and are therefore considered to function as an indirect defense. Selection should favor herbivores that are able to suppress these volatile emissions, and thereby make themselves less conspicuous to natural enemies. Silkworms leave secretions from their spinnerets while feeding on mulberry leaves. We ablated the spinnerets of silkworms to limit the secretions. The leaves infested by ablated silkworms emitted higher amounts of GLVs than those infested by intact silkworms while the amounts of other volatiles were similar, indicating that the spinneret secretion specifically suppressed GLV production. We found a novel enzyme that converted 13(S)-hydroperoxy-(9Z,11E,15Z)-octadecatrienoic acid, an intermediate in the biosynthetic pathway of GLVs, into its keto-derivative that cannot be used to form GLVs in leaves. Zenillia dolosa (Tachinidae), a parasitoid fly of silkworms, discriminated the difference in GLV emissions, and the flies laid fewer eggs when exposed to the volatiles from intact silkworm-infested leaves than when exposed to the volatiles from ablated silkworm-infested leaves. The genes orthologous to that encoding the enzyme were widespread among Lepidoptera. It is suggested that lepidopteran insects are able to feed on leaves in a stealthy manner by suppressing GLV production, as a countermeasure against induced indirect defense by plants.

The evolution of Zoraptera

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Abstract: Together with Dermaptera, Zoraptera is the first split among the polyneopteran orders. To understand the evolution of Polyneoptera, accumulating more knowledge on zorapteran species is essential. However in comparison to Phasmatodea and other related groups, there are still large gaps of information. Based on a broad taxon sampling from all continents where the group is known we conducted the first species level phylogeny, using partial sequences of 18S rRNA, Histone 3, 16S rRNA, and 12S rRNA genes. The resulting phylogenetic trees show that Zoraptera is divided into three major clades, and that two of them are composed of species distributed on different continents. The monophyly of these clades is at least partly supported by shared derived morphological features. The divergence age estimation and ancestral distribution area reconstruction unveiled an ancient origin and early radiation initiated in the Permian. The plate tectonics theory suggests that the present distribution of Zoraptera was mainly established by vicariance, rather than dispersal. The three major clades likely originated on the Pangaea supercontinent, or alternatively on the Gondwana and Laurasia supercontinents. Their ancient origin explains previously found conspicuous interspecific divergence variation of the spermatozoa morphology, genital apparatus, sperm structure, and mating behavior, in striking contrast to a highly conserved general body morphology. We also compiled data of available reproductive features and reconstructed the character evolution. Although homologies in the genital character system are not fully established yet, the analyses revealed repeated acquisitions and/or losses of a hyper-elongated intromittent organ, mating hooks, and tergal protuberances. We will discuss desiderates and introduce a part of our latest projects aiming at a better understanding of the evolution of Zoraptera.

Olfactory receptors tuned to volatile mustard oils in flies

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Abstract: Plant toxins are effective defenses because they are aversive to most insects. The same molecules, however, are co-opted as host-finding cues by specialist herbivores. Although these behavioral shifts are central to our understanding of herbivorous insect diversification, it is not well understood how these behaviors evolve. We addressed this in Scaptomyza flava, a herbivorous drosophilid fly that shifted to toxic mustard plants (Brassicales) less than 10 million years ago and lost the ancestral attraction to yeast volatiles as well as the attendant chemoreceptors. We first found a gain-of-function behavior: S. flava, but not its close microbe-feeding relatives Drosophila melanogaster and S. pallida, is attracted to mustard host-plant odors, including volatile mustard oils (isothiocyanates or ITCs). Our genomic analysis then uncovered three S. flava paralogs of an olfactory receptor gene (Or67b) that likely experienced recent positive selection. We then tested whether these candidate chemoreceptors could underlie the observed attraction to volatile ITCs. Our in vivo recordings revealed that two of the S. flava Or67b proteins (Or67b1 and Or67b3) – but not the homologous Ors from microbe-feeding relatives - responded selectively to volatile ITCs. These Ors are the first ITC chemoreceptors other than TRP channel family (e.g., the TrpA1 ‘wasabi’ receptor) known from any animal. Remarkably, S. flava Or67b3 was sufficient to drive olfactory attraction toward butyl ITC when expressed in an attractive olfactory circuit. Our study illuminates that ancestrally aversive chemicals can be co-opted as attractants through gene duplication, leading to the origin of hedonic valence shifts in herbivorous insects.

Evolutionary relationship between endopolyploidy and fecundity in termite queens

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Abstract: Extreme reproductive specializations are exhibited in social insects under the reproductive division of labor. Female fertility of them ranges from sterility (workers or soldiers) to hyperfecundity (queens). In termites, queen fecundity varies greatly between lineages with different lifestyles: queens in species with foraging lifestyle, which is observed in the advanced clade show much higher fecundity than those in wood-dwelling lifestyle, which is considered phylogenetically basal type. Recently, we reported that in a termite, queens exhibited higher polyploid levels than the nonreproductives in their fat body, the organ producing a lot of yolk protein precursors, vitellogenin. Moreover, we found that the polyploidization was occurred along with ovarian development of the queens. In general, endopolyploidy or somatic polyploidy is often attributed to the increasing cellular size or gene expression owing to the increase in availability of DNA templates; therefore, the fat body endopolyploidy can accelerate egg production, via promoting vitellogenin synthesis.

In this study, in order to investigate the relationship between the fecundity and ploidy level in the fat body of the queens, we conducted ploidy analyses on three foragings and three wood-dwelling termites via flow cytometry. In all the species, the fat body of queens contained significantly more polyploid cells than that of other nonreproductive females, even considering their body size effect. On the other hand, the male fat body, which is not involved in yolk production, did not show consistency in the rate of polyploid cell among the species studied. Then, we compared the relative ploidy levels of queens, which is the standardized polyploid level of queens relative to the polyploid levels of conspecific female workers that represent nonreproductives, and found that highly fecund queens in foraging termites exhibit higher levels of endopolyploidy in their fat body than those with less fecundity in wood-dwelling termites. These results suggest not only that endopolyploidy in the fat body of termite queens can boost their egg production, but also the level of endopolyploidy in their fat body is linked to their fecundity. Our study provides a novel insight into the evolutionary relationship between endoreduplication and caste specialization in social insects. In this talk, we will also discuss about what the polyploid index actually means, or the physiological significance of fat body endopolyploidy such as the regulation of gene expression, cell size and cell differentiations.

Genomic imprinting and the origin of termite eusociality

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Abstract: The concept of epigenetic inheritance provides the keys to many unsolved puzzles in a wide range of biology. Recent empirical studies have revealed that the transfer of epigenetic marks from parents to offspring can influence offspring phenotype independently of DNA sequence. Reproductive division of labor is a hallmark of social insect societies where individuals follow different developmental pathways resulting in distinct morphological castes. There has been a long controversy over the factors determining caste fate of individuals in social insects. It has been known that parental phenotypes influence the caste fate of offspring in termites. For example, female offspring of sexually matured queens and worker-derived males develop exclusively into queens, as do parthenogenetically produced daughters. Such heritable effects on caste propensity has been recognized as an evidence of genetic caste determination. Recently, we demonstrated that parental phenotypes influence the social status of the offspring not through genetic inheritance but through genomic imprinting. We conducted extensive field survey and genetic analysis of the termite Reticulitermes speratus and concluded that the caste system of this species cannot be explained by genetic caste determination models. Alternatively, we documented a genomic imprinting caste determination system in termites, in which queen- and king-specific epigenetic marks antagonistically influence the sexual development of offspring and thus determine their caste fate. Our genomic imprinting model accounts for all known empirical data on caste differentiation in termites and explains the evolutionary processes underlying diverse reproductive systems. According to the genomic imprinting model, the worker caste is seen as a ‘neuter’ caste whose sexual development is suppressed due to counterbalanced maternal and paternal imprinting. Importantly, a wide variety of species including lower and higher termites share the genomic imprinting caste determination system. The most parsimonious idea to explain this background would be that genomic imprinting is involved in the origin of termite eusociality. Our model further demonstrates that genomic imprinting played an essential role in the origin of eusociality.

Gut microbial pulse provides nutrition for parental provisioning to larvae during colony foundation in a termite

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Abstract: The success of aerial dispersal involves a tradeoff between propagule size and dispersal ability such that reducing weight may increase dispersal capability. Therefore, dispersing propagules such as plant seeds, fungal spores, and insect alates need to settle in new habitats with a very limited amount of resources. In termites, the time from alate dispersal to colony foundation is the most critical period in their life-cycle because a pair of males and females establish a new colony without any help from others. In addition, termites depend largely on gut microbes for their nutrition. However, little is known how termite founding pairs with limited resources manage to establish new colonies and raise first brood in association with their gut symbionts. Here we provide the integrated analysis of reproductive schedule, gut microbial fluctuation, and resource allocation of founding pairs in incipient colonies of subterranean termite, Reticulitermes speratus. We found a steep increase and rapid decrease of intestinal protozoa (hereafter gut microbial pulse) at the timing of larval hatching. Besides monogamous pairs same-sex (male-male and female-female) pairs found tentative colonies in this termite. A comparison of the patterns of changes in the amount of protein and lipid among different types of pairs revealed that the gut microbial pulse plays an essential role for parents to feed the first brood larvae. We also found that founders utilize the storage protein and lipid for brood production. Our study highlights the significant role of intestinal symbionts during the early stage of the termite life cycle.

Identification of an aggregation pheromone in a termite

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Abstract: Termites have developed a sophisticated chemical communication system that regulates various social activities. In most subterranean termites, workers forage for new wood resources to expand their nesting areas. When they discover a new edible wood, they gather and stay there, suggesting that an aggregation pheromone regulates this colonization process. Nevertheless, such a pheromone has never been discovered until today. This study successfully identified the aggregation pheromone that serves as the signal for the presence of nestmates and the place suitable for staying for a long time in the termite Reticulitermes speratus. Gas chromatography-mass spectrometry analysis combined with bioassays revealed that the workers utilize the mixture of an aromatic hydrocarbon, cuticular hydrocarbons, saturated and unsaturated fatty acids, and a steroid compound as the aggregation pheromone triggering long-term aggregation. Although the aromatic hydrocarbon can attract workers, all the other compounds enhanced the arrestment effects on the attracted workers when mixed. These results suggest that termite foraging workers produce the multicomponent aggregation pheromone by combining cuticular hydrocarbons with a volatile hydrocarbon and lipids, and that this pheromone enables the quick aggregation of the workers, contributing to efficiently feeding and dwelling in new dead wood. This work contributes to further understanding of the chemical communication underlying the social assembly in termites.

Royal homeostasis: the advanced maintenance systems exist in long-lived termite kings and queens

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Abstract: The trade-off between reproduction and longevity is the bedrock of the evolutionary theory of aging. The evolution of eusociality in termites has been attended by an increase in the intrinsic longevity of the royals (kings and queens) without sacrificing high reproductive activity. The extraordinary longevity of the royals, which contradicts the trade-off, has attracted much attention because it implies the existence of an anti-senescence mechanism. We performed comparative analyses of molecular homeostasis between long-lived royals and short-lived non-reproductive individuals in the subterranean termite <i>Reticulitermes speratus</i>. In this investigation, we found that the royals have advanced antioxidant and DNA-repairing system, which are important for maintaining molecular homeostasis, in comparison to that of non-reproductive individuals. In addition, we focused on environmental factors that influence physiological state in organisms. Termite royals reproduce in royal chambers deep inside the wood, which expects hypoxic environment in the royal chamber. We tested whether hypoxia influences the development of royal characteristics and found that hypoxia enhances survival and reproductive activity in the royals of <i>R. speratus</i> compared with those in control conditions. This result suggested that adaptation to hypoxic habitats accompanied with the development of anaerobic energy-producing systems, which avoid oxidative metabolic stress, may contribute to lifespan extension in the termite royals. Our studies provide new insights to the maintenance system of molecular homeostasis in long-lived termite royals.

Suppressive effect of prohydrojasmon on the western flower thrips (Frankliniella occidentalis) on greenhouse tomato plants

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Abstract: Frankliniella occidentalis is an important pest that transmits tospoviruses such as Tomato spotted wilt virus. F. occidentalis feeds by piercing plant cells with their mouthparts and ingesting cell contents through their stylets. Resistance in plants including Solanaceae against herbivorous insects depends on wound-response signaling via phytohormone jasmonate (JA). Thus, JA and its derivatives are phytohormones with essential roles in plant defense against herbivorous arthropods. Using an Arabidopsis–thrips system, Abe et al. (2008) revealed that endogenous JA enhanced resistance against thrips feeding via a JA-regulated defense response. Based on this finding, Abe et al. (2009) also showed that application of JA to Arabidopsis plants enhanced plant resistance to thrips; thus, JA induces acquired resistance against thrips feeding in Arabidopsis. Prohydrjasmon (PDJ), which is JA derivative, is registered for use as a plant growth regulator for accelerating ripening of tree fruits. We investigated the suppressive effects of PDJ sprays on F. occidental infestation of greenhouse tomato plants and the influence of these sprays on tomato growth, yield, and quality of tomato fruit under commercial-like conditions to help develop a novel control measure based on PDJ's repellent action with respect to this pest. In experiments conducted over two consecutive years, we evaluated how spraying with PDJ affected F. occidentalis infestations of greenhouse-grown tomato plants. Single or consecutive sprayings of 400 nmol/ml PDJ in the early growth stage of tomato plants significantly suppressed thrips infestation and feeding damage as well as spraying with spinetoram. Although initial plant growth was slightly inhibited by spraying with PDJ, no deleterious effects on tomato yields or fruit quality were observed. These results suggest that PDJ could be practically used as a repellent to control F. occidentalis infestation and primary tospovirus infection in commercial tomato growing greenhouses.

Are arthropod head segmentation mechanisms evolutionarily conserved?

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Abstract: Is the insect head segmented in the same way as the trunk? Studies using Drosophila have found differences in the expression of pair-rule genes and Hox genes between the head and trunk, suggesting different segmentation mechanisms between them. However, the insect head segmentation is poorly understood compared to the trunk, and the detailed mechanism-of head segmentation is unknown.

In other arthropods such as chelicerata, myriapoda and crustaceans, the head segment is formed by splitting of hedgehog (hh) stripes during embryonic development. Furthermore, it has recently been reported that msx1 is involved in splitting of the hh stripes in chelicerata.

In this study, we aim to understand whether the function of msx1 in splitting hh stripes is conserved outside od chelicerata. We performed functional analysis of msx1 and hh orthologs in the two-spotted cricket Gryllus bimaculatus, and found that these genes are involved in the segmentation of the anterior region of the head. This work provides the first evidence that supports the involvement of msx1 in splitting hh stripes in hexapods, and suggests that the anterior head region is formed by an evolutionarily conserved segmentation mechanism, that is splitting, throughout arthropods.

Interactions between air temperature and snow cover during overwintering produce extreme effects on the population dynamics of the alpine butterfly, Parnassius smintheus

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Abstract: We have been monitoring the dynamics of a network of 21 populations of this alpine butterfly since 1995. We show how the population dynamics are dominated by weather conditions early in the overwintering period (Nov.). Snow cover and temperature both act quadratically so that population growth is highest at mean values and lowest at extremes. There is also a strong interaction of these factors. Lab and field experiments show that warn, dry conditions result in premature emergence and cold, dry conditions freezing. Analysis of overwintering survival and temperature on the ground where eggs indicate that interaction between snow cover and temperature is only partly due to its effects on temperature at ground level and overwintering survival. Temperatures and snow cover negatively affecting population growth occur commonly, however the combination of these factors at very high or low levels represents an extreme event with large negative effects on population growth.

High evolutionary potential in the chemical defenses of an aposematic Heliconius butterfly

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Abstract: Chemical defences against predators underlie the evolution of aposematic coloration and mimicry, which represent classic examples of adaptive evolution. Yet, unlike color patterns, little is known about the evolutionary potential of chemical defences. Neotropical Heliconius butterflies exhibit incredibly diverse warning color patterns and widespread mimicry. Their larvae feed exclusively on cyanogenic Passiflora vines, can metabolize and sequester host plant toxins, as well as biosynthesize defensive cyanogenic toxins themselves. Here, we investigate variation of biosynthesized toxicity both in wild populations along environmental gradients and in common-garden broods and feeding treatments in Heliconius erato, together demonstrating considerable intraspecific variation and evolutionary potential in this important chemical defense trait. Among wild populations, toxicity varied markedly between populations from Central and South America. Within wild populations, the distribution of toxicity was consistently skewed, indicative of automimic “cheaters” that may exploit, and consequently deplete, the protection of the warning coloration. In a common-garden rearing design comprising more than 300 butterflies across 20 broods, variation in host-plant nutritional quality or cyanogen levels did not translate into differences in toxicity of butterflies feeding on these plants. Instead, toxicity had a significant heritable genetic component, in part explained by maternal inheritance. The evolvability of toxicity was high, suggesting that toxicity can evolve rapidly. Through its link with the evolution of warning color pattern mimicry, the high evolutionary potential of cyanogenic toxicity may have facilitated diversification and ecological speciation in Heliconius, highlighting the importance of understanding the evolution of chemical defense in aposematic and mimetic species.

Thermogenesis in a feeding matrix formed on carrion by Necrodes littoralis L. (Coleoptera: Silphidae)

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Abstract: Carrion beetles form a feeding matrix by spreading anal and oral exudates over cadaver surface. The matrix is a complex microenvironment emerging from the interactions between beetles, microbes that inhabit the matrix and the putrefying resource. Beetles contribute to its formation and maintenance mostly through exodigestion of carrion and manipulation of its microbial content. The matrix probably has several functions. We tested the hypothesis that the matrix, which is formed on carrion by Necrodes littoralis L. (Silphidae) produces heat. Using thermal imaging we demonstrated that heat produced in the matrix formed on meat by adult or larval beetles was larger than in meat decomposing without the insects. Larval beetles regularly warmed up in the matrix. These findings indicated that the spreading of exudates over carrion by adult or larval Necrodes beetles has thermal benefits for the insects and therefore may be considered as a new form of thermoregulation on carrion.

Moreover, by comparing thermogenesis and beetle fitness in larval colonies with and without the presence of adult beetles in the pre-larval phase, we found that formation of the matrix by adult beetles had deferred thermal benefits for the larvae. After adult beetles had prepared the meat in the pre-larval phase, thermogenesis of the matrix in the larval feeding phase increased, whereas development times and mortality of the larvae decreased. This behavior of the adult beetles brought distinct thermal benefits for their offspring and therefore may be classified as a new form of indirect parental care with an important thermal component.

At present we are experimenting to get a deeper insight into spatio-temporal patterns, mechanisms, determinants and fitness effects of thermogenesis in N. littoralis.

The significance of fungus-carrying organs, mycangia, in understanding the biology and evolution of ambrosia beetle-fungus symbioses

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Abstract: Ambrosia beetles farm fungi in tunnels deep within wood and rely on special fungal crops (ambrosia fungi) to survive and to nourish their young, but each generation must maintain the same domesticated cultivars despite generally flying to new trees to sow fungal gardens and establish their progeny. For more than fifty years, a diversity of pocket-like spore carrying organs (mycangia) have been known to facilitate this cultivar persistence in ambrosia beetles. However, the significance of mycangia in ambrosia beetle biology and evolution extends beyond transmission, and each ambrosia beetle lineage has unique mycangia that both enabled the inception of and currently define their symbioses. Understanding these fascinating organs is paramount to understanding the varied ambrosia beetle-fungus symbioses. Some ambrosia beetle lineages maintain strict associations with specific ambrosia fungi, and mycangia have enabled some ambrosia beetle lineages to still farm the fungi they first domesticated millions of years ago. Conversely, mycangia can also confer flexibility; some beetle lineages used their mycangia to capture already-domesticated fungi from other beetle lineages or replace ancestral cultivars with new ones, and some lineages continue to actively trade fungi. Patterns between mycangia and the fungi they carry make them valuable indicators for which fungi an invasive beetle can be expected to vector. Mycangia also likely exert significant evolutionary influence on the symbiosis. Most mycangia are lined with gland cells that secrete nutrients, which promotes the active and potentially selective growth of ambrosia fungi inside them. Mycangia shelter delicate ambrosia fungi from the environment and may have allowed the fungi to develop traits for nutrition and rapid colonization rather than dispersal and survival. Mycangia likely enforce genetic bottlenecks on the fungi that prevent selfish evolution and escape from symbiosis despite apparent sexual reproduction. These have proven to be perplexing pockets, however, and many mycangium mechanisms remain elusive. A short history of mycangium research is presented to contextualize our current knowledge and gaps in understanding, and the argument is made that mycangia should be appreciated as important components of the ambrosia symbiosis and an avenue for future research.

Dynamic analyses for the optimization of a pest control system based on vibrations

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Abstract: In many Hemipteran insects, vibrational communication is fundamental for reproduction in that it can provide cues that enable partner identification, location and courtship. If this communication fails, none of the previous actions will be possible and the species reproduction is compromised. From this concept, a new method of pest control, an alternative to pesticides, is currently under development: the vibrational mating disruption, which is based on the use of disturbance noise (DN, i.e., disruptive synthetic vibrations specifically designed to interfere with the mating communication).

In this study, we describe from an engineering point of view this method, applied in the field for the control of the grapevine leafhoppers Scaphoideus titanus and the Empoasca vitis. In order to prevent mating, the DN is continuously transmitted by a system of mini-shakers through the vineyard, from the trellis (i.e., poles and wires) to the grapevine leaves. The DN can disrupt the target species because of its specific frequency pattern and provide the respect of certain threshold of intensity. For these reasons, (i) we must reduce all the possible causes of dissipation and/or (ii) optimize the signal transmission at the source i.e. the mini-shakers. Since this method is applied in the field, many uncontrollable factors can contribute to dissipating the signal (materials, junctions, external perturbations just to name a few). Therefore, in the first instance, we decided to focus on the mini-shaker position to enhance its performance. In this study, we report our dynamic analysis of the shakers to suggest some changes, by varying the shaker assembly, stiffness, mass and position, and so generate improvements on the quality and the intensity of the signal to be transmitted. Both numerical (finite element) simulations and field measurements are shown to validate the proposed solutions.

Vibrational communication of the greenhouse whitefly Trialeurodes vaporariorum (Westwood) (Homoptera: Aleyrodidae)

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Abstract: Biotremology is a new discipline that studies the vibrational communication of animals. The applied biotremology investigates the control of insect pests of crops using vibrational signals (VS) to manipulate their behaviour (i.e., attraction, mating disruption, repellence).
The greenhouse whitefly (GW), Trialeurodes vaporariorum (Westwood) (Homoptera: Aleyrodidae) is considered one of the most harmful insect pests in greenhouses. The GW mating behaviour has been partially investigated and its vibrational communication is mostly unknown. A deeper knowledge of its intraspecific communication is necessary to evaluate the applicability of control methods.
In this study, we used the laser doppler vibrometer to record the VS, coupled with video recordings to link the signals production to the insect behaviour. VS were characterized in terms of spectral and temporal parameters and an ethogram was designed.
We identified three types of male vibrational emissions ("chirp", "pulses" and a Rivalry Signal), differently arranged according to the stage of the mating process, and one female responding signal here recorded and described for the first time. The GW showed to have a complex mating behaviour, consisting of four different stages: "call", "alternated duet", "courtship" and "overlapped duet". The analysis performed with the Markovian behavioural transition matrix showed that the "overlapped duet" stage seems to cover a crucial role to achieve a successful mating, in that strictly associated to the female acceptance.
This study demonstrates that vibrational communication plays an important role in GW mating process, therefore future studies should assess whether VS playbacks could be exploited to manipulate its behaviour. This would be the first case of pest control with vibrations in greenhouses.

Accessing biological control genetic resources: the South American experience

Authors: Mc Kay Fernando, Foundation for the study of invasive species, Argentina

Abstract: The Nagoya Protocol (NP) is a supplementary agreement to the Convention on Biological Diversity (CBD). It provides a framework for the effective implementation of the fair and equitable sharing of benefits arising out of the utilization of genetic resources. Biological control is one of many research activities that requires access to genetic resources. Historically, the principle of free multilateral use and exchange of natural enemies between countries has allowed prompt implementation of biological control programs against invasive alien species. However, this global benefit-sharing changed when countries adopted national ABS regulatory measures without undertaking a strategic planning process. At present, 8 South American countries are parties to the NP and 5 are not. Several points in the national ABS regulations are a cause for concern for research entomologists and biological control practitioners in South American countries. Complicated procedures to access genetic resources for non-commercial research such as classical biocontrol programs, uncoordinated redundant and bureaucratic procedures to control biodiversity research or utilization, and the lack of institutional capacities to facilitate ABS matters and a rapid turnover of officials, are some of the common difficulties shared by research entomologists and biological control practitioners in South America. Projects have even been abandoned due to difficulties and long delays in satisfying a country's provincial or national requirements and the various interpretations of how to protect their biodiversity. This presentation agrees with the objectives of the CBD and the NP in favor of a fairer and more equitable sharing of benefits arising from the use of genetic resources and the legitimate sovereign rights of countries and provinces over their genetic resources. However, it analyzes the unintentional negative consequences ABS provincial or national regimes can have on biological control research and practice. The present work aims to describe the present challenges for the access and use of biological control genetic resources in South America, particularly in Argentina.

Why Flies? Making the Undesirable, desirable

Authors: McAlister Erica, Natural History Museum, London, United Kingdom

Abstract: Flies have had a lot of bad PR. Their roles as Vectors dominate the news. But what about their roles in pollination, food webs, decomposition, biological control and just their natural splendour - how much is known about them and their ecological roles to other entomologists, researchers, the public and the Funders? And whose fault is it? Maybe we need to talk about our subject better?

SciComm has only recently been valued within many Academic departments as a useful and meaningful way of communicating research but there are still very few active scientists who regularly engage and communicate with a wider audience on their research topics. In this day and age, with less funding and a lack of understanding of key scientific topics can we afford to not get involved with more SciComm?

I will introduce how I balance the need to communicate my science and the subjects I study with my need to do my science, how I can show off the collections and value of them without it having a negative impact on other work areas, and how I can get folks to listen to me rant about the value of all flies, including the mosquitoes.

Systematics of the important but problematic wasp genus Psyllaephagus (Hymenoptera: Encyrtidae): parasitoids of lerp insects (Hemiptera: Psylloidea)

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Abstract: Species of the host specific, obligate parasitoid wasp genus Psyllaephagus (Hymenoptera: Encyrtidae) are the principal natural enemies of psyllids (Hemiptera: Psylloidea). The genus contains approximately 240 described species worldwide, of which 110 are known from Australia, where they comprise a poorly known fauna that parasitise lerp forming psyllids. As such, they are important for regulating natural psyllid populations as well as biocontrol of pest lerp insects. However, the taxonomy of the Australian fauna is in a state of confusion, with species being poorly described and mostly unidentifiable, due, in part to their tiny size and morphological complexity, but more so to the poor condition of type material and the absence of host records. Most Australian Psyllaephagus species are virtually unidentifiable due to their largely intractable taxonomy and historically poor descriptions based largely on trivial characters (colour, pattern) from often single specimens from undetermined hosts and patchy location records. This results in a misrepresentation of the true diversity of the Australian fauna and an almost complete lack of knowledge regarding host psyllid and plant associations. This lack of knowledge limits understanding of the evolution, ecology and true diversity of the group. It is likely that the taxonomy of Psyllaephagus can only be robustly resolved by employing a combined approach that integrates morphology, multi-gene sequencing and verified host data. Therefore, the three primary components of this PhD study are: 1) undertaking extensive field collecting and rearing of parasitoids from authoritatively identified host psyllids from across the continent; 2) generating a multi-gene sequence dataset for all specimens, and 3) examining the morphology of freshly collected, and pinned museum material, and comparing these to holotype material, particularly those that have associated host data. These components will provide an important framework to answer key questions regarding the biology, diversity, identification and host relationships of Australian Psyllaephagus.

The biological control triangle as a guide for selecting natural enemies for biological weed control

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Abstract: What evidence do we require to assure biocontrol is necessary, safe, and effective? To help answer this question, practitioners of biological control would like some simple heuristic that may not be optimal or perfect but is sufficient for their immediate goals. Here I propose the biological control triangle, which is an adaptation of the disease triangle used by plant pathologists to help envision and evaluate interactions among a host, a pathogen, and an environment. My modification of this framework incorporates (1) attributes of the enemy that confer virulence (including host specificity, colonizing ability, foraging ability, and feeding ability), (2) attributes of the host that confer susceptibility (including resistance and tolerance), and (3) abiotic and biotic drivers that create a permissive environment. Abiotic drivers include disturbance, temperature, moisture, wind, as well environmental cues such as photoperiod; biotic drivers include effects of neighboring plants, herbivores, carnivores, and mutualists. I also include practical considerations such as how easy a candidate control organism is to rear and redistribute. Progress requires more attention to the measurement and meaning of each attribute, transforming incomplete verbal definitions into variables and parameters that derive their meaning from a precise theoretical context. The biological control triangle offers a basis for understanding and predicting outcomes of invasion and biological control, identifying knowledge gaps, facilitating communication, and directing management of invasive plant species.

Transcriptional control of developmental timing

Authors: McKay Daniel, UNC Chapel Hill

Abstract: Systemic pulses of ecdysone trigger global changes in gene expression during developmental transitions and coordinates their timing between physically distant tissues. Gene expression changes induced by ecdysone are both tissue- and temporal-specific. The molecular basis for this specificity remains unclear. We investigate these questions through genetics and genome-wide profiling of ecdysone-regulated transcription factors during metamorphosis in Drosophila. Ecdysone regulates transcription through a genetic hierarchy. At the top of this hierarchy is the ecdysone receptor, a heterodimer of EcR and Usp. We have discovered that EcR binds extensively across the genome in a temporal and tissue-specific manner. In addition to its direct role in regulating gene expression genome wide, EcR induces expression of a set of primary response transcription factors. Genome-wide profiling of primary response factors indicates they also exhibit widespread binding. More importantly, we find that they play key roles in controlling accessibility of temporal-specific enhancers. By contrast, EcR does not control accessibility of enhancers. Instead, it differentially regulates their activity. The model that emerges is one wherein ecdysone triggers activation of primary response transcription factors through EcR; these factors then remodel the chromatin landscape in combination with tissue-specific transcription factors to drive temporal changes in lineage-specific gene expression programs.

Taking natural surveys to the lab: Describing infection patterns of a recently-discovered insect densovirus in a western North American Lycaenid

Authors: McKeegan Kelli[1], Smilanich Angela[1], Forister Matthew[1] and Teglas Michael[1], [1]University of Nevada, Reno, United States

Abstract: Understanding host-pathogen relationships in natural systems requires knowledge of the patterns of infection at the individual level. Studying the effects of life stage, host diet, and maternal infection status on disease progression helps inform us of pathogen transmission strategies along with the ability of the host to eliminate or tolerate infection. The Junonia coenia densovirus (JcDV) was first discovered in the buckeye (Junonia coenia) but has since been discovered to infect multiple species of Lepidoptera. JcDV is contracted orally by larvae and causes hypoxia and interruption of molting, often leading to death before adult emergence. The Melissa blue (Lycaeides melissa) is a multivoltine, sexually dimorphic butterfly that exists in genetically isolated populations across western North America. It specializes on native species of legumes (Lupinus, Glycyrrhiza, Astragalus, and Lotus genera), but has recently been found to incorporate feral alfalfa (Medicago sativa) as a novel host. In our preliminary indication that JcDV infects wild Lycaenids, we found compelling variation of viral frequency and load across populations of L. melissa adults. In this study, we reared larvae from wild-caught L. melissa females from a subset of populations, on different host plants. Larvae were infected with JcDV at the third instar and monitored for condition (i.e. mass) and survival. Additionally, frass was collected for a measure of virus eliminated into the environment, and a subset of larvae were sacrificed at 2-day increments post-inoculation to be screened for viral load. The results of this study help us describe the course of infection in this particular host-pathogen system, and uncover possible transmission strategies of the virus and disease resistance abilities of the host. By investigating the patterns of infection through manipulation in individuals, we can begin to understand the disease dynamics and ecological interactions of entomopathogens in the wild.

Using RNAi to Manage Invasive Wasps in New Zealand

Authors: McLaughlin Gemma[1] and Gilligan Josh[1], [1]University of Otago, New Zealand

Abstract: Invasive wasps Vespula vulgaris are extremely successful in New Zealand, where they reside at their highest densities on a global scale. The use of fipronil as an insecticide has worked with great success, but is limiting in terms of distribution, especially in their most populous regions, Nothofagus beech tree forests. Here, we attempt using RNAi with a variety of genes via both feeding and microinjection. Results varied with each gene; where krupple feeding subjects had no obvious uptake while individuals treated with cinnabar via microinjection displayed striking phenotypes. These findings provide insight into the viability of RNAi as a form of wasp control in countries where they reside as pests.

Native bee phenology: Quantifying phenological niches of bees in the Chihuahuan Desert, New Mexico, USA

Authors: McLaughlin Jade[1], Hallmark Alesia[1] and Rudgers Jennifer[1], [1]University of New Mexico, United States

Abstract: Understanding pollinator responses to climate change is increasingly important as we recognize how vital pollinators are to the global community. A more thorough understanding of the life history traits of these animals can help in predicting these responses and defining both current and future interactions between pollinators and their environments. Our study quantifies the phenological niches of bees in order to evaluate the risks of climate change to the disruption of plant-pollinator networks, particularly for specialist bees and the plants they pollinate. We analyzed data collected at the Sevilleta Long Term Ecological Research Program(LTER), where they have the world's longest continuously monitored bee community (2002 to present). This study has specimens collected monthly from February to October and has thus far resulted in the identification of over 300 species in the central New Mexico region. A monthly plant phenology dataset with species level resolution has been monitored concurrently with the bee data at the same location. By comparing plant and pollinator phenology with local climate data we ask the following questions: Do phenological niches change over time? Which biotic or abiotic factors influence phenological niches? How do phenological niches affect competition and coexistence?and Can we use phenological niches to predict future species interactions under climate change? The methodologies for quantifying and detecting phenological mismatch and its relationship to climate change are still in their early stages. Renner and Zohner (2018) suggest long-term data will be hugely influential in refining this area of research. We predict that precipitation will play a major role in bee seasonality due in part to the arid-land environments. Determining the phenological drivers of mutualist interactions could indicate if trophic asynchrony is occuring in the Chihuahuan Desert and its likelihood to occur in similar environmental regions around the world. Our results could influence understanding of pollinator seasonality and life histories, plant-pollinator mutualisms, the management of potentially threatened species, and agricultural impacts of native pollinators.

Natal origin, host plant use and mating: Reflections of “you are what you eat” in migrant Lepidoptera.

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Abstract: Many traditional techniques, such as mark-recapture or telemetry, are not particularly effective tools for studying the migration of insects. In this presentation we will discuss our ongoing research involving the use of naturally occurring stable isotope ratios (d13C, d15N and d2H) in various insect tissues to study different aspects of migration of two two noctuid pest species, the western bean cutworm, Striacosta albicosta, and the true armyworm, Mythimna (Pseudaletia) unipuncta, and the monarch butterfly, Danaus plexippus. We will describe how we are using novel isotopic approaches to address questions relating to natal origin, origin of mates based on spermatophores, larval host plants and habitat type, as well as the relative contribution of larval and adult food sources on lipid resources.

The scale of neighborhood effects on Solanum carolinense herbivore damage and reproduction

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Abstract: Associational effects (AE) occur when the frequency or density of plant neighbors affects the damage a focal plant receives from insect herbivores. While many studies have documented AE on individual plants, understanding the fitness consequences of AE requires isolating the potentially interactive effects of competitors on plant size and damage. Additionally, spatial scale is known to affect insect foraging decisions, so the strength of AE may vary with spatial scale of the defined neighborhood. However, it is not understood whether spatial scale affects the magnitude of AE or the degree to which the fitness effects of intra- or interspecific competitors are mediated by damage versus plant size. To answer these questions, we varied the frequency, intraspecific density, and interspecific density of the clonal perennials Solidago altissima and Solanum carolinense in a field experiment. Three times during the growing season, we measured the size and damage level of each of the 438 Solanum plants in the experiment. At the end of the growing season, we measured the plant biomass and total diameter of the fruits of each Solanum plant as correlates of asexual and sexual reproduction, respectively. We then used SEM to quantify the effect of a Solanum plant’s neighborhood (competitor density and frequency), damage, and size at each survey date on its neighborhood, size, and damage at the next survey date. We also quantified the effects of a plant’s neighborhood, size, and damage level at the final survey date on its final biomass and fruit production. We performed this analysis at nine different spatial scales by defining neighborhoods at nine different radii around each focal plant, ranging from 25cm to 300cm. We found both damage- and size-mediated neighborhood effects of Solanum density, Solidago density, and Solidago frequency on Solanum fitness; the presence of these effects depended on spatial scale. There were negative effects of Solanum density on Solanum damage (i.e., resource dilution), which resulted in positive effects on Solanum biomass and fruit production. The effects of intraspecific density on fruit production existed only at scales up to 100cm around the host plant and opposed the negative, size-mediated effects of intraspecific density on fitness existing at all spatial scales. We also found positive effects of Solidago density and frequency on Solanum damage (i.e., associational susceptibility), which resulted in negative effects on Solanum biomass and fruit production. Interspecific density effects on fruit production existed at scales up to 100cm around the host plant, and interspecific frequency effects on biomass and fruit production existed at scales up to 200cm. These negative effects reinforced the negative, size-mediated effects of interspecific density and frequency on Solanum fitness.

Developing synthetic sex distorters for the genetic control of an agricultural pest insect

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Abstract: The Mediterranean fruit fly (medfly), Ceratitis capitata, is one of the world’s most economically important agricultural insect pests. Currently, medfly control is mainly based on the use of insecticides and on the Sterile Insect Technique (SIT). SIT involves mass-rearing?, sorting and release of sterilized male flies that through mating with wild females locally suppress the wild population. X-shredding is a novel genetic control strategy based on CRISPR-induced shredding of the X chromosome during spermatogenesis and has been successfully applied to Anopheles gambiae the malaria mosquito. Here, we describe the development of an in-vivo CRISPR system in the medfly using Cas9 nuclease targeting the white eye gene during spermatogenesis and demonstrate highly efficient mutagenesis in progeny. We also describe the identification of abundant and X-chromosome specific CRISPR target sites and develop X-shredders targeting these sequences. Our best-performing X-shredder strains display 75% sex ratio distortion towards males. These results open new possibilities for developing sex ratio distorters in this important agricultural pest. The successful transfer of this system to the medfly represents an important step towards the development of novel genetic control approaches in this pest and the potential for its universal application in other pests with a XY male karyotype.

Plant genotypic variation and herbivore specialization influences plant-insect interactions across a geographic gradient

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Abstract: Anthropogenic changes, such as invasive species and climate change, strongly influence plant-herbivore evolution and these changes can result in the outbreak of weeds and pests, and a decline in native species. However, specialists and generalists herbivores have different constraints on their behavior, and we predicted that this would lead to different preference-performance relationships. We hypothesized that genotypic and geographic variation in plant traits would differentially influence plant resistance across a gradation of insect specialization.

We compared the responses of a polyphagous, an oligophagous, and a monophagous herbivore to genotypic variation in tall goldenrod, Solidago altissima. We compared how the highly specialized endophagous gall fly, Eurosta solidaginis, the moderately specialized ectophagous red aphid, Uroleucon nigrotuberculatum, and the ectophagous generalist chrysanthemum lace bug, Corythucha marmorata responded to differences in genotypic variation of tall goldenrod resistance.

We predicted that the greater the insect specialization, the stronger the relationship between oviposition preference and offspring performance would be. We used replicated plant genotypes from six populations in the USA and Japan to compare preference and performance of the three herbivores. We tested the prediction that the preference-performance relationship would be influenced by herbivore specialization and local adaptation. We also tested the prediction that the suitability of plant genotypes would differ for each of the herbivores, and that it would be influenced by variation in plant traits.

Overall, we found that insect specialization influenced insect preference for local and nonlocal plant genotypes. We also found that goldenrod genotypes varied in their morphological traits, and that this influenced insect preference and performance. Gall flies preferred the local plant population, however, it also preferred two nonlocal plant populations. Red aphids showed a preference to both plant population and plant genotype within population. Lace bug preference was positively influenced by the presence of galls, and therefore they preferred the same populations as the gall flies. We conclude that differences in the responses of specialist and generalist herbivores to variation in plant genotypes in plant traits influences their distribution and abundance.

How automation, machine learning, and DNA barcoding can accelerate species discovery in “dark taxa”: Overview

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Abstract: Insect biodiversity remains poorly understood although it comprises much of the terrestrial animal biomass, most species, and supplies many ecosystem services. One major obstacle is specimen-rich samples obtained with quantitative sampling techniques (e.g., Malaise trapping). Traditional sorting requires too much time. At the Center of Integrative Biodiversity discovery at the Museum für Naturkunde in Berlin, we work on specimen-based approaches that pick individual specimen from bulk samples for barcoding. We developed a robot (“DiversityScanner”) that detects, images, and measures individual specimens and moves them into the wells of a 96-well microplate. The images are used to train convolutional neural networks (CNNs) that are capable of assigning the specimens to common 14 insect “families”. To obtain biomass information, the images are also used to measure specimen length and estimate body volume. In order to obtain DNA barcodes, we have developed cost-effective barcoding techniques with MinION sequencers and bioinformatics tools for approximate species-level sorting. I here outline how the DiversityScanner can be a key component for automated species discovery in “dark taxa.” via a combination of automation, machine learning, and DNA barcoding. Two additional talks present more information on how to integrate morphology into the workflow and how the DiversityScanner works.

Detection of viral RNAs by Dicer-2 in Drosophila

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Abstract: Viruses are the most abundant intracellular parasites on earth, which can infect all cell types. Their impact is constant on our life from the diseases they cause as well as agricultural losses. Therefore, studying the mechanisms with which different organisms control viral infections is very important. The host's first line of defense - innate immunity - is initiated by the recognition of viruses as non-self. The key to this system is largely based on the detection of viral nucleic acids. In mammals, recognition of viruses can occur in two ways: inside the endosomal compartment by Toll-like receptors (TLR) or in the cytoplasm by RIG-I like receptors (RLR) as well as others cytoplasmic receptors. We aim to understand the dynamics of RNAi proteins during viral infection as well as the role of modifications of viral RNAs which could be recognized as non-self in the host cell.

In order to understand how viral nucleic acids are detected by the immune system, it is important to consider on the one hand (i) how the RNAi proteins (eg Dicer-2, R2D2 and AGO2) recognize viruses and then inhibit them and secondly (ii) the different types of nucleic acids generated during a viral infection. In Drosophila, the only known receptor for viral RNA to date is the protein Dicer-2, a key component of the RNAi pathway. Dicer-2 is an RNaseIII-like enzyme that cleaves duplex double-stranded RNA (dsRNA) by 21 bp called siRNAs. One of the strands of siRNA is then loaded onto the enzyme AGO2 in the RISC complex (RNAi Induced Silencing Complex). This strand will then guide the RISC complex towards the viral RNAs whose sequence is complementary, which will then be cleaved by AGO2 (an enzyme from the RNase H family). All viruses tested to date are subject to RNAi-dependent testing. Even if the RNAi pathway essential for antiviral immunity in Drosophila, the question of recognition of viral RNAs remains open.

Chemical diversity in plant – egg parasitoid interactions: a useful tool for biological Control?

Authors: Meiners Torsten, Julius Kuehn Institute (JKI), Federal Research Centre for Cultivated Plants, Germany

Abstract: Worldwide, in many crop systems a large number of parasitoids of arthropod pests have the potential for biocontrol of the pest organisms. However, their efficacy is often not high enough to warrant a substantial reduction of their hosts - and of yield losses. How can we enhance this efficacy? First, we need to understand the evolution and complexity of parasitoid – environment interactions. Plant - arthropod interactions have evolved in complex environments, formed primarily by the diversity of host and non-host plants. The functions of diverse areas next to crops are numerous because they allow the existence of alternative hosts, provide sites for aestivation or overwintering, and give nourishment to adults. However, a big part of this complexity is of chemical nature and plant chemical diversity might be used as a tool to enhance the efficacy of (egg) parasitoids. Parasitoids of crop pests have evolved physiological and behavioral mechanisms to cope with or even to utilize the chemical diversity of the crop environment for successful host finding.

Also in agroecosystems plant constituents fulfill a multitude of biological functions and determine the relationships between crops, pests and beneficial arthropods from the level of molecules to their function in the ecosystem and the agricultural landscape. In conservation biological control, strategies for conservation and enhancement of parasitoid efficacy need to be developed or improved that involve a positive effect of chemical diversity on beneficial arthropods. What is needed to make this happen? One option to achieve this is to adjust the composition of field margins or other non-crop areas in a way that they are supporting functionally populations of parasitoids of nearby crop pests. While commercial seed mixtures for birds, bees and butterflies exist, there are hardly any mixtures available supporting biocontrol. Seed mixtures for field margins or flowering areas including non-host plants are needed that support host search, maintenance and survival of beneficial arthropods and deliver ecosystem functioning and ecosystem services by providing the required chemical diversity. To achieve this a) the diversity of plant compounds from selected field margin or flowering area plants need to be investigated and b) the scent diversity of the entire flowering area needs to be determined and compared with overall arthropod biodiversity and specific multitrophic interactions. At the same time, it should be investigated how the composition of primary and secondary plant compounds varies depending on the abiotic environment and affects the arthropod communities in terms of plant quality, resistance and stress tolerance on the arable land and in the neighboring non-crop areas. This knowledge will allow deciding if chemical diversity in plant/ egg parasitoid interactions can be applied as biocontrol tool.

Comparative biology and behaviour of Trissolcus japonicus and Trissolcus mitsukurii at different temperatures

Authors: Mele Alberto[1], Avanigadda Dinvesh Sai[1], Martina Elisa[1], Simoni Filippo[1], Duso Carlo[1], Scaccini Davide[1] and Pozzebon Alberto[1], [1]University of Padua

Abstract: Trissolcus japonicus and Trissolcus mitsukurii are two Asian scelionid egg parasitoid that has been observed parasitizing Halyomorpha halys in Italy. These two parasitoid are active natural enemies of H. halys in Asia. In the North of Italy these two parasitoid species shows an overlapping distribution and are potentially engaged in an interspecific competition for the same resource represented by H. halys eggs. Differential response to climatic factors can influence the outcome of the competition. In laboratory experiments, we compared the life table parameters of these two egg parasitoid species under 3 constant temperatures (21, 26 and 31°C). We also compared behavioural response along increasing temperature from 5 to 25°C. The net reproductive rate of T. japonicus was greater than T. mitsukurii at 26°C and 31°C. The intrinsic rate of increase at 26°C and 31°C is similar between the two species, whereas the intrinsic rate of increase and the finite rate of increase was greater for T. mitsukurii at 21°C. Results suggest a better performances of T. mitsukurii at low temperature as compare to T. japonicus, while higher performances of the latter were observed temperature above 26°C. Behavioural response to increasing temperature suggest that T. mitsukurii activity start at lower temperature as compare to T. japonicus. Overall, of the result suggest that T. mitsukurii is more adapt to low temperature regimes as compare to T. japonicus that are expected to be advantaged under high temperatures conditions.

From a rare inhabitant into a potential pest – Status and outlook of the nun moth (Lymantria monacha) population in Finland based on pheromone trapping

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Abstract: Forests are being hit by climate change in various ways. This includes abiotic factors such as droughts, but also an increased risk of damage caused by biotic agents such as insects. There are numerous examples from cases where a pest insect has benefitted from endured growing season or from warmer summers. Similarly, new pest insects have been able to expand their range due to climatic conditions that have changed from hostile to tolerable.

Such seems to be the case with the nun moth (Lymantria monacha), Europe's most significant defoliator of coniferous trees. For centuries, the species has had massive outbreaks across Central-Europe while it has been only a rare inhabitant in Northern Europe. Recently, the nun moth population in Finland has not only expanded in range, but also grown more abundant.

Extensive field survey in 2019 showed that, so far, the northernmost individuals occupy forests near the 64 N degrees. The species was present in every trapping site below the latitude of 62 N degrees. More importantly, at some sites the abundance of the nun moth suggested that local forest damage may not be a distant scenario. Given the current climatic scenarios for Fennoscandia, it is likely that the nun moth populations will continue to grow, which is why systematic surveys on their abundance and range expansions are vital.

In the proposed presentation, I wish to illustrate the results from the first-ever conducted extensive pheromone survey of the nun moth in its northernmost range: abundance across the study area and range boundaries. In addition, I will discuss the efficacy of the trapping method as well as the future of the species and its forest damage potential, especially given the current climatic scenarios of Finland.

Irrigation decreases abundances of insects and spiders in Mediterranean vineyards

Authors: Melloul Emile[1], Rocher Leo[2], Gros Raphaël[2], Bischoff Armin[2] and Blight Olivier[2], [1]Avignon University, France, [2]Institut of Mediterranean Biodiversity and Ecology

Abstract: In a changing world, the identification of vulnerability and resilience factors of agroecosystems to climate change has become a major challenge. Globally, mean annual temperatures and drought periods are increasing which poses a threat to agriculture and related biodiversity. As a key sector of French agriculture, viticulture must be adapted to increase resilience to climate change. In southern France, the proportion of irrigated vineyards has increased in recent years to cope for higher evapotranspiration and lower rainfall. While irrigation is clearly beneficial to viticulture under water stress, the consequences on biodiversity of such artificial microclimatic conditions have not been studied. The objective here was to evaluate the effects of irrigation on inter-row vegetation and arthropod communities in Mediterranean vineyard systems. We selected nine pairs of vineyards in the Luberon region (Southern France), one irrigated and one unirrigated. In each vineyard, we sampled vegetation and arthropods (spiders, wasps, ladybird larvae and adults, wild bees, hoverflies) in two quadrats. We found a significant reduction in flower cover and abundance of different arthropod groups such as spiders, ladybirds, and wasps in irrigated vineyards. These results have important implications for the conservation of arthropod biodiversity and its associated ecosystem services in Mediterranean vineyards.

Determining contact chemical compounds responsible for host plant recognition in a belowground specialized phytophagous insect

Authors: Menacer Kathleen[1], Le Moal Clémence, Cabon Lilian, Hervé Maxime[1], Cortesero Anne Marie[1], [1]University of Rennes 1

Abstract: In phytophagous insects, key behaviors driving fitness are influenced by plant-related cues. Specialized species have therefore developed the ability to detect and recognize chemical cues produced and emitted by plants of their host range. Despite the considerable importance of belowground insects in ecosystems, determinants of their host plant selection remain poorly understood. We investigated host acceptance by larvae of the cabbage root fly (Delia radicum), a specialist of brassicaceous plants. We used Brassica rapa and Sinapis alba and two cultivars of each species to assess root damage caused by larvae. We also conducted feeding experiments on artificial substrates supplemented with root extracts and used bioguided fractionation to isolate the smallest active chemical fraction.

A contrast in root development was observed between infested and non-infested plants of all cultivars except for one mustard cultivar. All root extracts stimulated larval feeding on the artificial substrates. A feeding contrast was only observed between the two mustard cultivars and one subfraction (the most polar) appeared to contain the molecules responsible for this contrast.

This work supports the involvement of contact compounds in host acceptance by belowground insects and highlights similarities between above- and belowground insects in the mechanisms underpinning host plant selection.

Coding of behaviorally ‘‘meaningful’’ odors by which Conopomorpha sinensis Bradley (Lepidoptera: Gracillariidae) pinpoints its host

Authors: Meng Xiang[2], Ouyang Gecheng[1], Dai Jianqing[1] and Hu Junjie[2], [1]Guangdong Institute of Applied Biological Resources, China, [2]Guangzhou University, China

Abstract: Insect olfactory systems can detect important host signals efficiently from a complex odor background. Conopomorpha sinensis Bradley (Lepidoptera: Gracillariidae) as a host-specific pest of Litchi chinensis and Euphoria longan is periodically outbreaking in southern China. Little is known about the functions of individual volatiles and their combinations in the attraction of C. sinensis to these host taxa. In our study, we analyzed the behavioral and electroantennogram (EAG) responses of C. sinensis to eight major host volatile compounds and their mixtures. Both female and male C. sinensis exhibited an EAG response for all of the volatiles tested, and the volatile components were more stimulatory to female than to male C. sinensis. EAG responses of female antennal stimulation with component ß-guaiene were significantly different to components caryophyllene and ß-elemene, while odorant mixtures including compounds ß-farnesene and a-pinene significantly altered the behavioral and EAG responses of females. Further testing of the female and male behavioral responses to host volatile compounds were obtained in flight orientation studies using a wind tunnel. These findings demonstrate that C. sinensis behavior can be affected by single compounds or compound mixtures. The coding of behaviorally ‘‘meaningful’’ odors provides a new method for the biocontrol of C. sinensis.

IPM is Key to Effective Pest Management: New Biological Tools and Solutions For IPM in Cotton crops

Authors: Mensah Robert, Senior Principal Research Scientist (PSM) Ex Director, Australian Cotton Research Institute Formerly: NSW Department of Primary Industries Locked Bag 1000, Narr

Abstract: Since the 1960s, the control of cotton pests (particularly, Helicoverpa spp., sucking pests, mites etc) in Australia and most cotton growing countries has relied exclusively on the use of synthetic insecticides. The adoption of GM cotton with multiple toxins targeting Helicoverpa spp. has present to be a strong platform for IPM due to the selective toxicity of the Bt proteins. However, even these systems are challenged by potential for target pest resistance to the Bt proteins, which is still essentially a toxin based approach; and, ironically, altered pest complex due to reduced insecticide use. In GM cotton systems in Australia and other parts of the world, sucking bugs have emerged as important pests requiring targeted control or risking the problem of resistance. Sustainable IPM systems in both conventional and GM cotton systems requires a broader array of tools to manage pests and reduce primary reliance on synthetic insecticides This presentation focuses on new approaches to achieve this including innovative bio-control technologies, bio rational pesticides, new and safer pest control alternatives, use of refuge crops as a source of natural enemies, the use of selective insecticides, sampling regimes, decision support tools such as use of beneficial insects to pest ratio treatment thresholds which incorporate the action of existing natural enemies. This will enable growers to build long term self-sustaining IPM systems.

New Innovative Integrated Pest Management Tools and strategies For Cotton crops in Australia

Authors: Mensah Robert, Senior Principal Research Scientist (PSM) Ex Director, Australian Cotton Research Institute Formerly: NSW Department of Primary Industries Locked Bag 1000, Narr

Abstract: Sustainable integrated pest management (IPM) systems in both conventional and transgenic (Bt) cotton systems requires a broader array of tools to manage pests and reduce primary reliance on synthetic insecticides. This presentation focuses on new approaches to achieve this innovative bio-control technologies, bio-rational pesticides, new and safer pest control alternatives, use of refuge crops as a source of natural enemies, the use of selective insecticides, sampling regimes, decision support tools such as use of beneficial insects to pest ratio treatment thresholds which incorporate the action of existing natural enemies. This will enable cotton growers to build long term self-sustaining IPM system. The presentation will challenge the industry to think outside the square, look at the big picture and to think about the long term sustainability of cotton industries worldwide.

Since the 1960s, the control of cotton pests (particularly, Helicoverpa spp., sucking pests, mites etc) in Australia and most cotton growing countries has relied exclusively on the use of synthetic insecticides. The adoption of GM cotton with multiple toxins targeting Helicoverpa spp. has present to be a strong platform for IPM due to the selective toxicity of the Bt proteins. However, even these systems are challenged by potential for target pest resistance to the Bt proteins, which is still essentially a toxin based approach; and, ironically, altered pest complex due to reduced insecticide use. In GM cotton systems in Australia and other parts of the world, sucking bugs have emerged as important pests requiring targeted control or risking the problem of resistance. Sustainable IPM systems in both conventional and GM cotton systems requires a broader array of tools to manage pests and reduce primary reliance on synthetic insecticides This presentation focuses on new approaches to achieve this including innovative bio-control technologies, bio rational pesticides, new and safer pest control alternatives, use of refuge crops as a source of natural enemies, the use of selective insecticides, sampling regimes, decision support tools such as use of beneficial insects to pest ratio treatment thresholds which incorporate the action of existing natural enemies. This will enable growers to build long term self-sustaining IPM systems.

Conserved molecules involved in insect olfaction

Authors: Menuz Karen, University of Connecticut, United States

Abstract: The past few decades have witnessed an explosion of research into insect olfactory systems. The odorant response profile and behavioral significance of multiple receptors from two odorant receptor families have been characterized. However, most receptors are poorly conserved amongst insects, and few other molecules that contribute to odorant responses in olfactory neurons have been identified. Using RNASeq screens in Drosophila, we have identified a number of previously unstudied candidate genes with potential roles in olfaction. We found that one of these genes, a conserved ammonium transporter, acts as a non-canonical odor receptor for ammonia, an attractive odor for a wide variety of insects. Expression of ammonium transporters in the antennae of nearly all insect species examined suggests they could play a similar role in other species. Our recent work centers on a conserved calcium-activated chloride channel expressed in all Drosophila olfactory neurons, but not detected in the brain or other tissues. This ion channel allows for olfactory neuron odorant responses to closely track the level of fluctuating odorants, by enhancing signal termination. Together our approach is yielding an improved understanding of the molecular basis of olfactory signaling in the antenna, and could suggest novel targets for the development of future insect deterrents.

Ecostacking: the way forward for IPM

Authors: Menzler-Hokkanen Ingeborg[1], Hokkanen Heikki[2], [1]Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio, Finland, [2]Organizer, Finland

Abstract: Despite great advances in IPM, global pesticide use has largely continued unaffected, with negative implications for farmer livelihoods, biodiversity conservation, and the human food systems. Recently, the whole concept of IPM has been challenged due to its ambiguity, inconsistencies in implementation, insufficient engagement of farmers, and lack of basic understanding of its ecological concepts. Ecostacking as a concept makes full use of the benefits accruable from ecosystem services via stacking and conservation of functional biodiversity in cropping systems. Stacking implies combining in a synergistic manner the beneficial services of functional biodiversity from all levels and types. This is a comprehensive approach, where the various ecosystem service providers are fully integrated with the rest of the cropping system including agronomic practices. Ecostacking as an approach aims to stimulate the scientific community to develop, design, and implement integrated systems for optimised provision of ecosystem services and the use of plant protection tools, with focus on ecological, economic, and social sustainability of the integrated system.

Caste- and sex-based differences in brain anatomy in the Eastern subterranean termite, Reticulitermes flavipes

Authors: Merchant Austin, University of Kentucky

Abstract: Termites demonstrate a complex division of labor in which individuals develop into one of multiple castes that each possesses a unique role within the colony. Castes show significant differences in the number and type of tasks that they are able to perform, ranging from versatile workers to soldiers that are specialized for colony defense and little else. Given the role of the brain in controlling behavior and sensory processing, are these extreme behavioral differences reflected in differences in brain anatomy between termite castes? Using a deformation-based morphometric analysis, I compared brain anatomy across major castes found in the Eastern subterranean termite, Reticulitermes flavipes. In addition, I investigated the possibility of sexually dimorphic brain anatomy within castes. Significant differences in brain anatomy were found among castes, localized in distinct regions of the brain. Altogether, these results represent the first steps towards understanding the neural basis of caste in this complex group.

Duox determines insect gut symbiosis by stabilizing respiratory network

Authors: Mergaert Peter[1], Shigenobu Shuji[4], Ohbayashi Tsubasa[2] and Kikuchi Yoshitomo[3], [1]Centre national de la recherche scientifique (CNRS), France, [2]Centre national de la recherche scientifique, France, [3]National Institute of Advanced Industrial Science and Technology (AIST), Hokkaido center, Japan, [4]The National Institute for Basic Biology (NIBB), Japan

Abstract: Many insects harbor in specific organs large numbers of symbiotic bacteria, which produce essential nutrients for their host. How the respiratory activity of this large population of aerobic symbionts is maintained and oxygen is efficiently transported to the symbiotic organ is unclear. In insects, oxygen is delivered to organs by the tracheal system consisting of a tubular epithelial network containing a luminal chitin and protein matrix. Here we show that the proliferation of symbiotic Burkholderia insecticola in the midgut crypts of the stinkbug Riptortus pedestris triggers the formation of an extensive network of tracheae enveloping the symbiotic organ. We found that the expression of the gene encoding the ROS-producing dual oxidase (Duox) is tracheae-specific and its down-regulation by RNAi results in the loss of dityrosine crosslinks in the tracheal matrix, a collapse of the tracheal system and a disruption of symbiosis. Down-regulation of the hypoxia-responsive transcription factor Sima or the regulators of tracheae formation Trachealess and Branchless produces similar phenotypes. On the contrary, Duox-dependent ROS did not directly contribute to epithelial immunity in the midgut in response to symbiont or pathogen. Thus, symbiotic bacteria form a strong oxygen-sink in the insect body and the establishment of a tracheal network assures oxygen homeostasis in symbiosis. In addition to known roles in immunity and in the formation of diverse extracellular matrices, Duox is also a crucial enzyme for tracheae stability by establishing a dityrosine network of luminal matrix proteins. We expect that these are conserved functions in insects.

Movement of insects among patches modifies the relationships between insect density and plant patch size.

Authors: Merwin Andrew[1], Inouye Brian[2] and Underwood Nora[2], [1]Baldwin Wallace University, United States, [2]Florida State University, United States

Abstract: Predicting the relationship between insect density (individuals per unit area) and plant patch size is a longstanding goal of insect ecology with potential implications for conservation and pest management. An early conceptual model—the resource concentration hypothesis—suggested that larger patches of plants should have higher densities of insects. However, experimental and observational studies have found all possible relationships—negative, positive, and no relationship—underscoring the need to identify insect, plant, and landscape characteristics that can reconcile these disparate observations. One commonly overlooked factor with the potential to influence the relationship between insect density and patch size is inter-patch movement. For example, in landscapes where insects can readily move among patches, insect abundance in larger patches could reduce the number of potential immigrants to neighboring patches of other sizes and, thus, potentially influence the insect density-patch size relationship. Using a correlated random walk model with simplifying assumptions, we show that in landscapes with multiple patches of different sizes, where insects move among patches through matrix habitat, equilibrium density is higher in large patches compared to small patches (i.e. resource concentration). By contrast, in landscapes with only one patch, where insects cannot move among patches of different sizes, our model shows that larger patches have lower equilibrium insect densities than smaller patches (i.e. resource dilution) when comparing across landscapes. Further, we show that these patterns depend critically on the perimeter-to-area ratio of plant patches rather than area per se. Thus, our model highlights the need to not only consider the geometry of a given plant patch, but to also consider the landscape of patches and the potential movement of insects among them when attempting to predict relationships between the insect density and patch size.

Management of brown marmorated stink bug in Georgia

Authors: Meskhi Nikoloz, National Food Agency, Ministry of Environmental protection and Agriculture of Georgia, Georgia

Abstract: In Georgia Brown Marmorated Stink Bug (Halyomorpha halys) populations were observed during the 2015 season with the first significant damage to hazelnut reported a year later. In addition to hazelnuts, BMSB also has the potential to inflict severe damage to other crops, such as maize, apple, peach, etc.

Since 2017, within the frame of the official program, National food Agency has administered large scale control measures against BMSB in western Georgia. For the monitoring, pheromone traps have been used and in 2017, more than 20000 traps have been installed throughout the whole country. Based on data obtained from monitoring, chemical treatment has been carried out with the help of special NFA equipment. From chemical insecticides synthetic pyrethroids were used.

At locations where the state has enacted measures, the harvest was preserved and pest population decreased

Aphid biocontrol in greenhouses using cocktails of natural enemies

Authors: Messelink Gerben[1] and Bloemhard Chantal[1], [1]Wageningen University & Research BU Greenhouse Horticulture, Netherlands

Abstract: Aphids are among the most challenging pests to control with biological control agents in greenhouse crops. Their fast reproduction soon results in high densities that are difficult to control. Even the presence of one single aphid species often requires releases of several species of natural enemies (parasitoids and predators) to achieve effective control. An additional complexity is the fact that crops are usually attacked by several species of aphids that differ in vulnerability for natural enemies. A common practice in that case is to release cocktails of parasitoid species that each target different aphid hosts. However, it is hardly understood how this diversity of aphid hosts affects the performance of specialist aphid parasitoids. In greenhouse trials with sweet pepper, we studied how mixed populations of green peach aphids, Myzus persicae, and foxglove aphids, Aulacorthum solani, influence the control by specialist and generalist parasitoids. The presence of unsuitable aphid hosts distracted specialist parasitoids from their suitable aphid host and reduced control efficacy. In contrast, unsuitable aphid hosts could still be controlled by parasitoids through non-consumptive effects of parasitoids that developed within suitable aphid hosts. Thus, diversity of aphid species can have both positive and negative consequences for biological control with parasitoids. The control efficacy of parasitoids was further evaluated by releasing cocktails of parasitoids (Aphidius ervi, Aphidius colemani, Aphidius matricaeriae, Aphidius gifuensis and Praon volucre) for the control of either the green peach aphid or the foxglove aphid in a sweet pepper crop. The performance of the different aphids parasitoids appeared to vary strongly throughout the season. Overall we conclude that releasing cocktails of aphid parasitoids might be a good strategy to ensure complementary effects, but mixtures may need to be adapted for the species of aphids present in crops and time of the year.

Natural variation in an odorant receptor alters neural activity and underlies preference for human odor in Aedes aegypti

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Abstract: Mosquitoes use olfaction to target hosts for bloodmeals, and some show innate preference for the odor of specific hosts. Here, we leverage the recent evolution of a human-preferring subspecies of the yellow fever mosquito (Aedes aegypti aegypti) from a generalist ancestor (Ae. aegypti formosus), and use the tools of functional genetics and functional imaging to gain insight into odor coding. In a unique approach, we use genetic complementation (i.e. hemizygosity) tests to measure the effects of four alleles sampled from wild populations on both odor-guided host preference behavior and the activity of primary sensory neurons in the antennal lobe. We functionally confirm a role for AaegOr4 in preference for humans, where AaegOr4 alleles sensitive to the human odorant sulcatone increase preference for human odor compared to an insensitive allele. Additionally, our data suggest that the effects of AaegOr4 are strongest for a human subject showing naturally high sulcatone levels. Functional imaging confirmed that variation in the ligand-sensitivity of alleles measured in vitro correlates with neural activity in vivo.

Because host odors are complex blends comprised of tens to hundreds of individual compounds—each of which may be emitted from many sources in the environment—host discrimination must rely on the integration and coding of unique blend information. Nevertheless, our results demonstrate that the peripheral perception of a single odorant can significantly alter host preference behavior in Aedes aegypti, and represent a functional test of evolved behavioral differences between natural populations.

Uncovering the role of circadian transcription factors in regulating the overwintering dormancy of the Northern house mosquito, Culex pipiens

Authors: Meuti Megan E., The Ohio State University Department of Entomology Columbus, OH, United States

Abstract: Females of the Northern house mosquito, Culex pipiens, are the major vectors of West Nile virus, but during the winter they do not bite or transmit disease. Instead, they divert energetic resources from reproduction towards survival and enter a reproductive diapause. Although we know that the short daylengths of late summer and early fall are the environmental cue that cause females to initiate diapause, we do not understand precisely how mosquitoes and other animals measure daylength. Currently my lab is determining whether circadian transcription factors, vital components of the daily timekeeping machinery in all animals, are involved in measuring daylength and initiating seasonal responses in this disease vector. Our findings show that some circadian transcription factors and their predicted targets show altered daily expression profiles in female mosquitoes exposed to long day, diapause-averting conditions and short day, diapause-inducing conditions. Furthermore, suppressing expression of circadian transcription factors with RNAi prevents short-day reared mosquitoes from entering diapause while knocking down other genes associated with the clock prevents mosquitoes from becoming reproductively active. Ongoing work focuses on connecting the circadian clock to the hormonal pathways, such as Juvenile Hormone and insulin signaling, that are known to regulate diapause. In this way, we hope to identify novel targets that will allow us to manipulate the seasonal biology of Cx. pipiens by either tricking them into going into diapause during the summer, or preventing them from entering diapause in the fall.

Insects and other Invertebrates as Pharma

Authors: Meyer-Rochow Victor Benno, 1. Department of Genetics and Physiology, Oulu University, Oulu SF-90140, Finland; and 2. Department of Plant Medicals, Andong National University, Andong GB 36, South Korea

Abstract: Insects and other invertebrates have been used since time immemorial as a healthy food item. They were credited with potential to ease the problem of global food shortages (Meyer-Rochow 1975), but historically their role in traditional healing methods has been an even greater one. Bioactive honey, anti-rheumatic and anti-inflammatory bee venom, meloid beetles' cantharidin and Chinese cockroaches come to mind. Based on studies on erectile dysfunction and testosterone in rats silkworm pupal extract has been likened to Viagra-like effects (Oh et al. 2012). Umemura (1943) lists 28 species of Lepidoptera used therapeutically in Japan and In Germany just over 100 ys ago beetles of 13 families played some therapeutic roles. Bengaline, an isolate of scorpions in India, has been shown to exhibit antiproliferative and apoptogenic activity against human leukaemic cell lines (DasGupta et al. 2010). Insects and other arthropodes produce the broadest repertoire of antimicrobial peptides (AMPs), which must be considered alternatives to conventional antibiotics (Meyer-Rochow 2017).

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Honeybees and hornets are on the menu: nutritional value

Authors: Meyer-Rochow Victor Benno[1], Ghosh Sampat[3], Jung Chuleui[2], [1]1. Department of Genetics and Physiology, Oulu University, Finland; and 2. Department of Plant Medicals, Andong National University, Andong GB 36, South Korea, [2]1Agricultural science & technology research institute, Andong National University, Andong, GB, Korea 2 Department of Plant Medicals, Andong National University,, [3]Department of Plant Medicals, Andong National University, South Korea

Abstract: Different species of honeybees and hornets have received acceptance as edible insects among several populations of Asia and Africa. In order to explore the proximal background of human entomophagy, understanding these insects' nutritional benefits is of considerable importance. We examined the nutritional contents, including amino acids, fatty acids and minerals from different developmental stages of honeybees and hornets. Bees and hornets were found to contain protein which is comparable if not superior to the conventional foods of animal origin. Seventeen proteinergic amino acids were detected and quantified with similar patterns of distribution in these species. A different pattern was found for fatty acids. The higher proportion of mono and polyunsaturated fatty acids in the lipid fraction of the hornets could not only have nutritional but also medicinal benefits like reducing cardiovascular disorders, and inflammations. The presence of a high level of iron, calcium, and zinc and moreover the high K/Na ratio could supplement the requirements of these minerals and help mitigating mineral deficiencies especially among those of the population with inadequate nutrition. Further discussion involved issues like the extent of production of brood without stressing adult bees or hornets, utilization of drones and development of industrial production system. The results could help understanding the prospects of these edible species in the mainstream food system.

Miniaturization to the Extreme: The Compound Eye of a 0.65 mm Long “3-Eyed” Gall Midge (Diptera; Cecidomyiidae)

Authors: Meyer-Rochow Victor Benno[1], Yamahama Yumi[2], [1]1. Department of Genetics and Physiology, Oulu University, Finland; and 2. Department of Plant Medicals, Andong National University, Andong GB 36, South Korea, [2]Hamamatsu University School of Medicine

Abstract: Cecidomyiid midges of the genera Trisopsis and Lestodiplosis possess three compound eyes. The single dorsal compound eye of our only 0.65 mm long cecidomyiid specimen contained 90 ommatidia and represented the fusion product of left and right dorsal moieties jointly covering an area at the top of the head of 7000 µm2. Each of the two latero-ventral compound eyes on either side of the head consisted of approximately 35 ommatidia that did not differ anatomically from those of the dorsal eye (with the exception of the interommatidial angles, which measured 10-12° and thus much narrower than those of the dorsal eye). With regard to photoreception Diptera are interesting subjects. Not only has the compound eye of Drosophila been one of the genetically most-researched photoreceptors of animals generally, but because moreover the dipteran compound eye possesses an ‘open rhabdom’, which for biophysical reasons faces limitations when it comes to miniaturization. In a 0.7 mm size cecidomyiid midge with one dorsal and two lateral compound eyes, the retinal layers of both the dorsal and the lateral eyes were extraordinarily thin, only measuring approximately 12 µm, but all ommatidia were capped by 8 µm thick and 8-10 µm wide corneal lenses with a dense and regular coverage of 160 nm high corneal nipples. Despite being a species of the order Diptera, for which open rhabdoms are characteristic, our tiny cecidomyiid possessed the fused type of rhabdom with microvilli measuring 65 nm in diameter. It is postulated that dspite the reduction in body and eye size, rhabdomeres could not be scaled down as they had already reached their functional cross sectional limit of 1.5-2.0 µm in Diptera the size of Drosophila. A further reduction would have rendered the rhabdom ineffective as a waveguide. As the tiny insect was a swift flyer and on the basis of the eye‘s anatomy it is discussed what the insect could possibly see with its tiny eyes.

Kampinos WetLIFE: Protection and restoration of wetlands in Puszcza Kampinoska Natura 2000 site in Poland, creating habitat for butterflies and dragonflies (LIFE19 NAT/PL/000746)

Authors: Miazga Michał, Regional Environmental Center, REC Poland, Poland

Abstract: The Kampinos Forest Natura 2000 site has the largest complex of wetland habitats in central Poland. Well-preserved habitats now cover just 5% of the primaeval wetland area, after land reclamation over the past 150 years severely lowered groundwater levels. The site is especially vulnerable to extended dry periods and increasing fluctuations in water levels caused by climate change. Through this project, Kampinos National Park is restoring over 6000ha of habitat through the removal of non-invasive species, improvements to the hydrology, creation of ponds and naturalisation of man-made water courses to benefit species in need of strict protection including butterflies such as the scarce large blue (Maculinea teleius) and large copper (Lycaena dispar) and large white-faced darter (Leucorrhinia pectoralis).

Intracellular Burkholderia symbionts of eriococcids Acanthococcus aceris and Gossyparia spuria (Hemiptera: Coccomorpha)

Authors: Michalik Anna[5], Bauer Eugen[1], Michalik Katarzyna[3], Kalandyk-Kolodziejczyk Malgorzata[4], Kaltenpoth Martin[1] and Szklarzewicz Teresa[2], [1]Department for Evolutionary Ecology, Institute for Organismic and Molecular Evolution, Johannes Gutenberg University Mainz, [2]Department of Developmental Biology and Morphology of Invertebrates, Institute of Zoology and Biomedical Research, Jagiellonian University, [3]Department of Developmental Biology and Morphology of Invertebrates, Jagiellonian University, Kraków, Poland, [4]Department of Zoology, University of Silesia, Katowice, Poland, [5]Jagiellonian University, Poland

Abstract: Hemipterans are known as hosts to bacterial or fungal microorganisms that supplement their unbalanced diet with essentials nutrients. Among them, scale insects (Coccomorpha) are characterized by the large diversity of symbiotic systems. Numerous investigations have revealed that they may be associated both with bacteria (e.g. Tremblaya phenacola, Tremblaya princeps, Uzinura dispidicola, Wolbachia) as well as fungi (Ophiocordyceps). We analyzed using microscopic and molecular approaches, symbionts of two scale insects belonging to Eriococcidae family – Acanthococcus aceris nad Gossyparia spuria. Histological and ultrastructural studies have shown the presence of numerous, small, rod-shaped bacteria in the cytoplasm of fat body cells. Based on their 16S rDNA sequence, these bacteria were identified as bacteria Burkholderia (Betaproteobacteria). Metagenome sequencing has indicated that the symbionts of Acanthococcus aceris and Gossyparia spuria possess highly reduced genomes (<900KBp) with a low GC content (~38%), making them the smallest Burkholderia genomes yet sequenced. Overall, the genomic repertoire of the symbionts is congruent in terms of gene content and synteny, highlighting a convergent reductive genome evolution in these bacteria. Compared to free-living Burkholderia, the symbiotic strains have less genes involved in housekeeping functions, while retaining genes for essential amino acid biosynthesis, indicating potential roles for their hosts similar to other nutrient-supplementing insect symbionts. The transovarial transmission of bacteria Burkholderia between generations also confirms their crucial role in the biology of eriococcids analyzed.

This work was supported by the DS/MND/WBiNoZ/IZ/4/2014 from the Ministry of Science and Higher Education in Poland and Consolidator Grant of the European Research Council ERC CoG 819585 “SYMBeetle”.

Symbiont loss and replacement in Fulgoromorpha (Insecta, Hemiptera)

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Abstract: Nutritional symbiosis with heritable bacterial or/and fungal microorganisms is widespread within sap-sucking hemipterans. These symbionts provide essential amino acids and vitamins that are lacking in the diet of their host insects, which makes them necessary for their growth and reproduction. Within Fulgoromorpha, Sulcia (Bacteroidetes) and Vidania (Betaproteobacteria) are regarded as their ancestral symbionts, maternally transmitted and co-diversifying with hosts for over 200 million years. However, the literature data indicate that additional, more recently acquired bacteria or fungi may co-reside with, or sometimes replace, these two ancient bacterial symbionts.

We combine microscopic (LM, TEM, FISH) and molecular (amplicon sequencing, molecular cloning, metagenome sequencing) approaches to characterize the symbiotic systems of several species belonging to the following families of planthoppers: Dictyopharidae, Derbidae, Achilidae, Cixiidae, Tettigometridae, Issidae, Delphacidae and Flatidae.
The ancestral nutritional symbionts Sulcia and Vidania are present in all tested representatives of families Dictyopharidae, Cixiidae and Tettigometridae as well as in some of Achilidae, Issidae and Delphacidae. In some families ancestral bacterial symbionts are associated with additional gammaproteobacteria such as: Sodalis (some Dictyopharidae, Issidae, Delphacidae, Tettigometridae), Arsenophonus (some Dictyopharidae) or Purcelliella (Cixiidae) or fungi (some Issidae). Members of Derbidae family and some representatives of Achilidae lost the Sulcia symbiont and retained only Vidania. In the issid Issus coleoptratus Sulcia was lost and replaced by fungal symbionts which co-reside with bacteria Vidania. In turn, representatives of Flatidae family are host to fungal symbionts only. The most diverse, in respect of symbiont composition, is the family Delphacidae. Our investigations revealed that members of this family: (1) may possess both Sulcia and Vidania, (2) besides ancestral symbionts, may host Sodalis, or (3) may harbor fungal symbionts exclusively.
Our investigations confirmed the hypothesis that during the evolution of Fulgoromorpha both loss and symbiont switching /replacement took place.

This work was supported by Sonata 13 grant No. 2017/26/D/NZ8/00799 from National Science Centre, Poland

Symbiotic systems of treehoppers (Hemiptera: Cicadomorpha: Membracoidea: Membracidae). Ultrastructure, distribution and transovarial transmission

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Abstract: Treehoppers live in mutualistic associations with symbiotic microorganisms which supplement their diet with essential amino acids. Many microscopic and molecular studies have allowed to reveal that most auchenorrhynchans harbor two ancestral symbionts bacterium Sulcia and betaproteobacterium (e.g. Nasuia in leafhoppers and treehoppers). Some of auchenorrhynchan species harbor additional symbiotic microorganisms, e.g. gammaproteobacteria Arsenophonus and Sodalis, in others the betaproteobacterium or both ancestral symbionts have been lost and replaced by other bacteria or yeast-like microorganisms.
We examined symbionts of three species of treehoppers: Centrotus cornutus, Gargara genistae and Stictocephala bisonia. In all the examined species, large elongated organs termed bacteriomes are present in the close vicinity to the ovaries. The bacteriomes are composed of numerous large bacteriocytes that are densely packed with symbiotic bacteria. The external region of the bacteriome contains bacteriocytes filled with large pleomorphic bacteria Sulcia. The internal region is occupied by bacteriocytes with large lobated bacteria Nasuia. In C. cornutus, between the bacteriocytes with bacteria Sulcia and Nasuia, bacteriocytes with elongated bacteria Arsenophonus are localized. Bacteria Arsenophonus co-reside also in bacteriocytes with bacteria Nasuia. In G. genistae, instead of the bacteria Arsenophonus, the small almost spherical bacteria Serratia are present both in their own bacteriocytes and in bacteriocytes with bacteria Nasuia. The presence of autophagosomes and lamellar bodies in the bacteriocytes with bacteria Arsenophonus and Serratia in all the examined individuals indicates that these microorganisms undergo autophagic degradation. In all of the examined species of C. cornutus and G. genistae, in the cytoplasm and nuclei of all the cells of the bacteriome numerous small rod-shaped bacteria Rickettsia are present.
Our observations indicate that all symbionts are inherited in a way typical of auchenorrhynchans, through the infection of the posterior ends of ovarioles containing vitellogenic oocytes. The symbiotic microorganisms leave the bacteriocytes and begin to migrate towards the ovarioles. The bacteria gather around the posterior ends of the ovarioles and enter the cytoplasm of follicular cells which surround the oocytes. Subsequently microorganisms enter the space between the oocyte and follicular epithelium (perivitelline space). Symbionts closely adhere to each other and aggregate in an accumulation, termed a ‘symbiont ball’.

ACKNOWLEDGEMENTS:
This work was supported by research grants: MINIATURA 1 research grant DEC-2017/01/X/NZ8/01025 from the National Science Centre and K/ZDS/008068 and N18/DBS/000013.

Landscape effect on bioaccumulation of pesticide residues in local food webs in agroecosystems

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Abstract: One of the main reasons the existing strict European regulation of pesticides use fails in protecting ecosystem health is that natural dynamics and ecosystem functioning are often overlooked. For example, no empirical study to date has investigated how landscape composition affect bioaccumulation in local food webs in agroecosystems through a multiple-residue mixture of pesticides. This knowledge is essential for designing highly functional landscapes that would minimize pesticides' incorporation into food webs and negative impacts of pesticides on the environment, biodiversity, and human health. We explored the presence of pesticides in the groups soils, plants, rodents, and spiders within fruit orchards and vineyards. We found the concentration of pesticides to be highest in spiders as predicted by the biomagnification hypothesis. The spectrum of pesticides found in the studied groups, however, contained pesticides not locally applied. Widespread occurrence of multiple pesticide residues could be due to transport from the surrounding conventional fields or as "ghosts" from past treatments. Moreover, application of illegal pesticides and product counterfeits can be also a possible reason. However, each group contained some pesticides that were detected exclusively in that given group and that were not applied in a focal agroecosystem. In spiders and rodents, this 'group-specific pesticide composition' suggests that also spillover of spiders and rodents or spillover of their prey from surrounding agroecosystems and non-crop habitats to the focal agroecosystems might be an important source of pesticide transfer to local food webs.

The protease network that regulates innate immunity in mosquitoes

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Abstract: The mosquito immune system kills harmful pathogens and maintains a healthy microbiota. If overzealous, it however negatively affects the mosquito's blood feeding frequency, fecundity, and survival. Striking the balance is therefore key to mosquito fitness and thus vectorial capacity. Mosquito humoral immune reactions, including opsonization and melanization are regulated by proteolytic cleavage of thioester-containing proteins (TEPs) and pro-phenooxidase (proPO), respectively. Proteolysis in this system is performed by Clip-domain containing proteinases (cSPs), and regulated by non-functional proteinase-homologs (cSPHs), and serine proteinase inhibitors of the serpin family. However, the interplay of these factors is potentially complex, as each of these factors belong to large protein families, with nearly 20,000 individual molecular interactions possible with the mosquito hemolymph. To identify the critical interactions between the cSP, cSPH, serpins, TEP and proPO proteins that regulate mosquito immunity, we performed a meta-analysis of 256 transcriptomic datasets of Anopheles gambiae, the African malaria mosquito.
We assembled a co-transcription network, consisting of 178 nodes of six types based on protein families, and 1229 individual links between all nodes. To test whether this network can predict immune system function of individual putative immune factors, we experimentally tested the function of CLIPB4, the cSP node with the highest weighted degree centrality in the network. Detailed biochemical and genetic analyses confirmed that CLIPB4 is required for melanization in the mosquito hemolymph, directly cleaving proPO as well as upstream cSPs. As a visualization tool, the aggregated network highlights the complexity of the system, consisting of several highly branched protease cascades with positive and negative feedback loops. As an analysis tool, this network can be utilized to infer the potential biochemical interactions required for humoral immune system function in mosquitoes.

Reconstructing evolution of ancestral anatomies in Hymenoptera using PARAMO pipeline

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Abstract: Ancestral character state reconstruction has been long used to gain insight into the evolution of individual traits in organisms. However, organismal anatomies (= entire phenotypes) are not merely ensembles of individual traits, rather they are complex systems where traits interact with each other due to anatomical dependencies (when one trait depends on the presence of another trait) and developmental constraints. Comparative phylogenetics has been largely lacking a method for reconstructing the evolution of entire organismal anatomies or organismal body regions. Herein, we present a new approach named PARAMO (Phylogenetic Ancestral Reconstruction of Anatomy by Mapping Ontologies, Tarasov and Uyeda 2019) that takes into account anatomical dependencies and uses stochastic maps (i.e., phylogenetic trees with an instance of mapped evolutionary history of characters, Huelsenbeck et al. 2003) along with anatomy ontologies to reconstruct organismal anatomies.
Our approach treats the entire phenotype or its component body regions as single complex characters and allows exploring and comparing phenotypic evolution at different levels of anatomical hierarchy. These complex characters are constructed by ontology-informed amalgamation of elementary characters (i.e., those coded in character matrix) using stochastic maps. In our approach, characters are linked with the terms from an anatomy ontology, which allows viewing them not just as an ensemble of character state tokens but as entities that have their own biological meaning provided by the ontology. This ontology-informed framework provides new opportunities for tracking phenotypic radiations and anatomical evolution of organisms, which we explore using a large dataset for the insect order Hymenoptera (sawflies, wasps, ants and bees).

Action of species-selective JH-receptor agonists on insect development

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Abstract: Juvenile hormone (JH) maintains larval character of insect juveniles by activating the Kr-h1 gene through a JH receptor complex (JHR) comprising Met and Tai proteins. Metamorphosis to adults requires absence of JH and Kr-h1 expression during the final juvenile stage in both hemimetabolous and holometabolous insects. Administering JHR agonists at this time prevents adult development. Synthetic JH mimics that presently serve to control pest and disease vectors display poor selectivity toward target species. To develop selective means for insect control, we screened a chemical library of 90K compounds for activators of JHRs from diverse target species. We have found compounds that bound Met, stimulated assembly of the JHR complex, and blocked adult development in a species-selective manner. When treated with the specific JHR agonists, last-instar hemimetabolous larvae molted to a doomed extra larval instar, whereas treated pupae of holometabolans either formed second lethal pupae (beetles) or arrested without producing viable adults (mosquitoes). In contrast, development of honey bee pupae was unaffected by the compounds targeting other species. Our data demonstrate that novel, species-selective compounds for insect research and control can be developed.

Exploring and predicting multitrophic interactions between plant, whiteflies, parasitoids, and endosymbionts under changing climate

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Abstract: The impact of elevated CO2 levels, air temperature and relative humidity on the multitrophic interactions between plant, sap-sucking insects, and their antagonists and symbionts has not been studied in detail. Whitefly Bemisia tabaci is an important sap-sucking insect pest on a wide range of host plants globally including tomato where it causes direct damage by feeding and indirect damage through virus transmission. Biological control of whiteflies using parasitoids in European greenhouses is a standard practice. In addition, bacterial endosymbionts (ES) of B. tabaci also play an important role in the interaction between plant, whitefly, parasitoids, and the environment. At the moment studies investigating endosymbionts' role in whitefly biology under future climate scenarios currently do not exist.

In our study, we investigate the effects of physical consistent elevated CO2 levels, relative humidity and temperatures on multi-trophic interactions, including effects on the tomato plant, B. tabaci pest, its natural enemy (Eretmocerus), and endosymbionts. We peer into the underlying mechanisms using RNA sequencing techniques and identify differentially expressed genes in both tomato and whitefly to gain a better understanding of how the plant-whitefly system responds to climate change, parasitoid presence, and ES composition. Further, we combine the information on metabolic changes obtained through analysis of gene expression profiles with traditional life parameters of plant, whitefly, and parasitoids to get a comprehensive picture of multitrophic interactions under climate change effects.

The direct outcome of this study is a detailed prediction of climate change effects on the very important global pest and their associated multi-trophic interactions. These predictions together with a detailed molecular understanding of plant's and insect's biochemical responses to whitefly colonization under current and future environmental conditions will help create novel whitefly control methods. Additionally, these predictions are crucial in developing effective and sustainable climate change adaptation strategies for policy support as well as ensuring food security like vegetable production.

Minimum dispersal distance and ecological apparency mediate colonization of Arctostaphylos host plants by Tamalia gall aphids

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Abstract: Fire is an important ecological process in chaparral plant communities in California. Arctostaphylos shrubs (Ericaceae) typically germinate following wildfire, providing new opportunities for specialist Tamalia gall aphids (Aphididae) to establish populations on fresh growth. Following wildfire at a study site in the Cascade foothills of northern California, I tested the hypotheses of minimum dispersal distance and ecological apparency to predict relative rates of colonization by a gall-inducing aphid (Tamalia coweni) and its inquiline aphid (Tamalia inquilina). Methods included mapping the spatial distribution of 500 host plants in a 1-hectare study population using a high-precision Trimble Global Positioning System (GPS) instrument, as well as Geographic Information System (GIS) software. These data yielded estimates of the frequency and timing of plants first colonized by gall-inducers, as well as the frequency of inquilines subsequently invading galls.

Results show that, beginning in 2008, less than 4% of the 135 juvenile plants were colonized by Tamalia aphids. The proportion of plants with aphid galls has increased continuously: 75% had been colonized by 2018. Assuming Tamalia aphids establish galls on young plants (sinks) from existing populations on mature plants (sources), my results are generally consistent with a minimum dispersal distance hypothesis. Colonization rates of host plants are a function of their height, which is consistent with the ecological apparency hypothesis. Inquilines can disperse and colonize new habitats efficiently, in synchronization with their gall-inducing host aphids. These findings have implications for patterns of evolutionary diversification in both gall-inducer and inquiline lineages.

Developing a molecular diagnostic test to detect parasitism in a highly-invasive lepidopteran

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Abstract: The Oak Processionary moth (OPM) is a species native to central and southern Europe but is an invasive species, and serious forestry pest, in several northern European countries (Germany, the Netherlands, and the UK). OPM is a defoliator of Quercus (Oak) species and potential human health threat due to small urticating hairs which produce a pseudo-allergic response in humans. In London, OPM have been present since 2006, with a breeding population establishing and expanding. Concerns about the financial and environmental cost of nest removal and pesticide application have led to calls for alternative control measures, including biocontrol with parasitoids such as Carcelia iliaca.

Here, extracts of OPM larval samples with known parasitism status were used to test four LAMP primer sets. The results show the successful development of a LAMP based diagnostic assay that successfully amplifies C. iliaca from ground OPM lysate, excluding the need for complicated DNA extraction. Being able to gather C. iliaca distribution data from ground OPM samples allows for the development of predictive models to understand the ecological variables that allow for the presence of C. iliaca. This information would inform integrated pest management decision making frameworks for land managers.

Spatial responses of parasitoids to host patches, resource concentration or dilution?

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Abstract: Importation biological control, the introduction of a specialist natural enemy from the region of origin of an invasive pest or weed, has been practiced for more than 100 years and has provided some iconic success stories, but also a number of failures. To improve both the success and safety of biological control in the future it is important to consider all opportunities that can help to transform biological control into a more predictive science. Once established, whether or not an imported natural enemy can reduce the abundance and distribution of an invasive host, likely depends on a suite of life history and behavioral traits that include phenological synchronization and foraging efficiency among many others. One key aspect of foraging efficiency is how individuals respond to the patchy distribution of hosts in a spatially fragmented environment when facing potential competition and predation risk. Another is what distributions of natural enemy foraging effort lead to the greatest temporal reduction in mean host density among patches. Here we explore the current theoretical framework for natural enemy foraging behavior and find some evidence that a weak resource dilution distribution of natural enemies among patches might be an important trait for improving the success of importation biological control.

Off- and early season, biological control of Mediterranean fruit fly Ceratitis capitata with entomomathogenic nematoded

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Abstract: The purpose of the study is to investigate the efficacy of commercially available entomopathogenic nematodes (EPNs) Heterorhabditis bacteriophora Poinar, Steinernema Carpocapsae Weiser, and Steinernema feltiae Filipjev for the off-season control of the Medfly Ceratitis capitata (Diptera: Tephritidae). In laboratory experiments we investigated the efficacy and residual activity of EPN on soil substrate with organic content and moisture level similar to that of an orchard at a temperature of 19 ± 1 ° C. Steinernema feltiae and to a lesser extent S. carpocapsae, had a significant residual activity of up to two weeks. Whether the observed residual activity is due to the recycling of nematodes in recurrent additions of medfly larvae to the substrate (100 larvae every 14 days, three times) or to the residual duration of the nematodes themselves on the substrate requires further investigation. The ability of the three species of nematodes to move into artificially infected fruits, oranges and apples, laying on the soil substrate, was also assessed. The number of medfly pupating on the substrate in all three nematode treatments was significantly lower than in the control treatment. In conclusion, preliminary laboratory experiments showed that a single off-season application of S. feltiae or S. carpocapsae at relatively low doses (1.5mi /m2) can significantly reduce the overwintering larvae of madfly both in the soil and in the fallen fruits. In other experiments we explored whether application of a new formulation containing S carpocapsae on the canopy of orchards, early in the season (spring) can provide additional control via infestation of the adult flies as they emerge from the soil.

Presence, seasonal abundance and molecular studies on genetic and bacterial diversity of insect vectors of Xylella fastidiosa in olive orchards from Greece

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Abstract: During 2017 and 2018, samplings were carried out in several locations of Greece, distributed in 15 regional units, to study the presence of insect vectors of Xylella fastidiosa in olive orchards. In every location, samples were taken from the canopy of olive trees and from the ground vegetation cover, with a sweep net. In total, more than 40 Cicadellidae species were identified. However, none of them belonged to the subfamily of Cicadellinae. Five Aphrophoridae (Philaenus spumarius, P. signatus, Neophilaenus campestris, Aphrophora alni and Lepyronia coleoptrata) and one Cercopidae species (Cercopis sanguinolenta) were identified from the ground vegetation and the same Aphrophoridae species (except L. coleoptrata) were also found on the trees' canopy. Philaenus spumarius was found in nine out of the 15 regional units surveyed and was the widest distributed species.

In 2018 and 2019, detailed sampling throughout the year were performed in four areas of Greece in order to study the seasonal abundance of nymphs and adults of P. spumarius and N. campestris. Both species were present in olive orchards during spring and autumn while during summer months were absent. Their population densities greatly varied among the orchards sampled. A representative portion of the captured spittlebugs were analyzed with molecular methods and the analysis confirmed the absence of X. fastidiosa in the tested individuals.

Genetic divergence and/or relatedness within or between the different P. spumarius, P. signatus and N. campestris populations, was examined using molecular methods in 92, 24 and 62 adults from different populations of three species respectively, collected from different areas of Greece. Fragments of the mitochondrial genes Cytochrome Oxidase I (COI), cytochrome b (cytb) and of the nuclear gene Internal Transcribed Spacer (ITS) were amplified and sequenced. In addition, molecular experiments were carried out for examining the bacterial composition and diversity. One hundred fiftyfive, 28 and 81 collected adults from different populations of P. spumarius, P. signatus and N. campestris respectively, were screened for the presence of the secondary endosymbionts Cardinium, Rickettsia, Arsenophonus, Hamiltonella and Wolbachia. Among the different insect species and populations within the insect-species studied, the infection status and frequency of the endosymbionts varies significantly. The highest endosymbiont diversity is found in P. spumarius. There is no evidence for the presence of Cardinium in any of the three examined insect species. P. spumarius harbors Rickettsia, Arsenophonus, Hamiltonella and Wolbachia, P. signatus harbors only Rickettsia and N. campestris harbors Rickettsia, Hamiltonella and Wolbachia. Moreover, a multilocus sequence typing (MLST) approach has been used for the individuals harboring Wolbachia.

Nest boxes for birds increase insectivory in apple orchards

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Abstract: The use of nest boxes for attracting insectivorous birds can be a strategy of conservation biological control. We evaluate this issue in cider-apple orchards from Asturias (NW Spain) by comparing bird insectivory and arthropod abundance on apple trees between orchards with and without nest boxes occupied by birds. We also monitored adult birds to identify the preys they feed to nestlings. Nest boxes were mainly occupied by great and blue tits. Insectivory, estimated from bird attack on plasticine caterpillar models, was higher (36-47%), and arthropod biomass was lower (49%), in orchards with occupied nest boxes. According to the preys, blue tit was the species with higher predation rate on apple pests. We showed that nest boxes can help to increase the biological control of apple pests.

Antiviral RNAi Response against the Insect-Specific Agua Salud Alphavirus

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Abstract: RNA interference (RNAi) is the cornerstone of antiviral defense against arboviruses in mosquitoes. More specifically, it is understood that mainly the small interfering (si) and PIWI-interacting (pi) RNA pathways are involved in the control of these viruses. In contrast to arboviruses, little is known about the interaction of insect-specific viruses (ISVs) and the RNAi pathways. Due to their persistent nature and prolonged co-evolution in the insect host, it is safe to hypothesize that ISV-RNAi interactions differ compared to arboviruses. While investigations into this area further contribute to the characterization of ISVs, it also highlights potential intersections that might in the long run affect vector competence of mosquitoes for arboviruses of public health concern. Additionally, it could shed light on essential changes needed for an ISV to make the switch to becoming an arbovirus.

In this study we investigate the interactions of a recently isolated insect-specifc alphavirus, Agua Salud alphavirus (ASALV) with its mosquito host. Through the knockdown of transcripts of the different key RNAi pathway proteins, we show the antiviral role of Ago2, Ago1 and Piwi4 proteins against ASALV in Aedes aegypti-derived cells. Data from knockout cells further confirmed the main antiviral role of the siRNA pathway.

Taken together, ASALV interactions with the mosquito RNAi response differ from those of arthopod-borne alphaviruses in some aspects, although they also share some commonalities. Further research is needed to understand whether the identified differences can be generalised to other insect-specific alphaviruses.

LIFE ROsalia: Conservation of saproxylic beetles in the Carpathians in Romania (LIFE19 NAT/RO/000023)

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Abstract: The Romanian Carpathians are considered a biodiversity hotspot in Europe, with large, forested areas, including old-growth forests. Past forestry practices, such as selective logging resulting in forest high grading and removal of ancient or decaying trees has reduced the heterogeneity of forest structure and composition. These practices led to forest habitats with few veteran trees and a small amount of deadwood, which the protected group of saproxylic beetles rely on for completing their complex life cycles. The LIFE ROsalia project is improving habitat conditions for five saproxylic beetle species (Rosalia alpina, Osmoderma eremita, Cerambyx cerdo, Morimus funereus, and Lucanus cervus) in the forests of the Putna-Vrancea Natura 2000 site by demonstrating conservation actions for increasing the connectivity of favourable habitats for the beetle species. Actions include providing artificial and natural deadwood habitats, clearing overgrowth, and establishing a participatory monitoring system with foresters using a citizen science approach.

Surveying the acoustic biology of longhorned beetles (Coleoptera: Cerambycidae)

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Abstract: Many species of longhorned beetles (Cerambycidae) stridulate audibly by rasping the posterior margin of the pronotum over a stridulatory plate, or pars stridens, on the mesonotum. The function of stridulation is largely unknown, but individuals may stridulate when encountering conspecifics, and are especially likely to stridulate when disturbed. These “chirps” frequently range into ultrasonic frequencies, and we hypothesized that they may be a disruptive response to bat predation. We have recorded chirps of diverse species of longhorned beetles to determine how the acoustic properties of the chirp correlate with evening activity periods (and thus bat activity), species (suggesting intraspecific communication), or individual morphology. Additionally, we have coupled our approach with scanning electron microscopy (SEM) to observe the structure of the pars stridens in each species. Our preliminary results suggest that the properties of the pars stridens are similar within species, but they may vary considerably even among closely related species.

Molecular mechanisms of juvenile hormone biosynthesis and metamorphosis in Gryllus bimaculatus

Authors: Mito Taro[1], Watanabe Takahito[1], Noji Sumihare[1] and Ishimaru Yoshiyasu[1], [1]Tokushima University

Abstract: Juvenile hormone (JH) acid methyltransferase (JHAMT) plays a crucial role in JH biosynthesis. We previously reported that Myoglianin (Myo) suppresses JHAMT expression to down-regulate JH production in the cricket, Gryllus bimaculatus.

To improve our understanding of the role of Myo, we generated myo gene knockout (KO) crickets and characterized the phenotype of myo KO nymphs. We found that supernumerary nymphal molts were observed in the myo KO nymphs. The myo KO nymphs subsequently failed to cause the juvenile-to-adult transition. We further found that a significantly increased expression of JHAMT was detected in the myo KO fourth instar nymphs. In addition, JH titers were elevated in myo KO nymphs.

Next, we examined the function of JH and ecdysteroid target genes, Krüppel homolog 1 (Kr-h1), Broad complex (Br-C) and E93, in the metamorphosis of hemimetabolous G. bimaculatus. Depletion of Kr-h1 or Br-C at the sixth instar nymphs induced precocious adult moults. In contrast, E93 knockdown prevents final (eighth) nymphs transitioning to adults, instead producing supernumerary nymphs.

Our results suggest that the regulatory mechanisms underlying pupal transition in holometabolous insects are evolutionarily conserved in hemimetabolous G. bimaculatus, with the penultimate and final nymphal periods being equivalent to the pupal stage.

A New Genus of Cerocephalinae (Hymenoptera: Pteromalidae) from Madagascar

Authors: Mitroiu Mircea-Dan, Universitatea “Alexandru Ioan Cuza” din Iasi

Abstract: A new genus of Cerocephalinae with brachypterous females is described from Madagascar based on material from Muséum national d’Histoire naturelle Paris. Although its morphology is not in complete agreement with the current subfamily diagnosis, the new genus is classified in Cerocephalinae based on the following shared features: head globose, with interantennal concavity bearing sharp carina and parascobal area strongly raised; antennal shape and structure, with no anellus, six funiculars and completely fused clava; and the shape and structure of pronotum and gaster. The new genus is compared with all previously described genera of the subfamily and the limits of Cerocephalinae are discussed.

Circannual rhythms in two Anthrenus carpet beetles: comparison between spring- and autumn-pupation types

Authors: Miyazaki Yosuke[1] and Watari Yasuhiko[1], [1]Ashiya University, Japan

Abstract: The circannual rhythm is a biological rhythm with a period of about one year. Circannual rhythms in insects have mainly been reported in pupation of the varied carpet beetle, Anthrenus verbasci. This species has a long larval duration and pupates every spring. The circannual pupation rhythm of A. verbasci shows self-sustainability, temperature compensation of the period, and entrainability to a zeitgeber (photoperiodic change), which indicates that a circannual clock of A. verbasci is an endogenous oscillator. Although this rhythm has been reported since the early time of the circannual rhythm research, circannual rhythms have been rarely reported in other insects and no interspecific comparisons have been made. We focused on A. nipponensis of the same genus. This species has been reported to pupate in autumn. If there is also a circannual rhythm in the pupation of A. nipponensis, it is considered that the properties of rhythm can be compared between two species of the same genus with half a year difference of pupation phase. Therefore, we investigated whether circannual rhythm is exhibited in pupation when larvae of A. nipponensis are kept under various constant conditions. Moreover, we compared circannual rhythms of pupation between A. verbasci and A. nipponensis.

Behavioral mechanisms for the evolution of termite nest construction

Authors: Mizumoto Nobuaki[1], Bardunias Paul[2], Pratt Stephen[1] and Bourguignon Thomas[3], [1]Arizona State University, United States, [2]Florida Atlantic University, United States, [3]Okinawa Institute of Science & Technology Graduate University, Japan

Abstract: The nest structures built by social insects are complex group-level patterns that emerge from interactions among individuals following simple behavioral rules. The theory of complex systems predicts that there is no simple one-to-one relationship between variations in collective patterns and variation in individual behaviors; therefore, it is essential to know how actual behavior evolves to change pattern formation. In this presentation, we discuss the role of behavioral rules in the evolution of collective building in termites.

First, we show that the evolutionary divergence of termite tunneling patterns is achieved by quantitative tuning of shared behavioral rules, rather than the acquisition of novel behaviors. We compared tunnel formation between two closely related species, Reticulitermes tibialis and Heterotermes aureus, and found that H. aureus builds more highly branched tunnels than R. tibialis. Our behavioral analysis and data-based modeling revealed that these species share the same behavioral repertoire, but a quantitative difference in the probability of sidewall excavation leads to diverse tunneling patterns. In contrast, we also found that Paraneotermes simplicicornis, which evolved tunneling independently, possesses a distinct behavioral repertoire, but shows convergence of branching patterns with R. tibialis.

Second, we inferred the evolutionary process of termite shelter-tube construction through phylogenetic analysis. Although the use of shelter-tubes in natural conditions is variable, most modern species have the potential to build shelter-tubes. With this information, our ancestral reconstruction suggests that the behavioral rules for shelter-tube construction evolved once in the common ancestor of modern termites, and are shared among species.

Together, these results elucidate the complex relationship between individual behavior and group-level patterns; in some cases, distinct behavioral rules can produce similar group-level patterns, but in others, a common rule set can yield the evolution of distinct patterns via parameter tuning. Our result emphasizes the importance of direct comparative studies of both individual behaviors and group-level patterns.

Wildflower strips and their management affect resource availability and utilisation by parasitoids

Authors: Mockford Alice[4], Urbaneja Alberto[1], Westbury Duncan B[4], Tena Alejandro[2] and Ashbrook Kate[3], [1]Institut Valencià d'Investigacions Agràries (IVIA), [2]Instituto Valenciano de Investigaciones Agrarias, Spain, [3]School of Science and the Environment, University of Worcester, United Kingdom, [4]University of Worcester, United Kingdom

Abstract: The use of wildflower strips to provide carbohydrate resource for parasitoids and enhance pest regulation has become a cornerstone of habitat management for pest regulation. However, how wildflower strips and subsequent management might influence resource availability and utilisation by parasitoids has never been studied.

In a randomised block experiment, three treatments were applied in the alleyways between the rows of trees in three Spanish orange orchards: i) a control treatment where naturally occurring vegetation was managed under standard farm practice; ii) a standard management treatment, where sown wildflower strips were cut once a year; and iii) an active management treatment, where sown wildflower strips were cut three times a year.

Wildflower strips under standard management prevented the seasonal decline of available nectar observed in the control and active management treatments and instead, supported fructose feeding in parasitoids across all three seasons. The abundance of floral nectar and hemipteran honeydew in the alleyways and orange trees was consistently greater with the wildflower strips under standard management than with the control treatment or active management wildflower strips. In turn, the standard management wildflower treatment was associated with twice the abundance of primary parasitoids than with the control and active management treatments in both summer and autumn. In addition, in autumn, parasitoids were most likely to have recently fed on carbohydrate in the standard management treatment. Finally, increased carbohydrate feeding in parasitoids was associated with greater structural heterogeneity of the alleyway vegetation.

This study demonstrates that the nutritional status of parasitoids in a perennial crop, such as orange, can be improved by wildflower strips which could then enhance pest regulation services. Furthermore, the study emphasises the importance of investigating the management of wildflower strips when targeting specific resource requirements.

Creating a sustainable, 21st century IPM toolkit to combat a historic pest issue; Tipula larvae in agricultural settings.

Authors: Moffat Aisling, Teagasc, SRUC and the University of Edinburgh, Ireland

Abstract: Tipula larvae are important agricultural pests as their feeding cause's significant damage in cereals and grassland. A previously effective chemical has been withdrawn from use within the EU due to the associated risks, to both human health and the environment. Current control options are extremely limited. Our research aims to create a modern IPM toolkit for dealing sustainably with Tipula larvae infestations in grassland specifically. This involved a national survey across Ireland, which was conducted to determine (i) the Tipula species of agronomic importance, and (ii) the soil factors that limit larval survival/occurrence. Larval feeding experiments were established, with six plant monocultures and a mixed-species sward, to identify optimum grassland sward compositions for highly infested fields. Soil microbiome analysis from fields across Scotland and Ireland was also carried out to investigate the microbial communities present in fields with high and low pest pressure. This analysis will give insight into potential biocontrol agents for future control options, and will complete our IPM toolkit. Through better understanding the pest of interest, the role of soil properties and cultivar choice, we aim to provide farmers with an IPM toolkit for a pest with limited control options. (Refer to attachment for full draft).

Exogenously acquired sticky compounds influence herbivore selection in plants

Authors: Mofikoya Adedayo, University of Reading, United Kingdom

Abstract: Plant surfaces represent the first point of physical contact in plant-insect interactions and as such, various plant surfaces have evolved differing physicochemical properties to attract, repel and deter insects. Physical properties such as waxiness and leaf trichomes act as physical barriers against herbivory, some trichomes secrete secondary metabolites consisting of plant volatile organic compounds (VOCs) that are cues for plant selection for herbivores, gravid female insects, pollinators as well as natural enemies (parasitoids). Field scale studies in the Finnish subarctic provided evidence that semivolatiles compounds released by understorey shrubs Rhododendron tomentosum adhere to the surface of surrounding mountain birch (Betula pubescens) trees. Furthermore, laboratory tests show that these compounds may also adhere to the surface white cabbage Brassica oleracea and confer some resistance to oviposition by the diamondback moth, Plutella xylostella even under pollution conditions. These findings provide evidence that companion aromatic plants may confer associational resistance to main plants in agriculture and forestry systems.

Exogenously acquired chemicals on plant surfaces confers herbivore resistance in forest and agriculture systems

Authors: Mofikoya Adedayo[4], Kivimäenpää Minna[2], Holopainen Jarmo[1] and Blande James[3], [1]Department of Environmental and Biological Sciences, UEF, Finland, [2]Natural Resources Institute Finland, [3]University of Eastern Finland, Finland, [4]University of Reading, United Kingdom

Abstract: Plant surfaces represent the first point of physical contact in plant-insect interactions and as such, various plant surfaces have evolved differing physicochemical properties to attract, repel and deter insects. Physical properties such as waxiness and leaf trichomes act as physical barriers against herbivory, some trichomes secrete secondary metabolites consisting of plant volatile organic compounds (VOCs) that are cues for plant selection for herbivores, gravid female insects, pollinators as well as natural enemies (parasitoids). Field scale studies in the Finnish subarctic provided evidence that semivolatiles compounds released by understorey shrubs Rhododendron tomentosum adhere to the surface of surrounding mountain birch (Betula pubescens) trees. Furthermore, laboratory tests show that these compounds may also adhere to the surface white cabbage Brassica oleracea and confer some resistance to oviposition by the diamondback moth, Plutella xylostella even under pollution conditions. These findings provide evidence that companion aromatic plants may confer associational resistance to main plants in agriculture and forestry systems.

Some host trees properties contribute to variation in the Emerald Ash borer gut microbiome: Important ecological knowledge for applied biological control

Authors: Mogouong Judith[1], Guertin Claude[2] and Constant Philippe[2], [1]Cornell University, United States, [2]Institut national de la recherche scientifique Armand-Frappier Santé Biotechnologie Research Centre, Canada

Abstract: The Emerald Ash Borer (EAB), Agrilus planipennis Fairmaire, is an exotic insect pest native to Asia that causes environmental and economic damage to ash trees (Fraxinus spp.) in North America. This Buprestidae first detected in 2002 at Canada-U.S. border, is now known as the most serious pest in recent decades, particularly because of the environmental, ecological and economic impacts. The microbiome of wood boring beetles has been largely studied, and it now established that it may play crucial role for their host survival. Besides that, there is still lack of information on the mechanisms by which that microbiome maintains its role. More importantly, some concerns related to the drivers of that microbiome need to be addressed. Some environmental factors such as temperature and nutrition could act as determinants, and influence the composition of these insects' microbiome. One goal of our study was to address the following question: does host tree properties contribute to variation in the Emerald Ash borer gut microbiome structure? An approach based on the amplicon sequencing high throughput technique targeting the bacterial 16S rRNA and the ITS2 fungal internal transcribed spacer couple with different multivariate analyzes revealed the taxonomic structure of the insect's gut microbiome characterized by some ecological markers, and its plasticity when facing some variations in its environment. More specifically the bacterial and fungal communities associated with the host leaves (phyllosphere) appeared to play a determinant role in the variation observed in the insects' gut microbiome. Interestingly, our results suggest that most of the insect's gut fungal microbiome may be transitory probably acquired from the insect environment, whereas some specific bacterial taxa could be considered as habitual residents in the insect's gut microbiome. Moreover, the fungal microbiome was found more sensitive to those host tree properties. Our findings bring out some research questions such as what are the roles of the microorganisms found in the insects' gut? Or how important is the fungal community found in the gut microbiome? By improving the knowledge to the understanding of the microbial ecology, the future for potential biological pest management may be more efficient.

Effect of honey bee management strategies on Varroa destructor and small hive beetle (Aethina tumida) in Hawaii

Authors: Mogren Christina[1], Hausler Daniel[2], [1]University of Hawaii at Manoa, Plant and Environmental Protection Sciences Department, United States, [2]University of Hawai'i at Manoa, United States

Abstract: Beekeepers around the globe have to make informed management decisions when treating for hive pests. Varroa destructor, an ectoparasitic mite that feeds on the honey bee fat body, is considered the most devastating pest of the European honey bee (Apis mellifera). Varroa mites were introduced to the U.S. state of Hawaii in 2007 and are exclusively present on Oahu and Hawaii islands. To prevent further spread, state law prohibits the movement of used beekeeping equipment and live bees between islands. There are two main paradigms among beekeepers regarding varroa management; IPM (chemical control) using organic and conventional pesticides, and holistic (chemical-free options), which include the mechanical removal of drone brood. Integrated approaches may take advantage of Varroa sensitive hygienic traits as well. Small hive beetles (SHB, Aethina tumida) are colony parasites native to sub-Saharan Africa whose larvae tunnel through the combs and excrete a yeast in their frass that ferments hive products, making them unmarketable. Discovered in Hawaii in 2010, SHB is now ubiquitous across the archipelago, where current research is primarily focused on developing biocontrol agents. Hawaiian beekeepers can choose among various management strategies to combat varroa and SHB. For varroa, products registered for use in Hawaii include six organic and three conventional pesticides. No products are available that are registered for use against SHB in Hawaii, so standard mechanical methods for trapping and removal are the only option available to beekeepers. The goal of this project is to evaluate the effectiveness of IPM and holistic management practices against these economically important pests of honey bees in Hawaii.

Varroa mite and SHB levels were measured monthly under both management strategies on two islands: IPM and holistic for varroa on Oahu (varroa-positive) and holistic on Maui (varroa-negative). Varroa levels were assessed using an alcohol wash method, and SHBs trapped in Beetle Blaster (oil) traps were used to compare populations between colonies. Statistical comparisons were made between hive pest levels as well as IPM vs. holistic management paradigms.

There is relatively little research present on holistic management of honey bees, and results from this study will provide data directly to those that have a preference or restriction to this paradigm. Since IPM is not the only management option, the importance of knowing the capability of holistic pest control is significant to many beekeepers. This study is a foundation for future research on honey bee pest management options and how additional factors, such as nutrition, can integrate with management strategies to make them more or less effective.

Temporal shifts in nutrient quality of pollen collected by honey bees (Apis mellifera) in Kauai, Hawaii

Authors: Mogren Christina, University of Hawaii at Manoa, Plant and Environmental Protection Sciences Department, United States

Abstract: Honey bees were introduced to the Hawaiian Islands for pollination services and honey production in the 1850s, and since then have become ubiquitous across the archipelago. The honey bee queen rearing industry in the state is the largest in the world, with the subtropical climate allowing for year-round production. Many large mainland U.S. and Canadian beekeepers depend upon the availability of quality queens reared in Hawaii, particularly in the spring. However, the major native pollinating insects of endemic plants in Hawaii are beetles, which have different nutrient requirements for development and growth than honey bees. Since colonization by the Polynesians and later by Europeans, weed plants from regions to which honey bees are native have been continuously introduced, and honey bees are strongly suspected of serving as pollinators to these invasive plants. Pollination services are important for boosting yields of specialty crops such as Macadamia nuts and coffee, but it is not known to what extent honey bees forage upon native plants and whether this could be driven by nutrient quality of native vs. introduced plant pollen, in an ecosystem that evolved primarily with beetle pollinators. To determine the extent to which honey bees rely upon native vs. introduced plants, bee-collected pollen was analyzed from an apiary in Lihue, Kauai. Pollen samples were collected monthly, and sorted to color as a proxy for plant species. Each color group was identified to species using next-generation sequencing analysis of the ITS2 nuclear ribosomal gene and the macronutrients (lipids, protein, glycogen) and amino acids quantified. Statistical comparisons were made between native and introduced plant species pollen, and through time to see how nutrient values and plant species composition shifted throughout the year. Data will be presented in the context of future management considerations for honey bees in Hawaii, and how this may be used to inform beekeeping practices in subtropical island areas where European honey bees have been introduced.

A new bioassay to measure mosquito mortality and outdoor bite prevention strategies under semi field conditions

Authors: Mohamed Mgeni[1], Saddler Adam[1], Stica Caleb[1], Odufuwa Olukayode[1] and Moore Sarah[1], [1]Ifakara Health institute, Tanzania

Abstract: Introduction: The important component of mosquito-borne disease control programs worldwide is through the implementation of appropriate vector control tools. There is a gap in tools that provide protection against vectors that bite outdoors. Spatial repellents (SR) create a bite-free space through the evaporation of low doses of insecticides that repel and kill mosquitoes while requiring minimal compliance from users. These tools have demonstrated an ability to control both indoor and outdoor biting mosquitoes. Such tools must be evaluated in the semi-field system (SFS) prior to testing at the community level. We developed a bioassay to capture similar data as collected for insecticide-treated nets (ITNs) to inform mathematical models and predict the impact of transfluthrin SR on vectorial capacity.

Method: We treated hessian (jute) sacking with five doses of transfluthrin, 1g, 5g, 7.5g, 10g, 12g, and 15 g, or water for the control. The Ifakara Large Ambient chambers test (I-LACT). The I-LACT is a newly developed assay that simulates outdoor conditions and allows the recapture of all released mosquitoes. Each dose was evaluated in a block of four replicates, where volunteers were rotated while the treatment was fixed. Two blocks were conducted for each dose. Fifty pyrethroids susceptible Anopheles gambiae mosquitoes were released in each chamber where a volunteer sat in a plastic chair and allowed mosquitoes to feed. After an hour, mosquitoes were collected using aspirator held with access to sugar for 24 hours and scored as 1) fed alive, 2) fed dead, 3) unfed alive, 4) unfed dead. Feeding success and percentage mortality of free-flying mosquitoes was estimated and data were analyzed by generalized linear mixed-effects regressions with the binary distribution.

Result: There was a dose-response observed in both feeding inhibition and mortality induced by transfluthrin. For each 1g increase in transfluthrin, the probability of feeding decreased by 19% (OR 0.81(95% CI 0.80-0.83), $p<0.0001$) and the probability of dying increased by 38% (OR 1.38 (95% CI 1.31-1.45), $p<0.0001$). However, mosquito mortality stepped up from 10% to 58% when the dose was increased from 12.5 g to 15g while feeding success decreased from 30% to 15% between 10g and 12.5 g transfluthrin.

Conclusions: Transfluthrin treated material applied to houses with 15g per structure effectively reduces outdoor feeding and induces substantial mortality in pyrethroid susceptible mosquitoes. Therefore, products that release a similar concentration of transfluthrin may have an application for public health as they functioned as an “outdoor bednet” giving both personal protection (bite reduction) and community protection (mosquito mortality) sufficient to substantially reduce vectorial capacity of malaria vectors when applied at scale.

Integrated Pest Management of the Tomato Leaf Miner, Tuta absoluta (Meyrick) (Lepidoptera: Gelechiidae) in Tomato under green houses in Algeria

Authors: Mohammed Beddane, The directorate of agricultural services Phytosanitary inspection service, Algeria

Abstract: The tomato leaf minor (TLM), Tuta (Scrobipalpuloides) absoluta (Meyrick) (Lepidoptera: Gelechiidae) is one of the major devastating insect pests attacking tomato in many of the tomato-producing regions worldwide.
At present, depending on the cropping system and infestation intensity, the main control tools used against TLM rely too heavily on conventional insecticides that have led to the development of insecticide resistance .
In addition, the problems of using chemical control are further exacerbated by awareness of environmental pollution, toxicity to natural enemies and increasing risks to human and mammals (Tillman et al., 2000). Therefore, the use of insecticides has become subordinated to other control methods, such as biological control singly and/or in integrated with other methods as use of aggregation pheromones and biopesticides that have gained more credibility in the last decades (Senior et al., 2001; Agamy, 2003 and Mandour et al., 2012). Biological control using natural enemies would be the concerted use as a major component of any integrated pest management (IPM) program for controlling TLM. Egg parasitoid species of family Trichogrammatidae are considered efficient biological control agents and are widely used commercially for the suppression and control of lepidopterous pests on many crops (Agamy, 2003).

Being the progeny of a mother who lived in conventional orchards makes you more asymmetric than having a mother who lived in organic orchards in the European earwig Forficula auricularia.

Authors: Moiroux Joffrey[1], Le Navenant Adrien[2], Rault Magali[2] and Suchail Séverine[2], [1]Avignon University, France, [2]UMR IMBE, Avignon University, Aix Marseille University, CNRS, IRD - Avignon, France

Abstract: Organisms have to deal with many detrimental environmental factors throughout their development, such as stressful temperatures, competition or pollutants, which may result in developmental instability. For a long time, fluctuating asymmetry - i.e. small, random deviations away from perfect bilateral symmetry - has been used as a bioindicator to evaluate this developmental instability. When investigating the influence of any factor on fluctuating asymmetry, individuals are usually directly exposed during their development. In this study, we measured fluctuating asymmetry of several morphological traits in the progeny of European earwig females sampled before mating in conventional, integrated and organical orchards. Individuals which were used for measurements were thus never exposed directly to insecticides.
We observed a higher unsigned fluctuating asymmetry for six morphological traits in the progeny of females which were sampled in organic orchards, where chemical pesticides are not used, compared to the progeny of females which were sampled in integrated and conventional orchards, where chemical insecticides are allowed. Chemical compounds used for plant protection may thus have long-term effects on developmental stability of non-target insect species through maternal effects.

Understanding the Influence of Global Warming on Pest Management: Impact of Cross Effects between Temperature and Three Insecticides on Codling Moth Susceptibility

Authors: Moiroux Joffrey[1], Perrin Marie[2] and Delattre Thomas[3], [1]Avignon University, France, [2]Avignon University, France, [3]INRA, PSH Unit, Team Biological Control by Conservation, Avignon, France

Abstract: The frequency of insecticides' application is expected to increase with climate change since most of the insect pests are bound to appear earlier in the season, produce more generations because of a shorter development time at a higher temperature, and expand their distribution in the future. Temperature is known to influence the absorption, penetration, translocation and detoxification of pesticides by organisms. It is therefore necessary to investigate interactions between insecticides and temperature to predict possible outbreaks of pests in a climate change context and adapt pest management to future climatic conditions.
We conducted such an experiment on the codling moth, Cydia pomonella, one of the main pests in orchards worldwide that is commonly targeted with insecticides. Codling moth larvae were exposed to different concentrations of two chemical and one biological insecticides at five temperatures, and their mortality was recorded daily to assess the impact of cross effects between temperature and insecticides on this pest susceptibility.
We observed that larval mortality decreased as temperature increased for one of the two chemical insecticides, the emamectin. The lethal dose, 50% was indeed lower at 30 and 35°C than at 20 and 25°C. Preliminary results on the spinosad, a biological insecticide, are consistent with this result. Temperature did no influence larval mortality associated with the second chemical insecticide. Underlying physiological mechanisms are still investigated and will be discussed.
Our results highlight the disruption that may occur in pest management strategies because of the influence of high temperatures on the efficiency of pesticides. Such research is required to adapt application of pesticides to future climatic conditions.

Bioactive constituents, in vitro radical scavenging and antibacterial activities of selected Apis mellifera honey from Kenya

Authors: Mokaya Hosea[1] and Lattorff Michael[2], [1]International Center of Insect Physiology and Ecology. Jomo Kenyatta University of Agriculture and Technology, Kenya, [2]University of Nairobi; Martin-Luther-University Halle-Wittenberg

Abstract: There is limited information about the relative composition and health benefits of various honey consumed across Africa. This study aimed at estimating the bioactive constituents, in vitro radical scavenging and antibacterial activities of 16 kinds of honey obtained from different geographical locations in Kenya. Manuka 5 + honey was included for comparison. Some of the tested honey had biochemicals and bioactivities similar to or higher than Manuka 5 + honey. The honey exhibited DPPH radical scavenging ability, with several types of honey showing superior scavenging potential than Manuka 5 + honey, owing to their high phenol content. All types of honey inhibited the growth of E. coli and further showed a substantial amount of nonperoxide antimicrobial activity. The geographical origin of honey had an influence on its bioactive contents. Overall, these findings suggest that Kenyan honey has great therapeutic potential, and thus, its clinical application should not be overlooked.

What drives caterpillar abundance on individual trees: enemy pressure, leaf or tree growth, genetic traits, or phylogenetic neighbourhood?

Authors: Molleman Freerk[1], Walczak Urszula[1] and Melosik Iwona[1], [1]Adam Mickiewicz University in Poznań, Poland

Abstract: The abundance of insect herbivores on individual host trees can be driven by processes ranging from ongoing leaf development via recent microevolution to ancient phylogeny represented in the neighbourhood. To elucidate the relative importance of these processes, we sampled spring caterpillars (leaf-mining casebearers, semi-concealed, and free-living) from oaks (Quercus petraea) that varied in budburst phenology, trunk diameter, genotype, genome size, and phylogenetic neighbourhood. We found that free-living caterpillar abundance decreased with leaf age. Larger trees tended to show higher parasitism rates of herbivores. Casebearers were less abundant on more heterozygous oaks, but we detected no other effects of genotype or genome size on caterpillar abundance. In contrast to most previous studies, oaks growing among phylogenetic distant tree species had higher abundances of all three caterpillar guilds. This was not driven by the co-dominant species. Furthermore, in homogeneously phylogenetically distant neighbourhoods, parasitism tended to be lower. Lower parasitism, in turn, was associated with higher abundances of co-dominant caterpillar species. The overall dominating effect of phylogenetically distant neighbourhoods increasing caterpillar abundance further suggests that the consequences of growing amongst distantly related tree species may depend on factors such as geographic region and tree age.

Grant 2018/29/B/NZ8/00112 National Science Centre (Poland).

Collections-based genomics deciphers phylogeographic patterns in the Holarctic sawfly Pristiphora cincta Newman (Tenthredinidae)

Authors: Monckton Spencer K., Department of Biology, York University, Canada

Abstract: Sawflies in the subfamily Nematinae (Hymenoptera: Tenthredinidae) are cold-adapted insects that reach their greatest species richness in temperate, boreal, and arctic/subarctic regions of the Northern Hemisphere – a pattern that runs counter to that of most other organisms. In North America, most of their present range was covered by ice during the Pleistocene glaciations, meaning that they must have persisted in unglaciated refugia to the south, in Beringia, and possibly in other cryptic northern refugia. Along what corridors they repopulated the northern half of the continent, and from where, remain questions of great interest for understanding patterns of diversity for sawflies in particular and for North American insects in general. The holarctic species Pristiphora cincta Newman inhabits the temperate and boreal zones of North America and Eurasia, having seemingly crossed the Bering Land Bridge at least twice. As an herbivore on birch (Betula) and Vaccinium, it is hypothesized to have survived in small, geographically-restricted refugia on the peripheries of the Laurentide ice sheet, in Beringia, and in unglaciated parts of Eurasia. To evaluate the relative importance of these putative refugia, and to investigate present-day patterns of genetic diversity among populations of P. cincta, I use an approach called hyRAD to generate genome-wide RADseq data for pinned specimens sourced from natural history collections. With genomic data from representatives from across this species' range, I apply approximate Bayesian computation (ABC) to test ecologically-informed hypotheses about the phylogeographic history of P. cincta. I present the results of model-based phylogeographic analyses and interpret those results with respect to patterns of genetic diversity among populations, use of glacial refugia, and patterns of post-glacial recolonization. Broader implications for the diversity of Pristiphora Latreille, comprising more than 60 species in North America, are discussed, along with the potential to extend this study to include two other co-distributed species.

A Computational Approach for the Prediction of Relevant Olfactory Receptors in Insects

Authors: Montes Zaide[2], Reyes Alejandro[3], Molina Jorge[1], [1]1. Research Center in Microbiology and Tropical Parasitology (CIMPAT), Department of Biological Sciences, Universidad de los Andes, Bogota, Colombia, [2]1. Research Group on Computational Biology and Microbial Ecology. 2. Research Center in Microbiology and Tropical Parasitology (CIMPAT), Department of Biologi, [3]1. Research Group on Computational Biology and Microbial Ecology. 3. Max Planck Tandem Group in Computational Biology, Universidad de los Andes, Bogota, Colombia

Abstract: Insects are extremely successful organisms. A sophisticated olfactory system is in part responsible for their survival and reproduction. The detection of volatile organic compounds can positively or negatively affect many behaviors in insects. Compounds such as carbon dioxide, ammonium, indol, and lactic acid are essential for many species of mosquitoes in order to locate vertebrate hosts. For instance, in Anopheles gambiae the olfactory receptor AgOR2 is strongly activated by indol, which accounts for almost 30% of human sweat. Likewise, in some insects of agricultural importance, the identification of pheromone receptors such as in lepidoptera species has become a promising field for integrated pest management. For example, the disruption of the pheromone receptor, BmOR1, mediated by transcription activator-like effector nucleases (TALENs), remove completely the sensitivity to bombykol, affecting the pheromone-source searching behavior in male moths. In consequence, the identification of olfactory receptors in the genomes of insects is fundamental to improve our understanding of the ecological interactions, and to provide alternatives in the integrated pests and vectors management. Hence, the objective of this study is to propose a bioinformatic workflow to enhance the detection and identification of potential olfactory receptors in insects. Applying Hidden Markov Models (HMMs) and other computational tools, potential candidates for pheromone receptors in Lepidoptera were identified, as well as potential carbon dioxide receptors in Rhodnius prolixus, the main vector of Chagas disease. This study showed the capacity of a bioinformatic workflow with a potential to improve the identification of certain olfactory receptors in different Orders of insects.

Time of development of the forensically important carrion beetle Thanatophilus sinuatus (Silphidae: Silphinae) at constant temperatures

Authors: Montoya-Molina Santiago[1], Ruzicka Jan[1] and Jakubec Pavel[1], [1]Faculty of Environmental Sciences, Czech University of Life Sciences Prague, Czech Republic

Abstract: The species of the genus Thanatophilus (Silphidae: Silphinae) are recognized to be useful evidence for medico legal investigations primarily for the estimation of Post Mortem Interval (PMI). Thanatophilus sinuatus is a common carrion beetle found at early stages of decomposition on vertebrate carrion and human corpses across Europe. Regardless of the benefits for forensic sciences, thermal summation models are still unavailable for the species, therefore it cannot be used for PMI calculations. Thermal summation models or accumulated degree-days (ADD) methods are used as solid evidence to PMI estimation. The present study will provide information regarding developmental times of Th. sinuatus at five constant temperatures (16 °C, 18°C, 20°C, 21°C, 24°C). Immatures stages for the study were obtained from laboratory rearing under controlled conditions (16:8 h of light/dark period). Based on the data of temperature and development length a linear regression model was used to calculate the Lower Developmental-Threshold (LDT) and the Accumulated Degrees-Days (ADD). As expected, egg-adult development times decreased at higher temperatures. Results for each of the five developmental stages of Th. sinuatus from ovipositions to adult were: LDT(Egg) = 17.0 °C, ADD(Egg) = 12.0 ADD; LDT(Larvae1) = 17.4 °C, ADD(Larvae1) = 6.0 ADD; LDT(Larvae2) = 18.0 °C, ADD(Larvae2) = 5.9 ADD; LDT(Larvae3) = 16.9 °C, ADD(Larvae3) = 43.3 ADD; LDT(Pupae) = 16.0 °C, ADD(Pupae) = 46.4 ADD. As mentioned before, results are preliminary, but eventually they will provide critical data for the use of Th. sinuatus during criminal investigations.

High temperature survival and oviposition maxima of two forensically important flies

Authors: Monzon Michael[2], Hamilton George[2], Weidner Lauren[1] and Rusch Travis[1], [2]Rutgers, The State University of New Jersey, [1]Arizona State University

Abstract: The growth and development of blow flies (Diptera, Calliphoridae) is heavily influenced by the ambient temperature of their surroundings. Recent case and fieldwork from Canada and Australia indicate adult blow flies may access concealed carrion in automobile trunks. However, adult flies are incapable of egress even as the internal trunk temperatures far exceed the outside ambient temperature. This incubator experiment sought to determine the likely maximum temperatures for survival and successful oviposition in two forensically important blow flies of North America. The species investigated in this study were Phormia regina (Meigen) and Lucilia sericata (Meigen). Temperature treatments lasted for 24 hours for both studies. Both species were reduced to ~50% survival by 41°C. Similarly both species likely reach their survival threshold by 44°C. Preliminary body size analysis of L. sericata suggests females over 7mm in length may be more likely to survive extreme temperatures for sustained periods. Further, L. sericata consistently produced viable eggs until 43°C while instances of P. regina oviposition severely diminished passed 40°C. Our findings suggest heat was a more significant factor than species in both survival and oviposition trials.

Nano technology for prolonged flystrike control

Authors: Moradi Vajargah Mona[1], Song Hao[1], Zhang Jun[1], James Peter[1], Mitter Neena[1] and Yu Chengzhong (Michael)[1], [1]The University of Queensland, Australia

Abstract: Flystrike, caused by the Australian sheep blowfly Lucilia cuprina (Wiedemann) is amongst the most costly diseases affecting the sheep industry and a significant animal welfare concerns. Effective flystrike control relies heavily on two major methods; mulesing and insecticides. Mulesing is untenable because of sensitivity to animal welfare concerns, while for chemical development of resistance to blowfly control products.

We have developed a patented technology to fabricate novel hollow silica (SiO2) nano-capsules that can be loaded with active molecules to enable superior protection against insect pests. We investigated the relative toxicity of different prototype nanoparticle formulations loaded with ivermectin and cyromazine in comparison to the current commercial formulations. Bioassays were conducted using wool-serum system before and after artificial weathering to determine formulation parameters that provide the best efficacy. We showed improved effect following UV exposure for ivermectin and after wetting for cyromazine in comparison with standard formulations. Our particular FSN60 formulations enable 23% higher chemical loading than the other designs. So depending on the release dynamics, it is expected this can be used to achieve further improved longevity of effect with. This study will assist the development of novel, labour efficient, options for managing flystrike and countering resistance in sheep blowflies.

A tiger-moth tale and the Wallacean shortfall

Authors: Moraes Simeão, State University of Campinas (UNICAMP), Brazil

Abstract: Dysschema is the largest genus in the Pericopina, with 69 species. Taxonomic typological treatment and lack of understanding of geographical distributions contributed to a proliferation of publications and disputed validity of names in this group of tiger moths. Highly polymorphic Dysschema species with the tiger wing pattern were recently united in the “Dysschema eurocilia clade”. Only typological taxonomic treatment is available and ecological traits have not been used to delimit species displaying this tiger phenotype. Ecological niche modelling (ENM) and comparative morphological studies can clarify taxonomic scenarios, delimit species, and infer speciation mechanisms. We analyzed the genital morphology and wing patterns for the putative species in the ‘D. eurocilia clade’ and estimated the ecological niche using ENM. The morphological data and ENMs suggested an alternative hypothesis to previous taxonomic works on species within the ‘D. eurocilia clade’. The ENM models also revealed distribution patterns supporting the northern Andes as a geographical barrier between Central and South America, while the interconnected Andean valleys might represent areas of sympatry. Additionally, the predicted distribution showed that the South American species in “D. eurocilia clade” have distribution through the diagonal of open formations, which might represent a relict distribution known as the Pleistocene Arc.

Towards large-scale phylogenomic and morphological analysis of museum specimens

Authors: Moraes Simeão[5], Mayer Christoph[1], Ahrens Dirk[2], Buschbacher Keanu[4], Dietz Lars[3], Martin Sebastian[3] and Steinhage Volker[4], [1]Alexander Koenig Zoological Research Museum, [2]Arthropoda department, Zoological Research Museum Alexander Koenig, Bonn, Germany, [3]Centre for Molecular Biodiversity Research, Zoological Research Museum Alexander Koenig, Bonn, Germany, [4]Department of Computer Science, University of Bonn, Germany, [5]State University of Campinas (UNICAMP), Brazil

Abstract: Museum collections are repositories for biodiversity through space and time. To use museum specimens efficiently for scientific studies it is important to generate access to as much high quality morphological and molecular data per specimen as possible. Most of the hitherto applied approaches to generate large scale molecular data require good DNA quality and quantity, and cannot handle museum specimens due to the DNA damage occurring over time. We here present a target enrichment approach to sequence around 1700 loci across Lepidoptera for both new and old material. Using this approach we sequenced >500 loci for almost 130 year old material and more than 1000 loci for specimens collected 80 years ago and later. Additionally, an automated approach based on convolutional neural networks to efficiently identify species, or populations, and to generate data on morphological features for individual specimens based on whole drawer scans or specimen photos is in development. Using this approach we can automatically generate large amounts of morphological data, without the need of for example, placing landmarks, which is often a major bottleneck in such studies.

No geographic variation in chill coma recovery time of Ceratitis capitata adults after repeated frost events, in spite of population-specific survival costs

Authors: Moraiti Kleopatra[1], Papadopoulos Nikos T.[1], [1]University of Thessaly, Greece

Abstract: The Mediterranean fruit fly, Ceratitis capitata (Diptera: Tephritidae), is a chill-susceptible invasive, insect pest. Adults are capable of fully recovering after a short cold exposure at temperatures that induce a chill coma. However, the effects of repeated cold exposures on chill coma recovery time and post-recovery survival of flies remained unexplored. Here, we addressed the impact of three frost events in chill coma recovery time and post-recovery survival after a period of four days. We used adults from three temperate populations from different climatic zones from Greece (Thessaloniki and Chios Greece) and Israel (Yotvata). Flies (from F4-F5 generations were reared at 25oC up to adult day 10 and then exposed to three cycles of 4h exposures to 0oC (using slurry ice), each separated by 20h at 25oC with full access to adult diet and water. The recovery time was marked as the time needed for each individual to reach the upright position or fly. Our results reveal that multiple frost events evoke population-specific fitness costs in terms of survival of adults during the chill coma and repairing periods. Nonetheless, there is no geographic variation in both chill coma recovery time and short-term post-recovery survival after the three frost events.

Pollinating insects of oil palm in Colombia; habits, population dynamics and their relationship with the fruit set

Authors: Morales Rodriguez Anuar[1], Barrios Trilleras Carlos Enrique[1], Tejeda Rico German Esteban[1] and Diaz Castro Roberto Jose[1], [1]Cenipalma

Abstract: Insects mainly mediate pollination in oil palm. To identify the most frequent pollinating insects, their habits, and population dynamics, two plantations planted with oil palm Elaeis guineensis were selected in the municipalities of El Copey and Agustín Codazzi, Colombia. In these plantations, two plots were selected, and 10 male and 10 female inflorescences were reviewed; in these sampling, the species Elaeidobius kamerunicus, E. subvittatus, and Mistrops costaricensis were identified as the main oil palm pollinating insects. Subsequently, the behavior and habits of visiting the inflorescences by these insects in 20 male and 20 female inflorescences were recorded. It was determined that the activity of the pollinators begins around 7 am, reaching its highest activity at noon, and later the activity decreases, ceasing entirely around 5 pm. Finally, the population dynamics of pollinating insects in male and female inflorescences were monitored from December 2020 to March 2022. With the Spearman correlation, it was observed that the highest population densities in the female inflorescences were recorded in April and December with a positive correlation between the number of E. kamerunicus and the fruit set in the plots planted in Codazzi (r: 0.428; P-value: 0.047) and in El Copey (r: 0.415; P-value: 0.049).

Population dynamics of Leptopharsa gibbicarina and its relationship with biotic and abiotic factors in oil palm in Colombia

Authors: Morales Rodriguez Anuar[1], Barrios Trilleras Carlos Enrique[1], Díaz Castro Roberto Jose[1], Tejeda Rico Germán Esteban[1], [1]Cenipalma

Abstract: Leptopharsa gibbicarina is one of the most critical oil palm pests in Colombia. To determine the influence of environmental factors on the populations of L. gibbicarina, the population dynamics of L. gibbicarina were monitored in two oil palm plots in Agustín Codazzi and Copey north of Colombia, from December 2020 to February 2022. Data on the population dynamics of L. gibbicarina were correlated with precipitation, relative humidity, temperature, and biological control through Spearman correlations. No relationship was recorded between precipitation, relative humidity or temperature and the population fluctuation of L. gibbicarina (P - 0.05). On the other hand, a significant correlation was found between biological control and the population fluctuation of L. gibbicarina, being in El Copey -0.432 (p=0.045), while in Agustín Codazzi it was -0.223 (p=0.034). The main biological control agent was Beauveria bassiana among the other entomopatogenic fungi; several outbreaks were observed during the evaluation time. Beauveria bassiana has been isolated in all the samplings carried out and has generated mortalities close to 25%.

Keeping the baby with the bathwater: Mining and mapping raw reads using HMM improves accuracy and data recovery

Authors: Moran Kevin[2], Pooley Ashton, Valentine Michael and Skevington Jeffrey[1], [1]Canadian National Collection of Insects, Arachnids and Nematodes, Canada, [2]Carleton University, Canada

Abstract: Investigation into existing phylogenetic DNA dataset preparation pipelines revealed failure to recover data, improper contig assembly, and transcript re-use. PhyMMR, Phylogenetics through Markov Mapped Reads, was developed to resolve these issues. Coded in Rust, this dataset preparation pipeline brings significant improvements in data recovery, accuracy, ease of use, and lowers time required to produce an analysis ready dataset from months to days.

PhyMMR allows for the combination of transcriptome, genome, AHE and UCE data. Hidden Markov Modeling using HMMER, in combination with BLAST, is used to map raw reads to reference sequences. Mapped reads undergo a cleaning process involving end-trimming, cross-contamination check, and an outlier check prior to assembly. Using published UCE and AHE datasets, we demonstrate PhyMMR increases target data recovery by 1.5x to >20x compared to existing pipelines.

Use of PhyMMR resolves poorly supported nodes previously thought intractable. To illustrate this strength, we present a phylogeny of Diptera using publicly available data to assemble a dataset of 130 families and more than 250 subfamilies.

Cutting the knot: Untangling a paraphyletic Eristalinae (Diptera: Syrphidae) using phylogenomics

Authors: Moran Kevin[3], Ashton Pooley, Skevington Jeffrey[2], Young Andrew[4], Mengual Ximo[5] and Kelso Scott[1], [1]Canadian National Collection of Insects, Arachnids and Nematodes, [2]Canadian National Collection of Insects, Arachnids and Nematodes, Canada, [3]Carleton University, Canada, [4]University of Guelph, [5]Zoologisches Forschungsmuseum Alexander Koenig

Abstract: Next generation sequencing, in combination with the dataset preparation pipeline PhyMMR, cuts through the stubborn knot represented by the paraphyletic subfamily Eristalinae (Diptera: Syrphidae) to recover a new hypothesis of Syrphidae relationships. Eristalinae is revealed as a paraphyletic assemblage of five monophyletic clades: Eristalinae, Merodontinae, Cerioidinae, Volucellinae and Alipumilinae.

The study utilizes probes developed specifically for use with Syrphidae and samples 1302 orthologous genes. 136 of 145 described genera within Eristalinae are sampled, with the use of pinned museum specimens allowing for inclusion of rarer genera, for a total sampling of more than 300 taxa.

Multiple independent Australian-Chilean relationships are revealed, raising the question whether Syrphidae underwent Trans-Antarctic dispersal or Gondwanan vicariance.

Death does not escape the definition of time and space, at least in forensic entomology

Authors: Moreau Gaetan[1], Boudreau Denis[1] and Michaud Jean-Philippe[2], [1]Biology Department, Pavillon Remi-Rossignol, Universite de Moncton, Canada, [2]Royal Canadian Mounted Police (RCMP), Serious Crimes Branch, Airdrie, Alberta, Canada

Abstract: Time and space are indisputably two of the most important variables in forensic science, allowing to establish the chronology and circumstances of events, to understand the evidence obtained and, ultimately, to exonerate or incriminate individuals. These two variables also have singular characteristics and properties, their treatment being subject to different algebraic/statistical approaches than other variables of forensic importance such as temperature, cadaver exposure, precipitations, etc. In this presentation, theoretical and practical issues related to the handling of time and space will be discussed from the perspective of forensic research and applications. To this end, data on the ecological succession of Diptera and Coleoptera species on large vertebrate carcasses in Canada will be examined. Specifically, the analysis will focus on illustrating the temporal, spatial, and spatiotemporal dynamics of these datasets and highlight how forensics gains accuracy and mechanistic understanding when time and space are properly accounted for.

Trait-based approaches in urban ecology

Authors: Moretti Marco, Swiss Federal Research Institute WSL, Switzerland

Abstract: Cities worldwide are characterized by unique human stressors potentially leading to biodiversity changes through strong abiotic and biotic filtering. In this regard, functional traits (i.e. fitness-related individual characteristics) are considered good candidates to predict both biodiversity (B) response to stressors across taxa and regions, and to shade light on the mechanisms behind [direct and indirect] consequences on ecosystem functions (EF) and services (ES). However, most of our knowledge about BEF-relationships are still scares and mainly based on taxonomic components of biodiversity and (semi)natural ecosystems.
To advance in trait-based BEF/BES ecology in cities, we first need to identify the main filters and traits under selection, and then test their effects on measurable EF/BS.
In my talk, I will summarize key concepts based on theories and empirical studies that have investigated functional aspects of biodiversity in cities. I will illustrate 1) which traits are filtered from the regional to the urban species pool, 2) how this latter is further shaped by the distinct urban green space types, and 3) how the resulting species assemblages affect EF/ES. Finally, 4) I will present future perspectives, such as the importance of intraspecific trait variation to investigate species adaptation to urban characteristics and the potential role of trait-based approaches to bridge ecological and social science and improve conservation in the face of an urbanizing world.

BANKER-SHEET™: Development and improvement of a new release device of predatory mites

Authors: Mori Kotaro, Ishihara Sangyo Kaisha, ltd, Japan

Abstract: Although predatory mites are widely used for controlling small pest in crops, environmental stresses adversely affect their performance. The main barriers for the predatory mite population are as follows: 1) short of food (e.g. pollen, prey) over a long time after predatory mite release; 2) severe climatic environments and 3) side effects of pesticides. To solve these problems, we developed plant-attached shelters, Banker-Sheet™ that hold sachets of <i>Neoseiulus californicus</i> (McGregor) or <i>Amblyseius swirskii</i> (Athias-Henriot). The shelter is made of a water-resistant paper that protects against adverse effects of chemical application and rainfall, and acts as a buffer against temperature and humidity fluctuation. The basic features including shelter function has been studied (Shimoda et al. 2017; 2019). We conducted laboratory experiments to estimate the number of predatory mites released from Banker-sheet™ under different conditions. More mites (<i>N. californicus</i> and <i>A. swirskii</i>) were released from Banker-sheet™ than from unsheltered sachets (23 and 20 ?). <i>N. californicus</i> continued to release from Banker-sheet™ for more than one months at temperatures 17 and 15 ?. These results indicate Banker-sheet™ is potentially useful for protecting predatory mites against environmental stressors and enhances their release to crops. Banker-sheet™ with either <i>N. californicus</i> or <i>A. swirskii</i> (called Miyako-Banker™ and Suwaru-Banker™) became commercially available in Japan. We are going to apply this new device to various crops such as vegetables, fruit trees, and flowers. This research was supported by grants from the Project of the NARO Bio-oriented Technology Research Advancement Institution (Research program on development of innovative technology, 26070C and 28022C).

Molecular monitoring of Neoseiulus californicus released from sheltered slow-release sachets for spider mite control in a Japanese pear greenhouse

Authors: Mori Kotaro[2], Sonoda Shoji[6], Morishima Kaori[5], Osakabe Masahiro[3], Toyama Masatoshi[1], Aizawa Mineaki[5], Uesugi Ryuji[4] and Mikawa Yuya[5], [1]Institute of Fruit Tree and Tea Science, NARO, Japan, [2]Ishihara Sangyo Kaisha, ltd., Japan, [3]Kyoto University, Japan, [4]Tohoku Agricultural Research Center, NARO, Japan, [5]Utsunomiya University, Japan, [6]Utsunomiya University, Japan

Abstract: A novel system for spider mite control was developed with a slow-release sachet containing Neoseiulus californicus (McGregor) (Acari: Phytoseiidae) protected by a waterproof shelter. Monitoring the efficacy of the predator release system for spider mite control at a Japanese pear greenhouse requires discrimination of N. californicus from other indigenous phytoseiid mite species inhabiting the study site and subsequent identification of the released N. californicus. The report of our earlier study described a PCR-based method for discrimination of N. californicus species. For the present study, we first examined phytoseiid mite species composition in the greenhouse. Subsequently, we developed microsatellite markers to identify the released N. californicus. Finally, we installed the predator release system in the greenhouse and conducted a population survey of phytoseiid mites and spider mites. Results demonstrated that approximately one month is necessary for distribution of the released N. californicus on the leaves.

A Novel Repellent, Bemi-deotouchTM, to suppress infection of Tomato Yellow Leaf Curl Virus (TYLCV) transmitted by Bemisia tabaci (Hemiptera: Aleyrodidae)

Authors: Mori Kotaro[3], Kashima Takayuki[2], Morito Azusa[2], Ohnishi Jun[3], Sano Makiko[2], Kitamura Toshio[3] and Arimoto Yutaka[1], [1]Institute of Physical and Chemical Research, Japan, [2]Ishihara Sangyo Kaisha, ltd., Japan, [3]National Agriculture and Food Research Organization, Japan

Abstract: Bemi-detouchTM EC (acetylated glyceride; AG), food additive, was found to have 3 biological properties: repellency, mating disruption and anti-feeding activity against the adult sweet potato whitefly, Bemisia tabaci (Hemiptera: Alyeyrodidae). Tomato yellow leaf curl virus (TYLCV) is transmitted systematically by the only known natural vector B. tabaci, causing imajor economic loss of tomato production. But continuous field application of insecticides is not always feasible due to harmful effect on beneficial insects, deposition of pesticide residues on crops and the development of insecticide-resistant populations such as B. tabaci Q (MED Q1).

We found that the first function of AG was delayed initiation of plant sap ingestion caused by the adult repellency in the first 2 days in no-choice test. The second function was constant interference with adult feeding behavior, which resulted in a major reduction in honey dew excreta during the last 5 days of 7-days observation periods. In no choice test, the proportions of TYLCV-infected grape tomato seedlings treated with AG and water were 65 % and 94%, respectively after releasing viruliferous female for 7 days. In this test periods, almost no dead female was shown on the AG-treated leaf. Efficacy of AG to suppress TYLCV-infection were superior to most conventional insecticides. This compound shows no harmful effect on beneficial insects. AG is currently launched as a novel repellent pesticide in Japan.

This work was supported by Cabinet Office, Government of Japan, Cross-ministerial Strategic Innovation Promotion Program (SIP), "Technologies for creating next-generation agriculture, forestry and fisheries" (funding agency: Bio-oriented Technology Research Advancement Institution, NARO)

Addressing global challenges with unconventional insect ecosystem services: why should humanity care about insect larvae?

Authors: Morimoto Juliano, University of Aberdeen, United Kingdom

Abstract: Insects provide a wide range of services, the most widely known being pollination. However, our idea of insect services overlooks the full range of services that can be provided by insects, largely because services provided by life-stages other than the adult are often neglected. In this presentation, I will provide a collection of unconventional ecosystem services provided by insect larvae which highlights the importance of considering life stage-specific services in a holistic view of insect ecosystem services. More specifically, I discuss recent advances that revealed how insect larvae can degrade plastic, which is one of humanity's greatest environmental pollutants, and how larvae can be used to produce biofuel to help overcome the increasing contribution of the fossil fuel industry to climate change. I then discuss how toxic compounds produced by the larvae of some insects provide potential new medicines for clinical treatment and lastly, I discuss a unique example of how the larval stage of insects is entrenched into the cultural values of Aboriginal communities in Australia. By acknowledging life stage-specific ecosystem services provided by insects, my aim is to raise awareness of unconventional services that can underpin innovative solutions to contemporary global challenges, which can ultimately help create more sustainable and culturally diverse societies.

Chemical defenses of the yacon leaves

Authors: Morimoto Masanori, Kindai University, Faculty of Agriculture, Department of Applied Biological Chemistry, Nara, Japan

Abstract: Asteraceae plant species produce sesquiterpene lactones (SLs) probably as defense chemicals against herbivores. The Asteraceae crop, yacon (Smallanthus sonchifolius (Poepp. & Endl.) H. Rob) is a perennial plant species, and its enlarged roots are used as a foodstuff. Since this plant species exhibits high tolerance to herbivores, its SLs probably produced by their leaf trichomes were postulated to exhibit insect antifeedant activities. Thus, yacon leaves were rinsed with dichloromethane (DCM) to obtain the rinsate, and the residues were further extracted by DCM to obtain the DCM extract. Tests using dual choice leaf disks bioassay revealed that the rinsate contained several insect antifeedants against the tested insect pest, common cutworm (Spodoptera litura). The main constituents of the rinsate were isolated by silica gel flash chromatography using a hexane-ethyl acetate solvent system and active principles were identified as uvedalin (5-acetoxy-4-epoxyangeloyloxy-6-methylcarboxygermacrenolide) and its oxidative congener, enhydrin (5-acetoxy-10-epoxy-4-epoxyangeloyloxy-6-methylcarboxy germacrenolide), both of which are melampolides based on spectroscopic data. These SLs exhibited showed marked insect antifeedant activities, and thus, can function as defense weapons of yacon plant. The author further explored SLs and found parthenolide (10-epoxy-6-methyl germacrenolide) and erioflorin (6-epoxy-4-methacryloxy-6-methyl germacrenolide) from Tanacetum parthenum L. and Helianthus strumosus L., respectively, as insect antifeedants with moderate activity. Their SAR suggested that the substituents as well as the germacrenolide skeleton is critical for the activity. The volatiles from yacon leaves was measured by GCMS sampling the head-space method using PDMS-SPME fiber. Comparisons of volatiles within intact leaves, mechanical wounded leaves and common cutworms damaged leaves were evaluated. Also, the microorganisms on the leaf surface were separated using by the selected growth mediums for fungus or bacteria/yeast. The relationship with these separated microorganisms and productivity of defense chemical is discussed.

The Effect of Ant-Produced Compounds on Microorganisms

Authors: Morris Ashley[1], Pereira Roberto[1], [1]University of Florida, United States

Abstract: Sociality in insects is linked to efficient, multi-generational brood care, enhanced foraging, and protection against predators through a large number of constituents. Although beneficial, sociality involves crowded conditions that favor the quick introduction and transmission of pathogens. The ability for animals that live in group settings to detect and fight potential outbreaks is an essential adaptation for social insects, as evolution selects for the entire colony and not the individual members.

Many ants (Hymenoptera: Formicidae) have evolved chemical defenses to combat viral, bacterial, and fungal infections. Some of these compounds are extremely specialized against certain pathogens, while others are general and serve multiple purposes. Examples include the piperidine venom alkaloids and cuticular hydrocarbons produced by the Red Imported Fire Ant – RIFA (Solenopsis invicta Buren).

We isolated RIFA alkaloids and hydrocarbons through a hexane and water extraction. The solution containing alkaloids and hydrocarbons was pipetted at different quantities onto circular discs. Plates were sprayed with a bacterial suspension of Bacillus thuringiensis or Bradyrhizobium spp. or with a fungal suspension of Beauveria or Metarrhizium.

The combined effects of the venom alkaloids and cuticular hydrocarbons inhibited Bt, Bradyrhizobium, and Beauveria growth. Further experiments are planned with other microbes.

Attraction by stored product insects to microbial volatiles as an underexploited source for behaviorally-relevant compounds in food facilities.

Authors: Morrison William[3], Scully Erin[2], Maille Jacqueline[1], Yan Zhu Kun[1], Ponce Marco[1] and Kim Tania[1], [1]Department of Entomology, Kansas State University, United States, [2]USDA Agricultural Research Service, United States, [3]USDA-ARS Center for Grain and Animal Health Research, United States

Abstract: There has been a push to diversify postharvest IPM programs away from regular fumigant applications. One class of alternative IPM tactics is behaviorally-based management, where semiochemicals are deployed to manipulate pest behavior in ways that support food production, such as attract-and-kill or push-pull. However, apart from mating disruption, no behaviorally-based strategies exist commercially for stored products. A key challenge includes finding semiochemicals that can manipulate stored product insect behavior with the large amount of already-attractive food cues in the background at food facilities. One potential source for these are microbes. Because food facilities are generally well-sanitized, microbially-produced volatile organic compounds (MVOCs) represent a unique stimulus in an otherwise saturated background. Further, response to MVOCs may be conserved in postharvest insects because their historical food sources includes caches of food stored in damp locations for long periods by small mammals, birds, and other insects. Thus, we evaluated attraction by several species of stored product insects to MVOCs in the wind tunnel as well as release-recapture experiments. We also characterized the volatiles by dynamic headspace collection and GC-MS. After tempering grain to one of three moisture levels (12–19%) and incubating for one of three intervals (9–27 d), we evaluated the response of the insect community, and characterized microbial damage by using near infrared spectroscopy and DNA extractions. We found that Rhyzopertha dominica and Sitophilus zeamais responded positively to MVOCs in multiple assays. Our results show that MVOCs hold promise in manipulating the behavior of stored product insects. Future work should tie these behavioral responses to specific target genes.

Pheromone-based attract and kill strategies to restore IPM programs to apple orchards

Authors: Morrison William[3], C. Leskey Tracy[4], Short Brent[2], Lee Doo-Hyung[1], [1]Gachon University, South Korea, [2]Trece, United States, [3]USDA-ARS Center for Grain and Animal Health Research, United States, [4]USDA-ARS, Appalachian Fruit Research Station, Kearneysville, WV 25430, United States

Abstract: Brown marmorated stink bug (BMSB) is an invasive pest in the USA, Canada, Chile and a number of countries in Europe. Feeding by this species can lead to serious, if not catastrophic levels of injury if left unchecked. Indeed, in the USA, insecticide treatments in affected fruit orchards increased > 4x following its invasion. To reduce these inputs, we have developed spatially precise attract and kill strategies for BMSB that exploit its perimeter-driven behavior and attraction to and retention on host plants baited with pheromonal stimuli. In apple orchards, perimeter row apple trees spaced every 50 m and baited with the BMSB aggregation pheromone and pheromone synergist and provisioned with a killing agent (weekly insecticide treatments or long-lasting insecticide treated nets) resulted in acceptable levels of injury equivalent to that of conventional spray programs. These tools along with other IPM tactics offer the means to manage this invasive species more sustainably.

The role of endophytic entomopathogens in modulating plant-microbe-insect interactions

Authors: Mounger Jeannie[1], Birge Traci[2], [1]Biodiversity Unit University of Turku, Finland, [2]Finland

Abstract: During recent years, endophytic entomopathogens, such as Beauveria bassiana and Metarhizium anisopliae, have been acknowledged to show biocontrol potential against insect herbivores in different crops. Despite the reported negative effects of endophytic entomopathogens on insect herbivores, the exact mechanisms behind these outcomes are still largely unknown. Furthermore, while the harmful side effects of chemical pesticides on the natural enemies of the pests and pollinators are well explored, very little is known about the potential role of endophytic entomopathogens in steering higher trophic level ecosystem services, such as those conducted by the natural enemies of pests or pollinators. Given this, the aim of our ongoing project is to test how endophytic entomopathogens modulate plant-microbe-insect interactions. As a model plant-herbivore-microbe system, we use oilseed Brassica rapa, its most important pests (pollen beetle, Meligethes aeneus and flea beetles, Phyllotreta spp.), and entomopathogenic fungi (B. bassiana and M. anisopliae) which are known to be able to colonize tissues of oilseed rape plants as asymptomatic endophytes. We are currently running the first set of replicated greenhouse experiments to test the biocontrol potential of the fungi directly as entomopathogen and indirectly via phytohormone signaling pathways of its host plant. After this, we will determine if endophytic entomopathogens have bottom-up effects on natural enemies of pests as well as on pollinators.

Fungal grass endophytes reshape their hosts: Non-chemical plant traits as potential drivers of insect preference

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Abstract: Systemic seed transmitted Epichloë endophytes are considered mutualistic defenders of their host grasses. Epichloë endophytes have shown to increase host resistance against various abiotic and biotic factors (e.g. herbivores) and can provide their hosts with competitive advantages compared to endophyte-free conspecifics. Much of the research on the defensive mutualism in grass-endophyte system has focused on the bioactive alkaloids produced by Epichloë endophytes. Here we examine non-chemical plant traits that are altered by the endophyte symbiosis and may affect exploitation behaviour of the insects visiting the plants. Epichloë species in natural population of tall fescue (Schedonorus phoenix, syn. Festuca arundinacea) can change e.g. coloration, phenology and architecture of its plant host. We concentrate on plant traits that involve changes in tactile or visual cues for the insects. We discuss how differences in non-chemical plant traits can affect exploitation behavior and plant choice of (herbivorous) insects resulting in uneven distribution of herbivores between endophyte-symbiotic and endophyte-free plants.

Bacterial diversity and community structure differences between ‘Candidatus Phytoplasma solani’ infected and non-infected insect vectors in North Italy vineyards

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Abstract: In the present study, we described the bacterial diversity and community structure of the ‘Candidatus Phytoplasma solani’ infected and non-infected insect vectors (Cicadella viridis, Dictyophara europaea, Euscelis incisus, Euscelidius variegatus, Philaenus spumarius, and Psammotettix alienus), newly discovered in northern Italy alongside the main vector Hyalesthes obsoletus and a known host but non-vector, Cicadella viridis. A total of 300 individuals were captured with sweep entomological net and pooter in mid-June 2018 and transferred to the laboratory in 100% alcohol for molecular analyses. ‘Ca. P. solani’ was detected by nested PCR-based amplification of the stamp gene using as templates the total nucleic acids extracted from the insect specimens. Depending on the result of this PCR, specimens were separated into the “infected” and “non-infected” groups. A total of 14 individuals per species (7 specimens per group) were sent to Personal Genomics (Verona, Italy) for Illumina sequencing of the V3-V4 hypervariable region of the bacterial 16S rRNA gene

Biological control of Hyalesthes obsoletus Signoret, the main insect vector of 'Candidatus Phytoplasma solani', using entomopathogenic nematodes and fungi

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Abstract: Hyalesthes obsoletus Signoret is a univoltine, polyphagous species completing its complex life cycle, including the nymph subterranean cryptic stage, on herbaceous wild plants in European countries. In vineyards, it occasionally transmits 'Candidatus Phytoplasma solani', an obligate parasitic bacterium associated with Bois noir disease of grapevine, from its preferred host plants to grapevine. As no effective control measures targeting phytoplasmas are available, main strategies to manage the disease is based on the vector control. In the case of H. obsoletus, insecticide treatments on grapevine canopy are completely inefficient due to its life cycle. Consequently, the control of this planthopper focuses on its nymphs living on the host plant roots. In the present study, the control activity of entomopathogenic nematodes (EPNs; (Steinernema carpocapsae, S. feltiae, Heterorhabditis bacteriophora) and fungi (EPFs; Beauveria bassiana, Metarhizium anisopliae, Paecilomyces fumosoroseus, Lecanicillium muscarium) against H. obsoletus nymphs and adults were evaluated by laboratory bioassays and semi-field trials. Statistical analyses demonstrated that the majority of the examined EPNs and EPFs are able to control H. obsoletus nymphs and adults, exhibiting a range of effectiveness. In all the conducted trials, S. carpocapsae and P. fumosoroseus were found as the most effective biocontrol agents among EPNs and EPFs, respectively. Interestingly, considering their ability to colonize the soil after their inoculation, EPNs and EPFs can reduce the H. obsoletus population density for long time. Ecological competency and conditions that can impede or enhance the EPNs and EPFs performance should be investigated to optimize their performance in field conditions.

Role of the microbial community of Ips typographus in the outbreak dynamics in the Dolomites

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Abstract: In the last years, a series of unfavorable weather conditions, including the storm Vaia, caused severe damages to conifer forests of the Dolomite region. Consequently, Norway spruce-dominated forests got more susceptible to infestations by the European spruce bark beetle Ips typographus. Microorganisms play an essential role in the beetle's biology, like development, fitness. Here, we aimed to improve our knowledge on the composition and the role of the microbial community associated with I. typographus, using a high-throughput sequencing approach. Particularly, we focused on the role of microorganisms in overcoming the conifer's host defense system. Beetles from three regions of the Dolomites – Eastern Tyrol, South Tyrol and Belluno were sampled and compared to populations from the Apennines, Russia, Romania, and Croatia, for potential Pleistocene refugia of I. typographus. Sequencing was performed using an Illumina MiSeq platform for the amplification of a partial fragment of the 16S rRNA gene. Pairwise comparison of the alpha-diversity showed a significant difference among locations. Similarly, the bacterial community composition varied among the sampled regions. The genus Erwinia showed a high abundance in all regions. This genus is known for its role in increasing the tolerance against the conifer monoterpene myrcene. Such dominance could explain the outbreaks of I. typographus in the Dolomites. Furthermore, the endosymbionts Wolbachia and Spiroplasma are known for their antagonistic relationships and involvement in reproductive performances of the host insect; their relative abundance in the I. typographus populations will be discussed. Our results increase our understanding of symbiotic interactions in I. typographus

Structure of population Chironomidae Larvae in coastal lakes

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Abstract: The study was realized in 10 coastal lakes, among which three types were selected: freshwater (Wicko Przymorskie, Jamno, Sarbsko, Liwia Łuża, Dołgie Wielkie), transitional (Kopań, Gardno) and brackish (Łebsko, Ptasi Raj, Resko Przymorskie). Samples were analyzed from two years. Chironomidae larvae in the studied coastal lakes were represented by 11 taxa. Lake Łebsko was the most abundant in species, while the lowest number of taxa was recorded in Lake Liwia Łuża. The results of the zoocenotic indices, i.e. alpha biodiversity and evenness for particular lakes, were comparable. The beta diversity (Wittaker index) for the area of the southern Baltic coast was low and amounted to 0,563. The results of the value of Chironomidae larvae dominance showed that in freshwater and brackish water lakes, Chironomus plumosus was the most abundant species, while in transitional lakes Procladius Skuse was the most abundant. Chironomus plumosus was dominant in biomass of all types. Brackish lakes had the highest density of Chironomidae larvae, medium values in freshwater lakes and the lowest in transitional reservoirs. Biomass was highest for freshwater lakes, medium for brackish water lakes and lowest in transitional lakes.

Host plant and developmental stage impact prevalence and load of a viral pathogen, Junonia coenia densovirus, in wild butterflies

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Abstract: Incorporation of novel host plants can result in profound changes for insect herbivores. Characterizing variation in pathogen pressure across herbivore populations using native or novel host plant species may provide insight into the tritrophic outcomes of host range evolution. The Baltimore checkerspot butterfly, Euphydryas phaeton (Nymphalidae), recently incorporated an exotic plant, Plantago lanceolata (Plantaginaceae), into its host range. We investigated the consequences of this dietary expansion for interactions between E. phaeton and a naturally occurring entomopathogen, Junonia coenia densovirus (JcDV), across the course of herbivore development, which includes an obligate overwintering diapause during the larval stage. We quantified viral prevalence and loads in populations using either P. lanceolata or a native plant, Chelone glabra (Plantaginaceae) during three stages of the life cycle: post-diapause, pre-diapause, and diapause. We found that viral prevalence was higher in post-diapause caterpillars, pupae, and adults, compared to early-instar caterpillars in the pre-diapause and diapause stages. However, early-instar larvae that were infected with JcDV harbored higher viral loads, relative to their body size, compared to late-instar larvae, pupae, and butterflies. In addition, viral loads were substantially higher in post-diapause herbivores utilizing the exotic plant, P. lanceolata, compared to the native C. glabra, while host plant effects were minimal during earlier developmental stages. These results demonstrate that viral prevalence and burdens can vary considerably across the life cycle of an insect host and suggest that host plant mediated effects on herbivore susceptibility to infection may be most evident or consequential during later stages of development in this system.

Self-medication and host range expansions

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Abstract: Self-medication is an important defense that some animals display when attacked. Since plant chemistry provides the basis for protection, sequestering insects may be best poised to exhibit this behavior. We investigated immunity and sequestration of two butterflies, the Baltimore checkerspot and the white peacock, in response to infection by an entomopathogen. Populations of both butterflies have recently incorporated a new host plant, Plantago lanceolata, into their diet and are capable of sequestering iridoid glycosides (IGs) from their host plants, including P. lanceolata. We reared infected and uninfected caterpillars on the new host plant and on their native host plants to understand the interaction between immunity, sequestration, and viral outcomes. In the Baltimore checkerspots, we found that high sequestration of IGs was correlated with lower viral loads. Interestingly, high sequestration also reduced immunity. Similar results were discovered with the white peacocks, and while we did not directly measure sequestration, viral loads were lower on P. lanceolata compared to the native host plant, which does not contain IGs. Although we did not measure self-medication behavior, our results suggest that these caterpillars may engage in self-medication, and future work will elicit whether they do, and whether this behavior may influence host range expansion.

Can Nematodes be used as a biocontrol option of the Potato leafminer (Liriomyza huidobrensis) pupae?

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Abstract: Although agriculture is crucial to economic growth in South Africa, it faces several challenges, most include pests and diseases that lead to crop losses. Such losses significantly hinder securing of food and hunger reduction. Therefore, a major concern is finding effective, environment-friendly control measures for insect pests. Potatoes are among the four most widely consumed vegetable crops worldwide, with more than 315 million ha being grown yearly. The South African potato production industry contributes 60% of the total percentage of vegetables grown in the country, and 4% of total agricultural produce. However, potatoes are infested by various pests and diseases, like the devastating leaf miner, Liriomyza huidobrensis Blanchard (Diptera: Agromyzidae). The aforesaid leaf miner, since the early 2000s, has become the most important pest of vegetable crops nationwide. The highly invasive species damages solanaceous crops, causing up to 70% loss. The damage caused by the leaf miner is direct, resulting from the female flies feeding on the leaf mesophyll during oviposition, with the larvae mining the leaves, and indirect, induced through pathogens entering through perforations that act as vectors of plant diseases. L.huidobrensis has developed resistance against a wide range of synthetic insecticides, hence the need to find an integrated pest mangement programme.The use of Entomopathogenic nematodes (EPNs) for the control of L. huidobrensis larvae has proven to be advantageous. In this study, two South African local EPN species, namely, Heterorhabditis baujardi and Heterorhabditis bacteriophora, were tested for their ability to infect and kill L.huidobrensis pupae at 25 °C. The initial results showed that Heterorhabditis baujardi was effective against L. huidobrensis pupae, resulting in 72% mortality while Heterorhabditis bacteriophora was ales effective with 50% mortality. Heterorhabditis baujardi was able to reproduce within the pupae and the second-generation nematodes were observed. This study demonstrated the high potential for the use of locally isolated EPNs for the control of Potato Leafminer pupae in South Africa, but further research is needed.

Involvement of juvenile hormone in the maternal induction of diapause in the parasitic jewel wasp, Nasonia vitriepnnis .

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Abstract: Diapause is a neurohormonal-controlled cessation of development or reproduction, and which usually involves the acquirement of hardiness against several environmental stresses. In most inset species, diapause is induced under shortening day-length and averted by lengthening day-length. Such an ability which respond to day-length (photoperiod) is termed by photoperiodism. In several insects, diapause induction occurs in respond to photoperiodic conditions which individuals have experienced by themselves. However, in some cases, diapause induction occurs in respond to photoperiodic conditions in the previous generation, i.e., maternal induction of diapause. Although it is considered that the involvement of hormonal change in the determination of diapause fate, little is known about the hormone which regulates maternal physiology to produce diapause-destined progeny. Several studies showed that the essential role of the juvenile hormone (JH) in diapause induction. JH is an acyclic sesquiterpenoid that is synthesized at and released from an endocrine organ, the corpora allata (CA). Although it is considered that diapause induction is regulated by the production or secretion of JH in the CA under photoperiodic regulation, the role of JH in physiological states of adult insect which determine progeny's diapause fate is unknown. The parasitic jewel wasp, Nasonia vitripennis (Hymenoptera: Pteromalidae) is a cosmopolitan parasitoid wasp and shows a clear photoperiodic response in maternal induction of diapause. When adult females are exposed to long-day conditions, they lay eggs that develop to adulthood without developmental interruption. In contrast, when adult females are exposed to short-day conditions, they lay eggs that are destined to enter diapause at the final (4th) instar larval stage.

In current study, involvement of JH in the maternal induction of diapause was investigated in N. vitripennis. First, we measured the mRNA abundance of 6 genes involved in JH biosynthesis under long- and short-day conditions. The level of juvenile hormone acid methyl transferase (JHAMT) mRNA was lowered by a short-day exposure, whereas mRNA levels of other genes were nearly identical between photoperiods. The effect of JHAMT RNAi on induction of diapause producers was also assessed. JHAMT RNAi increased the proportion of diapause producers, irrespective of photoperiodic conditions. Topical application of JH III, the Hymenopteran JH, lowered the proportion of diapause-destined progeny both in females reared under short-day conditions and females exposed low temperature. The role of JH in maternal induction of diapause will be discussed.

The role of the juvenile hormone in the photoperiodic response in a jewel wasp, Nasonia vitripennis

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Abstract: Most temperate multivoltine insects enter diapause, a hormonally controlled developmental suspension, in response to the approaching harsh season. The circadian clock is involved in the perception of daylength as a seasonal cue and the endocrine effector regulates diapause induction. In some insect species, diapause induction is determined by environmental states that the mother received. Although maternally regulated diapause is common among insects, the maternal endocrinological mechanisms are largely veiled. To approach this issue, we used the parasitic jewel wasp Nasonia vitripennis, which produces non-diapause-destined offspring under long days and diapause-destined offspring under short days. We focused on the maternal physiological machinery to determine offspring diapause fate. Comparative transcriptomics and RT-qPCR revealed possible involvement of the juvenile hormone (JH) biosynthetic cascade in maternal diapause regulation. JH acid methyltransferase (jhamt) was typically downregulated under short days. The haemolymph JH concentration was reduced under short days. RNAi targeted at jhamt reduced haemolymph JH concentration and induced wasps to produce diapause-destined offspring even under long days. In addition, RNAi targeted at circadian clock gene period up-regulated jhamt expression. These results indicate that diapause in N. vitripennis is determined by maternal jhamt expression and haemolymph JH concentration in response to day length.

Fungivore-induced fungi volatiles attract parasitoid wasps Orthocentrinae (Hymenoptera: Ichneumonidae) as fungivore enemies: behavioral and electrophysiological responses of wasps to host cue

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Abstract: Tritrophic interactions between plants, herbivores, and carnivorous parasites are good models for understanding interspecific interactions of organisms in the food chain. Many studies have determined the function of plant infochemicals in plant-herbivore-parasitoid interactions; however, information about fungi infochemicals in fungi-fungivore-parasitoid interaction is less. This is because of the difficulty of reliable and long-term investigations as it concerns interspecific interactions surrounding these fungal species and the natural ecosystems surrounding these fungal species are fluctuating and complicated.

We previously reported that female parasitoid wasps, Orthocentrinae (Hymenoptera: Ichneumonidae) exhibited parasitic behavior on the larvae of the fungivorous flies Neoempheria spp. (Diptera: Mycetophilidae) (Mukai and Kitajima, 2019). Neoempheria spp. is one of the most ruthless insect pest of mushroom in Japan, and the breeding system of this fly has been developed using the commercial mycelial block of shiitake, Lentinula edodes (Agaricales: Omphalotaceae). We reared these insects in the laboratory, and investigated the host-locating behavior of parasitoids and the fungi infochemicals cues in fungi-fungivore-parasitoid interaction. Preliminary observations suggested that parasitoids get attracted to the odor of fungi and fungivorous flies. Odor preference experiments using Y-tube olfactometer showed that the parasitoid females exhibit a response to the odor of a piece of mycelial block of shiitake. The parasitoid females exhibited even stronger preference to a piece of mycelial block which have been consumed by larvae of the flies. GC-MS analyses revealed that the fluid extract of the fungivorous larva-infested mycelial block was different from that of the noninfested mycelial block. We also performed GC-EAD analysis, which revealed that the parasitoid females exhibited electrophysiological antennal response to some special odor components released from larva-infested mycelial block. It is speculated that the chemical information derived from the fungi or ingestion by larvae of fungivorous flies comprises reliable and detectable host-locating cues used by parasitoids to search for hosts. We provided the first observational and experimental evidence that fungivore-induced fungi volatiles mediated the fungi-fungivore-parasitoid tritrophic interaction.

“Vampires” or “Cows” - A new look at mosquito behavior

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Abstract: Mosquitoes are known for their blood feeding behavior and resulting disease transmission and most past and current research focused on this aspect. However, only females feed every few days on blood, and blood is mainly or solely used for egg production. In contrast both, females and males, need daily sugar meals. Sugar is their main energy source, influences longevity and fecundity, host seeking behavior and ultimately blood feeding and disease transmission. Sugar feeding is not random; mosquitoes have clear preferences and are attracted to favorable sources over long distances. In the absence of nectar and fruit, some mosquito species are able to divert to plant tissue feeding exposing them and parasites in their gut to an array of phyto-chemicals including toxins. Another aspect of neglected adult mosquito behavior is diurnal “resting“ in vegetation. For mosquitoes, surviving the day in adverse conditions is not trivial. An important aspect of vector competence of mosquito populations is the percentage of mosquitoes “old enough” to transmit diseases. Especially in arid and semi-arid habitats, suitable sugar sources and resting sites are bottlenecks. Thus, ornamental and invasive plants can provide both sugar and shelter and may accordingly increase vector competence. Recent research shows that this neglected mosquito behavior provides new opportunities for control. A new promising paradigm is Attractive Toxic Sugar Baits (ATSB). This approach exploits the daily quest of mosquitoes for sugar. Plant based attractants, sugar as a feeding stimulant, and an oral toxin applied as a spray on non-flowering vegetation or enclosed within bait stations attract and kill mosquitoes.

Effect organic farming on the relationship between predator diet diversity and pest control services in vineyards

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Abstract: Evidence shows that pest control services are enhanced by natural enemy abundance and diversity, notably under organic fields. However, little is known about the mechanisms behind these relationships. Here, we investigated how the natural enemy diet variability expected under different landscape and local contexts can explain variation of pest control services. We collected and sequenced the gut content of 2880 arthropod predators in 10 French vineyards in 2015. Five vineyards were conducted under organic farming and the other ones under conventional farming, distributed along a gradient of proportion of semi-natural habitats (from 1 to 75%). We showed that the diet of predators is more diverse under organic farming, this can in turn explain the higher level of pest control services. In addition, we extrapolated the locally observed pattern of pest control services to estimate landscape-scale levels of natural pest control services.

The role of USAID in monitoring spread of Tuta absoluta and its management

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Abstract: The South American tomato leafminer, Tuta absoluta, a native of South America, was accidentally introduced to Spain in 2006. Since then it has invaded most of Europe, Africa, Central Asia, Middle East, Afghanistan, India, Nepal, Bangladesh, and Myanmar. It also invaded Panama, Costa Rica, and Haiti in Central America and the Caribbean. Currently it is posing a serious threat to North American countries, even though they have posted some quarantine regulations to prevent its introduction. Since 2012, the IPM Innovation Lab, a USAID-funded program, has been involved in monitoring and modeling its spread and conducting awareness and management workshops in its host countries and in national, regional, and international conferences. One of the key findings of this program is that T. absoluta can spread long distances through infected tomato seedlings and fruits.

Implementation of IPM packages for tropical crops by the IPM Innovation Lab

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Abstract: The Innovation Labs funded by USAID address agricultural and related problems in developing countries by connecting scientists from the U.S.A. and host countries for collaboration. The IPM Innovation Lab has been in operation since 1993; in the early years, it addressed individual components of different crops and institutionalized their development. For the past 15 years, however, it has been concentrating on IPM package development and implementation for selected crops. In this, scientists develop a matrix of problems of a crop faced by the farmers in a country and tackle the problems that do not have a local solution. This led to the concept of IPM package development for selected crops, tackling problems and incorporating components of solutions into it. The IPM Innovation Lab has developed IPM Packages for most tropical high value vegetable crops, and some cereal, fruit, and legume crops. In recent years, it has regionalized most and globalized some of them.

IPM package for the management of Mango pests and diseases in Bangladesh

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Abstract: Mango (Mangifera indica L.) is a major fruit crop grown in the tropical and sub-tropical regions of the world including Bangladesh. Various insect pests and diseases affect mango production. About twenty arthropod pests, of which nineteen insect and one mite pests are reducing yield of mango in Bangladesh. Seven diseases causing pathogenic microorganisms are also responsible for the low yield of mango. Among the insects, mango hoppers (Idioscopus spp), mango fruit weevil (Sternochaetus frigidus), mango fruit fly (Bactrocera dorsalis) and mango mealy bug (Droshicha mangiferae) are major pests of mango. Among them mango hoppers and mango fruit fly are mainly responsible for most of the damage. The major diseases caused by pathogenic microorganisms include the anthracnose disease (Colletotrichum gloeosporioides) in the field conditions and fruit end rot (Lasiodiplodia theobromae) in post-harvest situations. These pests and diseases are causing both quantitative and qualitative losses and in addition act as export barrier. Excessive use of chemical pesticides leads to the development of pesticide resistance with various adverse effects on the environment and human health. In this paper, integrated pest management components widely practiced by farmers for mango production in Bangladesh are described. For instance, foliar spray of powder formulation of Beauveria bassiana @ 5.0g/L of water at flower initiation stage, Imidachloprid (Confidor 70WG) insecticide @ 0.2g/L of water before flower opening stage and again foliar spray of powder formulation of Beauveria bassiana @ 5.0g/L of water at pea stage; and fruit bagging with double layer brown paper bag before forty-two days of harvest found to effectively reduce hopper and fruit fly infestations, respectively. In addition, pruning of infected parts and spraying of Bavistin @2g/L 2-3 times at 15days intervals for anthracnose; three sprays of Mancozeb (Indofyl M-45) @2g/L of water for sooty mold; and hot water treatment for fruit end rot disease are successfully practiced in Bangladesh. This IPM package maximizes the marketable yield and marginal benefit cost ratio.

Tapping into existing networks or going it alone? Citizen science for plant health monitoring and surveillance

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Abstract: Monitoring and surveillance of plant health, bee health pests or vectors of human and livestock pathogens is mostly the responsibility of Government. For plant health pests there are portal inspections and crop / forest surveys. These approaches fulfil two different roles. Portal inspections are normally to detect potential incursions of pests into the country; whilst, surveys are to demonstrate to authorities (in Europe the EU) that the country is free from certain pests. An example of the latter, would be surveys to maintain EU protected zone status. However, both approaches are akin to 'finding a needle in a haystack'. Resource limitations mean that only a very small proportion of plant imports or cropping / forestry area are examined.

Ireland as an island off of another island on the edge of Europe, should have good plant and animal health biosecurity. Most invasive species, with a few exceptions, move through Europe East to West. We can therefore prepare in advance for potential pest invasion and provide alerts to industry and the public. In recent years in Northern Ireland, plant health pests have been detected by entomological recorders and enthusiasts. These include: horse chestnut leaf miner (Cameraria ohridella) detected in 2014 by an ecological consultant, box tree moth (Cydalima perspectalis) collected in a moth trap in 2018 by a recorder and spotted wing drosophila (Drosophila suzukii) swept from the wild in 2019 by a museum curator. Due to local connections in the entomological community, these were rapidly reported to the authorities. Another example is that of ash sawfly (Tomostethus nigritus). This species, first recorded in Ireland in 2016, causes spectacular defoliation of ash trees and was brought to our attention through a BBC news television report. Subsequently, we have sought to use ash sawfly as an examplar for a tree pest invasion and to explore the value of citizen science to monitor both incursion and spread. Three approaches are being considered. The first is use of traditional media such as television, radio and newspaper articles. This approach was used with some success in Northern Ireland to map the distribution of the New Zealand flatworm, an invasive predator of earthworms commonly found in gardens. Second, is the use of existing networks reporting on Facebook or through national biodiversity recording apps. Lastly, is use of Tree Check (www.treecheck.net), which is a more tailored approach specific to tree health on the island of Ireland.

Economic burden of Tomato Leaf Miner Tuta absoluta in tomato production in Kenya and Uganda

Authors: Muriithi Beatrice, International Centre of Insect Physiology and Ecology, Kenya

Abstract: The significance of the effects of pests in Agricultural production cannot be underestimated. There have been several efforts of controlling these pests, chiefly the use of pesticides. However, the continuous use of synthetic chemicals not only causes pests resistance and resurgences but also, presents high human and environmental risks. This study aims at examining the economic, health and environmental impact of pests on smallholder farmers in selected counties in Kenya and Uganda. Economic Impact Quotient (EIQ) and gross margin analysis was used on a random sample of 316 farmers in Kenya and 345 farmers. The results showed the average gross income of a farmer was $3282 in Kenya and $895 in Uganda. The potential tomato production in both countries was seen to be affected by the invasion of Tuta absoluta. The opportunity cost lost was valued at $8 and $646 in Kenya and Uganda repectively using NPV through the most persimistic scenario, while BCR had $1 and $5 in Kenya and Uganda respectively.

Economic and Poverty Impacts of Biological Control of Cereal Stemborers in Kenya

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Abstract: A biological control (BC) program was initiated by icipe and partners to respond to severe stemborers invasion in cereal farming regions of sub-Saharan Africa including Kenya. Four natural enemies: Cotesia flavipes (Cameron), C. sesamiae (Cameron) (Hymenoptera: Braconidae), Telenomus isis (Polaszek) (Hymenoptera: Scelionidae) and Xanthopimpla stemmator (Thunberg) (Hymenoptera: Ichneumonidae) were released to suppress economically important stemborer pests; Busseola fusca (Fuller), Sesamia calamistis Hampson (Lepidoptera: Noctuidae) and Chilo partelus (Swinhoe) (Lepidoptera: Crambidae). An economic surplus model was applied, based on time-series data on production, market and, Geographical data (GIS), to evaluate the economic and poverty impact of the BC program in Kenya. Findings show that the BC intervention contributed to an aggregate monetary surplus of $US 0.74 billion to the economy. The net present benefit of $US 141.52 million, the Internal Rate of Return of 113.08% and the Benefit-Cost Ratio of 276:1 justify that the program was worthwhile. On average, the BC program gains would lift out of poverty 57,400 persons every yearly. Wide promotion and up-scaling of the BC program should, therefore, be encouraged.

Biogeography and diversification patterns in a hyper-diverse and worldwide distributed group of moths

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Abstract: Megadiverse insect groups hold great potential to understand the processes that have led to the current uneven distribution of biodiversity. Understanding how and why some groups have become more species-rich than other groups, and how past biogeography may have shaped their current distribution, are important questions that many evolutionary biologists have long tried to solve. We address how diversification patterns and biogeography may have played in favour of a hyper-diverse Lepidoptera lineage, the geometrid moths, by studying its most species-rich clade. The tribe Boarmiini contains c. c. 200 genera and c. 3000 species. We inferred the evolutionary relationships of Boarmiini based on a dataset of 346 taxa, with up to eight genetic markers under a Maximum Likelihood approach. Their biogeographic origin was inferred using the Dispersal-Extinction-Cladogenesis (DEC) model, and the estimation of diversification rates was studied using the Bayesian analysis of macroevolutionary mixtures (BAMM). The monophyly of Boarmiini is strongly supported. The results indicated that boarmiines probably appeared in Laurasia c. 52 Mya, followed by dispersions throughout the Oriental, Australasia, African and Neotropical regions. Given the current distribution of most of the genera, we suggest that multiple dispersals have played an important role in their biogeographic distribution. Most of the dispersion patterns have occurred in the Eocene, which was characterized by intense geological activity and climate changes. In addition, diversification analyses showed a relatively constant diversification rate for all Boarmiini, except in one clade leading to one of the species-rich geometrid genera, genus Cleora. The identification of such burst in diversification rate, which is geographically limited, allows focusing future research to understand the evolutionary properties that may explain such phenomenon. Extreme polyphagy and habitat restriction of Cleora may be among the most important success factors.

Beyond case studies: a meta-analysis to identify patterns of diversification in the Neotropics

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Abstract: Biogeographic patterns of diversity in the Neotropics have long been characterised but their origin remains unclear and many hypotheses have been proposed. The so-called “Gentry-pattern” characterises groups which species richness either peaks in the Andes or instead peaks in the Amazon basin. Antonelli & Sanmartín (2011) suggested that this pattern could be explained by the presence of a barrier preventing exchanges between regions, which thereby diversified separately. Here, we explore the hypothesis that the large Pebas wetland that covered western Amazonia during the first half of the Miocene isolated Andean lineages from Amazonian lineages. Using 21 groups of Neotropical Nymphalidae butterflies we performed ancestral biogeographic state estimations under a unified model to assess 1- the dynamics of diversification in the Andes versus Amazonia, 2- the timing of interchanges between regions. According to Antonelli & Sanmartín (2011) we expected to the two regions to diversify in isolation until the Pebas started draining about 8-11 Ma.

Bottom-up and top-down effects are altered by interacting global change drivers: a case study in marine coastal habitats

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Abstract: Anthropogenic disturbances, such as nutrient pollution and habitat fragmentation, have significant impacts on natural ecosystems and their associated food webs. Salt marsh coastal ecosystems are particularly threatened by human impacts and are being lost at an alarming rate. Salt marshes are important for conservation because of the critical ecosystem services they offer, including erosion control, water filtration, nurseries for fisheries, and carbon sequestration. Arthropod communities in saltmarsh ecosystems are threatened by human impacts, including sea level rise, habitat loss, nutrient subsidies, and extreme weather events, such as hurricanes. Some disturbances are felt throughout the food web (e.g. hurricanes), whereas other disturbances are mediated via effects on host plants (e.g. nutrient subsidies). Our studies over the past two decades have found that the impacts of these disturbances on insects/ spiders and their rate of recovery are dependent on trophic level, life history, and diet breadth. While we understand impacts of single disturbances relatively well, we have very little understanding of how multiple disturbances interact to affect insect communities.

We found that generalism in diet and habitat use can lead to stable predator populations across different kinds of anthropogenic disturbance. For example, nutrient inputs consistently lead to increased populations of generalist predators, but sustained, high-inputs of nutrients eventually lead to ecosystem collapse. Diet generalism also sustains predator populations in edge habitats, but only in combination habitat generalism. When predators have specific habitat requirements, they are negatively impacted by habitat edges even when their food can be found in abutting habitats. Finally, when predator diets are so general as to include different food webs (multichannel omnivory), this can increase population stability through disturbance events. After a hurricane, spiders that were multichannel omnivores recovered most quickly because they were able to switch over to epigeic prey when herbivores were not abundant. While fewer studies have examined the interactive effects of different anthropogenic factors on organisms, we found that recovery of multichannel omnivores after hurricanes is enhanced in fertilized plots. Predators are declining globally with ramifications for important ecosystem processes. Here we show that predator persistence in the face of global change is impacted by diet and habitat breadth.

Nutrient subsidies increase food web recovery following a major disturbance by a hurricane

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Abstract: Anthropogenic disturbances, such as nutrient pollution, have significant impacts on natural ecosystems and their associated food webs. In particular, the timing and amount of nutrient inputs can have variable effects on food web structure, particularly stability. However, how anthropogenic nutrient pollution interacts with recovery from natural disturbances is not well studied. In the midst of our multi-year experiment investigating the effects of long-term nutrient presses and short-term nutrient pulses on food web interactions, a natural disturbance, Hurricane Sandy, directly affected our study site. This unplanned hurricane event allowed us to measure how food web stability in the form of resilience to environmental perturbation interacted with nutrient loading. We found that food webs in all treatments were negatively affected by the hurricane disturbance, but that food webs in our nutrient subsidy plots recovered from the hurricane more quickly than control plots. Notably, we found no significant differences in recovery between our long-term nutrient press and short-term nutrient pulse treatments. We found that anthropogenic disturbances, such as nutrient pollution, affect how natural systems recover from a natural disturbance.

Phylogenomics of Chrysidoidea: will family relationships finally be resolved?

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Abstract: Chrysidoidea is one of the least-known superfamilies of Aculeata, and there has not yet been a molecular phylogenetic analysis that has included a representative from all seven extant families. Chrysidoidea is noteworthy in an evolutionary and ecological context in part due to the many differing feeding habits and life histories. Additionally, the phylogenetic placement of Chrysidoidea at the interface between ‘Parasitica’ and Aculeata places them at an interesting junction. I will explore practices in data choice and analysis, and show how methodological decisions can change the outcomes of analyses, affecting the evolutionary inferences we draw from phylogenomic data.

Distribution and integrated pest management options of Brown Marmorated Stink Bug Halyomorpha halys (Hemiptera: Pentatomidae) in hazelnut orchards in the Republic of Georgia

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Abstract: Distribution of Halyomorpha halys (BMSB) in commercial hazelnut orchard was investigated during two consecutive years in two commercial hazelnut orchards located in western Georgia (Samegrelo region). One of the orchards was surrounded by dense wild vegetation while the second orchard was bordered by a river, arable and open lands. Different BMSB management strategies including “Attract and Kill” (A&K) approach, border sprays (BRD) and grower’s standard management practices (GS) were compared at each site with untreated blocks used as a control treatment(CTR). Phenology of BMSB was similar during both years with the first BMSB adults observed near the end of April and adults and all instar nymphs observed from July 20 (950 DD13.9) to the end of September. Finding of the 2nd instar nymphs near the end of September supports hypothesis on the presence of minimum two generations of H. halys in Georgia. The A&K treatment was very effective in killing high numbers of stink bugs through the growing season and demonstrated higher effectiveness in management of BMSB than the Grower’s standard insecticide program. Similarly, applications of pyrethroid insecticides around the perimeter of the orchard also protected the interior better than Grower’s standard program. Effectiveness of evaluated management strategies was highly impacted by the orchard surrounding vegetation. The influx of bugs from outside of the orchards was documented by high numbers of captured BMSB in the monitoring traps placed outside and inside of experimental plots. Evaluation of hazelnut quality showed that percentage of healthy kernels increased from the orchard perimeter to the interior of managed blocks. Corking damage of nuts by H. halys was associated mostly with the perimeter of the orchard and was higher on nuts collected from trees located near the edge. Percentage of healthy kernels was the highest in the A&K blocks in both years; however the overall quality of nuts in all treatments during the 2019 season was better than in 2018. The BMSB management decisions in hazelnut orchards should be firmly based on the documented populations of bugs but growers should also factor in the potential influx of BMSB from surrounding areas. With wild vegetation around, the A&K stations placed around the orchard performed better while in case of open surroundings effective protection was achieved by A&K and/or border treatments.

Predator induced changes in insect-plant and pathogen plant interactions

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Abstract: Pests and diseases can seriously affect strawberry production. Anthocorids are major predators in strawberries, but can puncture the plant for water, and they insert their eggs in plant tissue. To test the hypotheses that predators can induce resistance in strawberry plants against specialist and generalist herbivores as well as against a fungal disease two experiments were done. In both experiments, plants that had had a 24-h exposure to O. majusculus, removed before the onset of the experiment, were compared to intact plants. In the herbivore experiment, fecundity of the aphid generalist Macrosiphum euphorbiae and the strawberry specialist, Chaetosiphon fragaefolii reared on preexposed or intact plants was assessed. In the second experiment, mildew growth on exposed or intact plants was assessed. In both experiments leaf samples were taken for gene expression analysis. The chemistry of intact and preexposed plants will be compared to understand if and how induce resistance may affect specialist and generalist aphid species and powdery mildew. It was found that predator preexposure reduced fecundity of M. euphorbiae, while no effect was found on C. fragaefolii. Mildew growth was not affect by predator preexposure treatment according to a visual assessment. Results of effects on pests and diseases as well as any changes in plant chemistry will be reported and discussed.

Geographic variation of photoperiodic control of nymphal development and adult diapause induction in native and invasive populations of the brown marmorated stink bug, Halyomorpha halys

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Abstract: Facultative winter adult diapause in Halyomorpha halys is regulated by a long-day photoperiodic response. Day length influences also nymphal development which slows down at the critical (near threshold) day lengths. We compared photoperiodic responses of one native (Andong, South Korea) and three invasive (Torino, Italy; Basel, Switzerland; and Sochi, Russia) populations in a laboratory common-garden experiment. Nymphs developed and emerging adults were reared at 24 °C and a range of photoperiods with day lengths 14.0, 14.5, 15.0, 15.5, and 16.0 h. The critical day lengths of the photoperiodic responses of both sexes fell between 14.5 and 15.0 h in the native Korean and between 15.0 and 15.5 h in the invasive European populations. The differences between three invasive populations were not significant, although populations originated from distant regions. Moreover, the difference between Korean and European populations was much smaller than it was expected. The microevolution was possibly 'too slow to keep up' with the rapid spread of the invader across Eurasia. It is expected that soon the critical day length of invasive H. halys populations will gradually change to adopt better to the local conditions. At present, the critical day length for diapause induction of 15 h 15 min can be used to model phenology, further spread, and response to climate change for all European populations of the pest.

The research was funded by the Russian Science Foundation (project No. 21-16-00050).

Evaluation of a combination of thiamethoxam and pirimiphos methyl for the control of insect pests in stored grain

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Abstract: A study was conducted to determine the efficacy of a new dust formulation containing 0.36% thiomethoxam and1.6% pirimiphos-methyl (Simba) as active ingredients. The new formulation was tested against common storage insect pests of stored maize under laboratory and field conditions. In the laboratory trial 100g of maize and wheat held in 0.25 litre kilner jars were treated with doses of the cocktail thiamethoxam/pirimiphos methy at labeled rate of half dose 0.1 and 4.4 mg/kg, normal dose 0.2 and 8.9mg/kg, double dose 0.4 and 17.8 mg/kg respectively. A commercial product traded as Actellic Gold® with similar molecules as the test product but applied only as normal dose was used for comparison. The untreated controls of maize grain were prepared the same way but without insecticide The jars were arranged randomly on metal shelves in the controlled temperature room according to the insect species and storage period For the field trial, the same rates were applied in 10kg maize grains held in hessian mini jute bags. The bags were placed in a store simulating farmer storage conditions. All treatments plus control were replicated four times. In the laboratory bioassay trial exposure of Sitophilus zeamais (Motsch), Prostephanus truncatus (Horn) and Tribolium castaneum (Herbst) adults to all doses of test product in the 4,8,12,16,20,24 weeks interval resulted in mortality of 100% for all the species up to the end of the trial. No significant differences in the mortality between all dosage rates tested and the standard was detected giving a good comparison between the two products. During the entire storage period, practically no grain damage and weight loss were observed in the grains treated with either Actellic Gold® dust or normal and double dose rate of Simba dust. It is concluded that Simba dust was very effective against the three test insects at all the application rates tested in the laboratory and dosage rates of 0.2 and 8.9mg/kg and 0.4 and 17.8 mg/kg under field trial over the six month storage duration. The new product (Simba dust) is therefore recommended for registration as a potential grain protectant.

Fluctuating environments impact physiological fitness in an invasive insect species Bactrocera dorsalis (Diptera: Tephritidae)

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Abstract: The incidence and severity of environmental stressors associated with global climate change are increasing and insects frequently face variability in temperature and moisture regimes at variable spatio-temporal scales. Coincidental with this, is increased thermal and hydric stress on insects as warming increases vapour pressure deficit (VPD), the drying power of the air. While the effects of mean temperatures on fitness are widely documented, fluctuations in both temperature and relative humidity (RH) are largely underexplored. Here, we investigated the effects of dynamic temperature and RH fluctuations (around the mean [28 °C; 65% RH]) on low and high thermal tolerance of laboratory reared adult invasive Bactrocera dorsalis (Hendel) (Diptera: Tephritidae), measured as lower and upper thermal activity limits, chill coma recovery time (CCRT) and heat knockdown time (HKDT). Our results show that increased environmental amplitude significantly influenced low and high temperature responses and varied across traits tested. The highest amplitude (d12°C; 28% RH) compromised lower thermal activity limits, CCRT and HKDT while enhancing upper thermal activity limits. Similarly, acclimation to d3°C; 7% RH compromised both low (lower thermal activity limits and CCRT) and high (upper thermal activity limits and HKDT) fitness traits. These variations in fitness indicate significant roles of combined thermal and moisture fluctuations on B. dorsalis survival under changing ambient environments. This likely suggests B. dorsalis thermal fitness losses under climate change. These results are significant for B. dorsalis population phenology, management, quantifying vulnerability to climate variability and may help modeling future biogeographical patterns.

Remote Detection of Powder-Tagged Insects with Hyperspectral Lidar

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Abstract: We showcase a hyperspectral lidar used for in situ remote monitoring of powder-tagged honeybees, Apis mellifera. The experiment was ongoing from 08 to 20 o'clock for one day, and the insect activity over time and distance from the beehive was logged. Our ambition is to inspire for further entomological studies using similar technique.

Benefits of cooperation and its life-history costs in Pine Sawflies

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Abstract: In many socially behaving organisms the costs and benefits of cooperation are likely to vary with changes in ecological and social conditions. However, these trade offs between contribution to cooperative act and life-history traits have rarely been quantified, especially under multiple biological interactions. We investigated these aspects experimentally with haplodiploid social Diprion pini pine sawfly larvae that perform cooperative chemical group defence. The benefit of this system is that there is genetic and phenotypic variation in the cooperative behaviour and relatedness among cooperating individuals. We can also manipulate the levels of cooperativeness as well as social and ecological environments experimentally, and measure responses in reproductive and life-history traits. In several factorial rearing experiments and behavioral assays, we tested investment to cooperative defense and its correlated fitness effects under various conditions by manipulating diet, attack intensity and social environment. We found that cooperation increases survival of the group against predators, but investing to cooperative defence behaviour imposes several lifehistory costs. Cooperative behaviour and the magnitude of its life-history costs are further shaped by interactive effects of host plant quality and social environment (kin-structure and sex-ratio of the group). Together these results provide much needed experimental evidence that both ecological and social interactions can shape the adaptive value of cooperative behaviour and maintain variation in cooperation and cheating. Thus, to form ecologically realistic syntheses of adaptive processes and persistence of cooperation, we need tighter integration of experimental and theoretical work that takes into account multiple interactions that comprise an individual's selective environment in nature.

How to make trees good or bad for herbivores?

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Abstract: A plant should be good for herbivore arthropods if it is nutritious, does not have too many defence chemicals and does not attract too many predators of the herbivores. A plant bad for herbivores would then be the opposite: low in nutrients, high in defence chemicals and frequently visited by the predators. We wanted to study is it possible to manipulate plants to be better or worse for herbivores. We did this experiment in lowland tropical primary rainforests of Papua New Guinea. We used as experimental trees several species of Ficus which differ in their constitutive and induced defences. We used various methods to manipulate the Ficus trees. We increased the emission of volatile organic compounds (VOCs) that attract predators by spraying methyl jasmonate (MeJA). We reduced the attraction of predators by applying an inhibitor of MeJA, diethyldithiocarbamic acid (DIECA). With nitrogen fertilization (ammonium sulphate) we increased the nutrients of the tree. Finally we prevented vertebrate predator access with exclosure cages, and access of ants with glue on tree stem and poisonous baits. We had five different method combinations as treatments which were in our hypothesis from best to worst: 1) DIECA + fertilization + cage, 2) DIECA + fertilization, 3) control, 4) MeJA + cage, 5) MeJA. We have so far finished two experiments lasting 6 months and involving each 4 Ficus species. We collected from the trees before, middle and after experiment samples of leaves, arthropods, VOCs and soil, measured plant growth, and estimated the amount of herbivory. The early results show that the treatments worked as we expected: the amount of herbivory was highest in trees which were made good for herbivores, and lowest in trees that had a treatment to make the tree bad for herbivores. These results did not depend on the original level of constitutive defence of the Ficus tree. At least in some Ficus species there seemed to be a trade-off between growth (stem diameter and height) and emitting more VOCs due to the MeJA treatment. There appeared to be much more variation within and between species if the increased herbivory of DIECA + fertilization treatments affected the tree growth. There were also differences between species and treatments in e.g. VOC emissions and arthropod communities. The answer to the question in the title is that with the treatments in this experiment we managed to make the Ficus trees better or worse for herbivorous arthropods.

Phytoseiid mites benefit from conventional and integrated management as well as from higher amount of vineyards in the landscape

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Abstract: Biodiversity and ecosystem services in vineyards are strongly influenced by viticultural practices and landscape composition. Phytoseiid mites are important natural enemies of pest mites and therefore deliver important pest control services in vineyards.

In this study, we examined the relative effects of local management (organic versus integrated in Leithaberg (Austria)/ conventional in Bordeaux (France)) and the landscape composition (proportions of vineyards and semi-natural habitats within a 500 m landscape buffer) on phytoseiid mite densities in vineyards.

Compared to organic vineyards, phytoseiid mites benefited from conventional management and integrated management, respectively in Bordeaux and Leithaberg. The population densities were promoted through higher proportions of vineyards in the surrounding landscape. The influence of the management type on phytoseiid mite populations was probably caused through the higher region-specific pesticide use in organic vineyards resulting in lower phytoseiid mite densities. Especially the frequent application of the fungicides copper and sulphur in organic vineyards was probably crucial, due to their well known detrimental non-target effects on phytoseiid mites. The positive effects of surrounding vineyards may result from relative stable and interconnected phytoseiid mite populations in viticultural landscapes, which facilitates the recovery of locally diminishing populations in single vineyards by aerial dispersal of the phytoseiid mites.

Taste sensing by the maxillary palp in silkworm larvae

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Abstract: Taste sensing is essential for host-plant selection in herbivorous insects. Classical behavioral observations in the 1970s suggested that they select their diet at the surface of host plant leaves. Recently we found ultra-sensitive gustation by the maxillary palp of silkworm larvae, which enables them to identify the host mulberry leaves at the surface prior to biting (Tsuneto et al., bioRxiv). We also found that a subset of chemosensory neurons in the maxillary palp of silkworm larvae detects key mulberry compounds including chlorogenic acid, quercitrin glycosides, and ß-sitosterol with atto-/femtomolar sensitivity. Only if these three compounds are detected by the maxillary palp does the larva make a test bite, which is required for initiation of feeding. However, the neuronal and molecular basis of taste sensing by the maxillary palp still poorly understood.

Here we report the detail of taste responses by the maxillary palp towards feeding stimulants and deterrents. Electrophysiological recording reveals the ultra-sensitivities of the maxillary palp towards some sugars and secondary metabolites known as feeding deterrents. A test bite was inhibited when mulberry leaves treated with a leaf-surface extract from non-host plant leaves, suggesting that sensing of feeding deterrents by the maxillary palp inhibit test biting. Furthermore, we report a repertoire of chemosensory receptors in the maxillary palp revealed by RNA-seq. These results illuminate the role of the maxillary palp as an ultra-sensitive identifier for host-plant leaves. We also discuss the mechanism of host-plant selection by the maxillary palp that equips ~30 gustatory sensory neurons.

NPF signaling regulates feeding preference in the two-spotted cricket, Gryllus bimaculatus

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Abstract: Animals need to take appropriate nutrients by feeding to exert precise biological processes. In 1938, Richter and his colleagues have already proposed that animals can recognize their required deficient nutrient, which is called “self-selection”. So far, in both vertebrates and invertebrates, feeding behavior is thought to be regulated by endocrine control involving neuropeptides and biologically active peptides secreted from the central nervous system. As the vertebrate Neuropeptide Y (NPY) is a factor regulating feeding behavior, Neuropeptide F (NPF) is a homologue of NPY, which has been suggested to regulate feeding behavior in invertebrates including insects. In the desert locust, Schistocerca gregaria, the body-weight is decreased by NPF knockdown and increased by NPF injection as a consequence of changes in the amount of food intake. In the fruit fly, Drosophila melanogaster, the knockdown of NPF reduced the amount of sucralose intake. Together, NPF signaling regulates the amount of food intake and is involved in response to carbohydrates. However, it remains unclear whether or not NPF signaling is involved in the selection of nutrients. Here, we aim to elucidate the mechanism of feeding behavior, in particular, feeding preference, in the two-spotted cricket, Gryllus bimaculatus.

We firstly demonstrated the effect of a high-carbohydrate diet (C-rich diet) intake on NPF signaling. The transcriptional level of NPF was increased by C-rich diet intake but not only by normally fed diet. We next confirmed the effect of NPF signaling on the amount of food intake. RNAi-mediated silencing of NPF decreased the amount of C-rich diet intake. We further confirmed whether or not NPF signaling is involved in nutrient-selective behavior. The knockdown of NPF by RNAi reduced a proportion of the amount of C-rich diet to that of a high-protein diet (P-rich diet). In addition, we observed that locomotor activity was increased after dsRNA-treatment of NPF. The current data show that response to dietary carbohydrate is involved in NPF signaling in the crickets along with activation of NPF signaling. In conclusion, NPF is an important factor controlling the decision mechanisms of feeding preference, possibly involving the decision-making in the dietary choice between carbohydrate and protein accounting for the choice between herbivores and carnivores in the omnivorous insect.

Effects of Stunted on energy homeostasis in the two-spotted cricket, G. bimaculatus

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Abstract: As a heterotrophic organism, dietary products provide all the energy that is essential for digest, metabolisms and physiology activities. Fat body, where is the main peripheral tissue responsible for energy storage and expenditure, secretes several bioactive peptides for delivering energy-related information to central nervous system and triggers following systemically metabolic alterations. Stunted has been identified as one of the fat body-producing peptides, delivering signals by triggering insulin release. However, the roles of Stunted and its receptor in energy homeostasis are not clarified yet.

Here we report that the role of Stunted and its receptor, Methuselah, in energy homeostasis was addressed. RNA-sequencing revealed the strong abundance of Methuselah in the corpora cardiaca. As indicated in the fruit fly Drosophila melanogaster, Stunted is involved in the metabolic processes including insulin signaling in insect, possibly accompanied by AKH signaling, leading to the idea that reinforces the importance of fat body-brain axis in insect metabolisms.

Corpora cardiaca, a key organ regulating feeding behavior by Adipokinetic hormone and its high homologous peptide in the two-spotted cricket, Gryllus bimaculatus

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Abstract: Like most heterotrophic organisms, feeding behavior of insects is generated by the appropriate composition and amount of energy uptake and energy expenditure. Self-selection, proposed by Curt P. Richter in 1942, described a close relationship between appetite and dietary needs in many animals, which make insects perfect targets to study on energy requirements and its regulatory mechanism in vivo by observing feeding behavior individually. Adipokinetic hormone (AKH) is a neuropeptide that regulates feeding behavior and energy homeostasis in insects by supporting the mobilization of lipids. Our previous report revealed that knockdown of AKH receptor in the two spotted cricket, Gryllus bimaculatus, altered feeding behavior in the following aspects, 1) enhancement of starvation tolerance; 2) increase of feeding frequency and food intake; 3) decrease of locomotor activity in the cricket. However, the influences of feeding behavior by alteration of AKH itself has not been elucidated yet.

In this study, we identified cDNAs encoding AKH (GbAKH) and its high homologous hormone AKH/Corazonin-related peptide (GbACP) and found their predominant expression in the Corpora cardiaca (CC). Injection of synthetic GbAKH and GbACP altered feeding behavior accompanied by the following aspects, 1) inhibition on food intake and excretion; 2) elevation of carbohydrate level in the hemolymph; 3) moderate alteration in food preference. Interestingly, single knockdown of GbAKH or GbACP precursor did not alter lipid mobilization, which is possibly due to their collaborative contribution to control feeding behavior. Besides, interferences of GbAKH and GbACP signals seemed to regulate other neuropeptide signals in the midgut, which would be eventually involved in feeding behavior as observed in other insect enteroendocrine control. Here we hypothesized that the hemolymph carbohydrate elevation induced by GbAKH and GbACP signals in CC, consequently leading to alterations of neuropeptides expression in the midgut and following adjustment of feeding behavior in order to maintain energy homeostasis. In this study, we proved the possibility of the CC-midgut axis in the two-spotted cricket to regulate feeding behavior that is mainly directed by GbAKH and GbACP signals.

Nutrient selective behavior under endocrine control in the cricket

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Abstract: Animals are needed appropriate diets for normal growth and development. The omnivorous insects such as orthopteran species exert the nutrient selective behavior. Bioassays of macro-nutrient selective behavior using the two-spotted cricket Gryllus bimaculatus were carried out by the application of synthetic peptides and by RNA-interference knockdown of the neuropeptide signaling. Data revealed that Insulin-like peptide, Adipokinetic hormone (AKH), and Neuropeptide F, among all identified neuropeptides, play central roles in the nutrient selective behavior in this species. For example, protein selective behavior, as observed in the mated female, is regulated by insulin-like peptide, and lipid selective behavior is regulated by AKH. Further, such biased requirements for specific macro-nutrients are modified by the metabolisms in the fat body in addition to the endocrine control in the central nervous system including brain and corpora cardiaca (CC). These facts indicate that interplay between peripheral tissues such as fat body and central nervous system including brain-CC is crucial for successful nutrient selection. In addition, systemic nutrient conditions might be perceived by lipid and carbohydrate levels in the hemolymph via CC where produces AKH. Taken together, CC might be a hub tissue generating an endocrine network to maintain energy homeostasis involving nutrient selective behavior.

Imidacloprid toxicity in a dipteran pollinator, Eristalis tenax, supports trends of higher toxin tolerance among dipterans

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Abstract: Imidacloprid is a neonicotinoid neurotoxin that remains the most used insecticide worldwide. It persists in the environment long after the initial application, resulting in chronic exposure to non-target insects. To accurately map the dose-dependent effects of these exposures across taxa, toxicological assays need to assess various natural modes of exposure across relevant indicator species. However, due to the difficulty of these experiments, contact bioassays are frequently used to quantify dose. Dipterans remain underrepresented, despite their importance as pollinators. Here, we developed a novel naturalistic feeding bioassay to precisely measure imidacloprid ingestion and its toxicity for acute and chronic exposures in a dipteran pollinator, Eristalis tenax. We found them to be 2 to 3 orders of magnitude less sensitive than honeybees to acute exposure. Severe locomotive impairment (likely to be fatal in the wild) or death is only seen at much higher dosages than imidacloprid residues measured in nectar and pollen. Flies which ingested dosages lower than 12.1 ng/mg still showed consistent intake volumes and learned improved feeding efficiency over successive feeding sessions. Feeding ability was compromised at higher dosages due to severe locomotive impairment, but no direct antifeedant effect was observed. The similar imidacloprid sensitivity to other dipterans such as the fruitfly and housefly suggests a phylogenetically conserved component to pesticide tolerance that merits further investigation. The absence of obvious adverse effects at sublethal dosages also underscores a need to develop better tools for quantifying animal behaviour to evaluate the impact of insecticides on foraging efficiency in economically important species.

Role of circadian clocks in dopaminergic neurodegeneration

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Abstract: Patients suffering from neurodegenerative disorders, including Parkinson's disease (PD), frequently report circadian dysregulations and sleep problems. However, no causal link from circadian disturbances to vulnerability of dopaminergic (DA) neurons and PD has been demonstrated. Overarching goal of this study is therefore to understand the effect the circadian clock in Drosophila melanogaster exerts on the DA system and its underlying mechanisms. We have previously shown that DA neurons in the protocerebral anterior medial (PAM) subcluster are selectively vulnerable to oxidative stress in a toxin-induced model of DA neurodegeneration using H2O2. Based on this knowledge, here we establish time-of-day-dependent vulnerability of PAM neurons to oxidative insults and dissect underlying genetic and neuronal mechanisms. Our results demonstrate the critical role of circadian clocks in modulating dopaminergic neurodegeneration via specific neural circuit.

The global distribution of fall armyworm haplotypes and their implications to migration behavior

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Abstract: Fall armyworm, Spodoptera frugiperda (J. E. Smith), is an important agricultural pest native to the Americas that has recently been introduced into the Eastern Hemisphere where it has rapidly spread through most of Africa and much of Asia. The long-term economic consequences of this invasion will depend on how the species and important subpopulations become distributed upon reaching equilibrium, which is expected to be influenced by a number of factors including climate, geography, agricultural practices, seasonal winds, among others. Much of our understanding of fall armyworm movements have come from the mapping genetically defined subpopulations in the Western Hemisphere, particularly in North America where annual long-distance migrations of thousands of kilometers have been documented and modeled. In contrast, fall armyworm mapping in much of the rest of the world is relatively incomplete. Here we describe the global distribution of selected genetic markers and haplotypes relative to seasonal wind patterns and climate suitability estimates in order to assess the migratory relationships between populations.

Established non-native forest pests and pathogens in Australia — accumulation, response to detection, and impact

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Abstract: Geographic isolation and a robust biosecurity system render Australia free from many devastating exotic pests and pathogens found in other countries. Nevertheless, around 260 non-native pests and pathogens of arborescent hosts have established in Australia since 1885. Although the risk of invasive species arriving and establishing in Australia is increasing through increased trade and travel, the rate of establishment of non-native forest pests and pathogens has remained relatively constant over the last 130 years, with non-native species accumulating at a rate of about two per year. The majority of these affect host genera exotic to Australia, including the main plantation species, Pinus radiata; few are pests of Australian native genera. Eighteen percent of these pests and pathogens have caused moderate to significant impact or resulted in ongoing management costs in commercial plantations, native forests or amenity trees. Asian and European species accounted for two-thirds of Australia's non-native forest pests, and were equivalently represented numberically, temporally and compositionally. Asian species were more polyphagous and more frequently established in northern Australia. Earlier-establishing species were more polyphagous and had broader Australian and global non-native distributions. Thirty-four new detections of forest pests and pathogens were made since 1996, the majority (71%) via passive surveillance: 24% by public, 12% by industry, and 34% by researchers. This highlights the need for ongoing awareness campaigns and adequate systems for passive surveillance detection, reporting and response. There has been an increase in detections in recent years from active surveillance, but the majority of exotic forest pests and pathogens were not detected early enough to attempt eradication. Early detection is key to successful eradication, yet only one pest of arborescent hosts has been successfully eradicated from Australia, the nematode Bursaphelenchus hunanensis. All forest/tree stakeholders (industry, all levels of government & environment) need to be involved for forest biosecurity to be effective.

Associates of Megastigmus spp. (Hymenoptera: Megastigmidae) in eucalypt galls: a Leptocybe spp. biocontrol perspective

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Abstract: Species of Megastigmus Dalman (Hymenoptera: Megastigmidae) have been identified as potential biocontrol agents against Leptocybe spp., worldwide eucalypt galling pests originating from Australia. During the last two decades, Megastigmus zvimendeli and M. lawsoni from Australia have established as biocontrol agents in the invasive range of Leptocybe spp.; and many non-Australian species have been recorded in Africa, Asia, Europe and South America as local associates of Leptocybe spp. We conducted a survey of Megastigmus species and their co-inhabitants from eucalypt galls in Australia. Molecular data identified at least sixteen Megastigmus species associated with eucalypt galls, and with several chalcid wasp families (e.g. Eulophidae, Mymaridae, Eurytomidae) and gall midges (Cecidomyiidae). The abundance and geographical distribution of Megastigmus species associated with Leptocybe spp. was determined based on our field collections. A combination of molecular and morphological results revealed that some of the recently described non-Australian species are synonyms of M. zvimendeli, accounting for the unrecorded spread of this species outside of Australia. Our work contributes to the understanding of eucalypt galling insect communities in Australia, Megastigmus biodiversity and the potential of these species as biocontrol agents for Leptocybe and other eucalypt galling species.

Hidden interactions as revealed by metabarcoding on internal DNA of herbivore larvae

Authors: Nakadai Ryosuke, Department of Environmental and Biological Sciences, University of Eastern Finland; Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan

Abstract: In nature, various interactions have occurred in a fraction of a second. To reveal those interactions, researchers have spent a lot of time on field observations. However, to get all information about interactions is technically difficult only by field observations, thus quite a lot of hidden interactions still exist. The recent development of metabarcoding methods now makes us possible to reveal the interactions intensively. In this presentation, I will talk about a study that has applied metabarcoding to study a terrestrial tri-trophic interaction (i.e., a plant-herbivore-parasitoid association). Specifically, the study examined whether partitioning of phenology or natural enemies may explain the coexistence of leaf cone moths (Caloptilia; Gracillariidae) associated with maples (Acer; Sapindaceae). Larval activity of 10 sympatric Caloptilia species found on nine maple species was monitored every 2–3 weeks for a total of 13 sampling events, and an exhaustive search for internal parasitoid wasps was conducted using high–throughput sequencing. Also, blocking primers were used to facilitate the detection of wasp larvae inside moth tissue. The result clearly showed considerable phenological overlap among Caloptilia species, with two clear peaks in July and September–October. Coexisting Caloptilia species also had largely overlapping parasitoid communities; a total of 13 chalcid and ichneumon wasp species attacked Caloptilia in a nonspecific fashion at an overall parasitism rate of 46.4%. In the last of my presentation, I will discuss the future possibility to apply this method for monitoring parasitoid effects on insect outbreaks.

Seasonal occurrences and species composition of Orius spp. (Hemiptera: Anthocoridae) on eggplants planted in okra fields at Kawasaki City Japan

Authors: Nakamura Akinobu[1] and Itoyama Kyo[1], [1]Meiji University, Japan

Abstract: Conservation biological control is the practice to conserve and enhance the resident populations of natural enemies through modification of the environment or of existing practices, and its importance has been increasing in recent years. Conservation of natural enemies within cropland is possible by means of insectary plants which provide them with the resources they need to survive. For example, the introduction of flowering plants in agricultural systems increases nectar and pollen resources that are required by some natural enemies. However, it is difficult to secure enough space to plant insectary plants in urban agriculture where the agricultural land is limited.

It is known that Orius spp. occur and settle in Abelmoschus esculentus (L.) Moench, when cultivated in open eggplant fields, and effects of suppressing the density of thrips in eggplant can be expected. We also have shown that Orius spp. can be found and colonized in okra field in Kawasaki City, Kanagawa prefecture, Japan, there is engaged in urban agriculture.

But the effects on other crops grown nearby okra have not been clarified. In this study, we compared the occurrence and species composition of Orius spp. in the test plot where eggplant was planted in the okra field and the control plot where only eggplant was planted. The occurrence of Orius spp. in eggplants was earlier than in the surrounding okra. The occurrence of Orius spp. in the test plot was higher than that in the control plot. In the test plot, the population of thrips was also large, but it decreased after the occurrence and establishment of Orius spp., confirming the density suppression effect on thrips. Dominant species was Orius sauteri at each plot and the surrounding okra in July, but Orius minutus replaced Orius sauteri in September. Our results would give important information about the application of okra as insectary plants in urban agriculture.

Hazard rating of Japanese larch forests for larch bark beetle (Ips subelongatus) using self-organizing map (SOM) and random forest approaches

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Abstract: The objective of this study was to evaluate the hazard ratings of Japanese larch forests to Ips subelongatus by considering environmental factors. Factors related to thinning, geographical factors and forest stand condition were collected at 16 study sites in Japanese larch stands where thinning was implemented. Using machine learning approaches, self-organizing map (SOM), one of the unsupervised classification methods, and random forest model, which predicted the probability of the tree mortality caused by I. subelongatus, hazard rating of Japanese larch forests after thinning was analyzed. Our results showed that stand age, thinning history, slope orientation, and soil moisture are the major factors influencing on abundance of dead trees killed by the beetles after thinning. There were more dead trees killed by in older forests than in younger forests, suggesting that tree vigor can influence outbreak of the beetles. The slope orientation was related to occurrence of dead trees, which was more on southeast-facing slope than at sites facing other directions. Also, the dead trees were more occurred in the forests with dry soil during the first 3 years after thinning. These results can provide useful information for improved the Japanese larch forests management against I. subelongatus after thinning.

Using Social Media to Communicate Scientific Research as a Public Health Entomologist

Authors: Natasha Agramonte, University of Florida - Emerging Pathogens Institute: Gainesville, FL, USA DeKalb County Board of Health: Atlanta, GA, United States

Abstract: Scientific research has several tried and true outlets for communication, such as publishing in scientific journals or presenting at national and international conferences, however scientists often struggle to communicate their work to the general public. Some organizations encourage outreach to local and state communities in the form of classroom visits, educator trainings, state fairs, and extension publications. While very helpful for establishing ties to the local community, these outreach efforts typically reach fairly small audiences. With the aid of social media, scientists can now reach much larger, international audiences easily. More importantly, social media platforms like Facebook and Twitter allow for a dialogue between scientists and non-scientists, which encourages nuance into the interpretation of research that is often lacking when science research is presented via news broadcasts or popular media. I document my own journey from science researcher uncomfortable in my interactions with the general public to communicating my research on Twitter, Reddit, and even on the Bill Nye show.

Economic and Social Impacts of Arthropod Biological Control

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Abstract: Biological control of insect pests is an integral tactic of modern integrated pest management. The number of studies quantifying the economic benefits of biological control remains small, yet estimates suggest biological control has immense value. Here we present economic concepts and discuss methods for placing an economic value on biological control services. We then summarize and synthesize the extant studies that have attempted to quantify the economic outcomes of the biological control of arthropod pest with natural enemies, with particular focus on introductory (classical) biological control. Introductory biological control projects targeting arthropod pests have an average benefit to cost ratio of 61:1 with an estimated net present value of $37.3M per successful project.

Temporal and spatial change in Phytophagous mite populations of Varanasi region

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Abstract: The past few decades have witnessed poignant changes in global climatic conditions. The major factor attributed to this is the elevated CO2 levels in the atmosphere. It has been observed that there has been an unprecedented rise in the CO2 concentration from 280ppm (pre-industrial era) to 400+ ppm in current times. Though CO2 forms an integral part of the carbon cycle on earth and it is an essential component for synthesizing the photosynthates by the plant; global warming is yet another result of the elevated CO2 levels triggering various catastrophic phenomenon leading to climatic variabilities like erratic rainfall, extended drought, and flood conditions. These altercations disturb the diversity, population dynamics, and status of pests and their natural enemies. In this light, we studied the dynamics of plant mite population in and around Varanasi district of eastern Uttar Pradesh, India. The phytophagous mites hold economic significance in agricultural crops and vegetables. The Varanasi district (1,535 square kilometers) predominantly is a major vegetable growing region. The first report of plant mites by Singh (1976) as an emerging pest in eastern Uttar Pradesh was in the early 1980s. Approximately four decades later since it was reported, the obvious climate change coupled with faulty agricultural practices has lead mites to invade different localities across the Varanasi district. Previously it was concentrated in and around the farms of Bishanpura locality but now it has gradually dispersed and established itself in other distant localities as well. The probable hotspots observed were Raja Talab, Rohaniya, Susuwahi, Mundadih, Lalpura, Pindra, Umraha and Tikri to name a few. The mites belonging to family Tetranychidae have been found in abundance in the above-mentioned areas. The major being Tetranychus ludeni, T. urticae, T. macfarlanei, T. neocalidonicus on different host crops. Another mite belonging to family Tarsonemidae, Polyphagotarsonemus latus, is a major pest on chili crop in this region. Eutetranychus orientalis has also become a major threat to locally grown fruits like papaya and guava. Among family Eriophyidae, Aceria cajani on Pigeonpea and Aceria mangiferae on Mango is causing severe damage around the district. Over the years it has been observed that the incidence of the above-mentioned mites has increased substantially in different seasons with more spatial expansion within the Varanasi region. The point here to consider is that previously these mites were not a major concern but various factors over the years have led to a considerable surge in their population causing greater economic losses to the farming community.

Beneficial Predators for Integrated Pest Management - a Bioinformatics Approach

Authors: Nauen Ralf[1], Bailey Emma[3], Crossthwaite Andrew[4], Rawlings Chris[3], Hassani-Pak Keywan[3], Field Linda[2], Williamson Martin[3] and King Robert[3], [1]Bayer AG, Crop Science Division, Germany, [2]Department of Biointeractions and Crop Protection, Rothamsted Research, Harpenden, United Kingdom, [3]Rothamsted Research, United Kingdom, [4]Syngenta, United Kingdom

Abstract: Insect pests contribute significantly to crop yield losses every year, and with a rapidly growing population to feed, finding ways to increase or maintain crop yields amongst insecticide resistance and restrictions has become increasingly challenging.

Biological control – the use of beneficial predators to keep pest populations under control – is a highly effective and therefore key component of Integrated Pest Management (IPM) strategies. Unfortunately, there is a knowledge gap surrounding beneficial predators, with much of the focus to date being on pest species. More information is needed with regards to the impact of insecticides on beneficial predators in order to implement sustainable IPM programmes. Insecticides are an unavoidable element of such programmes and so a better understanding of their interaction with beneficial predators would be advantageous. An added bonus of this increased understanding could be a potential decrease in the use of insecticides and consequently an increased longevity of their action in the field.

The aim of this project is to help fill this knowledge gap through the development of predator genomes. Many genomes are already publicly available for pest species, but very few beneficial predator genomes have been released. The first step will therefore be to sequence and assemble the genomes of key beneficial predators using the latest technologies. The genomes of these beneficial predators will then be compared to pest genomes. A novel insect-specific biological network will be developed for use with 'KnetMiner' (an application to explore large biological knowledge networks), which will identify novel links between species not necessary directly observed.

This comparison will allow us to look for evidence of co-evolution between predators and their prey and learn more about how they interact. For example, it has been theorised that predators may have evolved odour binding proteins to detect pheromones released by the pests, and the expansion of related gene families may provide evidence for this. Particular focus will also be given to genes/pathways which have been linked to insecticide mode of action and resistance. Identifying and exploiting genetic differences related to these pathways could help to design more targeted IPM approaches with the aim to leave the beneficial predator populations unharmed.

The knowledge gained from this project could contribute to the development of successful IPM strategies and help increase crop yields to feed a growing world population.

The alfalfa leafcutter bee, Megachile rotundata is more sensitive to N-cyano neonicotinoid, pyrethroid and butanolide insecticides than other managed bees

Authors: Nauen Ralf[1], Bass Chris[2], Hayward Angela[2], [1]Bayer AG, Crop Science Division, Germany, [2]The University of Exeter, United Kingdom

Abstract: Recent research has shown that several managed bee species have specific P450 enzymes that are preadapted to confer intrinsic tolerance to some insecticides including certain neonicotinoids. However, the universality of this finding across managed bee pollinators is unclear. In this talk I will outline work that demonstrates that the leafcutter bee, Megachile rotundata, lacks such P450s, and is >2500-fold more sensitive to the neonicotinoid thiacloprid and >100 fold more sensitive to the pyrethroid tau-fluvalinate and the butenolide flupyradifurone than other bee species. These findings have significant implications for the safe use of insecticides in crops where M. rotundata is used for pollination, and for ensuring that regulatory pesticide risk assessment frameworks are protective of this species.

Mechanisms of pyrethroid resistance and potential cross-resistance issues in clonal cultures of pea aphid, Acyrthosiphon pisum

Authors: Nauen Ralf[1], Müller Viola[3], Rottmann Antje[2], Buer Benjamin[2] and Lueke Bettina[2], [1]Bayer AG, Crop Science Division, Germany, [2]Bayer Crop Science, Germany, [3]University of Bonn, Germany

Abstract: Insecticide resistance is quite common in green peach aphid, Myzus persicae, and cotton aphid, Aphis gossypii, a fact reflected by 750 documented cases found in the Arthropod Pesticide Resistance Database (https://www.pesticideresistance.org). In total this database lists 922 aphid resistance cases for 27 species, but strikingly not listing any entry for the pea aphid, Acyrthosiphon pisum. The pea aphid is known as a global sucking pest of leguminous plants including peas, broad beans and alfalfa. It is also a model aphid species and its genome has been recently sequenced and annotated.

We recently collected a French population of A. pisum showing a significantly lower susceptibility to pyrethroids when compared to an insecticide susceptible reference strain. After separating and testing a number of clonal cultures we obtained a strain, PYR-R1, exhibiting high levels of pyrethroid resistance (RR>100-fold), but lacking any cross-resistance to other chemical classes of insecticides.

We investigated the molecular mechanism confering pyrethroid resistance in strain PYR-R1 by analysing the involvement of detoxification enzymes as well as possible target-site mutations in the voltage-gated sodium channel, known as the pyrethroid target site. Here we describe the molecular mechanism of resistance and its implications for resistance management.

Target-site and metabolic mechanisms of resistance in fall armyworm

Authors: Nauen Ralf[2], Boaventura Debora[1], [1]Bayer AG & University of Bonn, Germany, [2]Bayer AG, Crop Science Division, Germany

Abstract: Fall armyworm (Spodoptera frugiperda) is a polyphagous lepidopteran species, causing significant damage in several economically important crops, particularly corn. It is a major pest in North and South America, but very recently invaded the African continent and East Asia.

The control of this pest relies on synthetic insecticides and genetically engineered crops expressing Bacillus thuringiensis (Bt) crystal (Cry) toxins. However, fall armyworm developed resistance to different insecticide chemical classes and since 2014, field-evolved Cry1F-resistance has been observed in Brazil.

In this study, the molecular mechanisms conferring resistant to Cry1F was characterized in fall armyworm populations collected in Brazil and cross-resistance pattern with chemical insecticides and Bt toxins were investigated. Moreover, the involvement of detoxification enzymes as well as possible target-site mutations in different insecticides targets were analyzed and new gDNA-based diagnostic tools developed to support fall armyworm resistance management strategies.

Molecular and allelic variation of field evolved mechanisms of resistance to Cry proteins in fall armyworm

Authors: Nauen Ralf[2], Franz Laura[3], Mehlhorn Sonja[1], Horikoshi Renato[1], Boaventura Debora[1] and Head Graham[1], [1]Bayer AG, [2]Bayer AG, Crop Science Division, Germany, [3]Bayer AG, Germany

Abstract: Fall armyworm (FAW), Spodoptera frugiperda (Lepidoptera: Noctuidae), is a highly-destructive moth pest native to the tropical and subtropical Americas that preferably feeds on corn plants. FAW pest management strategies largely rely on the use of synthetic insecticides and transgenic crops, e.g., corn expressing Bacillus thuringiensis (Bt) insecticidal Cry proteins such as Cry1F. Corn hybrids expressing Bt proteins remain a cornerstone in FAW control in North/South America, though resistance is on the move. Resistance to Cry1F is rather widespread and in some cases cross-resistance to Cry1A.105, Cry1Ab and Cry1Ac was described. Cry1F resistance in FAW was shown to be linked to mutations in the ATP-binding cassette transporter C2 (ABCC2) gene. In Brazilian FAW populations we detected by pooled population sequencing several mutations at high frequency in the ABCC2 extracellular loop domain 4 (ECL4), including deletions, insertions, and amino acid substitutions. Other ABBC2 mutations such as splice disruption sites or premature stop codons resulting in a truncated ABCC2 have been described in North American FAW populations. Recent whole genome sequencing approaches revealed the absence of such mutations in invasive populations collected in Eastern Hemisphere countries. Here we discuss the molecular and allelic variation of ABCC2 mutations in FAW and their functional validation.

Beyond Apis mellifera – Using a phylogenomics approach to identify putative detoxification enzymes in different bee species

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Abstract: Insect and especially pollinator declines are a topic of great concern and debate in modern society. Although reasons are manifold, the use of pesticides has been heavily criticized and often blamed for decreases in pollinator diversity and abundance. Historically, risk assessment of crop protection products to bees relied on the honey bee Apis mellifera as a model organism due to its importance, broad availability and standardized methodology. Recently, the question arose whether or not the honey bee is a good surrogate species in risk assessment for the very diverse and complex clade of Anthophila.

Although huge effort is invested into developing new bioassays for different bee species, a problem remains the practicability and/or validity of these test systems as well as the availability of rare species for laboratory testing. This gap in methodology can in parts be filled by using the rapidly advancing field of genomics.

Leveraging the increasing amount of published genomic data, we conducted a phylogenetic approach to identify close relatives of the A. mellifera CYP9Q enzymes – a P450 subfamily previously shown to effectively detoxify certain bee-friendly insecticides – in different bee species and families. After functional expression of several candidate genes we investigated their activity against a range of fluorescent model substrates to compare substrate profiles and tested their ability to metabolize different chemical classes of insecticides.

These results provide us insights into the comparability of detoxification systems between different bee species and families, helping us to better understand and assess intrinsic toxicity of insecticides to bees covering a broad phylogenetic range.

A Genetic Understanding of Transporters Implicated in Insecticide Resistance and Toxicology

Authors: Nauen Ralf[2], Vontas John[1], Denecke Shane Michael[1], Vogelsang Kathrin[4], Vorgia Elena[1], Bao Hang Luong Ngoc[1] and Geibel Sven[3], [1]Institute of Molecular Biology and Biotechnology, Foundation for Research and Technology-Hellas, Heraklion, Greece, [2]Bayer AG, Crop Science Division, Germany, [3]Division Crop Science, Research and Development, Bayer AG, Monheim, Germany, [4]Division Crop Science, Research and Development, Bayer AG, Monheim, Germany

Abstract: Small molecule pesticides are currently the most effective way of controlling damaging arthropod pest species in both public health and agriculture. As a result, genes that alter the toxicity of these compounds due to target site alterations and over-expression of drug metabolizing enzymes have been the subject of intense investigation. Other detoxification mechanisms such as pesticide transport have been less well-studied. While rarely associated with high levels of resistance, various studies have shown that transporters can play roles in basal levels of detoxification even in susceptible populations by preventing compounds from reaching their targets. Furthermore, it can be inferred from pharmaceutical studies that certain transporters may be critical in helping compounds be effectively absorbed into the body. Here, we describe our recent progress on studying transporter proteins that act on insecticides. Through a combination of in silico, in vivo, and in vitro approaches we identify insect transporters that act on pesticides and in what tissue they mediate their effect. It is hoped that these data can begin to establish insects as a model for pharmacokinetic research and provide for a more rational pesticide design strategy.

Pyrethroid efficacy and P450-mediated resistance in the Malaria mosquito Anopheles funestus with special reference to transfluthrin

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Abstract: Insecticide based control of mosquitoes contributed globally to two-third of the malaria cases which have been averted between 2000 and 2015. However, chemical control heavily relies on pyrethroids, a class of insecticides acting on voltage-gated sodium channels (VGSC). Pyrethroids are frequently applied as indoor residual sprays, space sprays and incorporated in bednets, leading to high levels of resistance.

Resistance is driven by two major mechanisms: Target-site resistance based on mutations in the VGSC, and metabolic resistance based on elevated levels of detoxification enzymes. One enzyme class, cytochrome P450-monooxygenases (P450s) has been shown to be overexpressed in resistant mosquitoes such as Anopheles funestus where the duplicated P450 variants CYP6P9a and CYP6P9b were identified and shown to confer resistance to common pyrethroids, e.g., deltamethrin and permethrin. Whereas the volatile pyrethroid transfluthrin has been shown to be resilient to oxidative metabolism by these P450s due to a highly fluorinated benzene-ring instead of the common phenoxybenzyl-structure.

In contact bioassays we found that An. funestus FUMOZ-R is highly resistant to common pyrethroids such as deltamethrin and permethrin, whereas almost no cross-resistance towards transfluthrin was detected. We recombinantly expressed CYP6P9a and CYP6P9b using a baculovirus expression system and evaluated the oxidative metabolism of various pyrethroids. Our studies revealed sequential metabolism by hydroxylation and subsequent cleavage of the phenoxy-benzyl ether by both CYP6P9 variants. No such oxidative metabolic fate was observed for transfluthrin, suggesting that it is protected by its high fluorination and the lack of the phenoxybenzyl-ether. Indeed, in transfluthrin-metabolism assays no hydroxylated metabolites were found and we unveiled alternative routes of metabolism for this molecule. Furthermore, we elucidated the low RRs observed for permethrin, likely due to its enantiomeric composition. These novel findings will help to refine resistance management tactics to control highly resistant malaria vectors.

Exploring the genetic diversity of the predatory mite Amblyseius swirskii: biological control in a context of climate change

Authors: Navajas Maria[2], Lopes Ivinho[3], Migeon Alain[1], Tixier Marie-Stéphane[4] and Douin Martial[4], [1]INRAE, France, [2]INRAE, France, [3]Institut Agro Montpellier, [4]UMR CBGP, Institut Agro, INRAE, CIRAD, IRD, Univ. Montpellier

Abstract: Genetic variability is an important element for organisms to face variable field conditions. Phytoseiidae are predatory mites, well- known for their efficiency in biological control. In a recent study we show that climate change is affecting predators and preys fitness and distribution, which in turn affect biocontrol performance. Here we focus on Amblyseius swirskii, a mite used in biological control of small insect and mite pests and commercialized since 2005. Our study combines 12S rRNA, CytB and COI mtDNA sequences obtained from (i) mites issued from commercial rearing (several companies), (ii) mites collected in Israel (where the material source now commercially marketed is originated), and (iii) mites collected in several other countries where the species naturally occurs. A very low genetic diversity was observed in and between all populations except the one from Cape Verde that clearly differs. This suggests that (i) commercialized and natural populations now co-occur widely, even in natural environments and/or (ii) that commercialized populations have probably overpassed the natural ones except in remote areas (here Cape Verde) where commercial releases have not occurred. How much observed genetic differentiation results in different biological features needs deeper analysis, however the detection of diversity in remote natural populations may provide a source of novel traits useful to improve performance of this natural enemy. More broadly, this study questions the role of natural enemies' diversity to face new environmental situations as for example the capacity of resilience adapting to climate change.

Bacterial symbionts from the gut of the coffee berry borer Hypothenemus hampei (Coleoptera: Curculionidae): identification of potential “Trojan horses” for insect pest management

Authors: Navarro-Escalante Lucio[3], Benavides Pablo[1], Grueso Nathalie[5], Góngora Carmenza[3], Acuña Ricardo[4] and Mejía Santiago[2], [1]FNC-CENICAFE, Colombia, [2]Graduate Research Assistant Department of Entomology Colombia National Coffee Research Center - CENICAFE, Colombia, [3]Research Scientist Department of Entomology Colombia National Coffee Research Center - CENICAFE, Colombia, [4]Research Scientist Department of Plant Physiology Colombia National Coffee Research Center - CENICAFE, Colombia, [5]Universidad de Caldas

Abstract: The coffee berry borer (CBB) is an important insect pest of coffee crops worldwide. Despite the use of current integrated pest management strategies focused on cultural and chemical control, CBB is a permanent threat for coffee production, urging for more effective and safer insect control strategies. Since microbial symbionts play important roles in the biology of insects, there is a growing interest for understanding this complex insect-symbiont interactions and the application of this knowledge to develop future pest control methods, including delivery of RNA interference. Here, we described the diversity and dynamics of bacterial symbionts within the gut across life stages of CBB using high-throughput DNA sequencing of the 16SrRNA gene (metabarcoding) and culture-dependent methods in order to identify species with potential use for pest control. Additionally, we developed a proof of concept for the RNAi-mediated gene silencing in CBB using bacteria as delivery system. Metabarcoding analysis revealed a diverse bacterial microbiota dominated by genera Ochrobactrum (15.1%), Pantoea (6.6%), Erwinia (5.7%), Lactobacillus (4.3%), Acinetobacter (3.4%), Stenotrophomonas (3.1%), Akkermansia (3.0%), Agrobacterium (2.9%), Curtobacterium (2.7%), and Clostridium (2.7%). From these microbiota, we isolated 21 bacteria strains, including some of the most abundant genera above. We also show that bacteria-delivered RNAi effectors are able to silence CBB genes and offer an opportunity to develop a symbiont-mediated pest control for CBB.

RNA interference of PgCadh gene in Pink Bollworm (Pectinophora gossypiella) enhanced its mortality and suppressed resistance evolution against Cry1Ac

Authors: Nazeer Ahmad Jam[1], Jam Nazeer Ahmad Samina[1], Majeed Dilawar[1], [1]University of Agriculture Faisalabad, Pakistan

Abstract: Gene silencing through RNA interference in different insect pests has been targeted from previous few years. It has been exploited to inhibit growth of insect, induce mortality, avoids resistance evolution and increases the chances of insect susceptibility to Cry1Ac and pesticides. Here, two field collected populations of Pectinophora gossypiella (Multan and Faisalabad) and one susceptible and other resistant laboratory population was used for investigation. All populations were examined for PgCad1 gene expression that is involved in Bt resistance against P. gossypiella. The double stranded RNA (dsRNA) specific for PgCad1 gene in Pectinophora gossypiella was developed and employed through micro-injection using different concentration (1-3 ul/sample) to knockdown it in resistant population. The results showed that expression of PgCadh1 was up regulated in Multan, and laboratory reared resistant population as compared to Faisalabad and laboratory reared susceptible population. Down regulation of PgCad1 gene was observed in 3rd instar larvae upon application of PgCad1-dsRNA RT-PCR and real time PCR. Increased mortality was observed in 3rd instar larvae treated with dsRNA as compared to control insects treated with water and dsGFP. Present study showed that dsRNA can cause severe effect on the P. gossypiella and persuade RNA interference. The findings also confirmed that RNAi application is appropriate tool to cause mortality and to reduce the evolution of Cry1Ac resistance in P.gossypiella.

Insecticide Resistance management in Red Palm Weevil (Rhynchophorus ferruginous) management through RNAi

Authors: Nazeer Ahmad Jam[2], Manzoor Mujahid[1] and Jam Nazeer Ahmad Samina[2], [1]Punjab university, Lahore, Pakistan, [2]University of Agriculture Faisalabad, Pakistan

Abstract: Molecular and proteomic study was conducted on field evolved resistance of Red Palm Weevil (Rhynchophorus ferruginous) against Parathyroid group of insecticide (Cypermethrin). Cytochrome P450 genes have been associated with insecticides resistance. Field collected population of R. ferruginous from different provinces of Pakistan was investigated for insecticides resistance development against P450 gene. Insect bioassay indicated highly significant level of LC50 values among laboratory reared and field collected population against Cypermethrin. The laboratory reared resistant population, Sindh and South Punjab collected population showed high LC50 values as compared to susceptible, Baluchistan and KPK population. The expression of P450 gene through PCR showed enhanced level of P450 gene in different Instars as well as collected population. The dsRNA specific for CYP450 gene was designed and targeted through dsRNA in thoracic region of R. ferruginous through micro-injection. Gene expression and proteomic study confirmed the down regulation of P450 gene and associated protein in dsRNA treated population. The application of ds RNA specific for CYP450 also reduced insecticide resistance in R. ferruginous. The developmental parameters were highly affected in RPW treated with dsRNA as compared to control samples treated with water or dsGFP. These results support the RNAi application as a suitable tool for the management of insecticide resistance and control of R. ferruginous

Enhanced efficacy of sub-lethal dose response of native Polyhedroviruses and Spinosad for economical and sustainable management of Sopodoptera litura in Pakistan

Authors: Nazeer Ahmad Jam[3], M Bones Atle[1], Ahuja Ishita[1], Ahmad Malik Mubashar[2], Mushtaq Rashid[2] and Jam Nazeer Ahmad Samina[2], [1]NTNU, Norway, [2]University of Agriculture Faisalabad, Pakistan

Abstract: In the present investigation, laboratory trials were conducted to investigate the synergistic, additive or antagonistic effect of three sub-lethal dose rates (2 x 103, 4.5 x 103, and 6 x 103 PIB/Larva) of native isolated Nucleopolyhydrovirus (NPV) from Spodoptera litura and Spinosad (0.01 ppm) against 3rd and 4th instar larvae collected from three different geographical areas of Punjab (Pakistan). The difference in larval mortality, pupation, adult emergence and egg ecluson occurred. The higher but sub-lethal dose rate of NPV with Spinosad exhibited synergistic interaction, while the rest of combinations were additive in all the tested populations, showing the population of S. litura from Rahim Yar Khan Region least susceptible, and that of Faisalabad highly susceptible. It may be inferred that the mixtures of the correct sub-lethal doses of Spinoad + NPV can be a proven potential pest and insecticides resistance management (IRPM) strategy against S. litura in vegetable and major crop growing areas of Pakistan.

On the morphology of male genitalia in Onciderini (Coleoptera: Cerambycidae: Lamiinae)

Authors: Nearns Eugenio, USDA APHIS National Identification Services (NIS), National Museum of Natural History, Smithsonian Institution, Washington, DC, United States

Abstract: Male genitallic structures for representatives of 81 genera of Onciderini (Coleoptera: Cerambycidae: Lamiinae) were dissected and illustrated. Several distinct types of parameres were discovered. A cladistic analysis based on morpohological characters is discussed.

Avoidance and toxicity of ladybirds (Coleoptera: Coccinellidae)

Authors: Nedved Olda[1], Sakaki Samane[1], [1]University of South Bohemia, Czech Republic

Abstract: Avoidance reaction of ants Lasius niger to the extracts from Adalia bipunctata, Hippodamia undecimnotata, Coccinella septempunctata, Harmonia axyridis, Halyzia sedecimguttata and Tytthaspis sedecimpunctata differed slightly. Fresh carcasses of toxic and aposematic insect species remained longer than 24 hours: firebugs Pyrrhocoris apterus and ladybirds C. septempunctata, H. undecimnotata, H. axyridis (adults and larvae) and T. sedecimpunctata. Extracts from the invasive alien ladybirds H. axyridis were more toxic for fleas Daphnia magna than native European species: aposematic A. bipunctata > cryptic Cynegetis impunctata > aposematic C. septempunctata > slightly aposematic Calvia quatuordecimguttata. Three months old ladybirds H. axyridis were 3.8x more toxic than 2 and 4 weeks old. Melanic and non-melanic forms of H. axyridis were equally toxic. Extracts from one week old H. axyridis decreased the root length of germinating seeds of Sinapis alba to one third and from three-month-old ladybirds to one tenth of the control. Differences in toxicity among 13 colour forms of H. axyridis were small. Insectivorous tits Parus major showed strong avoidance of various adult ladybirds, larvae and pupae, but not the granivorous sparrows Passer montanus. Artificial plasticine larvae resembling real larvae confirmed less attack rate of aposematically coloured prey than of black and green larvae.

Assessing the conservation status of ladybirds: A roadmap towards conservation

Authors: Nedved Oldrich[8], Haelewaters Danny[4], Roy Helen E.[7], Losey John E.[5], Brown Peter M.J.[1], Pervez Ahmad[2], Soares António Onofre[3], Mishra Geetanjali[6] and Omkar Omkar[6], [1]Anglia Ruskin University, United Kingdom, [2]Biocontrol Laboratory, Department of Zoology, Radhey Hari Govt. P.G. College, Chamoli, Uttarakhand., India, [3]CE3C, Centre for Ecology, Evolution and Environmental Changes, Azorean Biodiversity Group, Faculty of Sciences and Technology, University of the Azores., Portug, [4]Ghent University, Czech Republic, [5]IUCN SSC Ladybird Specialist Group, [6]Ladybird Research Laboratory, Department of Zoology, University of Lucknow, India, [7]UK Centre for Ecology & Hydrology, [8]University of South Bohemia

Abstract: Insects face many human-mediated threats, including climate change, agricultural intensification, habitat loss, pollution, and biological invasions. Ecological impacts from these threats have altered the richness, abundance, and distribution of insect species, impacting their survival and compromising the numerous services they provide. The development and implementation of conservation strategies for beneficial insects such as ladybirds (Coleoptera: Coccinellidae) is hindered by a lack of knowledge of the conservation status of most species and the factors driving their population dynamics. Here we review the ecological threats faced by ladybirds, and current projects and actions that should aid the conservation and recovery of their populations. We also identify knowledge gaps in biodiversity assessment and conservation approaches, and suggest mitigating actions following Harvey et al. (2020) as a roadmap for ladybird conservation and recovery over short-, intermediate-, and long-term timescales.

Fire: death by a thousand cuts in aquatic insect community assembly of streams in western North America, concerted and confounded variables in space and time.

Authors: Nelson C. Riley[1], Frandsen Paul[2], Abbott Ben W.[3], Errigo Isabella M.[3] and Eichert Anna L.[3], [1]Department of Biology, Brigham Young University, United States, [2]Department of Plant and Wildlife Sciences, Brigham Young Univ, Provo, UT, USA, United States, [3]Department of Plant and Wildlife Sciences, Brigham Young University

Abstract: Megafires have burned vast stretches of wildlands in western North America in recent years during unprecedented drought. The summer of 2018 was particularly devastating in central Utah where several huge fires merged into one encompassing 610 km2 in the southern Wasatch Mountains. Within weeks remnants of an intense tropical storm dumped unseasonable amounts of rain on the fire scar in this arid watershed, triggering extensive flash flooding. These streams are tributaries of Utah Lake, the third largest freshwater lake in the contiguous western United States, whose ecology is currently a focus of renewed public scrutiny. All streams in the lake's southern watershed were impacted to varying degrees and a sampling regime for quickly documenting changes in both abiotic (86 sites) and biotic communities (18 sites) put in place. In this report we summarize progress on measuring macroinvertebrate recovery in these streams over the past three years using species effort analyses, rapid bioassessment protocols, and community estimates using environmental DNA. Asymmetric methodologies with confounded variables for judging community decline and recovery are briefly reviewed in a context of global insect apocalypse and climate change.

New insecticidal proteins with potential applications in future genetically engineered crops

Authors: Nelson Mark, Corteva Agriscience, United States

Abstract: Genetically engineered insect resistant crops have provided growers with valuable tools for protecting yield for more than two decades. The insecticidal proteins derived from Bacillus thuringiensis have served as the cornerstone for establishing this technology leading to widespread adoption. However, the ongoing risk of insects developing resistance to the proteins in these crops has continued to drive the discovery of new proteins that can replace or augment those currently in use. This talk will briefly review the history of transgenic insect control and highlight the discovery of new insecticidal proteins with the potential for transgenic insect control applications in the future.

Roofing the forest to learn more about drought-induced bark beetle attack

Authors: Netherer Sigrid, Institute of Forest Entomology, Forest Pathology and Forest Protection Department of Forest and Soil Sciences BOKU - University of Natural Resources and Life Sc, Austria

Abstract: Drought episodes are widely considered to stress host conifer trees and render them highly susceptible to scolytid attack. The Eurasian spruce bark beetle Ips typographus is the main biotic disturbance agent in European Norway spruce forests, causing vast amounts of salvaged timber in the recent decades. The constellations of predisposing factors differ with geographical region; yet, temperature sums available for generation development and drought variables have turned out to be relevant for bark beetle infestations at all sites. Predisposition assessment, simulation of bark beetle phenology and of drought proxies such as the transpiration deficit are useful tools in bark beetle risk assessment. The fundamental questions however remain, how primary attack of Norway spruce depends on finding and acceptance of trees as hosts by bark beetles and in which way drought mediates tree defence capability. An ongoing drought manipulation experiment addresses constitutive and induced resistance against biotic attack, including resin flow, hypersensitive reaction on blue stain fungus inoculation, and the accumulation of defence compounds such as terpenes and monophenols in the bark. Volatile compounds, in particular the composition and concentration of terpenes, are gustatory and olfactory cues strongly affecting beetle attraction and repulsion. In my talk I will present novel results gained from the field experiments involving measurement of climate and soil parameters, tree physiological stress and tree defence markers, in particular bark and volatile compounds, as well as bark beetle attack under controlled test conditions.

When moon and sun intertwine: Characterizing the role of the circadian clock in endogenous lunar timekeeping of a marine midge

Authors: Neumann Jule[2] and Kaiser Tobias S.[1], [2]Max Planck Institute for Evolutionary Biology, Germany, [1]Max Planck Institute for Evolutionary Biology

Abstract: Life on earth evolved in recurring environmental cycles caused by the sun and the moon creating predictable, fluctuating environments. In anticipation of these regular changes, organisms have developed their own timekeepers – so-called biological clocks. Marine midges of the genus Clunio (Diptera, Chironomidae) time adult emergence to the lunar cycle by a circalunar clock. However, mechanism of such endogenous (semi)lunar timekeeping remains elusive. Three functional principles of the circa(semi)lunar clock have been proposed – two of which involve the circadian system: (1) A counting mechanism based on light-dark (LD) cycles, (2) a beat wave resulting from the superposition of a circadian and a circatidal rhythm, and (3) A (semi)lunar oscillator running independently of the circadian system. In our experiments, we find evidence that the semilunar period changes linearly with non-24h T-cycles, suggesting involvement of a counter mechanism in Clunio. Experiments conducted in LD 6:6 indicate that Clunio counts endogenous circadian oscillations rather than LD-cycles. In a broader evolutionary context these results strengthen the idea that circalunar clocks are based on different functional principles when comparing circalunar clocks of dipterous insects with those of marine annelids. These divergent clock principles may indicate multiple evolutionary origins of circalunar clocks.

Role of a Niemann-Pick type C2 transcript (Vd40090) in Varroa-honey bee interaction

Authors: Nganso Beatrice

Abstract: Chemical cues are well-known to play a crucial role in the interactions between the honeybee and its most devastating parasite, the invasive ecto-parasitic Varroa destructor mite. However, the chemosensory machinery that mediates this interaction remains unknown. Recently, via transcriptomic and proteomic analyses, we identified twelve putative soluble carrier and membrane-bound chemosensory proteins. Specifically, three transcripts were found to be foreleg-specific, while the other two transcripts were expressed in both the forelegs and gnathosoma. Silencing highly expressed and foreleg-specific transcript (Vd40090), which encodes a Niemann-Pick disease protein type C2 (NPC2) protein using RNA interference caused significant behavioral and physiological changes. Silencing effectively disrupted Varroa host selection, acceptance and feeding as well as significantly impaired the expression of reproduction-related genes leading to reduced mite reproduction within worker brood cells. Overall, our results clearly indicate the crucial role of this putative odorant carrier protein in Varroa-honeybee interaction.

Beyond Scientific Journals: Broadening the societal impact of entomological science discoveries

Authors: Ngumbi Esther, University of Illinois at Urbana-Champaign, United States

Abstract: Science continues to provide answers to the most persistent challenges our global societies face, including climate change, public health, and food insecurity. Yet, many of these novel scientific solutions, including those arising from entomological research, are only meaningful to the science community. Approximately 3 million scientific articles are published every year. Yet, on average, only ten people read a given scientific article in its entirety, so clearly, the public is not being reached. Considering this disconnect, it is crucial for graduate students, post-docs, early career, and seasoned scientists to learn the art of sharing their research findings beyond the scientific journals. In this talk, I will explore other avenues researchers can use to disseminate their findings widely and outline the art of writing and pitching impact-full science-related opinion pieces. By widely spreading our scientific results, we can build bridges between entomological research and society and allow communities, activists, private industries, and policymakers to build on our findings and discoveries.

How honest signaling and co-evolution between bees and their hornet predators has shaped bee communication

Authors: Nieh James, UCSD, United States

Abstract: Predators have shaped the evolution of multiple bee signals and how bees can detect signals. These adaptations include alarm communication, stop signals, and olfactory eavesdropping. I present recent work by my collaborators and myself on how predators affect the signaling of different honey bee species (Apis cerana, Apis florea, and Apis dorsata) to understand how important selective pressures, predation and peril, have shaped the evolution of honey bee communication.

Use of vibratory signals as mating disruption strategy for pest control

Authors: Nieri Rachele[3], Berardo Alice[2], Pugno Nicola M.[3], Mazzoni Valerio[1], [1]Fondazione Edmund Mach Center for Research & Innovation, Italy, [2]University of Padua, [3]University of Trento

Abstract: Mating disruption is normally associated with pheromones and for this reason it is considered a typical chemical ecology strategy. However, recent progresses in the field of biotremology are conveying research in the use of mechanical stimuli (i.e., semiophysicals) for pest manipulation. Vibrational inputs are less impacting on the environment than pesticides and for this reason they are suitable for organic and integrated pest management. Since 2017, a 1 ha vineyard of Cabernet Franc is managed with vibrational signals to disrupt the mating behavior of two noxious leafhoppers, Scaphoideus titanus Ball and Empoasca vitis Göthe. The 24h/day transmission of vibrations with frequency pattern overlapping the two pests' mating signals, by means of special electromagnetic transducers, caused a significant reduction (30-50%) of both populations in the treated area, in comparison with an adjacent control vineyard. Similarly, the leaf damage was much lower in the treated area compared to the control. On the contrary, no negative effects were observed on predators (e.g. spiders and lacewings). A numerical approach on the mechanics of the problem has indicated the optimal trellis system setup (i.e., poles and wires characteristics) to maximize the signal transmission along the row and thus reduce the overall costs (i.e., to increase the active space and thus to reduce the number of transducers per row). This is the first demonstration of the efficacy of the vibrational mating disruption method in the field. In future, we aim at extending the experimental area to other European vine regions, in order to further validate the method.

Endogenous viral elements are abundant in arthropod genomes and give rise to piRNAs

Authors: Nigg Jared[1], Falk Bryce[1], [1]University of California Davis, United States

Abstract: Endogenous viral elements (EVEs) are genomic sequences derived from partial integrations of DNA and non-retroviral RNA viruses. In Aedes aegypti and Aedes albopictus, EVEs give rise to Piwi-interacting RNAs (piRNAs), raising the possibility that EVE-derived piRNAs may prime ping-pong amplification of virus-derived piRNAs during infection with corresponding exogenous viruses. We conducted a comprehensive survey of 48 arthropod species and found that while EVEs are abundant in arthropod genomes and often give rise to piRNAs, limited nucleotide identity between the majority of EVEs and currently described viruses likely limits the extent to which EVE-derived piRNAs direct ping-pong-dependent cleavage events during infection with these viruses. Nevertheless, a small number of EVEs share stretches of >20 uninterrupted nucleotides with corresponding viruses. In one such case, we found that the Diaphorina citri genome contains a 654 nt EVE with 86% nucleotide identity to Diaphorina citri densovirus (DcDV). Furthemore, we found that DcDV is targeted by ping-pong-dependent piRNAs during infection in D. citri. To further explore the potential roles of EVE-derived piRNAs, we constructed a recombinant cricket paralysis virus (CrPV) mutant by inserting 57 nt of sequence derived from DcDV and corresponding to the DcDV-derived EVE into the CrPV genome. We found that the presence of DcDV-derived sequence within the CrPV genome was not sufficient to permit targeting of the recombinant CrPV by EVE-derived piRNAs during infections in D. citri initiated either by microinjection or oral inoculation. Moreover, we found that DcDV was targeted by ping-pong-dependent piRNAs in D. citri populations lacking the DcDV-derived EVE. Our results represent the first report of ping-pong-dependent virus-derived piRNAs outside of mosquitoes and do not support the hypothesis that EVE-derived piRNAs are capable of targeting corresponding exogenous viruses.

Of monarchs and mitochondria: Effects of starvation and infection on flight physiology in the monarch butterfly

Authors: Niitepõld Kristjan[2], N. Kavazis Andreas[1], G. Appel Arthur[1], A. Parry Hailey[1], de Roode Jacobus[3] and R. Hood Wendy[1], [1]Auburn University, United States, [2]Department of Biological Sciences, Auburn University, United States, Finland, [3]Emory University, United States

Abstract: Migration poses an extreme energetic and physiological challenge to animals. Flying insects, in particular, consume energy at very high rates during migration. Thus, any disruption by external and internal stressors has the potential to hinder an insect’s ability to maintain physiological performance. Mitochondrial function lies at the base of organismal performance, health and fitness, but has been little studied in the context of migration. Here, we focused on two stressors, starvation and parasite infection, and assessed how they affect physiological performance at two levels: at the whole-animal level and at the level of mitochondria. Our study species, the North American monarch butterfly (Danaus plexippus) is well known for its annual migration between northern breeding sites and southern overwintering sites. The monarch suffers from infection by the protozoan parasite Ophryocystis elektroscirrha, which has been shown to reduce survival and flight performance. We subjected infected and uninfected lab-reared female monarchs either to an ad lib diet or 7 days of starvation, and then measured whole-animal resting (RMR) and flight metabolic rates, and after quick dissection of flight muscles, mitochondrial oxygen consumption. We measured maximum oxygen consumption rate (State 3), resting rate (State 4), and the respiratory control ratio, indicating mitochondrial coupling. All results were corrected for body size. Starvation had a strong negative effect on whole-animal resting metabolic rate, which may reflect reduced capacity to maintain basal physiological functions. Starved individuals also showed reduced peak flight metabolic rate, indicating poor flight performance. In contrast, infection did not affect RMR or peak flight metabolic rate. Starvation lowered mitochondrial maximum (State 3) oxygen consumption of muscle whereas resting oxygen consumption did not change, leading to lowered respiratory control ratio. Infection did not affect mitochondrial respiration. A correlation analysis showed that mass-independent mitochondrial maximum respiration significantly predicted mass-independent whole-animal flight metabolic rate at the individual level, supporting the hypothesis of a clear link between mitochondrial and organismal performance. Many of the results showed trends suggesting additive effects of starvation and infection, but these were statistically nonsignificant. Nevertheless, as infection may lead to lower resource intake, it may ultimately reduce physiological flight performance via energy shortage. In summary, monarch flight physiology is sensitive to nutritional stress, highlighting the importance of natural food resources prior to energetically expensive undertakings, such as migration. Compromised mitochondrial function may serve as a mechanism leading to reduced survival and fitness in flying insects in general.

Evolution of developmental patterns in the sex-specific wing reduction in Lepidoptera: a perspective from developmental constraints

Authors: Niitsu Shuhei[3], Sugimoto Takafumi[2] and Kamito Takehiko[1], [1]International Christian University, Japan, [2]National Agriculture and Food Research Organization, Japan, [3]Tokyo Metropolitan University, Japan

Abstract: The acquisition of wings is the most important evolutionary event in insects, and thus pterygotan insects have become the most flourish animals in the world. Flight-loss has occurred in nearly all winged orders. Such flightlessness or winglessness have evolved many times in neopteran insects in a response to a change according to ecological conditions. Wing reduction in insects has received considerable attention regarding its processes and mechanisms in group such as Orthoptera, Homoptera, Hymenoptera, Coleoptera and Diptera. In lepidoptera, female-specific wing degeneration occurs in many groups; that is, brachypterous (vestigial wing) and apterous (no wing) forms occur in 26 of approximately 120 moth families. It has been well known that sex-specific vestigial wing type, which shows normal development of pupal wing but after adult development, pupal wing sheet degenerates due to sex-specific programmed cell death. While the developmental processes that led to these wingless females is well known, why and how such similar processes are caused in each different lepidopteran family still remain to be understood. To elucidate this issue, we compare the developmental processes of wing reduction in several lepidopteran families, e.g., Psychidae, Lymantriidae and Geometridae. Through our study, we found that these developmental processes of wing reduction were quite similar among different lineages in Lepidoptera. Based on these results, we propose that similar developmental patterns were caused by developmental constraints which limited evolutionary changes and were originated from parallel evolution of winglessness in Lepidoptera.

RNA viruses in spider mites and potential interactions with the host RNAi

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Abstract: RNA viruses are abundant and diverse in eukaryotic organisms, and evolved as a main biological factor in ecosystem. Currently, only a small proportion of RNA viruses has been characterized, and this is unknown in a key agricultural pest family-spider mites (Acari: Tetranychidae). In order to investigate RNA virome in spider mites, we used a polyphagous species (Tetranychus urticae) and two species preferred to infest on citrus (Panonychus citri and Eotetranychus kankitus). Based on rRNA-removed RNA-seq data of three mite species, we identified eight (six new and two known) RNA viruses, including one of Kitaviridae, two of Dicistroviridae, two of Chuviridae, and three picorna-like viruses (Picornavirales: unassigned). Screening of virus-derived sequences in multiple species of citrus pests (n=10 per species) showed that Eotetranychus kankitus picorna-like virus and Tetranychus urticae mivirus may be present in multiple citrus pests. These results may reflect spillover of this virus to different arthropod species in this citrus-based ecosystem. To further investigate the impact of viruses to host RNA interference pathway, we sequenced small RNAs of three spider mites. All identified viruses of Kitaviridae, Dicistroviridae, and picorna-like viruses (Picornavirales: unassigned), showed 20-21 bp peaks of virus-derived small RNAs, and these small RNAs also had symmetrical distribution patterns in the genome and antigenome, implying that viral infections may trigger the RNAi responses as an antiviral defense mechanism in spider mites. Our study highlight the importance to investigate RNA viromes in spider mites and the interactions between viruses and mites as well as interactions among pest species in an ecosystem via viruses.

Neuronal control of juvenile hormone biosynthesis to regulate reproductive dormancy in the fruit fly Drosophila melanogaster

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Abstract: Reproductive dormancy is a process to suppress oogenesis and save energy in adverse environmental changes, such as low temperature and short-day conditions. In many insects including the fruit flies Drosophila melanogaster, reproductive dormancy is induced by downregulation of juvenile hormone (JH) biosynthesis in the corpus allatum (CA). However, it is still largely unclear how JH biosynthesis is downregulated under dormancy-inducing conditions at the molecular and cellular levels. In this study, we report that a subset of neurons projecting to the CA plays an indispensable role in JH-dependent reproductive dormancy in Drosophila melanogaster. When a transgenic RNAi specifically impaired a neuropeptide expressed in the CA-projecting neurons, oogenesis was not suppressed, leading to mature egg production even in dormancy-inducing conditions. In addition, we also found that the neuropeptide receptor is highly expressed in the CA. Knockdown of the neuropeptide receptor in the CA also produced mature eggs in dormancy-inducing conditions. Consistent with these results, the hemolymph JH titer was upregulated by the knockdown of the neuropeptide receptor in the CA. Collectively, we propose that dormancy-inducing conditions activate the CA-projecting neurons to downregulate JH biosynthesis in the CA, leading to reproductive dormancy.

Developing behaviorally-compatible monitoring traps for the invasive spotted lanternfly, Lycorma delicatula

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Abstract: The invasive spotted lanternfly, Lycorma delicatula, has been officially detected in a number of states in the USA. To date, it has been recorded feeding on important specialty crops including grapevines and apple and peach trees, with recent reports of vine death attributed to their feeding. To enable more sensitive and reliable monitoring efforts for this invasive pest species, we have studied dispersal behavior of both adults and nymphs and developed novel trap designs based on their movement patterns that not only reliably capture L. delicatula, but also reduce non-target captures.

Contrasting light environments bias attacks by predators on white and yellow colour morphs of the aposematic wood tiger moth

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Abstract: The wood tiger moth warns predators on its unprofitability by its conspicuous coloration. It comes in many varieties including white and yellow, often co-occurring within a population. As predators are expected to select for the locally most efficient warning signal, there is a perplexing range of polymorphism present in this species and as such, it presents an evolutionary puzzle. One explanation that could maintain such polymorphism, is the light influence of variable light environments. As predators use visual perception to process luminance and chromatic information in their environment, different light environments may alter visual cues and bias their decision making. Here we recorded natural forest irradiance profiles and created two contrasting light environments and tested the impact of light on the survival of an aposematic, colour polymorphic wood tiger moth (Arctia plantaginis) using blue tits (Cyanistes caeruleus) as predators. To assess bird decisions in a simultaneous choice test with real prey, we offered yellow and white moths to blue tits under conditions simulating open (i.e. bright) and/or forested (i.e. shady) light environments. Yellow moths were more likely to get attacked first in low light conditions whereas white moths got more often attacked in bright light conditions. Our findings suggest that deviance in chromatic and luminance information and light conditions can influence predators' decision making, and thus facilitate the maintenance of anti-predatory colour polymorphism in the wild.

The existence of a new cryptic species of Japanese pygmy mole cricket (Orthoptera: Tridactylidae) revealed by morphological study and mitochondrial DNA analysis

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Abstract: Pygmy mole crickets (Orthoptera: Tridactylidae) are small, blackish, grasshopper-like insects that have several interesting morphological characters. In Japanese fauna, four species are described within the genus Xya, namely alcicornis, nitobe, japonica and riparia. Among these species, in Honshu, the mainland of Japan, there are two species of pygmy mole crickets: Xya japonica that are widely distributed, and X. riparia that show limited distribution. In 2014, we found a new pygmy mole cricket with similar morphological features to X. riparia in a southwestern area of Japan. Thereupon, we performed a morphological comparison and a molecular phylogenetic analysis using the mitochondrial DNA of all of the pygmy mole cricket species, including the unknown species we found.

As a result, the morphological characteristics of the genitalia in the unknown species was similar to X. riparia, and was quite different from the other three species. However, the unknown species was different from the individuals in the Southwestern Islands due to an external white pattern on the legs and wings. Molecular phylogenetic analysis using mitochondrial COI and COII genes of 971bp by the Maximum Likelihood Method revealed that the unknown species holds a close relationship with X. riparia in Honshu, but belongs a different group from the X.riparia in the Southwestern islands. In this study, we have concluded that the unknown species is a new cryptic species of pygmy mole cricket, and is different from the X.riparia where it was found in the Southwestern islands.

On the generality of the diploid male vortex in parasitoid wasps with single-locus complementary sex determination

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Abstract: Most parasitoid wasps have complementary sex determination (CSD), which produces sterile or inviable males when homozygous at sex determining loci. Zayed and Packer (2005) have theoretically shown that small populations have elevated risks of extinction due to positive feedback between inbreeding and small population size, referred to as the diploid male vortex. Consistent with limited empirical support, a few modeling papers have suggested that diploid male vortices may not be as common as indicated by Zayed and Packer because balancing selection at sex determining loci tends to maintain high allelic diversity and because immigrants can introduce locally new alleles in spatially structured populations. However, the generality of the conclusion is yet uncertain, as these models were either developed for a particular system or based on models atypical for host-parasitoid interactions. The objective of our paper is to attest the conclusion in several well-studied host-parasitoid models. We derived analytical expressions of the conditions for a diploid male vortex in a single population. Then, we developed stochastic individual-based versions of the models and tested the effects of various behaviors, diploid male fertility, temporal fluctuation in host populations, and spatial population structure on the likelihood of a diploid male vortex. We found that a small increase in dispersal probability, diploid male fertility, and female discrimination against diploid males as a mate and a small decrease in primary sex ratio can alleviate the risk of a diploid male vortex, even when host populations fluctuate with high amplitudes and synchronously. However, populations become more prone to extinction when the temporal dynamics of host abundance are autocorrelated. We conclude that spatially connected parasitoid populations may be more robust to a diploid male vortex than anticipated by Zayed and Packer. However, if future climate change induces more temporally autocorrelated host abundance, the likelihood of a diploid male vortex could increase substantially.

Revealing the bacterial diversity associated with Platypus cylindrus (Coleoptera: Curculionidae) on Portuguese cork oaks

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Abstract: The oak pinhole borer Platypus cylindrus Fab. (Coleoptera: Curculionidae) is an ambrosia beetle distributed across Eurasia and the Mediterranean area. In Portugal, it colonizes the trunks of the major forest tree species Quercus suber (Fagaceae). P. cylindrus was traditionally recorded as a secondary pest, with damages limited to dead and weakened trees. In recent decades, it has promoted cork tree death within a few years and been part of a complex multifactorial process of decline affecting cork oak forests involving several microorganisms. The associated fungi are well studied, and it is known that they can have an important adverse effect on the tree, but no knowledge exists about the bacteria in this specific interaction. The cause of the beetle outbreak remains still unknown leading to the formulation of the hypothesis of a new insect-symbionts interaction. The aim of this study is assessing the presence and the putative role in oak decline of the bacteria associated with cork oak and P. cylindrus. We provide an in-depth overview of the bacteria associated with this pathosystem by means of a culture dependent approach for strain isolation and phylogenetic identification of bacterial strains with 16S rRNA gene sequencing and multilocus sequence analysis (gyrB, atpD, infB), along with independent methods. The P. cylindrus bored galleries from five different cork oak trees, as well as the body and mycangia from male and female beetles were investigated. The whole set of wood and beetle samples revealed the presence of 68 distinct bacterial isolates, which were collected and used for sequencing. These allowed the construction of the phylogenetic tree, with the majority of the isolates belonging to two taxonomic groups: the Enterobacterales and the Actinobacteria. The largest set of Enterobacterales isolates were present only in the tree galleries and were allocated in a major group together with pathogenic strains from the Pectobacteriaceae family including Dickeya, Brenneria and Lonsdalea spp., collected from other Quercus spp. Beetle strains displayed high similarity levels with Curtobacterium sp., Microbacterium sp., and Brevibacterium sp. Furthermore, 16S metabarcoding complemented with a detailed overview of the bacteria, revealing specific ecological roles related to both the beetle and trees. The results highlighted a small sexual differentiation for the bacteria in the mycangia. Comparison between ASVs and full 16S sequences allowed the identification of a group of Pectobacteriaceae carried by the beetle. Lastly, prediction of metabolic pathways revealed upregulation in the galleries of carbohydrate and virulence factors. This study reports for the first time the bacterial community associated with the pathosystem Q. suber - P. cylindrus, contributing to highlight unique features of the cork oak-oak pinhole borer interaction in Portugal and compare them with other wood-boring beetle outbreaks and oak declines in different countries.

Pesticide-induced food and macronutrient limitation in beneficial predatory beetles in agroecosystems

Authors: Noreika Norbertas, Estonian University of Life Sciences, Estonia

Abstract: Pesticide usage is claimed as the main cause of insect declines. Beneficial predatory beetles are also exposed to indirect pesticide effects arising from reduced prey availability and quality. Our main aim was to investigate if higher food and macronutrient limitation in carabids are related to conventional agro-practices (especially pesticides). Individuals of different carabid species were collected by hand from 8 conventional and 8 organic oat fields scattered around Tartu, Estonia (three times). In the laboratory beetles were served with three semi-artificial diets: lipid-rich, protein-rich, sugar-rich. Consumption of each diet was evaluated after 24 hours (=test1). Afterwards, beetles were fed ad libitum for a week until full satiation. The procedure of test1 was repeated (=test2). The differences of consumed diets among two tests showed the level of food and macronutrient limitations in carabids within assemblages. Separately, pesticide residue analyses in beetle bodies were performed. Food and macronutrient limitations were more expressed in larger bodied, poorly dispersing species and for carabids from conventional rather than organic fields. 11 different pesticide residues were detected in carabid bodies from conventional fields. We conclude that reduced pesticide usage would improve carabid nutrition and fitness thus leading to higher efficiency in providing biocontrol service.

Approaches and tools to study the role of Juvenile Hormone in modulating insect behavior

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Abstract: Juvenile hormones (JHs) are sesquiterpenoids synthesized by the corpora allata (CA). They play critical roles during insect development and reproduction. JH titers in insects are often in the femtomole to picomole range, which makes it challenging to measure them by most typical analytical techniques. In addition, to study processes that are controlled by JH, researchers need tools that can increase or decrease JH titers in vitro and in vivo. JH titers in insects can be easily increased by topical application of JH analogs (JHA), such as methoprene. On the other hand, purposely decreasing JH titers has been more difficult. In this presentation we will summarize the current knowledge on 1) Detection and quantification of JH from insect samples. 2) Approaches to manipulate JH titers. 3) New "omic-approaches" to modulate JH action and behaviour.

Epoxidation of juvenile hormone was a key innovation improving insect reproductive fitness

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Abstract: Methyl farnesoate (MF) plays hormonal regulatory roles in crustaceans. An epoxidated form of MF, known as juvenile hormone (JH), controls metamorphosis and stimulates reproduction in insects. To address the evolutionary significance of MF epoxidation, we generated mosquitoes completely lacking the enzyme that catalyzes the last step of JH biosynthesis, the P450 epoxidase CYP15 (EPOX). Strikingly, epox-/- mutants, which synthesized MF but no JH, completed the entire life cycle. While epox-/- adults were fertile, the reproductive performance of both sexes was dramatically reduced. Our results suggest that although MF can substitute for the absence of JH in mosquitoes, it is with a significant fitness cost. We propose that MF can fulfill most roles of JH, but its epoxidation to JH was a key innovation providing insects with a reproductive advantage.

Does thiamethoxam reduce circadian rhythmicity and lower activity in Bombus impatiens?

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Abstract: Bumblebees (Bombus impatiens) are economically and ecologically important wild pollinators in temperate regions of North America and recent declines are of major concern. One reason for the decline is agrochemical use affecting non-target organisms like bumblebees. Bumblebees can be exposed to agrochemicals either directly by coming in contact with treated crops or indirectly by drift from agricultural fields. An agrochemical class of concern for the bumblebees are the neonicotinoids and specifically thiamethoxam which has become a popular choice among farmers in recent years. Neonicotinoids act as agonists of insect nicotinic acetylcholine receptors (nAChR) within the central nervous system. One possible target of neonicotinoids poisoning is the nAChR dependent neurons regulating the bumblebee's circadian rhythm. . We investigate activity and the circadian rhythms of bumblebees after chronic ingestion of field realistic levels of thiamethoxam. Thiamethoxam treatments included 0nM, 1nM, 10nM, 100nM. Although we did not observe an effect on circadian rhythmicity, we observed declines in activity in all treatment groups with significant reductions in activity at the highest dose of thiamethoxam. Our results suggest that thiamethoxam concentration at high does may reduce pollination efficiency through a reduction in overall activity levels.

The Impact of Glyphosate on Mitochondrial Function in Honey Bee Spermatozoa

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Abstract: The western honey bee is the most commercially managed bee, because of its value to agriculture. During the last few years, colony declines have been being recorded worldwide. Agrochemicals can act as inadvertent contraceptives among bees, affecting multiple reproductive mechanisms in the male, resulting in lowered sperm count, sperm viability and sperm motility. However, there are no studies demonstrating the effect of agrochemical exposure to changes in male reproduction at the cellular level. Mitochondrial activity can be indicative of the spermatozoa longevity, motility, and its ability to capacitate. We hypothesized that mitochondrial activity will decrease with increasing concentrations of N-(phosphonomethyl)glycine (glyphosate) exposure. We used the mitochondrial stain MitoTrackerTM (green) to measure mitochondrial function after exposure to glyphosate at three different near field-level doses (3.2 nmol, 32 nmol, and 320 nmol) as would be noted in the nectar or pollen. MitoTrackerTM stains indirectly assesses mitochondrial activity, mass, cysteine abundant proteins (thiol proteins), certain glycoproteins and the impact of reactive oxygen species (ROS). Thus, higher MitoTrackerTM (green) stain intensity can be construed an index of mitochondrial activity in the spermatozoa. Our Results indicate that in the presence of glyphosate there is increased mitochondrial activity in the presence of glyphosate, compared control to treatments. However, this finding is independent of increasing glyphosate dosages in the range of 3.2 - 320 nM. Since MitoTrackerTM accumulation is independent of the membrane potential, we believe that near field-level doses glyphosate exposure results in significant stress and elevated production of ROS. The effects of glyphosate on the membrane potential will be considered in future studies on honey bee reproductive stressors.

Triatominae symbiosis: unique after all?

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Abstract: Kissing bugs (Triatominae) are obligate hematophagous (blood-feeding) insects and the only known vector of Chagas' disease (Trypanasoma cruzi). Like many organisms, kissing bugs host symbiotic bacteria within their guts (the gut microbiome) that are important modulators of host phenotype. However, compared to our comprehensive understanding of other symbiotic systems involving obligate blood feeders like tsetse flies, keds and lice, current research have not yet provided much insight into the symbiotic associations established by kissing bugs. The findings published so far often contradicts each other and fail to identify common drivers shaping Triatominae symbiosis. In our project, we have succeeded to sample over 500 Triatoma individuals of all life stages from their natural environment, i.e. pack rat (Neotoma albigula) nests, in Texas and southern Arizona. Using this extensive sample set, 16S rRNA gene amplicon sequencing, genomics and advanced visualisation techniques including TEM and confocal microscopy, we have investigated the natural host-microbiome relationship in multiple species of kissing bug. Our results bring the first visualisation of the microbiome assembly along with the identification of intracellular symbionts. Furthermore, being able to study individual microhabitats. i.e. pack rat nests, we conclude that ontogeny, species identity, and location are the primary factors influencing gut microbiome community composition. Contrary to previous reports on triatomine microbiomes, we demonstrate that there is a high degree of species-specific effect on the microbiome composition coupled with a positive correlation between microbiome dissimilarities and host phylogeny.

Microbiome convergency in kissing bugs and their predator relatives (Heteroptera: Reduviidae)

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Abstract: Reduvinae subfamily are the predator relatives to Triatominae (Heteroptera: Reduviidae), the vectors of Trypanosoma cruzi causing Chagas disease in humans and dogs. Phylogeny suggests that the obligate blood feeding strategy of triatomines evolved from the predatory habit of reduvids feeding on hemolymph of other invertebrates. Along with our attention to the epidemiologiacally important triatomins, we have decided to investigate one of the plesiomorfic traits of the reduvid ancestors that presumably facilitated the evolution of hematophagy, i.e. symbiosis with bacteria. In particular, we have sampled these two closely related bugs from sympatric populations and the exact same microhabitat, i.e. the nest of white-throated woodrats (Neotoma albigula), and profiled their microbiome using 16S rRNA gene amplicon sequencing. Microbiomes from Reduvius sp. (n=20) and two species of Triatoma (T. rubida and T. protracta; n=7) collected from Southern Arizona, US, were analyzed to explore the first hand knowledge on Reduvius-associated bacteria. Our results showed the presence of specific and shared taxa between Reduvius and Triatoma bugs. Compared to the triatomins, the predator microbiome however displayed a higher complexity and distinct dynamics. While the microbiome richness and diversity generally increase from the first to higher instars of Reduvius bugs, Triatoma species show significant decrease in the diversity indices throughout their ontogeny. Furthermore, beta-diversity analyses showed that Reduvius bugs have highly similar bacterial communities across the instars which is not the case in Triatoma.

Latitudinal life-cycle variations and their change in relation to climate warming in two Japanese crickets

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Abstract: Recent climate warming has affected some life-history traits of insects, including the number of annual generations and body size. The magnitude of changes in these traits may differ with latitudes within a species because of the differing cumulative effective temperatures for growth. In the present study, we estimated the change in the number of annual generations in Polionemobius mikado and Dianemobius nigrofasciatus over the last four and five decades, respectively, by comparing the body size of adults collected from a wide range of latitudes in Japan. These species are closely related in the family Trigonidiidae (Orthoptera), and distributed broadly in low-elevation grasslands in the Japanese archipelago. They have univoltine life cycles in northern Japan, but bivoltine ones in southern Japan with embryonic winter diapause.

The body size of P. mikado and D. nigrofasciatus collected in recent years showed a latitudinal saw-tooth cline, in the same way as the body size did four and five decades ago, respectively. The adult body size increases with decreasing latitude, but sharply decreases at a latitude where the number of annual generations increases.

In P. mikado, the cline shifted northward by 1-2° from 1970s to 2010s. The sum of effective temperatures for postdiapause embryonic development was greater in 2010s than in 1970s by approximately 200-400 day-degrees within each site because of global warming and heat island phenomenon. This difference of the sum of effective temperatures was comparable to that caused by an increase by 1-2° of latitude. Taken together, these findings suggested that the latitudinal range suitable for the bivoltine life cycle of P. mikado has expanded northward over the last four decades because of climate warming. In D. nigrofasciatus, however, no significant temporal change was observed in the cline between 1960s and 2010s, suggesting that the bivoltine life cycle had not expanded in the last five decades. Therefore, the effect of climate warming is not so simple and varies even between two closely related species with similar life cycles.

Transgenerational seasonal timer as an adaptation to spring short days in the pea aphid

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Abstract: Most aphid species adapt to seasonal environmental changes, by switching from viviparous parthenogenesis in spring and summer to oviparous sexual reproduction in autumn. Sexual generations are induced by short days. Under short-day conditions in the laboratory, however, the appearance of sexual morphs is suppressed by a transgenerational seasonal timer after hatching of stem mothers from sexually produced eggs.

In the present study, we examined whether the seasonal timer measures the number of days or the number of generations from hatching in the pea aphid, Acyrthosiphon pisum. To distinguish the number of days and generations, we reared two lineages in which either early-born or late-born progenies were allowed to produce the next generation. The ability to produce sexual morphs was completely suppressed in stem mothers, and gradually recovered over successive generations produced during a few months. It was shown that the duration of the seasonal timer depended on the number of days from hatching, but not on the number of generations from hatching, by comparing the duration until the recovery of the ability to produce sexual morphs between early-born and late-born lineages. Moreover, the duration of the seasonal timer depended on temperature, but not on photoperiod.

Then we tested a hypothesis that the seasonal timer suppresses an unseasonal appearance of sexual generations which is induced by short days in spring, by rearing A. pisum under natural photoperiods and temperatures.

Stem mothers with the operative seasonal timer produced only parthenogenetic progenies in spring. In contrast, parthenogenetic females with the expired seasonal timer produced sexual progenies besides parthenogenetic ones in spring. These results show that photoperiods in spring induce sexual morph production as those in autumn, and the seasonal timer suppresses unseasonal appearance of sexual generations in spring.

Climate variability differentially impacts thermal fitness traits in three coprophagic beetle species

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Abstract: While the impacts of extreme and rising mean temperatures are well documented, increased thermal variability associated with climate change may also threaten ectotherm fitness and survival, but remains poorly explored. Using three wild collected coprophagic species Copris elphenor, Metacatharsius opacus and Scarabaeus zambezianus, we explored the effects of thermal amplitude around the mean on thermal tolerance. Using standardized protocols, we measured traits of high- (critical thermal maxima [CTmax] and heat knockdown time [HKDT]) and -low temperature tolerance (critical thermal minima [CTmin], chill coma recovery time [CCRT] and supercooling points [SCPs]) following variable temperature pulses (d0, d3, d6 and d9°C) around the mean (27°C). Our results show that increased temperature variability may offset basal and plastic responses to temperature and differs across species and metrics tested. Furthermore, we also show differential effects of body mass, body water content (BWC) and body lipid content (BLC) on traits of thermal tolerance. For example, body mass significantly influenced C. elphenor and S. zambezianus CTmax and S. zambezianus HKDT but not CTmin and CCRT. BWC significantly affected M. opacus and C. elphenor CTmax and in only M. opacus HKDT, CTmin and CCRT. Similarly, BLC only had a significant effect for M opacus CTmin. These results suggest differential and species dependent effects of climate variability of thermal fitness traits. It is therefore likely that the ecological services provided by these species may be constrained in the face of climate change. This implies that, to develop more realistic predictions for the effects of climate change on insect biodiversity and ecosystem function, thermal variability is a significant determinant.

The diversity and ecology of viruses in the Drosophilidae, a ‘model’ insect family.

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Abstract: Drosophila have been model for insect-virus interaction since the symptoms of Drosophila sigma virus were first recognised in 1937. Drosophila experiments have since been instrumental in defining all of the major antiviral immune pathways of insects. However, the advent of high-throughput metagenomic sequencing has only recently allowed us to appreciate the diversity of viruses associated with the Drosophilidae. We have now identified over 100 RNA viruses - and around a dozen DNA viruses - associated with more than 20 species of Drosophila in the wild. These include virus lineages not previously recognised to infect insects (the dsRNA Partitiviruses) and entirely new virus families (the segmented +ssRNA Quenyaviruses).

We have used targeted metagenomics and PCR surveys to show that some of these viruses are highly prevalent (Galbut Partitivirus infects more than 50% of wild D. melanogaster and is detectable in all populations examined); some have naturally wide host ranges (Prestney burn virus has been seen in 12/15 Drosophila species surveyed); and some can have extremely high titres (over 50% of the coding RNA in a fly). However, we still know little of the costs associated with infection. Our experiments suggest a 20-30% reduction in lifetime offspring production is not unusual for females under laboratory conditions, but it is necessarily hard to estimate fitness effects smaller than a few percent - the magnitude that likely shapes evolution in the wild.

Honeybee colony strength is affected by spatial scale in fragmented landscapes in eastern Kenya

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Abstract: Landscape fragmentation at multiple scales and habitat loss has a direct effect on species persistence, productivity and survival. Little is known about the effect of the surrounding landscape structure on honeybee colony performance in Kenya. Here we focus on how patch size, shape, connectivity, composition and configuration affect honeybee (Apis Mellifera) colony strength characteristics in a semi-arid agro-ecological landscape in eastern Kenya. The research was done within 6 study sites of varying degrees of degradation, during the period from 2017 to 2018; mapped using high resolution fused bi-temporal Sentinel-1A and Sentinel-2A satellite systems with an optimized random forest algorithm. The influence of the surrounding landscape matrix was constrained to spatial scales with a radius of up to 3km around the apiary to mimic average foraging distances of honeybees. The results of linear mixed effects models showed that adult honeybee population, amount of pollen and amount of brood increased with landscape homogeneity comprised of semi-natural vegetation at short distances from the apiary (500m), while simpler patch geometries at 1km radius from the apiary also had a similar effect on the same hive parameters. Amount of honey increased during the long rainy season that occurs in May, whereas during the driest month of the year (January), pollen amounts largely decreased, demonstrating that seasonality had a role to play for honey and pollen production. There were hardly any eggs in January, in contrast to May which had a large increment in the number of eggs. In contrast to expectations, honeybees in moderately degraded landscapes demonstrated the most consistently strong colonies throughout the study period, perhaps due the heterogeneity of the landscape, therefore availing forage from grasslands, croplands, weeds as well as natural woody vegetation. Colonies in the least degraded areas exhibited the highest rate of absconding, probably due to the presence of large hive beetles which were found in large numbers in the hives. Our results suggest that semi-natural landscape homogeneity, as well as proportion of croplands were most influential at short distances from the apiary (<= 1km), while complexity of patch geometries was most influential at longer distances from the apiary (2km). These results have important implications on hive placement and location for optimal hive productivity as well as pest control in least degraded areas for improved honeybee colony strength.

Flowers, florivores, and floral visitors across elevation gradients

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Abstract: The pervasive effects of climate change on the biosphere are increasingly evident with many well-documented impacts on species ranges and phenological events. As ectotherms, the phenologies of plants and insects are highly sensitive to changes in temperature. The vast majority of studies of climate change effects on terrestrial organisms have focused on the responses of individual organisms to changes in temperature and precipitation patterns. Far fewer studies have examined the effects of climate change on biotic interactions, yet studies are vital for our understanding of how climate change has (and will continue to) alter communities and ecosystems. This talk explores how changing temperatures differentially alter the phenologies of members of a simple trophic community (cowparsnip – Heracleum maximum, insect herbivore – parsnip webworm, its parasitoid wasp – Copidosoma sosares, and the suite of insect pollinators) across elevational gradients, resulting in phenological matches in warmer years and mismatches in colder years. In cooler years, cow parsnips at higher elevations largely escape herbivory; in warmer years, cowparsnip populations at higher elevations experience reduced fitness due to substantially increased levels of herbivory.

Determining the genetics of diapause termination in the codling moth (Cydia pomonella L.)

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Abstract: Codling moth (Cydia pomonella L.) hibernates in a larval diapause stage and terminates diapause temporally heterogeneous during spring. Individuals terminating earlier in the season have a higher chance of completing several generations before returning into diapause, whereas individuals terminating their diapause later in the year have a lower chance of doing so. In the studies conducted at Laimburg Research Centre, two different codling moth populations were selected by inbreeding, which showed diapause termination which differed by several weeks (early and late), indicating an inherited genetic basis for these phenotypes.

As most studies are looking at downstream processes like transcriptomic or hormonal changes depending on the already started diapause termination, these studies are only meaningful to a limited extend for determining the environmental signal for diapause termination in the codling moth. Investigation of our selected populations populations showed, that the diapause termination signal is dependent on photoperiod and temperature. Crossing of distinct diapause-termination phenotype populations and genome sequencing can give valuable insights about genetic mechanisms responsible of diapause termination. Elucidating the genetic background of diapause termination in codling moth can help keeping track of the population dynamics in the field and therefore help pome fruit growers to adapt control treatments.

Re-surveys reveal biotic homogenization of Orthoptera assemblages as a consequence of environmental change

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Abstract: Biodiversity loss is a major global challenge. While population trends of vertebrates are well documented, insect declines have not been sufficiently studied and their drivers are still not fully understood. Repeating historical surveys can help to reveal the patterns and drivers of insect declines. We resurveyed 199 study sites in which Orthoptera assemblages had been recorded between 1986 and 1999 in south-west Germany. Our results show a significant increase in species per site (α-diversity), but simultaneously a homogenization of species communities (decreasing β-diversity). Habitat generalists became more frequent than specialized species and highly mobile species significantly increased in site occupancy compared to species with low mobility. Some Orthoptera species showed significant altitudinal range shifts, including species with positive trends (i.e. expansion to higher altitudes) and negative trends (i.e. extinction at lower altitudes). Protected areas had a high efficacy for conservation as trends in site occupancy were generally more positive in protected areas than in unprotected sites. Our results provide insights into the patterns and drivers of orthopteran assemblage turnover, including major effects of agricultural land use change and climate change. It is therefore critical to repeat historical surveys in order to understand global biodiversity change and implement the necessary actions.

Violet light increases Nesidiocoris tenuis population on crops.

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Abstract: Introduction: The minute pirate bug Orius sauteri and zoophytophagous plant bug Nesidiocoris tenuis have received attention as effective biological control agents against micropests. Banker plants are used to increase and maintain the populations of biological control agents by providing food resources. However, higher preference for banker plants can prevent the establishment of populations on cultivated crops. To develop a strategy for promoting attraction to cultivated crops, we previously investigated wavelength preference in O. sauteri. In a cultivated field, violet light promoted an increase in O. sauteri populations on cultivated crops and suppressed thrips density (Ogino et al., 2016), demonstrating that light illumination is a promising candidate for naturally attracting and maintaining natural enemies. In the present study, we examined attraction to light in N. tenuis to improve the establishment of its populations on cultivated crops.

Methods: We examined wavelength preference in N. tenuis using a six-arm arena equipped with six monochromatic light-emitting diodes (LEDs): ultraviolet (wavelength, 365 nm), violet (405 nm), blue (450 nm), green (525 nm), orange (590 nm), and red (660 nm). The behavior of the bugs on the arena was observed, and the wavelength for attraction was determined. Attraction to light was also investigated in tomato greenhouses. Banker plants were planted just inside each greenhouse entrance, and an LED was located at the innermost part of the greenhouse. N. tenuis adults were then released on the banker plants. The attraction effect in N. tenuis was evaluated by monitoring their movement toward tomato plants.

Results/Conclusion: 1) More N. tenuis individuals selected ultraviolet and violet light than other types of light. We assumed that violet light would selectively attract natural enemies, because it differs from the spectral preferences of most pest species. 2) More N. tenuis individuals were found on tomato plants in the LED-illuminated greenhouses than in the conventional greenhouses. In addition, more N. tenuis individuals remained near banker plants in the non-illuminated greenhouse, whereas in the illuminated greenhouse, bugs immediately dispersed from banker plants to crops and became uniformly distributed. In conclusion, light illumination is a promising strategy for attracting N. tenuis, which can promote controlling crop pests.

Wavelength preferences differ significantly among four species of thrips

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Abstract: [Introduction] Thrips are major pests of many agricultural crops. They cause severe damage by transmitting viral plant diseases. Since thrips have developed pesticide resistance, other pest control methods are necessary for successful integrated pest management. Exploiting the phototactic behavior of thrips by using colored sticky traps (i.e., yellow, blue, green) for monitoring thrips density, offers one possible approach. However, ideal color compositions for such traps are not known because the phototactic responses to specific light wavelengths have not been adequately studied in thrips species yet. This study analyzed wavelength preferences of four thrips species, Frankliniella occidentalis, Thrips palmi Karny, Thrips tabaci Lindeman, and Frankliniella intonsa, and elucidated the reasons for diversity in their wavelength preferences.

[Methods] Wavelength choice tests were conducted by illuminating a hexagonal arena with six monochromatic LEDs that covered the visible light spectrum of thrips. Phototactic behavior was evaluated using tracking analysis after recording the phototactic attraction to each wavelength. The spectral sensitivity of compound eyes was determined with the electroretinographic (ERG) method. A molecular phylogenetic tree based on the amino acid sequence of mitochondrial COI was constructed using neighbor joining. The implications of diversity in wavelength preference among thrips species were discussed.

[Results] Wavelength preferences: Four thrips species exhibited clear differences in their wavelength preferences. F. occidentalis and F. intonsa preferred shorter wavelengths (365–450 nm), including ultraviolet, whereas T. palmi and T. tabaci preferred the green wavelength (525 nm).

Spectral sensitivity of compound eyes: All four thrips species had bimodal spectral sensitivity curves that peaked at both ultraviolet and green wavelengths. The spectral sensitivity was consistent with the wavelength preference of T. palmi, but there was no correlation in other species.

Phylogenetic relationships: The phylogenetic tree indicated that F. occidentalis and F. intonsa are closely related, as are T. palmi and T. tabaci.

[Discussion] We found notable differences in wavelength preference among the four thrips species. However, spectral sensitivity did not correlate with wavelength preferences in F. occidentalis, F. intonsa, or T. tabaci. This indicates that the wavelength preference of thrips is related to the neural processing of light input signals from photoreceptors. The four thrips species have a wide range of host plants, and are common pests for many of them. The species that preferred ultraviolet wavelengths, F. occidentalis and F. intonsa, are often found on flowers, whereas those that preferred green, T. palmi and T. tabaci, are found almost exclusively on foliage. Therefore, our results indicate that wavelength preference is related to whether feeding is on flower nectar or leaf sap, rather than the host plant species.

Aggregation of host plants attract the specialist leaf beetle through change of the leaf chemicals

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Abstract: Recent many studies have strongly suggested that plant-plant interactions affect resource utilization in herbivores through change in leaf traits of host plants. Here, we investigated the effects of phenotypic plasticity in leaves of Rumex obtusifolius (host plant) in response to intraspecific and interspecific interactions on the distribution of Gastrophysa atrocyanea (specialist herbivore).

In the field, the presence of G. atrocyanea was positively correlated with the local population density of R. obtusifolius. In the cultivation experiments, plants in the intraspecific interaction treatment increased their leaf concentrations of condensed tannins and total phenolics, and G. atrocyanea consumed more of these leaves than leaves in interspecific or no interaction treatments. Similar results were observed in the field. In the mesocosm experiments, larger numbers of G. atrocyanea were distributed on R. obtusifolius exposed to intraspecific interaction than on plants not exposed to intraspecific interaction.

The previous understanding of the resource concentration hypothesis was that a high density of host plants makes it easier to find them, i.e. that ‘resource quantity’ is important. However, our results show that changes in the chemical composition of leaves due to intraspecific interaction with neighbouring plants, i.e. ‘resource quality’, is an important factor in determining the distribution of herbivores.

Object Detection of Camouflaged Insect by Artificial Intelligence

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Abstract: Insects are found everywhere and often blend into nature to protect themselves from their enemies or to ambush prey. Insects hiding in this way are often difficult to spot at a glance, not only by their natural enemies and preys but also by humans. On the other hand, the performance of artificial intelligence (AI) in image recognition has been improving dramatically. In this context, image recognition of camouflaged objects, which detects hard-to-find objects in an image, has been attracting attention. There have been few experiments on image recognition of camouflaged objects, focusing only on insects. In this study, we tried to recognize camouflaged insects by AI in object detection, an image recognition method. Specifically, we investigated the prediction accuracy of AI for camouflaged insects in experiments using a combination of YOLOX, the latest model of YOLO, a typical machine learning model for object detection, and TDGA AA, one of the methods for image data augmentation for AI. As a result of the experiment, we obtained promising results by the proposed method as a COD10K as an example.

Diversity of fungus gnat-pollination systems and the fine-tuned convergence in floral characters: a new pollination syndrome

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Abstract: Dipteran insects are among the most common visitor to the flowers, yet the communications and its consequence on floral adaptation is less understood compared to those involving other pollinators such as bees. The fungus gnat is the groups of tiny fly families belonging to Nematocera. As they feed on fungi, moss, and plant litter, they are abundant in humid forest. Because of their tiny body, fungus gnats are often regarded as ineffective as pollen carriers, though in recent years, it has been found that several plant families shares fungus gnats as pollinators, forming a pollinator guild in the Japanese flora (Mochizuki and Kawakita, 2018 Ann. Bot.). Notably, plants also shares floral characters: dark red display, flat flowers, exposed nectary, short stamen, and fermented scent.

In this study, we hypothesized the set of shared floral traits to be convergence towards fungus gnats, namely floral syndrome involving fungus gnat pollinators. To test the hypothesis, we investigated the pollinators of the species in the genus Euonymus and its evolutionary relationship to floral traits in a phylogenetic context. All the investigated five species with dark red flowers were pollinated predominantly fungus gnats, and five greenish-flowered Euonymus species and the outgroup white-flowered Tripterigium species were pollinated by bees, beetles, and Brachyceran flies. There were strong correlation among pollinators, flower color, morphology (stamen length), and floral volatile. Ancestral reconstruction suggested that fungus gnat-pollinated has originated at least four-times, each time the dark red flower has evolved, and the floral scent bouquet mainly composed of acetoin has occurred three-times. These result indicate that adaptation towards fungus gnat pollination drives unique floral syndrome.

The floral scent bouquet dominated by acetoin is not common in angiosperms, suggesting that fungus gnats are functional group of pollinators distinct from any other pollinator taxa. As sensory and preference of the flies may be diverse corresponding to their diverse life history, flies may contain several functional pollinator groups and involve distinctive, fine-tuned floral adaptations.

Coexistence of honeybees with distinct mitochondrial haplotypes and hybridized nuclear genomes on Comoros Islands

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Abstract: The Western honeybee, Apis mellifera, is a globally distributed species which has spread both naturally and by humans. Well-defined population sub-structure exist with different evolutionary lineages defined via the divergence in their mtDNA genotypes. The divergent lineages can interact through naturally occurring overlap in distribution ranges or secondary contact via human-mediated transport. Such contacts are characterized by preferential replacement of specific mtDNA genotypes. For instance, the Africanized honeybees in the Americas are characterized by complete replacement of the European bee mtDNA genotypes with African genotypes despite showing complete hybridization in the nuclear genome. Similar cases of preferential replacement of specific mitotypes are reported in La Réunion, an island located south-west of the Indian ocean, where European genotypes have been imported 30 years ago. However, few studies have investigated the population structure and diversity of honeybee populations existing as feral colonies with minimum human interference. Here, we are investigating the genetic diversity, genetic differentiation and population structure of isolated honeybee populations existing as wild colonies on Comoros islands, which is best suited as beekeeping is not well established and the islands are isolated from the continental plate. Using genotyping and phenotypic markers, we show that the wild honeybees of the Comoros Islands consist of two coexisting mitochondrial haplotypes. One belongs to the A-lineage, Apis mellifera unicolor, typical for the African continent, the other, the newly described L-lineage, is closely related to Apis koschevnikovi, a honeybee species native to Southeast Asia. The nuclear genomes of A. mellifera show complete hybridization with slight differentiation according to the island of origin, as evidenced by microsatellite markers and wing shape as a phenotypic trait. Our results suggest that the Asian honeybee has been introduced in Comoros islands. This introduction could have occurred during the human migrations of Southeast Asian people to Africa which occurred 6,000 years ago, reaching Madagascar and the Comoros Islands. The transported honeybee has since hybridized with African honeybees at the nuclear genome but still maintain the original mtDNA genome.

Diseases and pests emerging in domestication of some African stingless bees in East sub-Sahara Africa

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Abstract: We conducted a surveillance at 5 meliponicultures sites around the Eastern remnant rainforest in the East sub-sahara Africa to identify diseases and pests damaging managed colonies of five stingless bee species. Domesticated stingless bees included, H. gribodoi, M. ferruginea, M. togoensis, M. lendliana and M. bocandei. Using microbiology technics, we identify yeast or fungal infesting colonies nest. We also used molecular biology techniques, to tested for the presence of eight common honeybee pathogens among the reared stingless bee colonies. Furthermore, pests or predators infesting, and robbing colonies where also determine. Susceptibility to yeast or fungal pathogens, we isolated a disease-causing fungal Peyronellaea pomorum affecting involucrum and pillar in nest of M. ferruginea, M. togoensis, M. bocandei and M. lendliana. The fungal infestation mostly occurred during heavy raining season and infested nests dehydrates causing collapse of the colony. Nest absconding rate due to infestation was moderately higher in M. lendliana colonies (56.3±12.4) and proportion of damaged colonies was 33%. Susceptibility to eight common honeybee pathogens (Deformed Wing Virus, Black Queen Cell Virus, Kashmir Bee Virus, Israeli Acute Paralysis Virus, Chronic Bee Paralysis Virus, Acute Bee Paralysis Virus, Sacbrood Virus and Nosema microsporidia) showed presence only of Black Queen Cell Virus, in three stingless bee species (Hypotrigona gribodoi, Meliponula bocandei and Meliponula lendiliana). Black Queen Cell Virus was reported in 14.14% of all the sampled colonies; which support the notion that honeybee pathogens can possibly be transmitted to stingless bees. However, it remains unclear whether the pathogen has a detrimental effect on the stingless bee colonies. Susceptibility to pests, we identified two species of insects namely Aethina tumida and Megaselia scalaris. Olfactometer bioassays of both sexes of Aethina tumida adults to stingless bee species odors from intact colonies and separate hive components revealed both sexes strongly preferred intact colony, pot honey, and pot pollen odors, rather than propolis and cerumen odors. This result provides substantial evidence of the host potential of African meliponine bees for the Small hive beetles. Aethina tumida larvaes infestation was higher in M. togoensis (34.6±5.6) and M. bocandei (31.7±4.8) but absent in H. gribodoi colonies. The proportion of damaged colonies due to infestation by Aethina tumida larvaes was 100% in M. togoensis colonies and moderated in other species. Similarly, colonies infestation rate by Megaselia scalaris larvaes was higher in M. togoensis (30.4±6.1). The proportion of damaged colonies due to infestation was mainly higher by 75% in H. gribodoi, 68.75% in M. togoensis and 50% in M. lendliana colonies. Susceptibility to predators, three enemies were identified namely Apis mellifera, Philanthus sp (wasp), Elminia longicauda teresita (bird) preying on honey and forager bees.

Pollen or commercial diets? The honey bee response in presence of pesticides

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Abstract: The European honey bee (Apis mellifera) is primarily reared for honey production, but its benefits are substantially higher considering it is the most important pollinator of crops. This tremendous insect is confronting several environmental challenges, including the intermingled effects of malnutrition and pesticide exposure. Pollen is intuitively the healthiest choice for honey bee nutrition, but commercial substitutes are widely used to offset pollen shortages despite their unclear nutritional value. In the present study, we examined if honey bee reaction to chemical exposure is impacted by feeding pollen versus an artificial diet. Newly emerging bees were distributed into 3 groups of 6 cages, with each group receiving one of the following diets: pollen / sucrose, MegaBee / sucrose or sucrose only. On day-5, for each diet, 3 cages were kept pesticide-free to constitute the controls while the remaining cages were fed a mixture of chlorpyriphos and fluvalinate for 5 consecutive days to constitute the chronic chemical exposure treatment. To investigate if and how the different diets influence the honey bee reaction to pesticide exposure, we measured several physiological traits (body weight, fat body mass, hypopharyngeal gland development, hemolymph protein concentration, midgut proteolytic enzyme activity, hindgut protein content, and vitellogenin expression). We also examined the transcription levels of nutrition response genes, primary and secondary antioxidants, detoxification genes, immunity genes as well as acetylcholinesterase (AChE) which is the target of the organophosphate chlorpyriphos. Finally, to gain insight on the extent of alternative splicing in honey bee in response to environmental stress, we investigated the alternative splicing of few genes known to be highly spliced in drosophila.

Inter-drone competition drives the evolution of paternally-biassed gene expression related to female reproductive traits in the Cape honey bee Apis mellifera capensis

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Abstract: The Kinship Theory of Genomic Imprinting (KTGI) posits that, in species where females mate with multiple males, there is strong selection for a male to enhance the reproductive success of his offspring at the expense of other males and his mating partner. Reciprocal crosses between honey bee subspecies show strong parent-of-origin effects for reproductive traits, suggesting that males epigenetically modify the expression of genes related to female function in their female offspring. This effect is likely to be strongest in the Cape honey bee (Apis mellifera capensis), because a male's daughters have the unique ability to produce female offspring that can develop into reproductive workers or the next queen without mating. We used RNA-seq to identify transcripts that are over- or under-expressed in Capensis embryos, depending on the parental origin of the gene. As predicted, 21 genes showed expression bias towards the Capensis father's allele in colonies with a Capensis father, with no such bias in the reciprocal cross. A further six genes (0.003% of informative genes) showed a consistent bias towards expression of the father's allele across all eight colonies examined, regardless of the direction of the cross.

Consistent with predictions of the KTGI, two of the six genes are associated with female reproduction and one with gametogenesis.

On springtails (Hexapoda: Collembola): A morphofunctional study of the jumping apparatus

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Abstract: Springtails (Hexapoda: Collembola) are tiny organisms that lead a hidden life,style (e.g. they occurring deeper in the soil and in leaf litter). Springtails have a variety of interesting body morphology patterns, the most famous of which is their catapult-like structure that enables them to jump and flee from predators. This highly specialized jumping apparatus consists of the a mobile furca, which when at rest fits into a trigger, "the "retinaculum", on the ventral side of the abdomen. In this study, the morphology of the jumping apparatus of Orchesella cincta was investigated in detail using confocal laser scanning microscopy (cLSM) and MicroCT techniques for 3D reconstructions. In the following, the morphology of O. cincta with both flexed and extended furca was is analysed and described step by step. With the data obtained in this study, hypotheses can be made about 1) where and how the spring and hydrostatic pressure mechanisms are constructed originate; 2) which muscles act on the extension and flexion of the furca and 3) which muscles act on the retinaculum.

Characterising the epigenetic landscape of the Anopheles gambiae complex

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Abstract: Epigenetics is the study of inheritance coded outside of the genome. Although this field has grown rapidly in the field of cancer and diseases, it lags in entomology. In this study, we aimed to explore the little-known epigenetic landscape of the Anopheles gambiae complex, which contains several malaria vector mosquito species. This was done by examining whether larval heavy metal exposure would alter epigenetic markers in the accruing adults. This is because one member of the An. gambiae complex in particular, An. arabiensis, is adapting to breeding in polluted waters. Finally, we examined whether immune responses in the An. gambiae complex had an epigenetic basis, as the immune system underlies vector competence.

The epigenetic modulator and metal studies were limited to two laboratory strains of An. arabiensis, the insecticide susceptible SENN strain and the insecticide resistant strain selected from it, SENN-DDT. An. arabiensis larvae were reared in cadmium chloride, copper nitrate or lead nitrate treated water. In accruing adults, the m6A RNA methylation levels, and 5mC and 5hmC DNA methylation and Histone acetyl transferase activities were assessed using commercial kits. For the immune studies, two additional strains were included; the minor vector An. merus (MAFUS) and the non-vector An. quadriannulatus (SANGWE). Adult females of these two strains, in addition to SENN and SENN-DDT, were stimulated by being fed either a Gram-positive bacterium or a Gram-negative bacterium-spiked blood, and epigenetic markers were assessed by commercial calorimetric kits.

Under control conditions, RNA methylation differed significantly between males and females of the SENN and SENN-DDT strains. There were significant differences between the 5mC levels of males and females in the SENN strain. The SENN strain was also generally more sensitive to changes in methylation levels. HAT activity levels were also markedly affected by larval metal exposure, with a clear suppression of HAT activity in SENN and a marked increase in SENN-DDT.

Within the An. gambiae complex, basal RNA methylation levels differed in all three species, although there were no significant differences after immune stimulation. MAFUS had the highest basal and blood meal-induced levels of 5mC. SANGWE displayed the highest level of 5mC methylation in response to Gram-positive blood. 5hmC methylation, which is associated with demethylation and therefore gene activation, did not differ between strains at basal levels. SANGWE had the greatest amount of methylation in response to blood and Gram-negative stimulation. Differences in HAT activity, which also correlates with gene activation, was greatest in response to blood. Upon Gram-positive stimulation, the two An. arabiensis strains had significantly higher levels of HAT activity than the An. merus and An. quadriannulatus strains. This study provides some of the first evidence of the role of epigenetic architecture in the An. gambiae complex.

A survey of ticks and tick borne parasites in commercial cattle at Lafia, Nasarawa State, Nigeria

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Abstract: Ticks and tick borne parasites are a major constrain to good livestock productivity in the Sub-Saharan Africa including Nigeria. This study aimed at determining the prevalence of ticks and tick borne parasites in cattle at Shinge Livestock Market Lafia Nasarawa State Nigeria. Ticks and blood collected from randomly selected cattle were examined using standard entomological, parasitological and haematological procedures. Out of the 200 cattle examined 112(56.0%) were tick infested. A total of 1,152 ticks were collected from all cattle examined. Rhipicephalus (Boophilus) decoloratus 948(62.3%) was the most abundant species infesting cattle breeds followed by Amblyomma variegatum 383(25.2%), then Hyalomma rufipes 184(12.1%), while Rhipicephalus sanguineus 7(0.5%) was the least tick species encountered. There was a very high significant difference ($P < 0.00001$) on species abundance. The bovine blood examined showed a 70.5% parasitic infection by two genera (Babesia and Anaplasma). Babesia bigemina 80(36.0%) was most prevalent, followed by Anaplasma marginale 77(34.7%), while Babesia bovis 65(29.3%) was the least prevalent. There was no significant difference ($P = 0.6848$) in prevalence rate between tick borne parasites. Haematological investigation showed that blood indices examined were within standard ranges. It is therefore recommended that dips be introduced at strategic points to herders for easy access to de-tick their animals.

Larvicidal Efficacy of Capsicum chinensis (Hot Pepper) Powder Against Mosquitoes Larvae in Lafia Local Government Area, Nasarawa State, Nigeria

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Abstract: Mosquitoes spread more diseases than any other known arthropod and have shown resistance to conventional insecticides despite several control efforts prompting the need to explore alternative control measures such as the use of bio-larvicides which are environmentally friendly. To this end, the study on larvicidal efficacy of Capsicum chinensis powder against mosquitoes larvae in Lafia Local Government Area, Nasarawa State, Nigeria was carried out through collection of wild field mosquitoes larvae from May to July, 2018. Fresh Capsicum chinensis fruits were collected from a farmland and dried under room temperature and further processed to fine powder from which varying concentrations were used against the larvae including the control group. The larvae were exposed at 24, 48 and 72 hours respectively based on WHO susceptibility protocol. Anopheles gambiae larvae were susceptible (100% mortality) to the various concentrations of the powder at the end of the 72 hours exposure period while Culex quinquefasciatus were resistant (0% mortality). There was significant difference ($P < 0.0001$) in mortality rate of An. gambiae larvae in relation to concentrations while there was no significant difference ($P = 1$) in mortality rate of Cx. quinquefasciatus across concentrations. LD50 and LD90 values for An. gambiae at 24 hours were 2.4mg/mL and 0.10mg/mL respectively; 0.1mg/mL and 0.26mg/mL respectively at 48 hours and 0.00mg/mL and 0.01/mL respectively at 72 hours. This study shows that Capsicum chinensis powder is a promising bio-larvicide for controlling An. gambiae while Cx. quinquefasciatus will require higher doses of Capsicum chinensis before they may be susceptible.

Survey of mosquitoes in students hostels of Federal University of Lafia, Nasarawa State, Nigeria

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Abstract: The presence of mosquitoes in academic environment is a great threat to students well-being due to transmission of mosquito-borne diseases. Thus, the study survey of mosquitoes in students hostels of Federal University of Lafia was carried out between August and October, 2019 using Prokopack Aspirator. A total of 114 mosquitoes species belonging to 4 genera: Anopheles, Culex, Aedes and Mansonia. The predominant was Culex quinquefasciatus 65 (57.0%) followed by Anopheles gambiae 41 (36.0%) then 3 (2.6%) Aedes aegypti and Mansonia uniformis respectively while Anopheles squamosus and Anopheles coustani were the least 1 (0.9%), showing a high significance difference between the six species ($P < 0.0001$). The abundance of mosquitoes was more in male hostel 79 (69.3%) than in female hostel 35 (30.7%). Therefore, the mean abundance of mosquitoes between female and male hostels showed a significant difference ($P = 0.03636$). Blood fed female mosquitoes collected were 72 (69.2%) followed by those gravid 20 (19.2%) then unfed 9 (8.7%) while the least was half gravid individuals 3 (2.9%). Hence, the abundance of female mosquitoes in relation to their abdominal conditions showed a very high significant difference ($P < 0.0001$). The number of mosquito specimens collected during the study period was relatively low due high amount of rainfall flooding breeding sites in the area. This is the first study on mosquitoes population in the Institution's students hostels which will serve as a baseline data for mosquitoes control in the University environment. Students should avoid human-vectors contact through constant use of insecticides and treated bed nets.

Bioecology and qualitative analysis of the likelihood of Introduction of Tuta absoluta Meyrich (Lepidoptera: Gelechidae) via Export of Tomatoes from Nigeria to the USA

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Abstract: The bioecology, damage characteristics of the tomato leaf miner, Tuta absoluta and the phyto-sanitary risks associated with export of fresh tomatoes fruits from Nigeria into the mainland USA was investigated. This pest is neither known to occur nor has been previously established in the USA although a closely related species, Keiferia lycopersicella (tomato pinworm) is present. Tuta absoluta is highly polyphagous and damaging on solanaceous crops and can survive in all tropical and sub-tropical conditions in the USA; presenting a potential risk to established vegetable crops in Florida, Texas and Alabama as well other states with similar environments. The impact of the pest could be very severe causing up to 100% yield loss and leading to increased tomato prices, bans on trade of tomatoes including seedlings, increase in synthetic insecticide applications, disruption of integrated management programmes of other tomato pests and general increase in crop protection cost. The high biotic potential, adaptability to various climatic conditions and the speed of spread could impact heavily on the livelihood of local tomato growers if introduced. The female T. absoluta lays about 260 eggs during its life time and it infests the apical buds and tomato leaves with visible mines. Egg eclosion at 26-30ºC and 60-75 % RH occurs in 5-7 days and the emergent larvae under these conditions pass through four instars in about 20 days and thereafter pupates in the soil. The consequence of introduction and entry potential through imported fresh fruits are high and the outbreak risks based on climatic conditions marching the pest etiology and host biotics as well as pest survival between crops could also be high. However, outbreak risks can be greatly reduced to the level meeting the phytosanitary protection of the importing country, USA; given application and enforcement of appropriate mitigation especially quality assurance and sorting, storehouse and pre-shipment treatment with environmentally safe pyrethroid insecticide and single point mitigation by gamma irradiation at approved dosimetry at the port of exit.

Neuroendocrine studies for the identification of target sites for next-generation insecticides

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Abstract: The persistent and excessive use of synthetic neurotoxic pesticides in agriculture, silviculture, animal husbandry and vector management created several difficulties on pest control: insecticide resistance, negative ecological impact, accumulation in the environment and food, etc. The use of many compounds has been phased out given their high environmental impact and/or the spreading of resistant populations. This is an alarming situation, given the reduction of the available options for the control of harmful arthropod species. Hence, there is an urgency in the development of novel eco-sustainable compounds for their use in integrated pest-management strategies, in order to replace or complement synthetic insecticides. A promising avenue in the development of novel compounds is the research in insect neuroendocrine system (neuropeptides and their receptors). It has been proposed that they are a source of targets for new-generation insecticides, given that neuropeptides play central roles in vital physiological processes in arthropods. The first step in a neuropeptide-based control strategy is the structural and functional characterization of neuroendocrine system from harmful species.

Our group performed comprehensive characterization of neuroendocrine complement in harmful species such as kissing bugs (Rhodnius prolixus, Triatoma spp), stinkbugs (Halyomorpha halys, Nezara viridula) and a lepidopteran species that is a pest of stored food (Plodia interpunctella). Using transcriptomic and genomic approaches, we were able to identify conserved features and particular characteristics for groups and/or species. Furthermore, we used RNAi-mediated gene silencing in hemipteran species to study the physiological roles of understudied neuropeptide families such as Orcokinins, CCHamide and ITG-like. Interestingly, we found that these poorly studied neuropeptide families have fundamental physiological roles in the regulation of either post-embryonic development, reproduction, diuresis or stress response. Even though we performed basic entomology, we are able to propose that some of the studied neuropeptides could be good targets for further studies in the development of next-generation tools for the control of hemipteran pests.

Reduced pollen return to commercial bumblebee colonies poses threats to nest provision and long-term health after exposure to field realistic levels of a pyrethroid and an organophosphate

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Abstract: Bumblebees are important pollinators of crops and wild plants and threats to their decline poses a risk to the sustained provision of the they provide. Evidence suggests that exposure to field realistic levels of insecticides can affect bumblebee health and foraging behaviour, however most of these studies have investigated neonicotinoids only, with fewer investigating impacts on pollination services.

We exposed commercial bumblebee colonies to two widely used insecticide compounds; lambda-cyhalothrin (pyrethroid) and dimethoate (organophosphate) before foraging on potted oilseed rape plants in large exclusion cages. The results indicate that treatment didn't significantly affect individual foraging behaviour, visitation rates to the crop, or the yield of plants pollinated by bees from each treatment. There was, however, a significant effect of treatment on activity, with fewer bees leaving to forage from dimethoate colonies than from lambda-cyhalothrin and control. Additionally, significantly fewer bees from dimethoate and lambda-cyhalothrin colonies returned with pollen than control colonies. This suggests that over time, the health of colonies exposed to field realistic doses of these insecticides may deteriorate due to reduced activity and return of crucial pollen resources to the nest. Consequently, this may also pose a threat to the long-term sustained provision of important pollination services.

Weevil’s PGRP-LB circumvents endosymbiont immunogenicity and maintains host immune homeostasis

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Abstract: Peptidoglycan recognition proteins (PGRPs) represent a large protein family that is widespread from insects to mammals and play a pivotal role in immune response activation and regulation. However, while this family has been well investigated in pathogenic systems and conditions, little is known about their function in mutualistic associations. The cereal weevils Sitophilus harbors a Gram-negative intracellular bacterium, Sodalis pierantonius, which complements weevil’s diet with components lacking or in few amounts in cereal grains, and improves insect biological traits and invasive power. This bacterium is compartmentalized within specific host cells, the bacteriocytes, which form an organ around the gut, the bacteriome. This organ allows a fine-tuned regulation of host immune genes involved in endosymbiont control and host immune homeostasis.

We discovered recently in this association that pgrp-lb gene generates three transcripts with different cellular localization: A secreted isoform (extracellular) that is only expressed under pathogenic infection conditions; and, an intracellular and a transmembrane isoforms that are produced in the bacteriome. These last two isoforms specifically cleave the tracheal cytotoxin (TCT), an immunogenic peptidoglycan monomer released by the endosymbiont. The pgrp-lb silencing by RNAi results in TCT escape from the bacteriome to other insect tissues, where it chronically activates the host systemic immunity. To understand structural and functional specificities of the weevil’s PGRP-LB we recently have conducted X-ray crystallography and enzymatic studies of different PGRP-LB from endosymbiotic and non-endosymbiotic insect species. In this talk, I will present the main molecular and biochemical data obtained on this model system, and discuss how symbiotic evolutionary constraints may drive immune gene shaping and their adaptation to endosymbiosis.

Socioeconomic changes transform the pattern of biological invasions: history of invasions of beetles (Coleoptera) to Russian empire, Soviet Union and Russian Federation

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Abstract: Our research group has compiled the first inventory of alien beetles of European Russia (ER) (https://www.researchgate.net/publication/334279194_Inventory_of_alien_beetles_of_European_Russia). Using this information, I analyzed beetle invasions to ER in three historical periods: before 1917 (when this territory was a part of Russian empire), in 1917-1991 (USSR) and after 1991 (Russian Federation). These periods drastically differ from each other in socioeconomic characters and I have found out that the pattern of beetle invasions was also quite different. The main sources of alien species established before 1917 were Europe, W. Asia and N. Africa. Many beetle species spread because of import of goods from Mediterranean region. Then, in 1917-1991, the main sources were Central Asia and East Asia. It could be probably connected with the transportation of goods within the USSR: from the republics of C. Asia and from the Far East. The main source of beetle invasions after 1991 is China, which is obviously connected with the dramatic increase of import from this country. 54 species were first recorded before 1917, 45 species in 1917-1991and 85 species after 1991. In general, the number of newly established alien species grew from decade to decade, but decreased in the period of the decrease of import to the USSR in 1917-1960. The distribution of newly established alien beetle species depended on the structure of the country and on features of historical development. St.-Petersburg was the capital of Russian Empire and had the first place in number of alien species newly recorded for the ER before 1917. Then after the transfer of the capital to Moscow, the first place belonged to Moscow. Now the first place belongs to the city of Sochi. This resort region is now developing quickly, and alien beetle species are often introduced with imported planting material. The main pathways of beetle invasions were different in different periods. The overwhelming majority of species established in the period of Russian Empire were unintentionally introduced with stored products and organic substrates. Then the increase of international plant trade caused the increase in introductions with planting material (seeds, seedlings, potted plants etc.): 24% of alien beetle species firstly recorded in ER in 1917-1991 and 41% - after 1991 were unintentionally introduced with planting material. The ratio of introductions connected with the import of wood also increased from 4% (before 1917) to 12% (in 1917-1991) and 14% (after 1991). Alien beetle species established in the previous periods are connected mainly with stored products and occur mainly indoors. But many of currently established beetle species are connected with living plants, establish in the wild and can potentially affect native ecosystems. This current tendency increases the possible negative ecological impact of invasions of beetles. The study was supported by Russian Science Foundation, project ?16-14-10031

Improving our knowledge of global bee distribution

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Abstract: Insects, especially hyper-diverse lineages such as Hymenoptera, constitute the foundation of many ecosystems. We must know where insects live to conserve them, given recently-reported declines, lest we risk irreversible ecological damage. However, even bees, invaluable pollinators, lack a modern distributional synthesis based on empirical data. Here, we combine >5,800,000 public bee records with a uniquely-comprehensive 168,618-entry checklist of the ~20,000 bee species' distributions to reveal the global patterns of bee biodiversity while also examining the pervasive sampling biases which obscured this knowledge until now.

The route of infection influences the contribution of key immunity genes to antibacterial defense in the malaria vector Anopheles gambiae

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Abstract: Insects deploy several humoral and cellular innate immune effector mechanisms to clear bacterial infections. While antimicrobial peptides, melanization, phagocytosis and complement-mediated attack are often described as the main players in different contexts, several knowledge gaps remain as to their regulation, specificity and relative contribution to microbial clearance. This is further complicated by the fact that the vast majority of bacterial challenges in model insects have been established through an artificial route by pricking the cuticle to introduce microbes directly into the hemocoel. While this mode of infection has allowed the dissection of systemic anti-microbial immune responses at different levels, it is associated with two major pitfalls. First, microbes are often introduced at large numbers which might blur the readouts from distinct effector programs due to saturation effects; low dose infections are most likely the norm in field conditions. Second, this mode of infection may not allow sufficient priming of the systemic response whether humoral or cellular. Here, we will address the contribution of key immune genes to tolerance and resistance of A. gambiae mosquitoes to systemic Serratia marcescens (Sm) infections established through direct injection into the hemocoel or through oral feeding. Sm is a Gram-negative bacterium with a broad host range including plants, vertebrates and invertebrates, and its ability to efficiently colonize the midguts of insects and to invade the midgut epithelium reaching into the hemolymph makes it an attractive microbe to address whether the route of infection alters the contribution of key immunity genes to the systemic immune response. We will also address by RNA seq analysis what functional gene groups are differentially regulated in the midgut and fat body in response to oral Sm infections relative to infections established by cuticular pricking

Clip-domain serine protease homologs: key players in the proteolytic cascades regulating melanization

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Abstract: In Insects, key humoral immune responses such as antimicrobial peptide synthesis by the Toll pathway, melanization and complement-mediated attack are regulated by serine protease cascades composed mainly of clip-domain serine proteases (cSP) and their non-catalytic homologs (cSPHs). These cascades have been mostly studied in the context of melanization, an immune effector response that is triggered locally in response to cuticle injury or systemically following microbial invasion of the hemocoel. Despite being non-catalytic, cSPHs were shown initially to play critical roles in the insect melanization response by mediating the proper activation cleavage of PPO. Studies in the malaria vector A. gambiae revealed novel functions of cSPHs that extend beyond PPO activation to the regulation of complement activity. The substantial number of cSPHs and cSPs involved in melanization suggest that the protease cascades regulating this response are governed by a staggering complexity of interactions, especially that both cSPHs and cSPs form expanded gene families. Here, we provide an integrated view of mosquito cSPHs, their hierarchical organization and their critical role in controlling the proteolytic activation of cSPs. In fact, biochemical and genetic studies in our lab suggest that cSPHs are likely to interact with cSPs at different levels within the protease network that regulates melanization. Our data provide novel insights into the regulation of CLIP protease cascades in the mosquito hemolymph, which should help decipher the dynamic interactions between the cSP and cSPH components of these cascades.

Effects of Euscelidius variegatus Iflavirus 1 on fitness parameters and transmission ability of the phytoplasma vector E. variegatus

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Abstract: Virus-based biocontrol technologies have been discussed for decades as sustainable alternatives to synthetic pesticides in crop protection. New virus-based tools to control pests and plant diseases became a reality since the advent of NGS applied to viral metagenomic analyses of insect populations. In this perspective, we aimed at identifying potential biocontrol agents from the virosphere of phytoplasma vectors. Euscelidius variegatus Kirschbaum (Hemiptera Cicadellidae) is a polivoltine and polyphagous leafhopper and an efficient vector of phytoplasmas of agricultural importance (i.e. Flavescence dorée of grapevine). The transcriptomic analysis of an E. variegatus laboratory population reared in Italy (Torino, EvaTO) led to the identification of a new insect virus species ascribed to the Iflavirus genus. The +ssRNA virus was named E. variegatus virus 1 (EVV1). EVV1 infection appeared to be asymptomatic and had a 100% prevalence across EvaTO population. On the contrary, an E. variegatus laboratory population from France (Bordeaux, EvaBX) was found to be virus-free and used as a negative control. EvaBX individuals microinjected with EVV1 derived from EvaTO population (EvaVI) were able to vertically transmit the virus to offspring. In EvaTO rearing, the virus was present mainly in ovaries, but also in testes, hemolymph, Malpighian tubules and alimentary canal. It was also detected in the honeydew of infected individuals and on the surface of plants exposed to infected insects, but horizontal transmission appeared to occur only occasionally. We hypothesized that viral particles can penetrate the cuticle and replicate in the insect body only with a low efficiency. To evaluate the effects of EVV1 on newly infected insects, a rearing of EvaVI individuals was established. Longevity and fecundity of EvaVI insects were compared to those of EvaTO and EvaBX populations and related to viral loads. Preliminary results on EvaTO population showed that the virus was constantly detected both in phytoplasma-exposed and non-exposed vectors, but, interestingly, the virus load was significantly lower in FD-exposed insects. Phytoplasma acquisition and transmission efficiency of the three populations, reared under laboratory conditions, are under evaluation. New insights in EVV1-phytoplasma interaction might provide the unprecedented opportunity to promote the use of insect viruses as biocontrol agents against phytoplasma vectors. Moreover, the construction of infectious clones for virus-induced gene silencing (VIGS) could be used to manipulate the expression of the insect genes potentially involved in phytoplasma acquisition/transmission.

In vitro interactions between immunodominant membrane protein Imp of Flavescence dorée phytoplasma and protein extracts of its leafhopper vectors

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Abstract: Phytoplasmas are phloem-limited plant pathogenic bacteria that cause diseases in hundreds of plant species, producing severe economic losses to crops worldwide. Phytoplasmas are transmitted by Hemipteran insect species, belonging to the suborder Auchenorrhyncha (Fulgoromorpha and Cicadomorpha) and the family Psyllidae. Once acquired by an insect, phytoplasmas must cross its midgut membrane, spread in the hemolymph, colonize the salivary glands and enter the saliva in order to be transmitted to another plant. Since phytoplasmas are wall-less bacteria, membrane proteins are possibly involved with the internalization process in the host cell. In the present study, the involvement of immunodominant membrane protein (Imp) of Flavescence dorée phytoplasma (FDp) in the interaction with vector proteins was investigated. FDp is a grapevine quarantine pest and represents a major threat to the viticulture of several European regions. Scaphoideus titanus is the main natural vector of FDp to grapevine, whereas Euscelidius variegatus is commonly used as laboratory vector. In a previous work, we demonstrated that the external domain of FDp Imp selectively interacts with proteins from vector species rather than those from non-vectors. Nevertheless, the identity of the insect vector proteins interacting with FDp Imp is still unknown. Imp C-terminus domains of both FDp strains, covering the whole portion of the protein predicted to be exposed outside the bacterial cell, were synthetized together with His-tag, using an optimized E. coli expression system. Similar patterns of interacting insect proteins were obtained from both vector species, following pull-down procedure based on agarose beads conjugated with Nickel and saturated with His-tagged FDp Imp proteins. The insect proteins interacting with FDp Imp were trypsin-digested and analysed by mass spectrometry and the bioinformatic analyses are ongoing. Peptide identification was based upon the appropriate protein datasets, according to the NGS transcriptomes produced by our lab for both S. titanus and E. variegatus. Five E. variegatus proteins interacting with Imp were further characterized by measuring expression of their corresponding transcripts in different insect tissues and in healthy vs infected insects. The five genes were silenced to evaluate the effects on phytoplasma acquisition. The specific silencing of two of them, namely legumain and natterin-4-like, resulted in a significant reduction of phytoplasma multiplication in insects upon pathogen acquisition compared to control insects. As control of phytoplasma diseases is based on insecticides against vectors, this work is an initial step to elucidate key stages of FDp transmission specificity and vector infection mechanisms, which might be targeted to disrupt the epidemiological cycle, providing tools to integrate chemical treatments for more sustainable pest control.

Estimation of insect's flight parameters with entomological radar and radiosonde data

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Abstract: A variety of migratory insect pests arrive in Japan. To develop an overseas migration prediction model for pest management, we need to know flight parameters characterizing their migration process. To estimate the parameters, a x-band vertical looking radar (VLR) to monitor insects flying at altitudes in night was used. The study location was in an agricultural plain of 20×60 km surrounded by mountains in western Japan where rice and soybean are cultivated in summer. Daily radiosonde data observed at 2100 h local time over Fukuoka Meteorological Station 30 km northeast of the site were also used. Flight parameters were investigated for night events in September 2018 when many targets were recorded. Major targets in three nights were suggested to be mostly moths based on shape parameters of a2 and a4. Plots of target speed versus flight height indicated cluster of radar targets, and three patterns were found: (1) a lower speed side of the cluster perfectly followed radiosonde's wind speed profile line on 14 Sep, (2) the cluster was located 1-3 m/sec and more above the wind speed profile line on 25 Sep, and (3) the wind speed profile line ran through the cluster. To explain these patters, flight direction and orientation were examined. Targets' flight direction and orientation in the three cases corresponded to downwind direction at the cluster's height (NE, SW and SW on 14, 25, and 27 Sep, respectively: radiosonde data). However, variation of the orientation from the downwind direction was different: variation on 25 Sep, about ±25º, in case 2 was smaller than those on 14 and 27 Sep, ±35º in case 1 and 3, respectively. The results suggested that heading was toward downwind direction and that common orientation contributed to flight speed in case 2. Relationship between top height of the cluster in late September and the radiosonde's temperature profile suggested that temperature ceiling beyond which moths don't fly up is located around at a height of 14 ºC (case 2, 3). Since temperature at radar detection range 1461 m on 14 Sep was 18.2ºC in southwestern warmer winds, which is more than the threshold, many targets were observed up to the level and the temperature ceiling should be located over the radar range. Radiosonde data suggest a possible temperature ceiling is around 2200 m. Because the relationship between flight speed and wind speed as well as the temperature ceiling affect predicted migration paths, the approach to these important flight parameters with VLR and radiosonde nearby is important. The same estimation in different seasons and years is necessary for a further study.

Indoor resting behaviors of the dengue vector Aedes aegypti (L.) in northeastern Thailand

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Abstract: Aedes aegypti (L.) is a vector of several arboviruses, for example the dengue virus (DENV), which causes dengue fever and more severe forms such as hemorrhagic fever. As there is no cure, nor an effective vaccine for dengue, vector control is currently the only effective method of prevention. Vector control generally consists of elimination of breeding habitats and space spraying (fogging) for adult control. Both larval source reduction and fogging have proven ineffective to reduce dengue outbreaks. Targeted indoor residual spraying (TIRS) against adult mosquitoes has been proposed as an effective preventive measure. Effective TIRS depends on knowledge of adult mosquito resting behaviors. The objectives of this study were to determine Ae. aegypti indoor mosquito resting patterns in different rooms at different heights and to assess mosquito DENV infection status. The study was conducted in 120 houses in two rural sites in Mahasarakham province and 120 houses in two urban sites in Khon Kaen province during May to August 2019. A mechanical aspirator was used to collect resting mosquitoes on the walls at low (0-0.75 m), middle (0.75-1.5 m) and upper (>1.5 m) levels in the bedroom, bathroom, living room and kitchen in each house. Collections were done for 10 minutes at each level in the morning (08:00-12:00 hours) and in the afternoon (13:00-17:00 hours). Mosquitoes were pooled and DENV infection in pools was confirmed by real-time RT-PCR (qPCR). Although other mosquito species were collected, here only the results of Ae. aegypti are reported. A total of 1361 Ae. aegypti was collected and 751 (45%) females and 610 (55%) males were recorded. More than double the number of Ae. aegypti was collected in the rural sites (n=946, 70%) versus the urban sites (n=415; 30%). Ae. aegypti mosquitoes rested in bedrooms (n=550; 40%), bathrooms (n=447; 33%), living rooms (n=292; 22%), and in kitchens (n=72; 5%). Most mosquitoes rested at the middle height (n=1008; 74%) and at the lower height (n=310; 23%). Only 43 (3%) specimens were collected at the upper levels of the wall. There was no significant difference between number of mosquitoes collected in the morning compared to the afternoon (p>0.05). DENV was detect in one mosquito pool from a rural area in Mahasarakham province. Further statistical analyses are ongoing. Knowledge of indoor resting behavior of adult Ae. aegypti is important because it can be used to choose the most appropriate and effective vector control method, for example selectively targeting the adult resting population using TIRS. It is recommended that governmental vector control authorities assess TIRS as a strategy for dengue vector control and focus on walls at heights lower than 1.5 m in all rooms in both urban and rural areas.

Aedes mosquito infestation and their dengue virus infection in households in Northeastern Thailand

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Abstract: Aedes mosquitoes are vectors of several arboviruses that cause important human diseases, including dengue, zika, and chikungunya. There is no cure or effective vaccines against the diseases. Disease prevention is done by vector control. Entomological surveillance is a fundamental tool in monitoring and controlling vector borne diseases. Thailand, rapid Aedes larval surveys are the official method to estimate the house, container and breteau index. Pupal and adult surveys can provide more information and improve vector control, but they aren't officially implemented because they are challenging to carry out. The objective of this study was to determine mosquito infestation in households in northeastern Thailand, an area of endemic dengue, and to detect dengue virus (DENV) infection in adult collected Aedes mosquitoes.

The study was carried out in KhonKaen, Mahasarakham, RoiEt and Kalasin provinces in northeastern Thailand. Entomological collections were undertaken at consenting subject's household, and 4 neighboring houses, recruited from a prospective hospital-based case-control study. Mosquito larvae and pupae were collected from all positive containers. Adult mosquitoes were collected using a prokopack aspirator. Mosquitoes were identified to species. Here only species belonging to Aedes genus are reported. Adult mosquitoes were stored individually in in -80°C and processed for DENV detection and serotyping using RT-PCR. Adult mosquitoes were separated into head/thorax and abdomen. DENV detection were performed on pooled specimens using abdomen with a pool size of 1-10. Positive pools were confirmed by individual mosquito head/thorax.

A total of 1,493 households were included, of which 380 were subject's households and 1,113 were neighboring households. A total of 1,973 immature and 3,129 adult Aedes mosquitoes were collected. The majority, 97.4%, was Ae. aegypti and 2.6% was Ae. albopictus. The proportion of DENV adult positive pools were 38.7% (72/186). All four serotypes were detected from individual mosquito. The most frequent was DENV-3 with 38.0% (63/166), followed by positive with more than one serotype (26.5%; 44/166), DENV-2 (23.5%; 39/166), DENV-1 (7.8%; 13/166) and DENV-4 (4.2%; 7/166). KhonKaen had the highest percentage of DENV positive mosquitoes of the four provinces.

All four dengue virus serotypes are co-circulating in the study area at high levels indicating a high risk of dengue transmission. Understanding the distribution of the different dengue serotypes within a region is useful for planning control strategies. A combination of entomological surveillance and xenosurveillance of DENV presented transmission intensities in the mosquito-human cycle that could be a better indicator for dengue transmission and important for developing and improving effective vector control programs. Moreover, xenosurveillance will be a capable method to alert arbovirus and other pathogens circulating including new emerging diseases in future.

Seasonal variations in immunological and entomological indices to estimate dengue vector infestation, a longitudinal study in Northeastern Thailand.

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Abstract: The dramatic increase of arboviral disease incidence together with the global climate changes foresaw that human populations might be more and more confronted to vector-borne diseases.

Vector density is related to abiotic factors such as rainfall and temperature, and their seasonal changes may impact on the entomological indices and disease transmission surveillance. Due to their facility of implementation, house and container indices remains standard for dengue vector surveillance. However, immature-based indices may fail to assess vector density and dengue transmission risk in some contexts. Assessing dengue vector density by targeting adult mosquitoes can be difficult to implement and time-consuming. Immune response the Aedes Nterm-34kDa salivary peptide might represent a good marker of dengue vector exposure. The relation between the serological biomarker and the Aedes density and their seasonal variations need to be better described to help the vector-borne disease surveillance systems. Our study aims to assess the correlation between immunological and entomological indices. Then, data were analyzed together with the climatic factors to address the seasonal variation changes in Aedes density and to address the seasonal variations in immune response to a salivary biomarker of vector exposure.

Our study was carried out from September 2017 to September 2019 in Khon Kaen and Roi Et city. In each city, 18 clusters of ten houses were included. At each visit, blood sample were collected on filter paper from the same two individuals per house. Adult Aedes were collected using battery-driven mechanical aspirators during 15 minutes both indoors and outdoors, pupae and larvae were collected and containers were recorded at each visit. Three sentinel houses per cluster in each city were visited every month. In addition, all houses were visited every four months. Daily climatic data were collected at the subdistrict level for temperature, and humidity, except rainfall which was recorded at the city level.

At the submission time, only a portion of the total dataset was analyzed. The immune response to Aedes saliva was measured monthly on a total of 90 and 77 individuals from Khon Kaen and Roi Et cities respectively. Aedes collections were monthly perfomed in 80 houses in Khon Kaen city and 55 houses in Roi Et city. Every four months all of the 180 houses in each city were inspected for Aedes and a total of 251 and 248 participants were enrolled in Khon Kaen and Roi Et districts respectively. During the study period, 2217 and 1188 female Aedes were collected in Khon Kaen and Roi Et provinces respectively. Preliminary results suggest that entomological indices were higher during the rainy season in both provinces. We expect the immune response to the salivary biomarker to be correlated with entomological indices and their seasonal variations. The use of a serological marker to assess the Aedes exposure and might ease dengue vector surveillance.

Can insights into the metabolic costs of digestion in biocontrol insects help practitioners with post-release efficacy predictions?

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Abstract: Thermal physiology investigations that predict post-release establishment and control success have recently been gaining popularity in the field of weed biological control (biocontrol). These experiments generally involve classical methods that look at the agent's developmental or behavioural reactions to temperature. Most of the physiological processes within an insect's body, however, can be linked to the functionality of their metabolism or energetic costs of diverse processes. Consequently, metabolic physiological responses can help understanding of research organisms, but it is an area that has not yet been fully integrated into weed biocontrol programmes. This study aimed to determine the metabolic responses, costs of digestion (specific dynamic action [SDA]) and energy budgets in a widely-established biocontrol agent of water hyacinth in South Africa, Neochetina eichhorniae, over a range of temperatures. Respiratory rates were tracked over time throughout digestion of a host plant meal in order to determine how much energy was required to complete digestion, and how these costs change in different environmental conditions. Digestion can arguably be considered one of the most important aspects of a biocontrol agent's efficacy, as it determines feeding frequency and damage extent. Results have indicated that energy and digestion costs, including rates thereof, in N. eichhorniae differ greatly depending on the environmental temperature. We illustrate how these differences could have important knock-on effects on the efficacy of the agents in field sites with differing thermal regimes, potentially explaining the lack of establishment and adequate control in some. Furthermore, we advocate for the use of respirometry as a novel way to predict post-release efficacy.

A novel mode of action of the ectoparasiticide fluralaner on insect GABA receptors

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Abstract: Fluralaner is an isoxazoline ectoparasiticide used for tick and flea protection for dogs. In 2010, we reported for the first time that fluralaner (A1443) is a noncompetitive antagonist that inhibits agonist response in ?-aminobutyric acid receptors (GABARs) more potently than that in inhibitory glutamate receptors (GluClRs). Subsequently, we showed that the low sensitivity of GluClRs to fluralaner is attributable to a Leu conserved in transmembrane region (TM) 3. Recently, we sought to identify amino acid residues that contribute to the high sensitivity of insect GABARs to fluralaner. Housefly (Musca domestica) GABARs with amino acid substitutions in TM1–TM3 of the RDL subunit were expressed in Xenopus oocytes and examined for the effects of the substitutions on the sensitivity to fluralaner. The Q271L substitution in TM1 led to a significant reduction in the sensitivity to fluralaner. Whereas the I274A and I274F substitutions in TM1 did not change fluralaner sensitivity, the I274C substitution significantly enhanced the sensitivity to fluralaner. The L278C substitution at a position one a-helical turn below Ile274 resulted in a reduction in fluralaner sensitivity. Substitutions of Gly333 in TM3 caused substantial reductions in the sensitivity to fluralaner. Our data indicate that four amino acid residues (Gln271, Ile274, Leu278, and Gly333), which are in the outer half of the transmembrane subunit interface, are deeply involved in the antagonism of GABARs by fluralaner.

How to use species distrubution models for endangered species conservation? A case study of Boros schneideri

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Abstract: Boros schneideri is an endangered saproxylic beetle species in Europe, which is included in The Habitats Directive ANNEX II species list. In Latvia micro-reserves for species protection can be established.
B. schneideri has been found in Latvia for the first time in 2003 (Vilks 2003). Since then scientists from Lithuania, Latvia and Poland have described local factors affecting this species on micro-habitat level, such as light intensity, area and thickness of the remaining bark upon pine snags, presence of Ascomycota fungi mycelium on a trunk, trunk's circumference, tree species preference. Other important ecological factors are age of the forest stand, the presence of dead wood in different stages of decomposition, and the number of snags per forest stand and forest stand type.
This study aimed to identify landscape ecological factors affecting the occurrence of B. schneideri and to make the species' distribution models. To evaluate affecting landscape ecological factors, data of species' findings was obtained from Nature Conservation Agency of Latvia (DAP) and Latvia's State Forests (LVM) and data of forest stands – from State Forest Service (VMD). Together 353 findings were analyzed. Using ArcGIS program, we randomly selected ten times more absence points (3530) in forest covered areas. Around each point we made a square buffer with edge sizes 100x100m.
Species distribution model is affected by such factors as forest type, dominant tree species composition, forest age structure, fragmentation, distance from the forest edge and distance from the sea .
These models allow to determine the most important territories for needs of species conservation in Latvia. We believe these models allow to determine the most important territories in the whole range of distribution of B. schneideri with minor changes. Furthermore, it is possible to use these models for other endangered saproxylic beetle species such as Nothorhina punctata, Chalcophora mariana, Tragosoma depsarium, Ergates faber and others that live in pine forests.

Hard to catch: Experimental tests of escape mimicry in Adelpha butterflies

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Abstract: Preys that advertise predators about their difficulty of capture using conspicuous signals, and convergence of these warning signals among different hard-to-catch prey species, known as escape mimicry, seems to be more common in nature than supposed. Many authors have suggested that escape mimicry could evolved similarly to classical Batesian and Müllerian mimicry in chemically-defended species. As most research has focused on aposematism and mimicry related to chemical defenses prey, little is known about the mechanisms underlying escape mimicry evolution, such as predators' avoidance learning and generalization. We carried out the first experimental investigation of escape mimicry that uses bearing naturally occurring color patterns, those of the butterflies belonging to the neotropical genus Adelpha, which is potentially involved in escape mimicry. We tested bird capabilities to learn to avoid wing color patterns associated to an efficient escape mechanism. We subsequently tested whether birds generalized their avoidance learning to different, never experienced wing color patterns. Additionally, we compared avoidance learning and generalization of escaping preys to classical aposematism and müllerian mimicry (i.e. related to chemical defense). We evidenced that bird predators learned to avoid evasive preys and generalize this avoidance to their potential mimics. Finnally, we observed that avoidance learning on evasive prey was faster compared to that on distasteful preys, and generalization was asymmetric depending on the model that birds learned to avoid on the previous phase.
We conclude that an efficient escape mechanism is also a profitability feature that can be signaled to predators, and that appears more effective than the level of distastefulness tested in terms of predator's learning and generalization.

Value of Biological Control in Urban Eucalyptus Forests

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Abstract: Biological control programs in California have targeted members of invasive borer, defoliator, and sucking guilds of herbivores feeding on eucalypts. Herbivore species in each guild were subject to biological control. Estimates of the total number of eucalypt street trees in California ranged from a high of 476,527 trees to a low of 190,666 trees. The estimated mean value of an individual eucalypt was $5,978. Thus, the total value of eucalypt street trees protected by biological control in California ranged from $1,139,801,348 to $2,848,678.406 at a cost of $3,949,251.

Tri-trophic interactions among the eucalyptus weevil Gonipterus platensis (Coleoptera, Curculionidae), its egg parasitoid Anaphes nitens and Eucalyptus globulus

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Abstract: The eucalyptus weevil Gonipterus platensis (Coleoptera, Curculionidae) is a defoliator that has spread worldwide, causing economic damage to plantations of most Eucalyptus species. Biological control using the specific egg parasitoid Anaphes nitens (Hymenoptera, Mymaridae) often achieves satisfactory results, yet fails to control the weevil in colder regions. The work developed aimed at decoding the chemical ecology of this tri-trophic interaction. Different gas chromatography-mass spectrometry/ electroantennography/ olfactometry systems were used to detect, identify and test the biological activity of the organic volatile compounds (VOCs) emitted by Eucalyptus globulus, G. platensis and A. nitens. Results showed that Eucalyptus plants emitted 51volatiles that elicited antennal responses from G. platensis, 33 of which were identified with standards. In olfactometer tests it was established that three of these compounds, camphene, (+)-α-pinene and 2-phenylethanol attracted virgin females. Regarding the VOCs emitted by adult insects, three compounds were male specific, namely verbenene, cis-verbenol and trans-verbenol, while eight others were emitted by both sexes. Bioassays with A. nitens showed that parasitoid females were attracted to several compounds emitted by E. globulus, which were identified, as well as to G. platensis egg capsules and to female feces. The identification of several pheromone candidates of G. platensis was achieved and the host finding behaviour of A. nitens female wasps decoded. These breakthroughs allow for the design of new biotechnological monitoring and control strategies of the eucalyptus weevil, based on the use of VOCs, to manipulate the populations of the phytophagous insect and of its most efficient parasitoid. Acknowledgements: Thanks to Ulrike Eisenwiener, Dr. Bernhard Weissbecker, Dr. Gerrit Holighaus, Dr. Christine Rachow and Dr. Martin Gabriel, Department of Forest Zoology and Forest Protection, University of Göttingen, DE, for support with the electrophysiological and behavioural bioassays, and to Dr. Helena Santos and MSc. Mónica Almeida for assistance with the maintenance of a Gonipterus culture. Funding: Research supported by: RESOLUTION LAB at NOVA School of Science and Technology; CENSE (Center for Environmental and Sustainability Research) which is financed by Fundação para a Ciência e Tecnologia, I.P., PT (UID/AMB/04085/2019); Associate Laboratory for Green Chemistry, LAQV which is financed by national funds from Fundação para a Ciência e Tecnologia, I.P., PT (UID/QUI/50006/2019) and co-financed by the ERDF under the PT2020 Partnership Agreement (POCI-01-0145-FEDER-007265); and by PDR2020 project GO-fitoglobulus (PDR2020-1.0.1-FEADER-031159). Sofia Branco received a PhD scholarship from Fundação para a Ciência e Tecnologia, I.P., Portugal (FCT)—SFRH/ BD/84412/2012.

Use of data-driven models to predict to risk of invasion of pre-emergent pest species

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Abstract: A major pathway for the introduction of exotic invasive pests that impact the agriculture and natural resources of a region is through international trade of agricultural commodities and planting materials. Therefore, it is important to predict the likelihood that a pest may enter, establish and impact a new area. This knowledge allows to allocate the right amount of resources to identify and stop these pests before they reach or establish within our borders. In this session, we will discuss a framework of data-driven models to forecast the entry, establishment, and impact of pre-emergent pest species. Models used for this non-native pest forecast includes Self-Organizing Maps (SOM), a neural network algorithm using unsupervised competitive learning. We also examine the use of pest monitoring systems and the path forward in this new era of big data.

Hot, sour, and spicy: tolerance of bee parasites to high temperature, low pH, and pollen phytochemicals

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Abstract: Heat, acidity, and antimicrobial phytochemicals are three factors that can limit parasitic infection. The colony-level endothermy, acidic guts, and pollen-based diets of social bees provide unique opportunities to study how temperature, acidity, and dietary phytochemicals shape insect-parasite associations. We compared temperature, pH, and phytochemical tolerance between three trypanosomatid gut parasites from social bees and a related trypanosomatid from poikilothermic mosquitoes, which have alkaline guts and pollen-free diets.

Relative to mosquito parasites, bee parasites had higher heat tolerance that reflected body temperatures of hosts. Heat tolerance of the honey bee parasite Crithidia mellificae was exceptional for its genus, implicating honey bee endothermy as a plausible filter of parasite establishment. Whereas both honey bee parasites tolerated the acidic pH's found in bee intestines, mosquito parasites tolerated the alkaline conditions found in mosquito midguts. Bee parasites exhibited greater tolerance of chrysin—a flavonoid found in nectar, pollen, and plant resin-derived propolis. In contrast, mosquito parasites were more tolerant of cinnamic acid—a product of lignin decomposition present in woody debris-rich larval habitats.

Collectively, these results suggest that temperature, gut pH, and ingested phytochemicals could influence the distribution of trypanosomatids in insects and resistance to infection in pollinators.

Oral delivery of dsHvlwr is a feasible method for management of the pest Henosepilachna vigintioctopunctata (Coleoptera: Coccinellidae)

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Abstract: RNA interference (RNAi) techniques have emerged as powerful tools for the development of novel insect pest management strategies, such as for Henosepilachna vigintioctopunctata (Coleoptera: Coccinellidae) that is a major pest of Solanaceae crops in Asia. Our results showed the lesswright (lwr) gene of H. vigintioctopunctata (Hvlwr) had an ORF of 480 bp and encoded a 160-amino acid protein. Levels of Hvlwr expression were greater in fat body than in other tissue types. Silencing of Hvlwr led to greater H. vigintioctopunctata mortality rates and appeared to be time- and partially dose-dependent, likely as a result of the number of hemocytes that increased with dsRNA concentration, but decreased with time. Bacterially expressed dsHvlwr that was applied to detached plant leaves caused 88, 66, and 36% mortality in 1st instars, 3rd instars, and adults after 10, 10, and 14 days, respectively; when applied to living plants, bacterially expressed dsHvlwr led to greater mortality in 1st and 3rd instars, with no effect on adults. Bacterially expressed dsHvlwr led to improved plant protection against H. vigintioctopunctata, indicating the potential for use of Hvlwr as an RNAi target gene for the control of this pest species.

Mutations in the coat protein of a begomovirus result in altered transmission by different species of whitefly vectors: a way of virus evolution?

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Abstract: For many crop pathogens including viruses, high genetic variation provides them with potential to adapt to and prevail in a changing environment. Understanding genetic variation in viruses and their significance are a key to elaborating virus epidemiology and evolution. For the genetic variation of plant viruses, while its impact on virus-host interactions has been documented, how it affects virus-insect vector interactions remains elusive. Here we report the impact of mutations in the coat protein of squash leaf curl China virus (SLCCNV), a begomovirus, on the interaction between the virus and its whitefly vectors. We characterized mutations in the coat protein of SLCCNV and found several residues exhibited much higher mutation rates than the others. We assayed the impact of mutation on infectivity using agro-inoculation and found these mutations marginally affect virus infectivity. We further analyzed their functions using virus acquisition and transmission trials and found some of mutations resulted in altered transmission of SLCCNV by different species of the whitefly Bemisia tabaci complex. We then identified the key amino acid residue(s) involved and found that a single-residue mutation in the coat protein of SLCCNV was sufficient to significantly alter the whitefly transmission characteristics of SLCCNV. We examined the competition between different genotypes of SLCCNV in plant infection and whitefly transmission, and found that while mutations in the coat protein did not alter the fitness of SLCCNV in plants, they rendered the virus more competitive in transmission by certain species of whiteflies. Our findings indicate that mutations in the coat protein may play a key role in both the adaptation of begomoviruses to the changing vector populations and the evolution of begomoviruses.

Management of Colorado potato beetle in invasive frontier areas

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Abstract: Colorado potato beetle (CPB) is one of the most devastating invasive insects and it is native to North America. It feeds on several wild species of the genus Solamum, such as S. elaeagnifolium and S. rostratum Dunal, and is one of the major pests of potato and eggplant. Beginning in the early 19th century, CPB has rapidly spread across North America, Europe, and Central Asia. CPB was first reported to invade Xinjiang of China in 1993 and it was effectively controlled in Mori County. Since 2013, CPB has also been found in Jilin and Heilongjiang in Northeast China, and it likely migrated to these provinces from Russia. Thus, China has become the frontier for the global CPB spread, and risk management and monitoring systems for this pest are urgently needed. Here, we summarize pest management methods that are used in areas at the frontier of the CPB invasion, and put forward rameworks for further preventing and controlling of the spread of CPB. The management methods for CPB can also serve as an example for the control of invasive species mitigation in frontier areas.

Quality, quantity, or both? Agri-environmental measures and extensification mainly foster grassland pollinator species richness but less not overall insect biomass

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Abstract: A key target of agri-environmental schemes (AES) is increasing biodiversity. However, if and how insect biomass and diversity benefit from grassland AES is, not well known. Using Malaise trap samples from 72 grasslands, we investigated the effect of 1) on-site AES management (three levels: control, farm-wide, site-specific), 2) an index of land extensification (LEI), 3) plant species richness on insect biomass and species richness of all insects, Coleoptera, Diptera, Hymenoptera, Lepidoptera, Hemiptera and three pollinator groups (Syrphidae, Apiformes, Papilionoidea) derived by metabarcoding methods. Bayesian mixed models clearly indicated that site-specific AES and a high LEI positively influenced the species richness of pollinators. An increasing LEI additionally increased the number of all insects, Hemiptera and Hymenoptera species while especially Apiformes and Papilionoidea benefited from a high plant diversity. Moreover, we found an interaction of site-specific AES and the amount of AES in the surrounding landscape explaining differences in insect biomass and species richness of all insects, Coleoptera, Diptera, Hymenoptera and Lepidoptera. When the amount of AES in the surrounding landscape was low a high LEI was especially beneficial e.g., for Lepidoptera. We conclude that many grassland insects (especially pollinators) benefit from site-specific AES and extensive management.

From high-throughout hiccups to real biology for comparative insect genomics

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Abstract: The proliferation of new genome resources across the breadth of the insect phylogeny opens many new possibilities for comparative investigation of genome evolution and the genomic basis of key biological traits for insect development, physiology, and environmental interactions. Rapid improvements in long-read sequencing technologies and hybrid computational approaches are increasingly generating high quality genome assemblies, even from single individuals of small-bodied species. Yet, recent and new publications that go beyond resource documentation often still present biological findings from older, short-read-only technologies and fragmented assemblies. How can these datasets with different levels of quality, from different NGS eras, be reconciled and integrated? Second, it is all too easy to get lost in extended computational pipelines, with many steps at which data are filtered (excluded) and assumptions are made. How can we navigate our way through the pipelines to valid organismal insights? Here, I will discuss some notable lessons learned as an experimental geneticist who has thoroughly enjoyed a decade-long crash course on collaborating with computational biologists to get the most out of insect genomes. I owe particular thanks to the many excellent colleagues from the 1KITE, i5K, and Ag100Pest sequencing initiatives.

Analyzing evolutionary conservation of developmentally dynamic genes in the milkweed bug

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Abstract: Midway through embryogenesis, hemimetabolous insects undergo katatrepsis, a major tissue reorganization event wherein the extraembryonic tissues contract and reposition the embryo within the egg. Katatrepsis is energetically demanding and sensitive to perturbation, yet it is essential for the embryo to complete development. Gaining a greater understanding of the genetic basis of katatrepsis will clarify the nature of a defining embryological trait that has been recognized since the 19th century. Equally, understanding the genetic elements for katatrepsis that are broadly conserved or lineage-specific could contribute to the identification of new targets for molecular pest control strategies.

The milkweed bug Oncopeltus fasciatus is a representative of the species-rich Hemiptera and offers a highly tractable lab model for developmental genetics research, supported by a recent, high-quality genome project. Here, we will present our work to date on analyzing the molecular control of katatrepsis. In preparation for RNA-sequencing after RNA interference (RNA-seq and RNAi) experiments, we have generated high-quality, staged transcriptomes that span mid-embryogenesis stages, including katatrepsis. The use of multiple, sequential stages in our analysis – integrating staging by age and by morphology – is a powerful strategy to identify differentially expressed (DE) genes with changing expression (up- or downregulation) specifically during katatrepsis.

Furthermore, a key outcome of this dataset is the opportunity to analyze DE genes in terms of evolutionary age. Ongoing analyses thus involve assessing the taxonomic distribution of their orthologues through hierarchical, orthology clustering across the insects. The growing wealth of sequenced genomes within the Hemiptera also allows nuanced appraisal of whether lineage-specific genes are common to this order or restricted to the Heteroptera or Pentatomomorpha.

Ultimately, the goal is to determine (1) which genes have dynamic expression required for katatrepsis and (2) the extent to which these genes are evolutionarily old and broadly conserved or represent recent, lineage-specific innovations.

Advances on electropenetrography (EPG) studies with Neotropical pentatomids: waveforms and histology analyses

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Abstract: On the electropenetrography (EPG) technique, a sucking insect and its host plant make part of an electrical circuit where an electric current flow through the system. As the insect inserts its stylets into the electrified plant tissue the circuit closes; this makes the current flows through the insect-plant interface causing changes in the voltage of the system according to the stylet activity (e.g., stylet penetration, salivation, ingestion). The signals obtained are captured and recorded in graphical form (waveforms). By so doing, it is possible to determine the feeding site exploited by the bug (e.g., parenchyma tissue, vascular vessels, seed endosperm), the time spend by the bug on each feeding site, and the activities carried out such as salivation and ingestion. Correlations between each waveform with a specific feeding site are achieved mostly via histological studies. In the past 50 years, several species of sucking insects, mostly aphids and leafhoppers, had their feeding behavior determined using the EPG technique. However, the study of the feeding behavior of stink bugs (Pentatomidae) using the EPG is much more recent. Therefore, in this lecture we will discuss the advances on the use of the EPG technique to reveal the feeding process of Neotropical stink bugs, and the potential use of EPG as a tool to explore other research lines with these bugs.

Stink bug pests bioecology in the neotropics: host-plant interactions and implications for their management

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Abstract: Stink bugs (pentatomids) are polyphagous feeding on several species of plants, cultivated and non-cultivated. They feed by introducing the stylets (2 maxillae + 2 mandibles) into the plants to obtain nutrients and water. Feeding strategies include the salivary sheath, the cell rupture, and the osmotic pump feeding. Plants explored can be divided into hosts and associated plants. On host plants, bugs feed, nymphs complete development, and produced adults that continue breeding. On associated plants, however, bugs may feed, use them as shelter, lay eggs on, but nymphs do not complete development, and any resulting adults do not breed. Nymph and adult biology is variable on those plants, and the nymph to adult food-switch may have a variable impact to adult biology. Although polyphagous stink bugs show some degree of preferences for determined plant taxa, and less-preferred plants, often overseen, may show an important role in their bioecology. Considering any integrated pest management (IPM) programs, the multiple interactions of stink bugs with their host or associated plants should be taken into consideration. This is important because the information on host-plant interactions certainly helps to develop holistic tactics that will mitigate the deleterious effects of stink bugs on cultivated plants.

The underestimated role of pentatomid parasitoids in the neotropics

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Abstract: Stink bugs are pests of economic importance of extensive crops (commodities) in the Neotropics, particularly in Southern South America. They are abundant, have a broad geographical distribution, and cause severe damage. Main species include the Neotropical brown-stink bug, Euschistus heros (F.), the red-banded stink bug, Piezodorus guildinii (Westwood), the Southern green stink bug, Nezara viridula (L.), the green-belly stink bugs, Dichelops furcatus (F.), and D. melacanthus (Dallas), and the brown-winged stink bug, Edessa meditabunda (F.). The management of these pest species on crops is complex because they can cause economic damage in low numbers, and it is difficult to control by the commonly used insecticides. Therefore, biological control appears as the most important tactic to be implemented in stink bug management programs. Among the many natural enemies present on the various agroecosystems, egg parasitoids (Hymenoptera) and parasitoids of adult stink bugs (Diptera and Hymenoptera) are the most promising groups to be exploited as biological control agents of pest species. In the Neotropics about 30 species of egg parasitoids of stink bugs and more than 12 species of tachinid flies have been recorded. Efforts should be concentrated on conservation biological control. This biocontrol effort should be integrated with other tactics, such as the use of trap crops and semiochemicals. Landscape planning providing parasitoids with food, hibernation, and refuge sites favors their permanence, and cultivation spatially and temporally planned should be developed. Considering the biodiversity of the Neotropics, there is a tremendous potential to increase the use of biocontrol agents to mitigate pests.

Overwintering of Piezodorus guildinii (Heteroptera, Pentatomidae) populations at Southern latitudes of South America

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Abstract: Piezodorus guildinii (Westwood) is a soybean pest that causes significant economic losses in the Americas. The variability of overwintering (diapause) traits was evaluated in populations of the Southwest (SW) (33°55'-34°17' S, 57°13'-57°46' W) during 2 years-period (2011-2013) and of the Northwest (NW) (32º01'-33º02' S, 57º50' -57º24' W) during 1 year-period (2014-2015) regions of Uruguay. Samples were taken from different plant species (cultivated legumes, wild shrubs and trees), and from overwintering sites (leaf litter and bark). Alfalfa, Medicago sativa L. was the main host, with a collection period of 10-11 months in the SW and 12 months in the NW. Cluster analysis for each sex was carried out to group the months according to the similarity in diapause traits of populations (body size, body lipid content, immature reproductive organs, and clear type of pronotum band and connexivum in females). Female diapause in the SW was longer (beginning of autumn to end of winter) than in the NW (mid-autumn to mid- winter). Male diapause was longer (mid-autumn to mid-winter) in SW1 (1st year) than in SW2 (2nd year) and NW (late-autumn to mid-winter). Male diapause was shorter than female diapause in both regions. Differences were associated with maximum temperature at daylight hours = 12.1, being necessary maximum temperatures below 23.8 °C for females and 19.2 °C for males to initiate diapause. Earlier resumption of seasonal development in spring and later termination of activity in autumn may generate greater number of P. guildinii generations per year in the NW than in SW regions.

Natural genetic variation for life history traits: opportunities and constraints for insect breeding

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Abstract: The Arthropod phylum contains many species that can be used in human society, such as for biocontrol of agricultural pests and for exploiting organic waste streams in circular agriculture and economies. Many of these applications involve mass rearing of insects and it is fair to say that thus far not much attention has been given to both exploiting and maintaining genetic variation for traits that matter for the performance of the focal species. Moreover, the "desired traits" are often life-history traits that have co-evolved and have been shaped in the natural habitat. In this talk I will argue that taking lessons from life-history theory and quantitative genetics has the potential to strongly benefit the rapidly growing field of insect farming. Incorporating such evolutionary genetic knowledge will result in better designed breeding programmes and, importantly, realistic expectations on their outcomes.

Next-generation biological control: the need for integrating genetics

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Abstract: Secure and sustainable food production in terms of quantity and quality is a major challenge facing human societies. However, food security is continuously threatened by current and invasive pest species. In addition, regulations for the use of pesticides are getting stricter to ensure food safety and protect ecosystem health. Biocontrol of agricultural pests by using natural enemies has great potential to deal with these two demands. Biocontrol of novel exotic pests, however, often involves importing non-native natural enemies. Such practices are being restricted due to the Nagoya Access and Benefit Sharing regulations. The dependence on imported natural enemies can be reduced by optimizing existing and native biocontrol agents. A powerful way of optimizing biocontrol agents is the use of genetic knowledge. This not only entails classical selective breeding, but ranges from applying basic population genetic principles, to monitoring genetic variation during rearing and post-release, determining the genetic basis of traits, to advanced methods such as genomic selection. In this talk, I will outline the use of genetic tools and knowledge to improve the efficiency of biocontrol and present several cases of the wide range of application of genetics to improve biocontrol efficacy.

Overwintered Drosophila suzukii are the main source for infestations of the first fruit crops of the season

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Abstract: The mechanisms allowing the widespread invasive pest Drosophila suzukii to survive from early spring until the availability of the first fruit crops are still unclear. Seasonal biology and population dynamics of D. suzukii were investigated in order to better understand the contribution of the early spring hosts to the infestation of the first fruit crops of the season. We identified hosts available to D. suzukii in early spring and assessed their suitability for the pest oviposition and reproductive success under field and laboratory conditions. The natural infestation rate of one of these hosts, Aucuba japonica, was assessed over springtime and the morphology of the flies that emerged from infested A. japonica fruits was characterized under field conditions. Then, these findings were correlated with long-term monitoring data on seasonal reproductive biology and morphology of the pest, using a cumulative degree-days (DD) analysis. Field sampling revealed that overwintered D. suzukii females were physiologically able to lay eggs at 87 DD which coincided with the detection of the first infested early spring hosts. The latter were continuously and increasingly infested by D. suzukii eggs in nature from early spring until the end of May, in particular Aucuba japonica. Individuals emerged from most of these hosts were characterized by a poor fitness and a rather low success of emergence. In the field, only few summer morphs emerged from naturally infested A. japonica fruits around the end of May-beginning of June. However, field monitoring in orchards revealed that D. suzukii individuals consisted solely of winter morphs until mid-June. These observations indicate that overwintered D. suzukii females are the predominant source for the infestations in the first available fruit crops of the season. We discuss these findings in the context of possible pest control strategies.

Horizontal transmission of Metarhizium sp. conidia in Popillia japonica adults.

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Abstract: Microbiological control of pest populations has greatly developed due to the increasingly high restrictions applied to the use of chemical insecticides.

As regards fungal Biological Control Agents (BCAs), the transmission of infecting conidia from one individual to another is very important since it causes the spreading of infections within the pest population and the induction of epizootics (Lacey et al., 1994b; Hesket et al., 2010).

Two different Metarhizium-based commercial products available in Italy were used as source of inoculum in our experiments and horizontal transmission during mating between infected and uninfected Popillia japonica (Pj) adults was studied according to the following scheme: infected male x uninfected female (MixF), uninfected male x infected female (MxFi), infected male x infected female (MixFi), and uninfected male x uninfected female (MxF) as a control (Quesada-Moraga et al., 2008).

Horizontal transmission potential was also assessed in one-against-twenty experiments. Ten infected male and ten infected female Pj adults were individually brought in contact with twenty (ten males and ten females) uninfected Pj adults each.

Experiments showed 100% mortality by 19 days after treatment with the first product, while mortality associated with the second one was 30-65%.

The ability to transport and spread conidia in both male and female Pj adults was also analyzed and no difference between sexes was observed.

In one-against-twenty experiments final mortality achieved by a single infected male and a single infected female was 67% and 72% respectively.

Our tests confirmed that the inoculum can be transmitted from one infected adult to a healthy one during copulation, thus supporting the idea of an auto-dissemination of the fungus within the pest population that can induce epizootics.

Phylogeography of the invasive scarab beetle Popillia japonica

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Abstract: Popillia japonica Newman (Coleoptera: Scarabaeidae) is a scarab beetle native to Japan that in the last century invaded North America, the Azores and, more recently, Italy and Switzerland. It is a notorious agricultural pest that has been added to the 2019 EU priority pest list. Economic damage is due to larvae feeding on plant roots, and adults feeding on leaves, flowers and fruits. In order to limit the further spread of this pest urges to reconstruct its worldwide range expansion. The aim of the present contribution was to analyze the P. japonica population structure and phylogeography, with a special focus on its spatial movements.

The present work is based on sequence data from two different mitochondrial loci and nine microsatellite loci from P. japonica samples covering its global distribution.

Basing on mitochondrial data, the North American population of P. japonica appears to include two different maternal lineages, one grossly localized in the Great Lakes region and the other displaying a larger distribution for the rest of North America. The two lineages display very limited genetic variability, possibly due to a strong founder effect. Out of the 13 haplotypes found in North America, only 3 were identified in Japan, two of which being the most frequent overall in North America and having spread and differentiated to produce a series of ancillary haplotypes. It is therefore possible to hypothesize that these haplotypes characterized the original introduction, with others satellite being generated by casual mutation during the colonization process. These two most frequent North American haplotypes were identified only in a limited geographical region of Japan, in the center of Honshu island between the Ibaraki, Tochigi, and Gunma Prefectures. As such, this geographical region can be considered as the most likely origin of the invasive specimens associated with the first North American outbreak of P. japonica.

The Italian outbreak is characterized by the same haplotypes of the Azorean population, nevertheless their haplotypic frequencies are totally different. On the contrary, Italian and Swiss individuals share one and the same mitochondrial haplotype, suggesting a common origin from the Italian outbreak.

Microsatellite data suggest an old differentiation between Southern and Central Japan, with this latter region contributing to the invasion in the US. Popillia japonica in North America is subdivided in two different populations: the first one is mainly localized on the north-east coast and the second in the south-east coast of the continent. The more recent invasions in Italy and the Azores appear to be related to the US but displaying a marked genetically differentiation; Italian outbreak seems to be closer to north-eastern population while Azorean beetles were closer to south-eastern one.

Agroferstation and beekeeping: the LIFE VAIA project

Authors: Paolo Fontana[1] and Valeria Malagnini[1], [1]Edmund Mach Foundation

Abstract: Storms, floods, fires: the occurrence of extreme climatic events, with the dramatic repercussions they have on our territories, is the testimony of climate change in recent decades. The VAIA storm that hit North East Italy in 2018 caused extensive damage to mountain areas and their delicate ecosystems. Extreme weather events quickly create open spaces where there were forests. Agroforestry is a solution that can provide for the exploitation of the new habitat, both by introducing temporary crops and through the implementation of beekeeping. In fact, in these environments we can observe the rapid and abundant appearance of a nectarous and polleniferous flora.

A little known insect order: general information, collection, breeding and study of Italian and Mediterranean Embioptera

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Abstract: The Embioptera or web spinners, are perhaps the least studied and therefore least known insect order in Italy. In order to stimulate and facilitate new studies on these unique insects, general information on their biology, collection, breeding and study techniques and current knowledge on their presence in Italy and Europe are presented. A key to identify genera and an extensive bibliography are also provided.

A mobile phone application to survey and monitor the wild colonies of Apis mellifera

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Abstract: Although Apis mellifera have been reared by humans for millennia, it remains a wild animal) as reported by ancient authors and modern beekeepers and researchers. Until a few decades ago, wild colonies of A. mellifera were largely common. However, since the early 1980s there has been a rapid and underestimated rarefaction of the “wild” colonies due to a parasite, the fearsome Varroa destructor mite. The effect of the Varroa mite on unmanaged colonies was so strong that today in Europe most of the survived honey bees live in hives managed by beekeepers. Indeed, for many years it has even been thought that in Europe wild honey bees were disappeared. Rather surprisingly, there are no scientific studies on this phenomenon and the only available information deals with the number and distribution of honey bees colonies owned by beekeepers. In recent years, reports and interest in wild honey bee colonies have increased significantly and today we can say that even in many areas of Europe these colonies are still there. The app BeeWild intends to survey and monitor these wild colonies through a typical citizen science action.

Fruit fly invasion a global phenomenon with huge agricultural and trading implications

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Abstract: Fruit flies (Diptera: Tephritidae) comprise a major group of pests including several invasive species, such as the Mediterranean fruit fly, the oriental fruit fly and the peach fruit fly that threaten sustainable fruit and vegetable production worldwide. Because of the extremely high economic relevance invasion events have documented since the beginning of the last century. Intense government-mandated eradication campaigns are implemented after the documentation of an invasion event of a fruit fly of economic importance that almost always declared as successful. New invasion events following an eradication campaign often trigger debates regarding the success of the operation. The risks of arrival, establishment and range expansion of invasive fruit flies are expected to escalate because of global climate change, increased trade and human mobility. Establishment of an invasive fruit fly in a new area, besides having a huge direct impact on fruit and/or vegetable production, increases insecticide use and dramatically affects trading of fresh commodities and impose quarantine regulations. Incursion of invasive fruit flies in Australia, north America and Europe is estimated to result in losses of billions of Euros because of direct and indirect damage. And a single eradication campaign costs several million Euros. The current paper covers several aspects of the fruit fly invasion biology, including (a) historical perspectives, (b) the enormous impact on local, national and regional economies, (c) interception and detection efforts, (d) management of invasion event including eradication campaigns, and (d) predictive ecological and climatic modelling. The need for revisiting existing policies is also highlighted.

DNA barcoding and phylogeny of Afrotropical Rhiniidae (Diptera: Calyptratae) and placement of the enigmatic Prosthetosomatinae

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Abstract: The family Rhiniidae, represented by almost 400 species, is distributed in the Australasian, Palearctic, Oriental and Afrotropical region, with around 150 of the species occurring in the Afrotropical region. The biology of the Rhiniidae is poorly known and the phylogeny is not well understood. Adult flies are often seen visiting flowers and potentially play an important role as pollinators. In the Afrotropics at least six Rhiniidae genera are associated with termites, and some larvae apparently develop in termite nests as parasitoids, predators or scavengers, but in general the knowledge about this association is scarce. Identification of Rhiniidae species is challenging and relies heavily on male terminalia, which makes identifications of females difficult. Immature stages are largely unknown, with larvae only described for five species. Accurate identification of Rhiniidae species is important when exploring their biology and phylogeny, but also to aid in conservation and pollination studies. By building a reference library of DNA barcodes from voucher specimens, this study aims at linking conspecific males and females, and exploring the phylogenetic relationships within the Rhiniidae. COI barcodes were obtained for more than 60 species covering 14 of 16 genera recorded from the Afrotropical Region. Species limits and phylogeny was explored by reconstructing neighbor-joining, maximum likelihood and Bayesian inference phylogenetic trees and calculating genetic distances. COI barcodes enabled us to link females with their conspecific male morphotype and, combined with a sample of larvae from South Africa, to place the enigmatic Prosthetosomatinae in the family Rhiniidae.

Molecular armament: a first attempt at solving Polleniidae and Rhinophoridae phylogeny using molecular data

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Abstract: Recent attempts at resolving oestroid phylogeny employing limited taxon sampling have converged in retrieving monophyly for most families and subfamilies, and the deeper relationships among these are now stabilising. In this context, we reconstructed phylogenetic relationships within the parasitoid fly families Polleniidae (cluster flies) and Rhinophoridae (woodlouse flies) using two nuclear protein-coding loci (CAD and MCS, 3872 bp) with a broad and representative selection of the two target clades comprising 11 species of cluster flies and 62 species of woodlouse flies, as well as a selection of taxa representing the main oestroid lineages (Tachinidae, Sarcophagidae, Oestridae, Calliphoridae, etc.). We analyzed the dataset using Maximum Likelihood and Bayesian Inference.

As expected, analysis with these loci provide good resolution and strong support for distal nodes, though several basal nodes are weakly supported, as highlighted in previous literature. Polleniidae and Rhinophoridae are retrieved as monophyletic groups with strong support.

Cluster flies are divided in two lineages: a Pollenia clade and a Morinia + Melanodexia clade, with Morinia reconstructed as paraphyletic. Despite including only five species of Pollenia, monophyly of this genus is well supported and the only included Australian taxon takes up a position as sister to the remaining Pollenia species. The two included species of Morinia (i.e., an undescribed species from South Africa and the type species M. doronici) form a grade from which the North American endemic Melanodexia arose. The sister group relationship of Polleniidae and Tachinidae is confirmed with high support.

Our analyses confirm the division of woodlouse flies into two groups, which is supported by larval morphology: the Stevenia-group and the Phyto-group. The sister group to Rhinophoridae remains unclear, with two different hypotheses based on the analytical method used. All genera within Rhinophoridae emerge as monophyletic except for Rhinomorinia. Species assigned to Rhinomorinia are split into two clades corresponding to biogeographical distributions: the Palaearctic R. sarcophagina clusters as sister to Oplisa, whereas the Afrotropical species form a monophyletic group sister to all the remaining taxa of the Stevenia-group. This result leads to the resurrection of the genus group name Oxytachina for the Afrotropical clade.

The present phylogenetic reconstruction is the first molecular-based phylogenetic backbone for Polleniidae and Rhinophoridae at a world scale.

Redefinition of blowflies from a phylogenomic perspective

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Abstract: Blowflies (Diptera: Calyptratae, Calliphoridae) have been recognized since earliest times by humans as metallic-coloured, carrion-breeding flies. However, they exhibit a rich diversity morphologically and biologically, and the monophyly and general classification of this group have been debated for decades, making them the main challenge in tracing the phylogeny and evolutionary history of oestroid calyptrates. Following a modified 1KITE pipeline with a dipteran ortholog reference library of 3,755 genes, we conducted the most comprehensive analysis using transcriptomic data covering 11 out of 13 (formerly) recognized calliphorid subfamilies. The raising to family rank of Mesembrinellidae and Polleniidae was confirmed in our study. The remaining calliphorids sensu lato (including Rhinophoridae) emerge as monophyletic, while the carrion-breeding blowflies originated twice independently (Chrysomyinae and Calliphorinae + Luciliinae). Accordingly, a re-classification of calliphorids sensu lato is proposed based on the robust backbone phylogeny recovered in this study. The evolutionary history of oestroid breeding habits is also traced to understand the origin of these flies.

Females adjust maternal hormone concentration in eggs according to male condition in a burying beetle

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Abstract: In vertebrates and more specifically birds, there is good evidence that females adjust their allocation of hormones in response to prenatal environmental conditions, such as food availability or male phenotype, with profound consequences on life history traits. In insects, there is evidence that females deposit juvenile hormones (JH) and ecdysteroids (ESH) in their eggs, hormones that play a key role in regulating offspring growth and metamorphosis. However, it is unclear whether females adjust their hormonal deposition in eggs in response to prenatal environmental conditions. Here we address this gap by conducting an experiment on the burying beetle Nicrophorus vespilloides, in which we manipulated the presence of the male parent and the size of the carcass used for breeding at the time of laying. We also tested for effects of the condition (i.e., body mass) of the parents. We then recorded subsequent effects on JH and ESH concentrations in the eggs. We found no evidence for an effect of these prenatal environmental conditions (male presence and carcass size) on hormonal concentration in the eggs. However, we found that females reduced their deposition of JH when mated with heavier males. This finding is consistent with negative differential allocation of maternal hormones in response to variation in the mass of the male parent. We encourage further work to investigate the role of maternally derived hormones in insect eggs.

Cotton Insect Management in the Semi-Arid Region: Pest Management and Production Profitability.

Authors: Parajulee Megha, Texas A&M University, United States

Abstract: Cotton is a major agricultural crop in the Texas High Plains (THP), producing over 6.4 million metric ton of cotton per year. This represents an average of 30% of U.S. cotton and approximately 4% of world cotton. THP is a semi-arid region in south-central United States with characteristic low rainfall, with production agriculture supported by limited irrigation or solely rain-fed. As a result, the cropping system in this region is largely low-input and the producer decision-making in economically profitable input use is a challenge. Low cotton market price, increased nitrogen fertilizer price, and reduced water availability have forced farmers to move toward reorganizing available input resources to sustain their production enterprise, particularly arthropod pest management. The western flower thrips, Frankliniella occidentalis, is the most dominant thrips species affecting seedling cotton in THP, which is the most economic pest of cotton in this region. Cotton fleahoppers, Pseudatomoscelis seriatus, and western tarnished plant bugs, Lygus hesperus, are two important plant bug pests of cotton that feed on reproductive structures of cotton. Cotton fleahoppers are early season pests while Lygus bugs are mid- to late season pests in THP. Cotton squares up to pinhead size are most susceptible to fleahopper damage, and yield loss is most likely from feeding during the first three weeks of fruiting, whereas Lygus bugs mostly feed on developing bolls. A comprehensive field study was conducted to characterize the host-plant sequence and movement of these insect pests from non-cotton habitats to cotton. While grassy weeds and terminating wheat are responsible for thrips colonization in seedling cotton, cotton fleahopper and Lygus utilize several weed hosts during non-cotton season and move to cotton when non-cotton habitats are no longer a suitable host. Extensive field studies have established management thresholds for all three insect pests, whereas their impact on cotton production risks have been evaluated with various combinations of single versus multiple-species infestations under three deficit-water (near-zero, intermediate, and high) production scenarios. These studies are crucial because a significant component of IPM lies in adoption of new tactics by growers to improve profitability and production sustainability. However, producer decisions are complicated by uncertainty of production risks posed by the interaction of biotic (pests) and abiotic (water) factors. Because these three insect pests of cotton occur sequentially in Texas High Plains cotton, we experimentally discerned the population dynamics and damage potential of each insect species infesting the crop in isolation or in combination (sequentially), all under different water-deficit production scenarios. This allowed us to develop specific crop production models under various production settings which would help producers to optimize input resources for profitable cotton production.

Neem oil (Azadirachta indica) fabricated silver nano-particles as an eco-friendly tool for the control of Helicoverpa armigera – A case study

Authors: Parajulee Megha[2], Murugan K.[1], [1]Bharathiar University, India, [2]Texas A&M University, United States

Abstract: Helicoverpa armigera is a polypghagous insect pest that infests many crop plants. Indian neem (Azadirachta indica) tree is a versatile plant which possesses enormous insect control properties. Nanoencapsulations and nanoemulsions are the potential nanotechnology tools that can be used in managing biological systems, including insect pest control. In this study, neem oil nanoencapsulate silver nanoparticles (AgNPs) and neem nanoemulsions were tested against larval and pupal populations of the cotton bollworm, Helicoverpa armigera, and lethal concentrations (LC50 and LC90) were established. The silver encapsulated insecticidal nanomaterials performed as reducing and stabilizing agents. Results obtained from UV, XRD, FTIR, DLS, ZETA, SEM, TEM and EDX analyses showed quantitative and morphological characters of the synthesized nanoencapsulated silver nanoparticles. Neem essential oil, nanoemulsions and encapsulated silver nanoparticles showed significant larvicidal and pupicidal toxicity against the Helicoverpa armigera. Sub-lethal doses of nanoencapsulated silver nanoparticles and neem oil nanoemulsion treatment significantly affected the longevity and fecundity and also reduced egg hatchability. Treated insects displayed reduced food consumption as well as lower growth and nutritional indices such as efficiency of ingested and digested food materials (ECI and ECD) and concomitant reduction in the digestive enzyme activity (a-amylase, lipase and proteases, serine, cystein and aspartic proteinases). In addition, the insects egested lesser number of faecal pellets and time taken to pass out first faecal pellets were also diminished in the experimental insects. The results revealed that encapsulated AgNPs of nanoemulsified droplet concentrations (ppm level) might have affected the digestive physiology of insects. Overall, encapsulated AgNPs and nano-emulsions from plant essential oil have shown demonstrated potential for the development of safer alternative insecticidal formulations for the control of H. armigera.

Will an exotic, competitive egg parasitoid displace a native larval parasitoid?

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Abstract: Fopius arisanus Soman (Hymenoptera: Braconidae) is a generalist tephritid egg parasitoid from the Indo-Pacific region introduced to Brazil in 2012 to control the exotic fruit fly pest Bactrocera carambolae Drew & Hancock (Diptera: Tephritidae) in the northern region. Doryctobracon areolatus Szépligeti (Hymenoptera: Braconidae) is a native generalist parasitoid of second instar larval fruit flies from Central and South America. Because both species of fruit fly parasitoids share some genera of fruit fly hosts, we evaluated if the commercial release of F. arisanus could cause adverse effects (e.g., competitive displacement) on the native parasitoid. Host preference and competitive ability were compared using as hosts the native Anastrepha fraterculus Wiedemann (Diptera: Tephritidae) and the exotic Ceratitis capitata Wiedemann (Diptera: Tephritidae) fruit fly species. To evaluate host preference, choice and no-choice experiments were conducted with lines of F. arisanus reared from each of the hosts. Laboratory studies showed that F. arisanus accepted only 2-3% of the native hosts compared to 34-41% of the exotic hosts under no choice conditions, with similar results when given a choice of native and exotic hosts. The field cage choice study showed similar results when F. arisanus was reared on the exotic host, but when reared on the native host, F. arisanus parasitized more of the native host than when reared on the exotic host. However, both lines of the parasitoid preferred the exotic host. To evaluate competitive ability, experiments with both species together and separate were conducted in the laboratory and in field cages. Both experiments showed that F. arisanus had no measurable detrimental effect on the native parasitoid in either the native or exotic host. Indeed, the native parasitoid was consistently the superior competitor in native host even though it parasitized larvae while F. arisanus is an egg parasitoid. These results indicated that F. arisanus interacted minimally with the native parasitoid on the native host, and while it interacted with the native parasitoid on the exotic host, it did not detrimentally affect it. Thus, F. arisanus is unlikely to cause adverse effects on the native parasitoid, D. areolatus in Brazil.

Sacbrood virus suppression in Apis cerana by virus-derived dsRNA produced from Bacillus thuringiensis toxic to Galleria mellonella

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Abstract: Honeybees play an important role in the global economy by assisting in the pollination of food crops and by producing honey, and other hive products. The health of honey bees is inevitably threatened by a range of pathogens including bacteria, fungi, microsporidian parasites, and viruses. The Asian honey bee, Apis cerana is a native honey bee species in Korea, and has been noted for its strong resistance to Varroa destructor, however, it shows weakness to Sacbrood virus and Galleria mellonella. Recently, RNA interference (RNAi) has been suggested as a promising strategy for suppression of honey bee viruses. Also, Bacillus thuringiensis (Bt) has been widely applied for the control of lepidopteran pests such as G. mellonella, the greater wax moth. In this study, it was intended to develop dsRNA production platform using Bt. For this, the pBTdsVP1 vector which transcribes sense and anti-sense SBV vp1 gene under the control of Cyt1Aa sporulation-dependent promoter with STAB-SD sequence was constructed. This vector was introduced into Bt strain NT0423 expressing Cry1-types toxins. SBV replication was suppressed in the worker A. cerana ingested dsRNA produced from the Bt transformant. Crystal proteins from the Bt transformant showed high level of insecticidal activity against 4th instar larvae of G. mellonella. These results demonstrated that Bt-based dsRNA producing system could be exploited for the control of both SBV and G. mellonella simultaneously.

Transcriptome analysis of fat body from Japanese pine sawyer beetle, Monochamus alternatus, infected with the entomopathogenic fungus Beauveria bassiana ERL836

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Abstract: In forest, Japanese pine sawyer beetle, Monochamus alternatus, is a vector of pine wilt nematode causing pine wilt disease (PWD). Management of M. alternatus has been relied on chemical insecticides that cause environmental pollution and insect resistance. In this study, entomopathogenic fungi, the biological control agents were used to control M. alternatus, and the response of fat body from M. alternatus to the fungus was investigated. The virulence test was conducted using a spraying method with a conidial suspension at 1×10^7 conidia/ml. As a result, the mortality of M. alternatus was higher than 70% in seven isolates, including Beauveria bassiana ERL836. ERL836 showed the highest level of mycosis on insect body and the highest conidial thermostability. We investigated the response of fat body from ERL836-infected M. alternatus using RNA-seq. RNA samples were obtained from fat body of M. alternatus in 2 and 4 days after ERL836 treatment. On day 2 and 4, genes involved in muscle contraction were upregulated, however, genes involved in defense response were downregulated. Additionally, genes involved in ion-channel activity were downregulated on day 4. In conclusion, according to transcriptome analysis, it seems that genes related to defense and ion-channel activity are downregulated by ERL836 infection.

Dosage compensation in sexual and asexual stick insects

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Abstract: In species with differentiated sex chromosomes, genes on the X (or Z) will be present in different copy numbers in males and females. This creates a problem since for many genes expression is proportional to their copy number. To alleviate this problem, organisms have evolved several methods of dosage compensation to equalise expression between the sexes. Most model species show ‘complete dosage compensation’ whereby all genes on the sex chromosomes are up- or down- regulated dependent on which sex they are present in. However, recent studies using non-model species have shown that the extent of dosage compensation is in fact very variable.

The explanatory factors that influence the amount of dosage compensation are largely unknown. One proposed factor is the amount of differentiation between the sex chromosomes, with greater dosage compensation evolving as genes on the sex chromosomes diverge. X0 systems represent an extreme point in this continuum, since all genes on the X chromosome will be single copy in males; however the extent of dosage compensation in X0 systems has been largely unexplored. Here we examine dosage compensation across five X0 species of stick insect in the genus Timema. Using this approach we are able to i) quantify the extent of dosage compensation in each species, and ii) identify possible turnover and migration of dosage compensated genes from the X to autosomes.

Complementary to this approach, we also investigate the fate of dosage compensation in three asexual Timema species. In asexual species selection for dosage compensation has stopped, and thus we predict that asexual species will have evolved a reduced capacity for dosage compensation. Here we quantify this reduction and determine if this reduction is equal across the X chromosome or more pronounced among certain classes of genes.

Social cognition and behavioral integration in a model ant-myrmecophile partnership

Authors: Parker Joseph[1], Wagner Julian[2] and Naragon Thomas[2], [1]California Institute of Technology, Parker Lab, United States, [2]California Institute of Technology, United States

Abstract: Myrmecophilous lifestyles are often highly host-specific, and rely on chemical and tactile cues exchanged between host and symbiont that promote their behavioral interaction. The identities of these cues are for the most part unknown, and how they act as releasers for interspecies social behaviors is poorly understood. In this talk, I describe a model host-myrmecophile relationship that can be reconstituted in the laboratory and studied in high throughput. This system has enabled us to use machine learning to quantify behavioral interactions between the myrmecophile and other objects or organisms that partially or fully recapitulate the host ant phenotype. By gaining experimental control over myrmecophile behavior, we have been able to address the nature and function of ant body-derived cues that are perceived by the myrmecophile and underlie host recognition. We demonstrate a minimal set of cues that are necessary and sufficient to release stereotyped social behaviors that enable the myrmecophile to achieve integration inside the colony. Although in nature the myrmecophile is stringently associated with a single ant species, the ant body cues that trigger its symbiotic behaviors are not host-ant specific. We show how the myrmecophile shows no preference for its host ant in a choice assay, its fidelity towards its host being readily broken in the laboratory. The extreme host specificity of many myrmecophilous relationships may be enforced by colony cues other than those directly associated with the ant body, loosening constraints on social cognition and enabling the myrmecophile to perceive a broad range of ants as potential hosts. This behavioral strategy may be adaptive in allowing the myrmecophile to integrate into colonies in the face of variation in chemical and tactile cues associated with the ant body.

Cell type evolution of a rove beetle chemical defence system revealed by single-cell biology

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Abstract: Multicellular exocrine glands, where cells work collectively to synthesize bioactive secretions, provide a paradigm to study the evolution of novel cell types and biosynthetic pathways. We exploit a new unique model system – the defensive gland of the rove beetle Dalotia coriaria. This rove beetle has a large defensive gland at the dorsal abdomen tip consisting at least two cell types, which produce a cocktail of three different benzoquinones (D1 cells), or the hydrocarbon solvent undecane and two esters (D2 cells). To shed light on how these cell types evolved and whether they arose from pre-existing cell types, we perform bulk and single-cell comparative transcriptomic analyses (10x droplet-based sequencing and SMARTseq) of the beetles' gland segment and compare it to other non-gland bearing segments. In total, over 3000 genes are differentially expressed in the gland cells and can be assigned to different cell types. We use these data and harness the power of newly developed bioinformatic tools to assign transcriptional building blocks and reconstruct the molecular architecture of the glandular complex from pre-existing tissue. Additionally, stable-isotope experiments help to trace potential precursors and interfere the biosynthetic pathways on both molecular and biochemical level. Overall, we show how state-of-the-art single cell biology can be utilized to evolutionarily dissect the assembly of novel gland cell types with unprecedented molecular and transcriptional resolution.

Rove Beetle Genomes Provide Insight into Defensive Gland Evolution

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Abstract: Rove beetles (Staphylinidae) comprise the largest family in Metazoa with nearly 64,000 species. The vast radiation of rove beetles can be attributed in part to their shortened elytra that enhanced abdomen flexibility, thereby allowing occupation of diverse and novel habitats. A second key innovation was the evolution of a defensive tergal gland in the largest subfamily Aleocharinae. The gland can discharge volatiles through abdomen flexing to deter predators. The development of the abdominal gland has been proposed as a primary preadaptation for social insect symbiosis. Many lineages have convergently evolved into highly social, symbiotic organisms through repeated changes in morphology, glandular chemistry and behavior to assimilate into the complex societies of ants and termites. In this study we investigate the evolutionary "ground state" of aleocharine beetles through genomic, transcriptomic and chemical profiling. We present the near chromosome-level genome assembly of Dalotia coriaria, a new genetic model system, and draft genome assemblies of 12 other species. Genomic scans for conservation of genes, gene families and genomic architecture in tergal gland development were assessed within the higher Aleocharinae and the convergently-derived defensive glands of Tribolium castaneum. Genes previously characterized to be specific to the gland tissue and volatile production in T. castaneum were compared with differential expression of control and gland tissue, targeted RNA interference and quantification of gland volatiles with GC/MS in D. coriaria. We highlight common molecular processes underlying the evolution of the defensive gland in beetles and those specific to the aleocharines that were key to their diversification.

Myrmecophile assemblages as models for testing hypotheses in community ecology

Authors: Parmentier Thomas, Ghent University, Belgium

Abstract: Ant colonies house a hidden diversity of symbiotic arthropods. Gradually, we gained a profound understanding of how these so-called myrmecophiles interact with their ant host. They possess a range of chemical, morphological and behavioural tactics to be able to live in the hostile ant nest environment. Interestingly, myrmecophiles do not only interact with their ant host, but also strongly interact with other co-habiting myrmecophiles by predation and competition. In fact, myrmecophiles are often part of heterogeneous communities spanning different trophic levels. In this talk, I will lay out how these neat microcosm communities can be used as model systems to address general hypotheses on spatial ecology, ecological succession, community stability and the drivers of food chain length.

Nutrient value and safety of black soldier fly larvae fed on organic waste streams for use in animal feed

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Abstract: Fly larvae can be used to effectively reduce and valorise organic waste streams and produce value-added products such as a protein supplement for monogastric animal feed and lipids for biodiesel. The black soldier fly, Hermetia illucens L. (Diptera: Stratiomyidae), is commonly used in bioconversion due to its versatility and efficiency in reducing various types of organic waste, including fruit and vegetable waste and animal manure. The type of organic waste that larvae feed on can affect their nutritional composition and the presence of pathological microbes and heavy metals. This study investigated the nutritional composition of larvae that fed on three different types of organic waste. Freshly hatched neonates (90 mg), collected within three hours of hatching, were placed on 12 kg of pre-consumer waste, post-consumer waste or chicken manure and collected 15 days after egg hatch. The larvae were held at 28 ± 0.5°C and this was repeated for fifteen different batches of each waste type. Proximate analyses (crude protein, crude lipid content, ash and fibre), fatty acid analyses, amino acid analyses, microbiological tests and heavy metal tests were performed on larvae and on each waste batch. Nutritional composition, microbiological load and heavy metal presence of the larvae were related to the waste type that they fed on. The nutritional composition, performance and efficacy of waste reduction and bioconversion of the larvae on each waste type was compared. The nutritional composition of the larvae fed on different waste types was compared to the ideal nutrient composition of traditional protein sources for animal feed. Results to be discussed.

Assessment of the repellent effect of essential oils and volatile compounds against apple sawfly (Hoplocampa testudinea) in organic orchards

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Abstract: The European apple sawfly Hoplocampa testudinea (Klug) (Hymenoptera: Tenthredinidae) is a pest in apple orchards in Europe and in North America. In organic production, methods to control this pest have a low efficacy, and damages can reach up to 80%. However, since this pest causes damage during the blooming period, the use of insecticides is not recommended to preserve beneficial insects. Thus, disruption of host-plant finding before oviposition by using volatiles compounds is a sustainable way to control it. Inspired by the publication from De Almeida et al. (2017) who demonstrated a significant repellent effect of yarrow flower strips (Achillea millefolium L.) and sprayed yarrow essential oils, we assessed the repellent effect of essential oils and volatile compounds in organic orchards during two years. In 2018, the experiments were conducted in three organic apple orchards to test separately the repellent effects of the three essential oils (Achillea millefolium, Artemisia dracunculus and Cananga odorata) on apple sawflies, predators and pollinators. Taragon (A. dracunculus) and C. odorata essentials oils were selected because they respectively contain beta-ocimene and alpha-farnesene. Essential oils were diffused with 2 mL drilled vials put on white sticky traps. Captures were compared with the control treatment, i.e. traps without essential oil diffusion. A gradient of pest pressure was observed in the three experimental plots: from 10 to 155 apple sawflies were counted per trap in 15 days. No significant repellent or attractant effect of the three essentials oils on apple sawflies and pollinators was observed. In 2019, the experiments were conducted in two organic apple orchards to test separately the repellent effects of Achillea millefolium essential oil and a 50:50 blend of beta-ocimene and alpha-farnesene. Dispensers consisted of 1mL of a base matrix paste (SPLAT paste, ISCA Technologies) used to hold and release semiochemicals. Each 1 mL droplet was put in a plastic cup which was easy to hang on trellis wire. Apple sawfly damages were assessed at two dates. No significant repellent effects were observed. The discrepancy between literature and the present results may be explained by the quantity of repellent used. De Almeida et al. (2017) sprayed daily a solution at 4% of essential oil: apple sawflies were certainly exposed at a higher concentration of organic compound than in our experiments with passive diffusion only. The dynamics of diffusion of volatile compounds over time could also be involved.

Oviposition-related cues affect plant responses against herbivores, and life history traits

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Abstract: Plants can detect cues associated with the risk of future herbivory and modify defense phenotypes accordingly. However, our understanding of these early warning cues and associated plant responses is limited, both with respect to the range of cues to which plants respond and the nature of the responses. We assessed plant responses to different early warning cues, egg deposition and volatile emissions from neighbors infested with herbivore eggs, and measured changes in both defense and fitness-related traits. We show that exposure to oviposition–early warning cues promotes stronger defense responses to subsequent herbivory in Brassica species. Furthermore, exposure to these volatile cues induced earlier flowering and increased seed production in Brassica nigra, suggesting a strategy of reproductive escape. Our results thus document novel cues for plant responses, and show that plants respond to the threat of herbivore attack through changes in both defense and life-history traits to preserve fitness.

The crucial role of the circulatory system in maintaining the biomechanical properties of insect wings

Authors: Pass Guenther, Department of Integrative Zoology University of Vienna, Austria

Abstract: As every entomologist knows from experience, insect wings quickly stiffen and become brittle when they dry out. This is clearly due to a physical process, as it can easily be reversed by high humidity or prolonged immersion in water. The strong dependence of the flexibility and toughness of the insect wing cuticle on its hydration status inevitably involves also the problem of constantly replacing the loss of water caused by evaporation. Despite the importance of this topic for the biomechanics of the insect flight apparatus, only marginal notes on the water balance of the wings can be found in the literature. Studies on the ultrastructure of the wing cuticle support the hypothesis that the wing membrane, which consists almost exclusively of epicuticle, requires little hydration. On the other hand, the cuticle of the wing veins needs continuous hydration since it also contains layers of chitin-protein complexes and resilin. The necessary water is obviously supplied by the hemolymph which flows continuously through the veinal network of the wing. The influence of the hemolymph mass and the circulating flow in the veins on the aerodynamic properties of insect wings also requires further investigation.

Local adaptations or genetic diversity: which is more beneficial in a biocontrol agent population?

Authors: Paterson Iain, Rhodes University, South Africa

Abstract: Significant efforts are invested into ensuring that classical biological control agents are suitably adapted to the target pest population and the climatic conditions to where they are intended for introduction. The most effective biological control agents are assumed to be those that have a close evolutionary association with the target pest population and those that were collected in climatically similar areas to the introduced range. An alternative strategy to ensure that biological control agents are suitably adapted to the introduced range is to release a genetically diverse agent population that can adapt to the target pest population and climatic conditions of the introduced range over time. This could be achieved by collecting agent populations from a wide variety of target pest populations across a wide variety of climatic zones in the native distribution. Releasing the best adapted biocontrol agent and releasing a genetically diverse agent population on which evolution can act are mutually exclusive, so one of these approaches must be selected for each new biological control agent. Specific examples of weed biological control agents from South Africa, as well as an analysis of how genetic bottlenecks and founder population size effect success of the agents released in the country, indicated that neither of these approaches can be seen as a general rule. The relative importance of genetic diversity and local adaptation is dependent on the nuances of each individual biological control programme.

With or without increased competitive advantage in Pereskia aculeata, susceptibility to a biological control agent, Catorhintha schffneri, remains genotype specific

Authors: Paterson Iain[1], Egbon Ikponmwosa N.[3], Hill Martin[2] and Compton Stephen[4], [1]Rhodes University, South Africa, [2]South Africa, [3]University of Benin, Nigeria, [4]University of Leeds, United Kingdom

Abstract: Native species transported without their natural enemies to new habitats could invest more in fitness, as opposed to defence, which explains their invasiveness according to ‘Evolution of Increased Competitive Ability’ (EICA). We tested here native and invasive genotypes of Pereskia aculeata Miller as models to test for EICA and explore how ‘enemy release’ influenced the invasion success of the introduced populations. Plant growth parameters (height and shoot length) of fifteen genotypes, and the susceptibility of ten genotypes to a specialist herbivore, Catorhintha schaffneri Brailovsky & Garcia, were compared in common garden experiments. Introduced genotypes grew significantly taller than native-range genotypes. Furthermore, invasive genotypes were more susceptible to herbivory than the native genotypes, though the observed differences were not completely explained by ranges as EICA had predicted; nonetheless, the observed data partially support its predictions, because invasive genotypes generally and significantly grew taller more quickly and were more susceptible to damage from a specialist herbivore, C. schaffneri, than some native genotypes. Higher susceptibility to herbivore damage by the invasive genotypes suggests that C. schaffneri may be more damaging in South Africa where it is introduced as a biological control agent than it is in the native range.

Measuring success of aquatic weed biological control in Africa

Authors: Paterson Iain[2], Martin Grant[1], Coetzee Julie[1], Hill Martin[3] and Motitsoe Samuel[1], [1]Centre for Biological Control, Department of Zoology and Entomology, Rhodes University, Makhanda, South Africa, [2]Rhodes University, South Africa, [3]South Africa

Abstract: The economic, social and environmental impacts of invasive aquatic weeds have largely been quantified in Africa, where, uniquely, biological control is the primary method of control in many parts of the continent. However, post-release evaluations are still neglected, with the exception of South Africa, where the effect of releasing host-specific natural enemies has been quantified at different scales, including cellular, individual plant, population and landscape scales. In most cases, biological control has successfully reduced the invasion according to these metrics. While the reduction in the invasion is assumed to alleviate the negative impacts, this is not measured, and ecosystems are unlikely to revert to pre-invasion conditions after control has been implemented, in the absence of active restoration efforts. Studies that directly measure the economic, social and environmental benefits generated by aquatic ecosystems before, during and after biological control, will improve how success is quantified. The first studies of this kind, which have investigated the environmental benefits of biological control on aquatic ecosystems in South Africa, recommend that biological control programmes must be followed by active restoration practices. Further investigations into trophic structure and function will provide holistic aquatic weed management strategies for ecosystem recovery and restoration of invaded aquatic ecosystems in southern Africa and globally.

The Hymenoptera collections of the Finnish Museum of Natural History

Authors: Paukkunen Juho, Finnish Museum of Natural History, Finland

Abstract: The entomological collections of the Finnish Museum of Natural History (LUOMUS) contain about 9 million preserved insect specimens. The most abundantly represented groups are Lepidoptera, Coleoptera and Hymenoptera, followed by Diptera and the smaller orders. The Hymenoptera collections comprise approximately 1,5 million specimens of which 1 million belong to the Eastern Fennoscandian collection and 500 000 to the World collection. Most specimens in the Eastern Fennoscandian collection are from Finland, but also much material from the Russian part of Fennoscandia is included. The World collection contains specimens from all over the world, while the majority are from Europe and other parts of the Palaearctic region. Particularly well represented regions include Macaronesia, southern Europe and Russia. The collections have accumulated during two hundred years, mainly starting from the 1840s. The four most abundant superfamilies are Ichneumonoidea, Apoidea, Tenthredinoidea, Chalcidoidea and Formicoidea. Of the approximately 3500 Hymenoptera type specimens about 1000 are name-bearing types of several authors such as Wolter Hellén, Eitel Lindqvist and William Nylander. Approximately 15% of all the Hymenoptera specimens have been digitized by 2022, the majority of which are Finnish aculeates. The collections have been growing steadily by thousands of specimens every year during the past decade.

Population Genomics of the Antarctic midge (Belgica antarctica)

Authors: Pavinato Vitor[2], Edgington Hilary[1] and Michel Andrew[2], [1]The College of Wooster, [2]The Ohio State University, United States

Abstract: Phylogenetics show that Antarctica's terrestrial arthropods persisted throughout the repeated glaciation events of the Pleistocene. As ancient glacial-interglacial cycles are similar to current and future environmental changes, these arthropods are ideal systems to study the evolutionary responses to climate changes. The Western Antarctic Peninsula (WAP), which is home to the Antarctic midge (Belgica antarctica), had experienced a dramatic climate change. This species is an ideal candidate to study how ancient glacial-interglacial cycles have shaped genetic diversity, persistence and adaptation. Preliminary study showed two distinct evolutionary signals co-exist in the genetic makeup of Antarctic midge: 1) a signal of deep phylogeographic divergence among islands populations, and 2) signals of recent and frequent dispersion of individuals to nearby islands. This apparent paradox might indicate the role of local selection against migrants thereby maintaining locally adapted genotypes. Population genetics offers the framework to quantify the relative role of local adaptation and neutral processes in determining the species genetic diversity. We are going to show how methods for demography inference (neutral processes as admixture, population size changes, etc) can help us identify the last glacial-interglacial events that left recognizable signals in the species genome.

Population genomics and epigenomics reveal differential adaptations for biotype evolution

Authors: Pavinato Vitor[3], Shahid Saima[2], Wenger Jacob[1], Slotkin R. Keith[2] and Michel Andrew[3], [1]California State University, [2]Donald Danforth Plant Science Center, [3]The Ohio State University, United States

Abstract: Agroecosystems force intense selection pressures on biodiversity. For some species, these pressures present significant barriers to population stability and persistence, evidenced by low species and genetic diversity. As some species perish, others flourish in these constantly changing landscapes. Rapid insect pest evolution in agroecosystems negatively impacts crop production, as the failure of control causes severe economic losses. Evidence of the role of beneficial mutations in the evolution of pest resistance has been accumulated for several pest systems. However, little is known about the role of epigenetic modifications which could facilitate pest adaptation. We investigated the adaptation to host-plant resistance (HPR) in the soybean aphid, Aphis glycines. This aphid has adapted to soybean with natural resistance, but the mechanism of this virulence is unknown. We combined population genomics, transcriptomics, and a comparison of differentially methylated regions to identify genomic areas associated with virulence. Our combined data sets suggest an interplay between mechanisms associated with the evolution of virulence.

First Inventory of Coleoptera Fauna Associated to Mangroves Ecosystems from the Dominican Republic

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Abstract: This is the first faunistic inventory of mangroves ecosystems carried out in the Dominican Republic. The studied mangroves are from four species. The areas from Pedernales, a province at the southwestern region of the country, were selected as the locations to conduct the study, in which samples were taken during the dry season and the season with the highest humidity. The landscape is dominated by herbaceous plants, inaccessible lagoons, swamps, and a coastline overwhelmed by Sargassum. Different sampling techniques were utilized in terrestrial and aquatic habitats as part of a project that had as its main objective collecting invertebrates from a wide variety. Sweep nets, beating sheets, aquatic nets, bowl traps, and UV light tramps were used to capture the coleoptera. Preliminary data shows the presence of thirty families of and fifty more Coleoptera species. On the other hand, the result data is still not sufficient to reach a conclusion regarding which season possesses the most abundance and diversity of coleoptera. Moreover, the poor taxonomic information available about this entomofauna, make the identification of the aforementioned species more complex. Consequently, we recommend further research and studies in this region ensuring the inclusion of specialist from the abovementioned taxonomic groups.

Biocontrol Predators-in-first (PIF) strategies in greenhouse crops

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Abstract: The expiration of registration of broad spectrum and persistent pesticides and the availability of new more selective ones have allowed for the emergence of new IPM tactics in greenhouse crops. Nowadays, growers tend to prefer Inoculative Biological Control (IBC) or Conservation Biological Control (CBC), rather than repeated releases of natural enemies of greenhouse pests. Tools like modification of the crop environment or adaptation practices are developed to enhance early establishment and population growth of biocontrol agents on the plants before pest invasion or outbreaks. Examples of effective IBC/CBC techniques, as used by growers, are discussed.

Soluble proteins of chemical communication across arthropods

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Abstract: Since the discovery of odorant-binding proteins (OBPs) about four decades ago, a very large number of reports have been published on soluble proteins of chemical communication. However, nearly all the work has been focused on insects and very few studies have addressed other arthropods. Recently, at least two classes of soluble proteins, putative carriers for semiochemicals, have been identified and characterised in spiders, ticks and mites. Niemann-Pick type C2 (NPC2) proteins have been well characterised in vertebrates, where a single sequence is expressed in each species with a common function of carrier for cholesterol and fatty acids. In arthropods, instead, NPC2 proteins have undergone extensive duplication and differentiation, probably under environmental pressure, with a dozen or more members in each species, suggesting a role in chemical communication. In fact, these proteins, so far reported in Hexapoda, Crustacea and Chelicerata, are expressed in chemosensory organs and may represent the main class of soluble proteins of chemical communication in non-insect arthropods.

Another family of soluble binding proteins, named OBP-like for their sequence similarity to insect OBPs, has been found only in Chelicerata and Myriapoda, with only 4-6 members in each species. Despite their significant, although poor, similarity with insect OBPs, these proteins present a completely different structure. The six cysteines are paired in a pattern unlike the interlocked fashion observed in insect OBPs and this likely contributes to the peculiar folding of these proteins. Unlike their insect counterparts, in these proteins the N-terminus and the C-terminus are close and point in the same direction, brought together by a disulphide bridge between the first and the last cysteines.

We have focused our recent work on two species of ticks, the specialised honeybee parasite Varroa destructor and the generalist plant pest Tetranychus urticae. We have expressed and characterised representative members of NPC2 and OBP-like proteins with the aim of investigating the involvement of these soluble binding proteins in chemical communication or in other unrelated functions.

Harnessing endosymbionts for management of vectors and vector-borne agricultural pathogens

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Abstract: Insect pests represent a significant problem for agriculture as a result of economic losses resulting from direct plant damage and indirect losses resulting from the transmission of plant pathogens during feeding. Globalization has increased the prevalence of many pathogens during recent years, while increasing concerns associated with pesticide use have limited the efficacy of insect pest management programs. Citrus greening disease is one of the most destructive diseases of citrus worldwide. The putative causal agent, Candidatus Liberibacter asiaticus (Las), is transmitted by the Asian citrus psyllid, Diaphorina citri Kuwayama (Hemiptera: Liviidae). The goal of this project was to develop a novel, biological control-based tool for decreasing pathogen transmission by harnessing native D. citri microbial flora to reduce pathogen transmission. Here, we describe the development of a D. citri-derived Wolbachia culture and the establishment of a paratransgenesis system using genetically-modified Wolbachia to introduce a phenotype-altering transgene into D. citri. Development of this biological control-based strategy may have a significant impact on the epidemiology of vector-borne agricultural pathogens as a novel tool to disrupt pathogen transmission.

Extending the knowledge of the African savannah parasitic wasp fauna: the Braconidae and Ichneumonidae from the Quiçama National Park

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Abstract: The currently designated Quiçama National Park, 9 o 55'2 " south latitude and 13 o 52'37" west longitude, 70 km south of Luanda, is located in Quiçama municipality, Luanda province, Angola. It has a total area of 960,000 hectares of Savannah vegetation and its average temperature ranges from 27o to 28oC during the rainy season and from 23o to 24oC in the dry season. The Park is bordered by the Kwanza River (the largest in the country), the Long River and bathed by the Atlantic Ocean, with a humidity between 80% and 87% and its average annual rainfall varies between 400 mm, on the coast and 1000 mm, more to the interior . From January to April 2019, with monthly Malaise trap collections in the dry and wet savannah area of Quiçama Park we studied the Braconidae (954 specimens, 15 subfamilies) and Ichneumonidae (212 specimens, 8 subfamilies). Among the Braconidae are Cardiochilinae (316 specimens, 5 genera) and Agathidinae (229 specimens, 3 genera); among the Ichneumonidae, Campopleginae (104 specimens, 6 genera) and Cremastinae (57 specimens, 4 genera) were the most common in the samples. Our results are new species or first occurrences for Angola and even for the Afrotropical region.

Financial support: INCT-HYMPAR (FAPESP, CNPq, CAPES), INAGBE, INBAC

Evidence of ATP-binding cassette transporter (family C4) gene is involved in eCry3.1Ab resistance mechanism in western corn rootworm

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Abstract: Western corn rootworm (WCR), Diabrotica virgifera virgifera LeConte, has proved to evolve resistance to any control tactics in the field. In this study, we investigated the resistance mechanisms in WCR-resistant strain to the Bacillus thuringiensis (Bt) protein eCry3.1Ab by using double stranded(ds) RNA to knockdown WCR midgut genes potentially involved in resistance mechanisms. The genes ABC-transporter, Aminopeptidase-N, Cadherin, and Cathepsin-B, were found to be differentially upregulated in eCry3.1Ab-resistant WCR larvae. Initially, we compared the expression of those four genes with Green Fluorescent Protein (GFP) in WCR-resistant and susceptible strains by exposing neonate larvae to 1µg of dsRNA/cm2 of artificial diet for three days to perform RT-qPCR. The results showed that all those four genes were significantly knocked down in both WCR strains. Finally, WCR-resistant and susceptible larvae were exposed to eCry3.1Ab and dsRNA mixed together in 10-day diet overlay toxicity assays. We report the first case of partial restoration of WCR resistant larvae to susceptibility to eCry3.1Ab protein after feeding on eCry3.1Ab and ABCC4 transporter dsRNA mixed together. We also report that mortality observed in WCR larvae is the opposite of what was shown in lepidopteran in which susceptible insects became less susceptible to Bt protein after ABC transporter knockdown. ABC transporter is known to be involved in Bt resistance in several lepidopteran and in at least one coleopteran insect pes. Therefore, our results show evidence that ABC transporter may be involved in WCR resistance to Bt protein eCry3.1Ab

Insect Pathogens and their Control in Insect Rearing Facilities

Authors: Pereira Roberto, University of Florida, United States

Abstract: General discussion will be presented on the principal entomopathogens that may occur in large scale production of insects. The characteristics of the different pathogen groups, and the signs that may be useful in their detection, will be discussed in relation to preventive measures to be used in production systems. Decontamination and other corrective actions to control entomopathogens and contaminants in insect colonies will be discussed in relation to different production systems and the final use of insects in production..

New insights on corn borer resistance to Bt maize in Europe

Authors: Pérez Farinós Gema[1] and Ortego Félix[1], [1]Margarita Salas Center for Biological Research (Spanish National Research Council), Madrid, Spain

Abstract: Maize varieties derived from event MON810 expressing Cry1Ab toxin (Bt maize) are currently the only genetically modified plants approved for cultivation in the EU. Ninety-five percent of them are found in Spain, representing approximately 30% of the maize grown in the country. Bt maize effectively controls the maize pests Sesamia nonagrioides (Mediterranean corn borer) and Ostrinia nubilalis (European corn borer). Despite the widespread trend towards the development of resistance of target pests to Bt crops (Tabashnik & Carrière, 2019), both species remain susceptible to MON810 maize, with no cases of practical resistance detected in the field after 24 years of Bt maize cultivation (Bt176 between 1998 and 2005, and MON810 since 2003) (Farinós et al., 2018; Thieme et al., 2018).

Insect resistance management in Spain is based in the high-dose/refuge (HDR) strategy and in the implementation of monitoring programs, to assess the potential development of resistance of both target pests to Bt maize. Since 2016 monitoring is focused on the Ebro Valley (northeast Spain). This is Europe's only hotspot, where target pests have been exposed to Cry1Ab maize continuously since 1998 and the adoption rate of Bt maize is normally above 60%. A resistance evolution model for S. nonagrioides, developed considering biological, ecological and agronomical variables known to affect resistance development, showed that low initial adoption rates of Bt maize, as well as high compliance with the use of refuges by farmers (around 90% in the last 12 years), appear to have been key to prevent resistance (Castañera et al., 2016). Despite this, an allele of resistance was found in a S. nonagrioides field population in 2016 using the F2 technique (Camargo et al., 2018). The resistance evolution model was updated with this new information and it showed that resistance did not seem to be evolving faster than predicted, although the frequency of resistance was triple the value recommended for an effective implementation of the HDR strategy, so vigilance must be maintained.

The sustainability of Bt maize cultivation in the EU faces several challenges, the most important being the uncertainties of EU policy for GM crops and the reduced set of tools available for resistance management, since pyramided Bt maize varieties cannot be used. Thus, it is essential the strict compliance of refuges, as well as continuing the monitoring of resistance evolution in the Ebro Valley.

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Performance of the Mediterranean corn borer Sesamia nonagrioides (Lepidoptera: Noctuidae) on cultivated and wild host plants: implications for Bt maize resistance management in Spain.

Authors: Pérez Farinós Gema[1], Martín Camargo Ana[1], Arias-Martín María[1] and Castañera Pedro[1], [1]Margarita Salas Center for Biological Research (Spanish National Research Council), Madrid, Spain

Abstract: The Mediterranean corn borer Sesamia nonagrioides (Lefèbvre) is an important maize pest restricted to the Mediterranean area that is effectively controlled by maize varieties derived from the event MON 810 that express the Cry1Ab toxin (Bt maize). The continued cultivation of Bt maize in Spain exerts high selection pressure on the target pests, which could lead to the development of resistance to this crop. Provision of refuges of non-Bt plants to prevent the development of resistance is an essential point in the high-dose/refuge (HDR) strategy. In this work we analyze whether two cultivated plants (rice and sorghum) and four wild plants (johnsongrass, cattail, common reed and giant reed), reported as hosts of S. nonagrioides, are suitable for larval development and oviposition of this pest compared to maize. The results provide information on the possibility that these plants can be used as unstructured refuges for Bt maize, and therefore on their role in delaying resistance development to this crop.

We carried out different types of bioassays to assess: i) the larval performance of S. nonagrioides on all seven hosts, and ii) the larval feeding preference and the oviposition preference between the three cultivated hosts, maize, rice and sorghum. Females of S. nonagrioides laid eggs on all seven plants. However, bioassays conducted with plant pieces or whole plants showed that the larval cycle could only be completed in the three cultivated plants and in johnsongrass. Females showed a strong preference for ovipositing on maize plants in comparison with sorghum or rice. Although neonates chose to feed on sorghum rather than maize in two-choice bioassays, both larvae and adults had a better performance when larvae fed with maize throughout their larval stage.

Our results suggest that none of the alternative hosts of S. nonagrioides tested here should be used as an unstructured natural refuge for Bt maize in Spain, nor be considered within the HDR strategy in this species, as some of the necessary requirements to effectively delay resistance development would not be met.

Nectar-inhabiting bacteria affect attraction and fitness of egg parasitoids

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Abstract: Floral nectar is ubiquitously colonized by a variety of microbial organisms among which yeasts and bacteria are the most common. Microorganisms inhabiting floral nectar can alter several nectar traits, including nectar odor by producing microbial volatile organic compounds (mVOCs). Evidence showing that mVOCs can affect the foraging behavior of insect pollinators is increasing in the literature, whereas the role of mVOCs in altering the foraging behavior of third-trophic level organisms such as insect parasitoids is largely overlooked. Parasitoids are frequent visitors of flowers and are well known to feed on nectar. In this study we isolated bacteria inhabiting floral nectar of buckwheat, Fagopyrum esculentum, to test the hypothesis that nectar bacteria affect the foraging behavior of the egg parasitoid Trissolcus basalis via changes in odors of nectar. In behavioral assays, we found that T. basalis wasps were attracted towards nectar fermented by 4 out of the 14 bacterial strains isolated, which belong to Staphylococcus epidermidis, Terrabacillus saccharophilus (both Firmicutes), Pantoea sp. (Proteobacteria) and Curtobacterium sp. (Actinobacteria). Results of chemical investigations revealed significant differences in the volatile blend composition of nectars fermented by the bacterial strains. Our results indicate that nectar-inhabiting bacteria play an important role in the interactions between flowering plants and foraging parasitoids. These results are also relevant from an applied perspective as flowering resources, such as buckwheat, are largely used in agriculture to promote conservation biological control of insect pests.

Phylogenomic reconstruction of the Polideini (Tachinidae: Tachininae) through the lens of Ultraconserved Elements

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Abstract: The Polideini are a primarily New World tribe of the Tachininae with about 160 described species. They display strikingly diverse external morphological variation, a wide geographic distribution, and a broad array of host associations. The tribe, as currently understood, was defined by O'Hara in 2002, and its monophyly is well supported by morphological and molecular analysis using four nuclear loci. However, the true diversity of the tribe in the Neotropical region is still unknown. Limits of Neotropical genera are poorly defined and numerous genera and species remain undescribed. The Polideini provide an ideal case study to assess the ability of Ultraconserved Elements (UCEs) to resolve relationships in a rapidly diversifying and taxonomically confusing clade of insects. Using a recently developed UCE probe set designed to target families of the Oestroidea, we performed target enrichment and multiplexed sequencing of 77 representatives of the Polideini and outgroups, capturing an average of 630 loci per taxon. Using a maximum likelihood analysis, the Polideini were reconstructed as monophyletic, supporting previous morphological and molecular locus-limited analyses. Reconstructed relationships within major clades are robustly supported, however relationships between them are characterized by very short internode intervals suggesting a recent an explosive radiation of the Polideini. Nearctic Polideine were resolved as several clades well nested within Neotropical lineages suggesting a Neotropical origin of the tribe, with multiple colonization events of temperate regions. In addition, our results suggest that large-bodied spiny Polideine lineages have convergently evolved several times within the tribe. Our UCE-based phylogeny provides a foundation for understanding the evolutionary relationships within this morphologically diverse tribe, sets the stage to define limits of morphologically distinct and disjunct genera, and highlights the widespread morphological homoplasy throughout the Tachinidae.

Benefits of insect conservation measures in agricultural areas

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Abstract: Land-use changes in the 1950–1970's notably impacted modern intensive agricultural practices, resulting in a substitution of heterogeneous agricultural landscapes by homogeneous ones. Land consolidation led to the elimination of edges and other ecologically valuable structural elements that provided floral resources and nesting sites.

Habitat loss triggered critical changes in the insect communities. Within beneficial insects, pollinators, mainly wild bees, have been severely affected and suffered the highest decline, reaching up to 50%. Reviews carried out demonstrate that habitat loss, invasive species, parasites and diseases, non-sustainable use of pesticides, and climate change explain the reduction of insect abundance and diversity.

Here we present LIVINGRO™, a collaboration between Syngenta and nine universities. This agro-ecological program aims to build substantial and comprehensive scientific data from real-world field trials. The data will serve to test our hypothesis that the use of modern agricultural technology and best agricultural practices, together with ecological compensatory measures, can sustainably improve biodiversity and soil health in agricultural landscapes.

LIVINGRO™ examines the performance of crops and natural ecosystems across different geographies, and on a variety of perennial and rotational crops. The researchers will look at all orders of insects, whether they are living above ground or in the soil.

Differential influence of temperature on the toxicity of three insecticides between Cydia pomonella (L.) and two natural enemies: consequences of global warming on biological control in orchards

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Abstract: Insecticide toxicity may strongly vary with temperature and interspecific differences have been commonly reported for this relationship. A differential influence of temperature on insecticides toxicity between pests and their natural enemies may have important consequences on biological control in a warming world. This study aimed to investigate cross effects between temperature and three insecticides on the mortality of a major pest in orchards, Cydia pomonella, and two natural enemies in southern France, the predatory earwig Forficula auricularia and the introduced parasitoid Mastrus ridens. We observed a decreased efficiency of emamectin and spinosad at high temperature to control the codling moth while temperature did not influence chlorantraniliprole efficacy. Increasing temperatures however increased the toxicity of all insecticides on M. ridens, and of emamectin on F. auricularia. Such study provides insight to make recommendations for the use of these insecticides in combination with the use of natural enemies to control pests in a warming world. An alternating use of emamectin during early spring, when its toxicity is the lowest on F. auricularia, with chlorantraniliprole during summer could for example limit the risks of resistance appearance in codling moth populations while reducing insecticides impact on populations of natural enemies.

Post-fire trends of pollinators in the Aegean Archipelago, a biodiversity hotspot

Authors: Petanidou Theodora, University of the Aegean

Abstract: Fire is among the most important disturbances in Mediterranean ecosystems, and frequent enough to be considered as an integral characteristic of this Region and of other Mediterranean-type regions of the world. The increasing inflammability within these systems, as a result of climate change, will boost both the frequency and the severity of fires. In this talk I will present the results of a series of systematic studies carried out in three areas of Greece (two Aegean islands and a mainland) on the effects of wildfires on pollinator diversity, principally bees, considering fire history, fire severity, and post-fire recovery both in the short- and the long-term. The results show that fire history does not affect richness and abundance of bees, but it does shape their community structure, vis-à-vis functional traits (nesting habit, polylecty, body size). Regarding the effect of fire severity, major insect guilds (bees, sawflies, wasps) respond to fire severity at relatively small spatial scales (250-300 m) and in conformity with the Intermediate Disturbance Hypothesis; flies and beetles respond to larger spatial scales, their response being of decreasing type. The entire set of conclusions stemming out from these results constitute a valuable basis for forest management targeting to pollinator conservation.

The project LIFE 4 POLLINATORS: Educating about pollinators in the Mediterranean Region

Authors: Petanidou Theodora[1], Chroni Athanasia, Tsamparli Fereniki, Tzannetou Maria and Galloni Marta[2], [1]Department of Geography, University of the Aegean, Greece, [2]University of Bologna, Italy

Abstract: Despite consisting a major bee hotspot and world center of bee speciation, the bees and pollinators of the Mediterranean are poorly studied. What is particularly missing in all Mediterranean countries, however, is public awareness on the role of wild pollinators, as most of the existing awareness-raising initiatives there focus exclusively on honeybees. The EU LIFE 4 POLLINATORS project aims to safeguard the pollinators of the Mediterranean by focusing on public awareness of different stakeholders and the public in four Mediterranean countries making use of citizen science through developing a series of outreach tools. Here we will present some of the tools already in use by the project in Greece, particularly in the Aegean, such as mini bioblitzes, bee-hotels, and most importantly, a 3-D Mediterranean flower–pollinator garden. The garden consist of 13 different plant species models bearing flowers of different floral architecture, i.e. of diverse pollination syndromes, together with their pollinators; all pieces are 5x the natural size and constructed from recycled material, mainly paper. The garden gives immense possibilities for education on plant–pollinator relationships and for inspiration to animators and children to make stories out of natural history.

Transcriptome-based phylogenomics in Hymenoptera – achievements and problems

Authors: Peters Ralph S., Zoologisches Forschungsmuseum Alexander Koenig, Germany

Abstract: Analyses of transcriptome sequence data have been established in the last ten years to decipher phylogenetic relationships between taxa, and have also been applied to the insect order Hymenoptera and some of its subgroups (e.g., Chalcidoidea, Vespidae, Apoidea). Data sets usually span thousands of genes and millions of amino acid or nucleotide positions.

In several cases, analyses have helped to resolve relationships that had so far been unknown or controversial. In other cases, we still see unresolved relationships and significant conflict within data sets, incongruence between phylogenomic results and evidence from other data sources or we still face large gaps in the Hymenoptera tree due to coarse taxon sampling.

Analyses pipelines have many steps implemented that deal with data quality management, contamination issues, detection and avoidance of conflicting signal or confounding effects; steps are widely automized in order to be able to process very large data sets. However, while most analyses allow inferring well-supported and plausible trees, transcriptome-based datasets fail to resolve some of the hymenopteran relationships.

I will present the status quo of transcriptome-based phylogenies in Hymenoptera and summarize the achievements and problems; I will focus on the measures we take to target and solve those problems and will outline possible reasons why some of the problems still persist.

Sensitivity and specificity of two LAMP eDNA assays for Buprestid forest pests

Authors: Peterson Donnie[3], Kyle Kathleen[2], Pecori Francesco[1], Santini Alberto[1], Luchi Nicola[1] and Cleary Michelle[3], [1]Institute for Sustainable Plant Protection - National Research Council (IPSP-CNR, [2]Rutgers University, [3]Swedish University of Agricultural Sciences

Abstract: The early detection of forest pests using genetic tools is relatively new in forestry. qPCR assays have been used for forest pests, but they can take hours to receive results. LAMP eDNA assays are a rapid tool with results in 30 minutes. Buprestid pests are an emerging forest invader across the world and the early detection of these pests is vital to prevent their establishment. In our study, we designed and modified two LAMP eDNA assays for two Buprestids, both are major pests that if they are not detected early, they could spread further or establish in other European forests. We conducted specificity and sensitivity testing for a current LAMP design for the detection of one Agrilus. We then designed a new LAMP assay for the detection of another species. We found that both assays only amplified DNA of for the targeted species when tested against 12 other European Agrilus and another 12 non-Agrilus. We found both assays were highly specific for detection. The sensitivity of the assays was high, with a limit of detection of 20 femtograms/ul. The results of this study provide a promising tool that is specific and sensitive to the target organisms.

LIFE 4 Oak Forests: Structure and composition enhancement and its monitoring in 5 Natura2000 oak forest habitat types in Hungary and Italy (LIFE16NAT/IT/000245)

Authors: Petroncini Serena[2], Aszalós Réka [1], Frank Tamás [1] and Fidlóczky József[3], [1]Centre for Ecological Research, [2]Ente di gestione per i Parchi e la Biodiversità Romagna, Italy, [3]FENCON Ltd

Abstract: The biodiversity of oak forests is declining because of intensive commercial use. With the nature conservation interventions our goal is to promote the regeneration of the forests and to restore the diversity of forest structure, native tree species composition and micro habitats. As a results, the protected forest mammals, birds, insects, plants, and fungi will be preserved and their populations will increase.

Unlocking the potential of insect biomonitoring surveys using DNA-metabarcoding: Examples from two nationwide monitoring schemes in the UK

Authors: Petsopoulos Dimitrios[2], Evans Darren[1], Lunt Dave, Kitson James, Collins Larissa, Bell James, Boonham Neil and Morales-Hojas Ramiro, [2]Newcastle University, United Kingdom, [1]Newcastle University

Abstract: Insect monitoring schemes have enormous potential for understanding biodiversity declines, but to date have largely been underutilised. We evaluate the use of DNA-metabarcoding of samples from two insect monitoring schemes in the UK and compare them with conventional methods of identification. First, using archived aerial suction samples from the Rothamsted Insect Survey (RIS, collected between 2003-2018), we show that it is possible to successfully metabarcode stored samples over a 20 year period. Congruence with taxonomic identifications varied. Second, we used FERA yellow water-pan trap (YWT, 70 agricultural sites across the UK) and metabarcoded the ‘by-catch’ of non-target insects that would otherwise be discarded. We then examined changes in the seasonal patterns of insect biodiversity. Our results highlight how DNA-metabarcoding can add value to already established bio-monitoring schemes by: i) providing a way to non-destructively analyze archived samples, and therefore unlock their ‘hidden’ potential, and ii) increasing the breadth of taxa being monitored in traditional surveys by including hitherto overlooked by-catch species. We discuss the emerging trends of how species-interactions can be derived using these methods, ultimately leading to the construction and analysis of highly-resolved ecological networks that can then be used to better understand and mitigate insect declines.

Daily and seasonal temperature fluctuation in hollow urban trees – implications for saproxylic beetle conservation

Authors: Peuhu Elina[1], Hölttä Teemu[1] and Mattsson Teppo[1], [1]University of Helsinki, Department of forest sciences, Finland

Abstract: Hollow trees are a key habitat for biodiversity in many environments. A vast number of species live in or utilize trees during their lives. Certain species are specialized to tree cavities and are endangered. Ancient hollow trees have declined in great numbers due to land-use, forestry and agricultural changes, and the trees are still continuously declining. Previously, species assemblages living in hollow trees have been studied worldwide but some issues have been given less attention. For example, the effect of microclimate within hollow trees on saproxylic species existence is yet to be discovered. We measured hollow cavity temperatures in ten lindens (Tilia x vulgaris) in two city parks in Helsinki, Finland. We placed one temperature logger (iButton©) in each tree on the inner wall of the cavity just above the wood mould layer and one at a depth of 15 cm within the wood mould. Ambient temperature was measured with five loggers each attached to the bark of linden trees in the parks. Temperature was measured in 60-min intervals from May 14th 2009 to October 6th 2010 with an accuracy of 0.5 C. The most rapid daily temperature fluctuation was detected with ambient temperatures. Cavity temperatures followed ambient temperatures closely. Wood mould temperatures on the other hand reached their daily maximum during nighttime (around 22:00 in summer) and minimum close to midday. A similar trend in the delay for reaching maximum and minimum temperature was seen with seasonal changes. Average temperature in wood mould seems to be related to cavity size and the height of the opening from ground level. In the future, the relation between microclimate in tree cavities and saproxylic insect occurrences should be studied further to understand the environmental preferences of species assemblages in hollow trees and thus the most important trees for biodiversity.

Citizen Science and the Introduction of Spotted Lanternfly into Virginia, USA

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Abstract: Spotted lanternfly is a fulgorid hopper, closely associated with tree-of-heaven, but with a wide host range, notably grapes. This species was introduced into Pennsylvania in 2014, and it has expanded its range each year since. This was the first infestation outside of Asia. It is now established in parts of Virginia, Maryland, Delaware, New Jersey and West Virginia. Spotted lanternfly was first detected in Virginia in January 2018. This insect feeds on a broad range of species; winegrapes are a commercial crop at high risk. Because of the dispersed nature of host plants, difficulty in detecting in low densities, and high risk of economic impact, we instituted a Citizen Science approach with three main approaches: surveillance using brown sticky band traps, an online reporting portal, and an online training to meet quarantine requirements. Citizens were trained in use of traps and identification of spotted lanternfly. Subsequent visits to northern Virginia were made to follow up on proper use, and evaluation of catch. Advantages and disadvantages of current assessment tools will be discussed. For paper sticky traps, disadvantages included lack of sensitivity and selectivity. The online reporting portal was made available through various outlets. The goal was to provide specialists with knowledge of incipient infestations in the state. In spring of 2019, the state of Virginia established a quarantine for the infestation zone. This could have posed a problem for fruit growers and other shippers. On online training course was established to allow members of the public to obtain certification to inspect shipments, incorporating citizens not only in collection of data, but on meeting the resulting regulatory needs.

Pesticide usage and handling practices in the malaria endemic region of north-western Tanzania: Implications to the control of malaria vectors (Anopheles gambiae s.l)

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Abstract: Pesticides remain the mainstay for the control of agricultural pests and disease vectors. However, their indiscriminate use in agriculture ought to be the source of resistance among disease vectors against public health insecticides. We investigated the practices of farmers with regard to pesticide handling and usage and their impact on susceptibility status of An. gambiae s.l. to insecticides.

Methods
Data collection involved administration of questionnaires and observation of the practices. The surveys were complemented by bioassay tests to assess the susceptibility of vectors to pyrethroids (permethrin-0.75%, cyfluthrin-0.15%, deltametrin-0.05% and lambdacyhalothrin-0.05%) and DDT using WHO test kits. Molecular analysis was performed to identify sibling species of An. gambiae s.l and to characterize the knockdown resistance (kdr) genes.

Results
Forty eight pesticides were used for control of crop and livestock pests, 50% of these were pyrethroids. Pesticide mixing (cocktails), overspray and disposal of left overs in the mosquito breeding habitats were common practices. Susceptibility test results confirmed high phenotypic resistance among An. gambiae populations, mortality rate up to 54% against permethrin. Anopheles arabiensis was the dominant species (86%) followed by An. gambiae s.s (6%), kdr genes were not detected in all of the specimens tested.

Conclusion
The study found out that there is a common use of pyrethroids in agriculture and public health. The study also reports high phenotypic resistance among An. gambiae s.l against most of the pyrethroids tested. These findings are important for introduction of combined integrated pest and vector management (IPVM) strategies.

Chemical cues used by natural enemies of the green peach aphid (Myzus persicae) (Hemiptera) to locate their prey in canola fields

Authors: Phillips Andrew, Murdoch University, Australia

Abstract: The green peach aphid (GPA, Myzus persicae) is a serious pest of canola. Control of GPA has traditionally been achieved using pesticides, however, GPA has shown considerable ability to develop resistance to insecticides. Therefore, alternative methods of control are needed, such as biological control. Historically, biological control has not been successful for aphids in broad-acre crops, such as canola. Therefore, my project aims to explore ways to optimise biological control in canola by investigating the chemicals that natural enemies of the GPA use to find their prey in canola fields. Firstly, six canola fields in Western Australia were sampled to determine which natural enemies were present. Secondly, the volatile profile of canola would be sampled using GC-MS. Finally, the behavioural and electrophysiological response of the natural enemies to canola volatiles would be determined using Y-tube olfactometers and electroantennography (EAG). Preliminary results indicate that the most common natural enemies in canola fields are the parasitoid wasps and hoverflies. Other natural enemies present include lacewings, ladybird beetles and spiders. EAG results indicate that 2-Heptanone, cis-3-hexen-1-ol and Hexenyl acetate elicit a strong response from both hoverflies and wasps.

Phosphine resistance in two species of grain beetles, Tribolium castaneum and Rhyzopertha dominica in North America: Geographic Variation in Resistance Phenotypes and Genotypes

Authors: Phillips Thomas, Kansas State University, United States

Abstract: The lesser grain borer, Rhyzopertha dominica (F) (Coleotpera: Bostrichidae) and the red flour beetle, Tribolium castaneum (Herbst) (Coleoptera: Tenebrionidae) are two of the most destructive stored-product insect pests worldwide. Phosphine gas, or hydrogen phosphide (PH3) is an effective and widely used fumigant pesticide for controlling stored grain insects world-wide. Most likely due to long-term selection pressure, sub-optimal fumigation concentration or/and fumigation failure, phosphine resistant populations of T. castaneum and R. dominica have been reported in many countries. Phosphine resistance (PH3) was investigated for 29 populations of R. dominica from 8 states of USA and 4 provinces of Canada and 35 populations of T. castaneum from 12 states of USA, four provinces of Canada and one population from Thailand using both FAO discriminating dose bioassay and molecular marker analysis. Our results showed that the distribution of PH3 resistance in both species was varied and it was not related to geographic coordinates. However, PH3 resistance was highly correlated with R allele frequencies in both species.

Can we identify them before they disappear? Machine learning to scale insect identification

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Abstract: With only an estimated 20% of insects currently described and known, and anthropogenic impacts continually threatening insects, our process for identifying insects is flawed. Current methods require expertise in taxonomic groups, and a significant input of resources in generating morphological characters that ultimately describe the new species. We have developed a new method that addresses the massive scale of the problem by bypassing human expertise through computer vision and machine learning approaches. In our proof-of-concept, we developed a novel machine learning algorithm that integrated DNA and insect images on a large number of insect species (>1000 across four orders) to not only classify known species with high accuracy (>97%) but delivering the highest accuracies (~81%) to date in classifying unknown species to their correct genus (species that contained neither image nor DNA data in the training dataset). Next steps include extracting morphological information from the images that humans are unlikely to perceive and generate a new way of doing insect identification. The proposed approach can pave the way for more sustainable and scalable monitoring of biodiversity and can become instrumental in offering objective measures of the impacts of recent changes our planet is going through.

Comparative Genomics of Insect Development for Feed and Food Applications

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Abstract: Development time is a classic quantitative trait that can be influenced by genetic and environmental factors and is associated with fitness. This study evaluated genetic components of development time variation through selection experiments on three different experimental populations established from distinct Texas locations. There is was ample standing genetic variation in the species, with most genetic variation segregating within, not among, experimental populations. The selection response was biased such that wild flies appear to be more similar to strains selected for fast development. Genome-wide patterns of selection revealed SNPs with significant shifts in allele frequencies, including in traditional genes associated with regulating growth in Drosophila melanogaster. The presentation will highlight these genomic regions and their homologous regions in commercially relevant insects.

Do floral traits mediate indirect interactions between co-flowering Sierra wildflowers?

Authors: Picklum Devon[1], Richards Lora[1], [1]University of Nevada at Reno, United States

Abstract: Pollinators provide reproductive services to flowering plants by carrying pollen between individuals while collecting nutritional resources in the form of nectar or pollen. In diverse flowering communities, pollinators may visit several different species concurrently, which has direct consequences for plant fitness. Heterospecific pollen transfer represents a cost in lost male gametes and may prevent subsequent pollination if stigmas become clogged with the wrong species of pollen. In this way, plant species that interact indirectly via shared pollinators may experience impaired pollination services. Alternatively, plants interacting indirectly may facilitate each other when pollination services are enhanced due to increased abundance of pollinators. In natural settings, these indirect interactions can be context dependent, and may be influenced by floral traits (eg. morphology, reward type, or floral displays). Here, we investigate the pollination of two flowering species with multi-trait floral similarity to disentangle the role that floral traits play in shaping indirect interactions. Dodecatheon alpinum (alt. Primula tetrandra, Alpine shooting star) and Pedicularis groenlandica (Elephant head lousewort) share similar color, a pollen reward, specific behavioral requirements (buzz pollination), habitat preference, and are both predominately visited by Bombus (bumblebee) species. We first describe bee foraging behavior and pollen deposition, showing that bees move between these species where they co-occur. Pollen placement data and stigma samples show that these species partition pollen on bees' bodies imperfectly, leading to occasional heterospecific pollen transfer. We then measure floral trait similarity using fine-scale reflectance measurements and visual models and floral volatile profiles using dynamic headspace sampling and GC-MS. Visual modeling indicates these two plant species overlap in color to a bumble bee's eyes but vary within their populations. Lastly, we characterize indirect interactions between naturally co-occurring populations of P. groenlandica and D. alpinum. In this field-based approach, we measure co-flowering density and abundance, and look for resulting patterns of con- and heterospecific pollen transfer between these species across close, plot level, and landscape level scales. Together these data connect sensory traits, bee preference, and plant reproductive ecology, setting the groundwork to further understand the evolution of floral traits.

First evidence of long-lasting association between viruses and the Black soldier fly, Hermetia illucens

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Abstract: In insect farming, viruses have caused negative economic impacts to long-established species like honeybees or crickets. More recent models used in the insect industry, such as black soldier flies (Hermetia illucens, BSF) may also face viral diseases, but lack of knowledge about any natural pathogens of BSF leaves the industry unaware of any potential threats from viruses. As traces of contemporary and past viral infections can be mined in transcriptomics and genomic datasets, we undertook a bioinformatic approach to explore publicly available BSF data. A novel pipeline for the discovery of endogenous viral elements (EVEs) uncovered several EVEs in 3 BSF genomes. Some EVE sequences were found in all three BSF genomes, indicating ancient integration in the BSF genome. In a second approach based on transcriptome analyses, we uncovered an exogenous virus that we refer to as Hermetia illucens Toti-like virus 1 (HiTV1) and that is related to some of the EVEs. Of note, a short sequence, that is highly similar to one EVE, is expressed in BSF. Altogether, the results suggest that HiTV1 is an exogenous virus producing an active infection, and that related viruses have long been associated with BSFs.

Developing novel mode of action insecticides and repellents for mosquito control from medicinal plants

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Abstract: The emergence of resistance to pyrethroids and other conventional insecticides in mosquitoes is a global challenge that has prompted a need to discover novel mode of action insecticides. In response, we are exploiting the chemistry of cinnamodial (CDIAL), which is a natural drimane sesquiterpene enriched in endemic plants of Madagascar used in traditional medicines (Cinnamosma species). We previously demonstrated that CDIAL exhibited similar insecticidal potency against pyrethroid-susceptible and pyrethroid-resistant strains of Aedes aegypti. Moreover, CDIAL was a potent antifeedant and repellent against Ae. aegypti that modulated transient receptor potential ankyrin 1 (TRPA1) channels. Here we provide new insights into the chemical features of CDIAL that promote its insecticidal and antifeedant activities, as well as its molecular interactions with mosquito TRPA1 channels. Our results will be discussed in the context of developing novel mode of action insecticides and biorational repellents for controlling mosquito vectors.

Emerging biological control agents for bed bugs

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Abstract: Bed bugs have become widespread across the globe over the last several decades and pose significant health concerns for human populations. The development of resistance against commonly used chemical insecticides along with the spread of bed bugs to diverse environments has created an urgent need for new, effective, and flexible bed bug control tools. Microbial biological control agents have been used with success to combat a number of insect pests. However, despite its efficacy in other systems, this form of control has only explored against bed bugs to a limited degree. We previously determined that several species of environmental bacteria that are harmless to mammals are highly toxic when administered to bed bugs in the laboratory via an artificial blood-meal or through simulated wounding. This presentation will discuss up to date results of ongoing research to leverage knowledge of bacterial entomopathogen virulence, bed bug immune responses, and bed bug feeding behavior towards the development of effective biological control tools that are easily applicable under a broad range of settings.

In search of suitable predatory mites against the tomato russet mite Aculops lycopersici (Acari: Eriophyidae)

Authors: Pijnakker Juliette[3], Hürriyet Asli[1], Petit Clément[1], Vangansbeke Dominiek [1], Duarte Marcus [1], Moerkens Rob[1], Arijs Yves[4] and Wackers Felix[2], [1]Biobest, [2]Biobest Group NV, Belgium, [3]Biobest, Netherlands, [4]Private Company, Belgium

Abstract: The efficiency of nine predatory mite species (Phytoseiidae) in controlling the tomato russet mite Aculops lycopersici was evaluated on tomato plants in an experimental greenhouse. Neoseiulus californicus, Amblyseius andersoni and Neoseiulus fallacis showed the strongest pest reduction. Although these species had a low survival and the curative strategy did not totally eliminate the pest, plants remained healthy. These predatory mites could be used in a curative biological control strategy, but would be too expensive for growers due to the required repeated introductions, as the mites do not establish. Other predatory mites, like tydeoids, can survive on tomato and can reach high densities when pollen is supplied. High densities of the tydeoids Homeopronematus anconai and Pronematus ubiquitus were obtained in trials due to the weekly provision of Typha angustifolia pollen as alternative food. When the predatory mites were introduced and allowed to establish at an early plant stage, high tydeoid densities were reached. This preventative predator establishment proved successful in preventing the development of TRM. The predators did not sufficiently control eriophyid mites when they were introduced curatively. The potential of tydeoids for biological control of eriophyids as an alternative to chemical treatments is discussed.

Density-dependent polyphenism in sub-arctic populations of the winter moth Operophtera brumata: the thermal melanism hypothesis

Authors: Pincebourde Sylvain[4], Laksforsmo Vindstad Ole Petter[1], Uhd Jepsen Jane[3], Laparie Mathieu[2], Alsila Annika[3], Heinänen Emma[3], Gilles Yoccoz Nigel[7] and Anker Ims Rolf[1], [1]Department of Arctic and Marine Biology University of Tromsø (UiT) Tromsø, Norway, [2]INRAE, URZF, Orléans, France, [3]Norwegian Institute for Nature Research (NINA) Framcentre Tromsø, Norway, [4]Research Institut of Insect Biology, CNRS-University of Tours, France, [5]University of Tromsø - The Arctic University of Norway

Abstract: Density-dependent polyphenism of cuticle melanization is a widespread phenomenon in Lepidopteran larvae. In the sub-Arctic Fennoscandian birch forest, where the winter moth (Operophtera brumata) is expanding northward and exhibits 10-year cyclical outbreaks, crowding has been associated with the promotion of melanized spanworms. No such striking polyphenism has been reported at lower latitudes, possibly due to lower densities. However, dark pigmentation does not seem to prevail either in populations currently invading North America despite outbreak densities, which raises questions on the adaptive function of polyphenism in Fennoscandia. The evolutionary significance of melanism at high densities is not fully understood, but evidence is accumulating in a number of species that it can be associated with increased immunity, predator avoidance (camouflage, warning), or thermoregulation. In the winter moth, however, the camouflage and immunity hypotheses have been rejected, and melanization even appeared to increase vulnerability to enemies. We hypothesized that melanization might be an intra- and interspecific advantage over pale competitors during outbreaks if better absorption of solar radiation results in higher body temperature and earlier nymphosis (before total defoliation), especially at midnight sun latitudes. Such thermal melanism was tested by comparing metabolic rate and phenology among larval phenotypes. Metabolic rate was found to vary greatly but was 150% higher in melanized versus pale larvae under artificial light. The causal relationship with radiation absorption was further explored using respirometry with no light, and thermography. Preliminary results on the phenology of either phenotypes will be presented. Our findings suggest ecophysiological benefits of melanization that may offset its costs on resistance to enemies during outbreaks. Sliding selection regimes caused by cold summers and cyclic dynamics at the northern front likely contribute to maintaining phenotypic heterogeneity, a parameter largely neglected in attempts to predict expansions and invasions.

Effects of local microclimates on the phenology of the pine processionary moth, a forest pest invading urban areas

Authors: Pincebourde Sylvain[3], Poitou Laura[1], Laparie Mathieu[1], Backe Kristi[2], Robinet Christelle[1], Suppo Christelle[3] and Rousselet Jérôme[1], [1]INRA, URZF, Orléans, France,[2]North Carolina State University, Department of Entomology and Plant Pathology, United States, [3]Research Institut of Insect Biology, CNRS-University of Tours, France

Abstract: There is growing evidence that the phenology of many insects is impacted by climate change. Since temperature influences their development time, considering microclimates is crucial to deeply understand the variability in space and in time of insect phenology. The pine processionary moth (PPM), Thaumetopoea pityocampa, is a forest pest that has been invading urban areas due to the plantation of numerous ornamental pine trees. The PPM is expanding its distribution due to climate warming, but the phenological consequences are still unknown, yet time shifts and range shifts are most likely two interrelated responses to overcome climatic barriers. We conducted both field observation and field experimentation to explore phenology change compared to historical data and to determine the phenology variability across different microclimate conditions. We studied variability in a stand, between and across bioclimatic regions. Microclimate is suspected to vary in space due to different conditions at which pine trees are exposed (e.g., sun-exposed versus shaded trees, urban heat versus cool green areas), but it can also vary depending on microhabitat features such as the silk tent in which PPM larvae develop throughout winter, or the number of larvae in it. Temperature recorded in these tents can differ by up to 4°C from air temperature depending on the time of the day. Precisely estimating temperature inside tents and the factors of their variation is challenging, but the development of biophysical model based on these estimations will allow understanding larval development times and better predicting their phenology under climate change.

Living in the leaf microclimate: thermal ecology and biophysics of plant microcosms

Authors: Pincebourde Sylvain, Research Institut of Insect Biology, CNRS-University of Tours, France

Abstract: The surface of pant leaves hosts a huge diversity of interacting ectotherms. The ecophysiology of these tiny organisms, as well as the rate of biotic interactions, depends on the leaf surface temperature. Most of these organisms are tiny enough to be totally submerged within the leaf boundary layer, making them largely under the influence of the leaf functioning. The temperature of a leaf surface can deviate from air temperature sometimes quite strongly. In this presentation, I will detail the biophysical mechanisms determining the microclimate of arthropods living at the leaf surface. A comprehensive understanding of the leaf-air temperature deviations as well as the temperature heterogeneity at the within-leaf surface scale, is important to identify the extent to which ectotherms can exploit these thermal patterns to thermoregulate. Then, arthropod herbivore can fundamentally modify the functioning of the leaf when feeding on it; these changes have cascading effects on the leaf microclimate. These cascading effects can help explain the patterns of thermal adaptation among arthropod herbivores and predict the consequences of competitive interactions. From here, we can extrapolate on the role of the leaf microclimate in modulating prey-predator interactions at the leaf surface. Finally, the leaf microclimate can be placed in the context of climate change impacts: will the leaf surface provide ectotherms with a buffer of extreme heat or by contrast will it magnify the atmospheric changes? This knowledge of the leaf microclimate helps us determining the vulnerability of arthropods to warming.

Phenology of the pine processionary moth as an indicator of climate change

Authors: Pincebourde Sylvain[3], Poitou Laura[2], Laparie Mathieu[2], Robinet Christelle[1], Suppo Christelle[3] and Rousselet Jérôme[2], [1]INRA, URZF, Orléans, France, [2]INRA, URZF, Orléans, France, [3]Research Institut of Insect Biology, CNRS-University of Tours, France

Abstract: Insect development, reproduction and survival are closely linked to temperature. As a result, global warming could considerably impact the spatio-temporal dynamics of insects. However, it is often difficult to disentangle the effects of climate warming from the effects of other disturbances. The Pine processionary moth (PPM) is a major tree pest in Europe, which causes severe economic and public-health problems. It has become a model to understand the ecological impacts of climate change because its spatial distribution has expanded due to the increase of winter temperature which facilitated larval feeding and survival. Although the effect of climate change on the distribution of the PPM is clearly understood, potential phenological consequences are so far poorly documented. However, an increasing phenological variability is being reported, and atypical cycles up to 6-month early can now be observed in some areas. A better understanding of such phenological changes is crucial, not only for the better assessment of the effects of climate change, but also to optimize control methods and to limit urtication risks at unusual periods. We conducted field observations to compare current phenology with historical data and to determine the variability across different microclimate conditions. A phenological model was developed to predict future changes. While field observations were used to validate the model, its initial calibration was based on experimental data. First, the rate of development from egg to late instar larva was measured in controlled conditions at different temperatures. Second, the silk nest spun by larval colonies create a microhabitat that confers a thermal gain compared to ambient air. Correctly predicting PPM phenology therefore implied accounting for the microclimate the larvae are actually exposed to in the nests, which was estimated in semi-natural conditions.

Using the principles of ECOstacking to develop ecologically-based IPM approaches in apple agroecosystems in New England

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Abstract: One ecological approach to pest management involves manipulating the habitat by means of planting non-crop plants. Non-crop plants can be trap crop plants that can pull the pests away from the cash crop, and insectary plants that can attract and boost natural enemy populations. In 2018, we initiated a long-term project aimed at developing a permanent, low-cost, trap cropping system for multiple apple pests by grafting selected perimeter-row trees with 6 apple cultivars that are attractive to key pests including plum curculio, Conotrachelus nenuphar (Coleoptera: Curculionidae), and apple maggot fly, Rhagoletis pomonella (Diptera: Tephritidae). This type of IPM approaches can be readily implemented to support ecologically-based pest management via ECOstacking in support of more sustainable crop production.

Detecting the Unexpected: Invasive Insect Surveillance using Non-Destructive DNA Metabarcoding

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Abstract: Trap based insect surveillance forms a key component of plant biosecurity and pest management programs, aiming to detect newly arrived exotic taxa as well as track the population levels of established or endemic pests. However even when targeted lures are used, surveillance traps generally capture many more native species than the target pests and the extensive specimen sorting required prior to identification forms a major diagnostic bottleneck. DNA Metabarcoding has recently emerged as a high-throughput sequencing based method for conducting simultaneous, multi-species identification of complex mixed communities. By analysing bulk DNA extracts rather than single specimens metabarcoding circumvents the ‘needle in a haystack’ problem of previous identification methods and allows a dramatic scale up of both the quantity of traps that can be processed concurrently, and the number of species that can be actively monitored for.

Despite the wealth of information provided by metabarcoding assays, integrating novel multi-species diagnostics into previously highly targeted surveillance programs presents unique technical and regulatory challenges. Of particular concern is ensuring accurate species-level detections in the face of complex laboratory and bioinformatic pipelines, and how the incidental detection of invasive species that were outside the scope of the initial assay validation should be responded to. In order to address these issues, we have developed a non-destructive DNA metabarcoding assay that provides sensitive and rapid detection of high-priority pest insects for Australia, while maintaining the integrity of morphological specimens for later confirmation. We anticipate that adoption of non-destructive DNA extraction techniques will bridge the gap between new genomic methods and traditional entomological techniques and may bootstrap the acceptance of metabarcoding based diagnostics within international regulatory frameworks.

Odorant Receptors in the Housefly, Musca domestica

Authors: Pitts Jason[1] and Boyi John[1], [1]Baylor University, United States

Abstract: The common housefly, Musca domestica L, is a major worldwide pest and a potential mechanical vector for a number of human and animal pathogens, especially those that cause enteric diseases. As in all insects, houseflies utilize a highly-developed olfactory system to locate resources in the environment via host-emitted kairomones. Odorant receptors are molecular receptors that respond to volatile odors and comprise a large gene family in the housefly (MdomOrs). In this study, we compare MdomOrs with those of other Diptera, highlighting receptor evolution. We have characterized MdomOr expression profiles in adult antennae using RNA sequencing. While most MdomOrs show similar abundance levels in both sexes, a subset of conserved receptors appear to be differentially expressed. These receptors are closely related to a receptor in Drosophila melanogaster that mediates behavioral responses to a male-produced pheromone. In M. domestica, (Z)-9-tricosene is produced by females and induces courtship in males. We propose that these conserved MdomOrs are candidate pheromone receptors that are activated by components of housefly cuticular hydrocarbon pheromone blends. This study will help illuminate the functional roles of chemoreceptors in the chemical ecology of houseflies and advance efforts in their control.

Managed solitary bee advances for crop pollination

Authors: Pitts-Singer Theresa, USDA Agricultural Research Service Pollinating Insects Research Unit Logan, Utah, United States

Abstract: The enhancement of propagation and management protocols of Osmia lignaria and Megachile rotundata has assured the use of these pollinators for orchard and alfalfa seed crops, respectively. Open field, large field cage, and laboratory studies were conducted to track and assess female bees, their behavior, and their reproduction. Understanding visually- and chemically-mediated behavior of these bees has helped to increase the retention of bees within targeted crops, including the invention of a bee attractant for O. lignaria. Assessment of the number of bees released in fields and the number of females retained at bee shelters has informed stocking densities and pollination efficacy. Evaluation of the effect of an insect growth regulator (employed to control a seed predator) on M. rotundata reproduction provided the first evidence of its ovicidal activity that can great reduce sustainability of commercial populations. Certain fungicides used in orchards were applied to ground cover and showed disrupted nesting behavior for both M. rotundata and O. lignaria. Phenologies of O. lignaria from disparate geographical regions of the United States were shown to differ due to variations in larval and pupal develop times at natural and at common field temperatures. Affects of photoperiod and nutrition were examined for M. rotundata and showed the aversion of prepupal diapause when mothers were exposed to a relatively long photoperiod and when larvae fed on relatively small provisions, leading to theories on maternal control of offspring diapause fate. All results have important implications for successful and economically feasible commercial bee management.

Ecdysone is essential for cell differentiation in the ovary of the cockroach Blattella germanica.

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Abstract: The role of ecdysone in oogenesis has been deeply studied in holometabolous insects with meroistic ovaries, especially in Drosophila melanogaster, while in panoistic ovaries, the most ancestral ovary type, is still poorly understood. Using the hemimetabolous species Blattella germanica (German cockroach) as a model, which has panoistic ovaries, we have depleted the expression of the Ecdysone receptor (EcR) with RNAi, in order to characterize the role of ecdysone in ovaries of sixth instar nymphs, thus providing knowledge about the evolutionary changes or conservation of the ecdysone role in insect oogenesis. In sixth instar nymphs of B. germanica females, dsEcR treatment arrests the synthesis of ecdysone in the prothoracic gland, helping us to demonstrate that ecdysone is essential for the regulation of the germinal stem cells differentiation, as well as for the correct distribution of cells in the germaria of this cockroach species.

The Blattella germanica piRNAs key regulators of materno-zygotic transition.

Authors: Piulachs Maria-Dolors[3], Bau Josep[1] and Montañés Jose Carlos[2], [1]Department of Biosciences, University of Vic–CentralUniversity of Catalonia, , [2]Hospital del Mar Medical Research Institute (IMIM), Barcelona, Spain, [3]Institute of Evolutionary Biology (CSIC- Univ. Pompeu Fabra). Barcelona, Spain

Abstract: During insect oogenesis, a series of genes must be transcribed and translated on-site in the ovarian follicle at the right time to guarantee embryo development. In the last years, the sncRNAs have appeared as candidates to regulate mRNA expression and their importance in regulating the transition materno-zygotic was begin studied in insect species.

Between the small non-coding RNAs there are the piRNAs that have a length comprised between 26 and 31 nt, which is longer than that of miRNAs and siRNAs (21 to 25 nt). The piRNAs are involved in the control of transposable elements (TEs), as part of an evolutionarily conserved mechanism that protects the genome, preserving the fertility of the individual by ensuring the development of gametes. However, the role of piRNAs as regulators of mRNA expression is emerging, which opens a new avenue for functional studies.

Using small RNA libraries from cockroach Blattella germanica we identified the piRNAs expressed in adult ovaries during the first gonadotropic cycle and we have analyzed those piRNAs stored in eggs and those expressed just after the zygote formation. The analysis of this set of piRNAs is giving us information on how the oocyte keeps some mRNAs blocked waiting until zygote formation.

Influence of tilling on invertebrate food webs and their dynamics in wheat fields

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Abstract: The transition towards a more sustainable agriculture has become one of the main issues of our society. Developing new agricultural practices promoting ecosystem services that biodiversity provides, rather than using chemical inputs, is one of the considered solutions to increase agricultural sustainability.

Conservation agriculture is one of these promising agroecological farming systems, which notably proposes to limit soil disturbance and to foster the maintaining of a permanent vegetal cover in order to promote ecosystems services. We conducted a study to figure out how soil management in wheat field affect the biodiversity of species of direct agricultural interest (weeds, pests, beneficial arthropods), as well as the ecosystem services of regulation provided. We used molecular tools to assess precisely the diet of carabid beetles, and to unravel all trophic interactions, including all potential prey for carabids beetles. Thus, ecological trophic networks observed in conventional versus conservation wheat fields were constructed from the sequencing data's of predator gut contents.
We explored how soil management practices influence the structure of the trophic network. These ecological networks also give interesting insight in the seasonality and the compromise that can exist between ecosystems services.

Combining models of agricultural landscapes and soil-dwelling pest population dynamics to design novel management strategies against wireworms

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Abstract: Elaterid pest species exploit both cultivated and uncultivated areas in the agricultural mosaic. Understanding their movement from sources that sustain important populations, i.e. uncultivated areas, to vulnerable crops is central in the development of pest management strategies. Considering movement ecology and landscape ecology is then critical to design pest-resilient agroecosystems, particularly in the context of a dramatic reduction of the use of pesticides. The main objective of our study was to simulate the colonisation dynamics of click beetles and their larvae in agricultural landscapes, and discuss the implications for crop protection against wireworms.
First, we built a spatially-explicit and mechanistic model describing the pest population dynamics in both aerial and soil compartments along its life cycle. Larval and adult mortality, larval maturation, oviposition, and adult movements (in terms of diffusion and advection) were the main processes considered. Model parameterisation derives from a comprehensive review of the literature regarding the wireworm biology and ecology. Secondly, we modelled agricultural mosaics at two spatial scales: (i) the local level (i.e. a focal field and its adjacent land uses) comprising grasslands and arable crops, and (ii) the landscape level (about 2 km^2) using CAPFarm, a multi-year cover allocation simulator generating landscapes (here considering three land uses: arable crops, temporary and permanent grasslands) under agronomic constraints. In both cases, habitat quality was characterised in terms of carrying capacity. Combining these two framework components, we investigated how the spatial arrangement and dynamics of crops influence pest density distribution.
At the local level, model outputs show qualitative agreement with field observations. We outline how the balance between diffusion and advection can drive the population spillover on both sides of the transitions between land uses. We also demonstrate that spatiotemporal connectivity between grasslands affect the pest infestation levels within crops. At the landscape level, we studied correlations between metrics characterising the landscapes and levels of wireworm infestation to draw some interesting avenues to design beneficial spatiotemporal organisation of agricultural landscapes. Providing new insights into the role of grasslands in pest infestation in a dynamic agricultural mosaic, our findings bring an original contribution to the prospect of innovative landscape-scale strategies for pest management.

Providing the board and the lodging- How conservation agriculture can deal with its pests? Wireworms as case study

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Abstract: The sustainability of low-input and environment-friendly crop productions involve an overview of the services and dis-services that the agro-ecosystem could provide. Conservation Agriculture (CA), which combine the no-disturbance of soil, its permanent cover and crop diversification, has been introduced worldwide as a low-input system and is notably known to enhance soil physical properties such as erodibility, carbon storage or root penetration. This system, by not disturbing the ground, provides favourable conditions (i.e. "the lodging") for soil dwelling organisms including pests.

Wireworms, the larvae of click beetles (Coleoptera: Elateridae, Agriotes) are among the most notorious soil dwelling pests since long in Europe. Because of wireworms upsurge since 15 years, understanding their ecology and the factors influencing their pest potential have become a key issue in crop protection. Their life history traits lasting several years and taking place largely in soil, tillage may impact several parts of their life cycles. During the oviposition period in spring, females lay their eggs in the top soil layer as far as possible in a buffered environment such as litter or grass because of their own sensitivity to temperature fluctuation and eggs sensitivity to desiccation. After hatching, larvae are exposed to soil tillage, in particular to ploughing making them vulnerable to the predation or desiccation

In line with previous studies that put forward the hypothesis that reducing tillage will lead to a physically hospitable habitat to wireworms, the outcomes of our investigations in experimental platform or agricultural plots confirmed that reducing tillage rise wireworm populations. Previous studies also demonstrated the preference of click beetles for grass compared to bare soil and also the sensitivity of female to soil temperature variations. The outcomes of our monitoring showed that females lay their eggs in bare soil anyway and confirmed the population reduction under arable crops is due to the repeated disturbance of the soil.

Nevertheless, reducing tillage without combining it with soil permanent cover and crop diversification in association or sequence (i.e. rotations) only represents an incomplete implementation of CA. And both of these practices may, on one side, impact populations of ground and soil dwelling arthropods. For example, including cover crop such as Brassicaceae or buckwheat could reduce wireworms populations. On the other side, providing the "board" by covering soil with mulch or companion plant had been proven to lure wireworms away from the main crop and the mitigate their harmfullness.

Mutualism between the invasive mealybug Delottococcus aberiae and the mediterranean ant Lasius grandis in citrus crops

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Abstract: The exotic mealybug Delottococcus aberiae has become a key pest of citrus in Spain. D. aberiae excretes copious amounts of honeydew that can be exploited by ants. The aim of this work was to study the interactions between mediterranean ants and the invasive mealybug species. For this, we first sampled 16 citrus orchards in spring, summer and autumn of 2020 and 2021. The Mediterranean ant Lasius grandis represented 95% of the ant complex that attended the invasive mealybug. Ant attendance and absolute ant attendance (number of ants per colony) by L. grandis were positively correlated with the mealybug colony size. Finally, orchards with higher density of D. aberiae were associated with higher density of L. grandis. To further evaluate the benefit obtained by the mealybug from L. grandis attendance, we perform an ant-exclusion experiment in two additional orchards during two consecutive years. Ant-excluded trees reported lower D. aberiae density and damage, as well as a higher density of generalist predators. Overall, our results describe the mutualistic relationship between the Mediterranean ant L. grandis and the invasive mealybug D. aberiae and demonstrate that ant exclusion from citrus canopies can reduce D. aberiae damage up to 50% in Mediterranean citrus.

Testing the ‘Pay-back’ hypothesis in the field: Can bumblebee pollination ‘rescue’ seed production in cucumber mosaic virus-infected tomato plants?

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Abstract: The interactions between plants and associated insects are complex and often mediated by volatiles. Infection by viruses alters plant volatile signatures and consequently affects how insects interact with plants. In lab experiments cucumber mosaic virus (CMV) was shown to cause plants to emit volatile chemicals that attract bumblebees (Bombus terrestris) (Groen et al. 2016). Bumblebees are important tomato pollinators but do not transmit CMV. For wild plants under natural conditions, helping host reproduction by encouraging bee visitation, pollination and increased host reproduction might represent a ‘payback’ by the virus to susceptible hosts (Groen et al. 2016). Experiments in the summer of 2018 and 2019 tested this hypothesis for the first time under field conditions by comparing pollination rates and resulting seed set of CMV-infected and mock-inoculated tomato plants. In the field mock-inoculated plants produced similar numbers of seeds whether or not pollinators were excluded but CMV-infected plants produced a greater number of seeds when pollinators were allowed access to flowers. This is additional evidence supporting the idea that the virus is ‘paying back’ its susceptible host by attracting pollinators and aiding seed production. An additional aim of this work at Royal Horticultural Society is to further understand the interactions between plants, insects, and plant viruses in order to inform and benefit both amateur gardeners and the horticultural industry. Groen SC et al. PLoS Pathogens 12(8):e1005790

Problems and pitfalls of long-read sequencing in insect genomics

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Abstract: The advent of long-read sequencing technologies allow for a much more reliable genome assembly process than short-read sequencing ever did. More and more studies now focus on structural variations (e.g. insertions, deletions, inversions, tandem duplications, transposable element dynamics) between members of the same or closely related species.

Examples of new, unpublished genome data from a bee (Andrena vaga) and a butterfliy (Parnasius apollo) highlight different aspects of the state-of-art sequencing approaches: The apollo butterfly genome underwent a fourfold genome expansion in comparison to other papilionid lineages and exhibits a transposon content of >60%, with LINE elements forming the most abundant repeat class. The genome of the grey-backed mining bee (Andrena vaga) is similar in size, gene and transposon content to other bee genomes. Both genomes were also analysed intensively for gene and transposable element transfer from parasites, endosymbionts and food sources.

Phylogenomic analysis of Orthoptera sheds new light on the evolution of acoustic communication

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Abstract: Orthoptera (crickets, katydids and grasshoppers) is the most diverse group of organisms practicing acoustic communication extensively. Expectedly, it translates into highly diverse communication strategies. Yet, many species neither hear nor sing. Therefore, this group presents a unique opportunity to reveal important insights about the origin and evolution of animal communication. Using both transcriptomes and mitochondrial genomes, and an updated selection of relevant fossil species, we obtained a robust, time-calibrated phylogeny showing that Orthoptera broke silence 300 million years ago. Hearing likely evolved in the context of locating conspecific individuals based on their song. We show that the evolution of hearing and sound producing organs has followed complex and dynamic trajectories, with multiple origins and secondary losses, and that sexual communication using acoustic signalling alone was not a major driving force of orthopteran diversification.

At the miniaturization limit — results and prospects of studying the smallest insects

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Abstract: Size is one of the most important parameters of living and non-living things. Our age is an age of miniaturization. Miniaturization in electronics has made devices that used to occupy a whole room or even a building small enough to be carried in our pockets. But miniaturization is not only a trend in technology: it is also one of the trends in the evolution of life. Microinsects — the extremely diverse miniature insects less than a millimeter long — are one of the most intriguing components of this microworld. Having evolved to the size of unicellular organisms, the smallest insects managed not only to preserve structural complexity, but also to invent some novel features not found in larger insects. This talk is about comprehensive study of microinsects: from morphology to connectomics, from locomotion to genomics, and also about the potential benefits of the study of microinsects for solving fundamental scientific and biotechnological problems.

This study was supported by the Russian Science Foundation (project no. 22-14-00028).

Associative learning and memory in thrips

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Abstract: Associative learning is known in many groups of insects, but little is known about the learning abilities and memory of microinsects. Miniaturization causes many changes in the neural system, including reductions in the number of neurons. Nevertheless, associative learning has been shown in some groups of microinsects, mostly parasitic wasps; among non-parasitic microinsects, only beetles were also tested (Polilov et al., 2019); thrips (Thysanoptera), which are at most 2 mm long, have never been tested .

We designed an experimental setup for microinsects, based on the idea from Ofstad et al. (2011), where it was used for testing the visual place learning in Drosophila melanogaster. Our setup includes a thermal maze and an LED screen surrounding the maze. The temperature in the maze is too high for thrips, but the maze has four cooler spots (which the insect is supposed to find); the spots switch one by one together with the rotating visual stimuli on the screen. Thrips were experimented one at a time. Every experiment consisted of ten trials of searching, each followed by 1 minute of the thrips staying in the cool spot to memorize the visual stimulus. In addition, there were four tests of sector preference for each thrips: before the experiment, immediately after it, in 1 hour, and in 24 hours after the experiment. In these tests, the cool spots were switched off, while the visual stimuli on the screen were random. We checked whether the insect choses the target section (matching the stimulus) according to the visual learning it underwent.

Pairwise comparison of the lengths of the way in every trial shows that significant difference between test and control groups can be seen after 7 trials (t-test, $p < 0.05$). This may indicate that after seven trials the thrips form an association between the visual stimulus and the target spot; this association helps them find the spot sooner. Tests of sector preference performed immediately after all ten trials show that a majority of the insects follow the visual stimulus associated with the comfort spot in the maze (ANOVA Tukey test, $p < 0.05$). In the tests performed 1 hour later, the number of insects who preferred the target sector (supposed to match the cool spot) had decreased, but remained significantly different from the number of insects who preferred either of the three other spots ($p < 0.05$). The number of insects who follow the visual stimulus was also significantly higher in the 1-hour test than in the test before trials or in the control group ($p < 0.05$).

Thus, we have shown that thrips are not only capable of learning, but also have long-term memory that can be retained for at least one hour. Our study is the first to show such abilities in thrips . Learning capacity and retained principal cognitive abilities in these microinsects make them suitable models for cognitive and neurobiological experiments.

This study was supported by the Russian Science Foundation (project no. 19-74-10019).

Evolutionary genomics and implications of miniaturization in the parasitoid wasp Megaphragma amalphitanum

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Abstract: Body size reduction, also known as miniaturization, is an important evolutionary process that affects a number of physiological and phenotypic traits and helps animals conquer new ecological niches. However, this process is poorly understood at the molecular level. Here, we report genomic and transcriptomic features of arguably the smallest known insect – the parasitoid wasp, Megaphragma amalphitanum (Hymenoptera: Trichogrammatidae). In contrast to expectations, we find that the genome and transcriptome sizes of this parasitoid wasp are comparable to other members of the Chalcidoidea superfamily. Moreover, compared to other chalcid wasps the gene content of M. amalphitanum is remarkably conserved. Intriguingly, we observed significant changes in M. amalphitanum transposable element dynamics over time, in which an initial burst was followed by suppression of activity, possibly due to a recent reinforcement of the genome defense machinery. Overall, while the M. amalphitanum genomic data reveal certain features that may be linked to the unusual biological properties of this organism, miniaturization is not associated with a large decrease in genome complexity.

External morphology of the antennal sensilla of the smallest free-living insect Scydosella musawasensis (Coleoptera: Ptiliidae)

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Abstract: Miniaturization is a major evolutionary trend prominent in insects. Diminution of body size in some insect groups has resulted in insects comparable in size to some unicellular protists. The nervous systems and sense organs of insects have been considerably transformed by adaptation to extremely small size. The miniaturization-related changes in the complex multimodal sense organs of the antennae are of special interest in this context.

Scydosella musawasensis (Coleoptera: Ptiliidae) is the smallest free-living insect, with a body length of the smallest measured specimens only 325 µm. We have studied the antennal sensilla of S. musawasensis using scanning electron microscopy and described their sizes, external morphological features, and distribution. Eight different morphological types of sensilla have been revealed: sensilla chaetica, four types of sensilla trichodea, sensilla styloconica, and two types of sensilla basiconica. The numbers of sensilla of all types are identical in males and females. Comparative analysis with the available published data on the larger Coleoptera has revealed a decrease in the number of antennal sensilla with decreasing body size; S. musawasensis has only 124 sensilla per antenna. The revealed size-related trends in free-living insects have been compared with those determined earlier in the miniature parasitoid wasps Megaphragma spp. (Hymenoptera: Trichogrammatidae), which have a body size of about 200 µm. S. musawasensis has three times as many antennal sensilla as Megaphragma wasps, which demonstrate pronounced sexual dimorphism in the numbers and types of these sensilla.

Our data contributes to the morphological, functional and evolutionary context needed for understanding the effects of miniaturization on the structure of the brain and sensory organs of microinsects. Together with our earlier data, the results of this study reveal the universal principles of antennal miniaturization: extreme level of optimization combined with retention of high functionality of the antennal sensory system.

This study was supported by the Russian Foundation for Basic Research (project no. 19-34-90162).

Flight kinematics of the miniature parasitoid wasp Megaphragma amalphitanum

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Abstract: The study of insect flight is a large area of modern entomology, closely related to biomechanics and aerodynamics. Studying the flight of microinsects is a technically difficult task. Most work in this area has been done during the last few years.

Our group recentlyaccurately described the morphological and kinematic adaptations to flight at low Reynolds numbers in the miniature beetle Paratuposa placentis. Microinsects are a polyphyletic group, but many of them have acquired similar adaptations to flight at low Reynolds numbers, such as the bristled wings found in most flying microinsects. However, there are important differences in the details of structure of their wing apparatuses, which probably affect the mechanics of flight.

Some of the smallest body sizes among flying insects are found among parasitic wasps of the family Trichogrammatidae. The body length of one of the smallest species of this family, Megaphragma amalphitanum, is only about 250 μm.

We designed an experimental setup that made it possible to perform macro video recording of the flight of M. amalphitanum using four synchronized high-speed cameras. We reconstructed the kinematics of the flight using frame-by-frame triangulation of landmarks on the wing and body. The averaged wing cycle and pitch oscillations of the body were mathematically described in the system of Euler angles. The angles of attack speed of the wings at all stages of the wing cycle, and Reynolds numbers were calculated. Additionally, we reconstructed the flight trajectories of the wasps in spacious boxes and calculated flight speeds and accelerations.

M. amalphitanum is capable of active flapping flight at considerable speeds up to 1000 body lengths per second: average and maximum flight velocity are 0.06 and 0.25 m/s, respectively; maximum acceleration is 4.19 m/s2. The average Reynolds number during the wing cycle is about 3, which means that viscous friction forces are prevalent, and the leakiness between the bristles must be quite low. During both translations, the angle of attack and wing velocity are high: 50 degrees and 0.12 m/s during the downstroke and 80 degrees and 0.27 m/s during the upstroke. During the recovery stroke between downstroke and upstroke, the wings clap and move slowly at near-zero angles of attack, which apparently reduce the unwanted drag of the wings. Stroke amplitude is 140 degrees. Pitch angle reaches its minimum value at the end of translational phase of the upstroke (2 degrees). The maximum angle of attack is reached by the end of the recovery stroke (50 degrees). Deviation angle varies from 17 degrees during the downstroke to 125 degrees during the upstroke. Wingbeat frequency is 276 Hz.

The estimated aerodynamic features revealed in our study and unusual kinematics of the operation of the microwasp wings are an important adaptation to flight at ultra-low Reynolds numbers, under conditions of prevalent viscous friction forces.

This study has been supported by the Russian Foundation for Basic Research (project no. 22-74-10010).

Functional mapping of the ommatidia based on a complete reconstruction of the compound eye of Megaphragma (Hymenoptera: Trichogrammatidae)

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Abstract: Compound eyes are among the most complex and important sense organs. The structure and morphofunctional specializations of the ommatidia in insect compound eyes have been described for years using light and electron microscopy. The current understanding of the cellular organization is based mostly on 2D data collected on single retinotopic sections. The new age of 3D electron microscopy gives access to the precise cellular and subcellular reconstructions of whole eyes as well as synaptic configurations of the insect's visual system. That helps us better understand the analyzer–neuron interactions in visual processing modeling.

The whole head of Megaphragma amalphitanum was scanned on a double-beam microscope (FIB-SEM) with a resolution of 8 nm per pixel for all xyz measurements. As a result, we provide the first detailed complete 3D reconstruction of the compound eye at the cellular and subcellular levels. Our complex morphological analysis of each photoreceptor position, diameters and shapes of the rhabdoms, volumes of cell bodies and rhabdomeres, orientation angles of microvilli along the rhabdom axis, diameters and curvature of each of the lenses and general optic parameters calculations gives us unique data and constitute the first steps of functional mapping of the eye. The shapes and lengths of cones, degrees of lenses curvature, and shapes of the rhabdom are markedly different in the dorsal rim ommatidia and in the regular ones. Specialized microvilli orientation angle along the rhabdom in ommatidia of the dorsal rim area (DRA) most likely indicates an increased sensitivity to polarized light. Our findings show the strict morphological difference between the morphology of seven facets of DRA ommatidia and is consistent with cartridge connectivity trends reconstructed in collaboration with Dmitry Chklovskii team (Flatiron Institute).

The organization of compound eyes and possible functional mapping in minute wasps are of particular interest and show that even the smallest eyes retain functional specialization areas. Due to its small body size and unique adaptations of its miniaturized nervous system, Megaphragma can be used as a model for the study of brain neuroarchitecture.

This study was supported by the Russian Science Foundation (project no. 22-14-00028).

Wing folding and unfolding in featherwing beetles (Coleoptera: Ptiliidae)

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Abstract: Most adult beetles (Insecta: Coleoptera) are capable of folding their hindwings under the protective cover of the modified forewings (elytra) and unfolding them before flight. Beetles of the family Ptiliidae, which in most cases have a body length smaller than 1 mm and include the smallest free-living (non-parasitic) insects, are no exception: most ptiliids fly and are able to fold and unfold their bristled wings (a condition known as ptiloptery). This ability makes them unique among microinsects. The details of the two processes have been unclear, and the mechanics behind them remains almost a mystery.

We have studied the wings, mechanisms of their folding and unfolding, and various structures involved in these mechanisms, in representatives of different groups of Ptiliidae, and the analyzed distribution of resilin in the wings of some species, using light, scanning electron, and confocal microscopy and high-speed video recording. Our results show that ptiliids have two different types of positioning the folded wings; the wings are folded using a complex mechanism involving several structures and unfolded largely by the elasticity provided by resilin.

In the generally larger and less specialized basal genera, the wings are folded by bending along several diagonal lines and asymmetrically overlap at rest under the elytra, in a manner similar to Staphylinidae (Saito et al., 2014); in the other ptiliid genera, the wings are folded symmetrically, without overlapping, by bending at four points along lines subperpendicular to the axis of the wing. The setae, especially in the smaller, more advanced genera, are also folded, by bending at their bases, and lie subparallel to the wing blade. In the genus Ptenidium the wings have an additional fifth bending line.

The complex mechanism of folding and unfolding the feather-like wings involves several elements of the microsculpture of the elytra and different elements of the pterothoracic and abdominal dorsum, especially abdominal tergites.

Remarkably, the wings of ptiliids contain only a single cavity, situated basally in the petiole and in the proximal portion of RA4 in the wing blade, and no cavities within any other veins. Therefore, the folding and unfolding of the wings largely depend on the flexibility and resilience of the cuticle, and can only partly be guided by changes in the pressure of the haemolymph within the veins.

The distribution of resilin in the wing is uneven: it is concentrated in the areas that bend during folding and unbend during unfolding. Resilin must also play a role in the flexibility of the wing during flight. In the studied ptiliids the wings in flight can bend at an amplitude of at least 17 degrees.

Our results show that ptiliids have evolved a set of features that make their miniaturized wings easily foldable and unfoldable. These features may have contributed to the evolutionary success of ptiliids as the smallest free-living insects.

The study was supported by the Russian Science Foundation (project no. 22-14-00028).

Colony Decline Influenced by Highbush Blueberry Pollination Services in New Jersey, USA

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Abstract: On-farm pollination treatments were established to verify colony decline during blueberry pollination services. Four treatments were replicated 3 times, with hives placed on: 1) large farms, 2) small farms, 3) large farms followed by cranberry pollination, and 4) control (no pollination services). Hives were measured throughout the 3-4 week pollination period for brood growth, weight, queen rightness, parasite and disease incidence, and pesticide residues. Colony weight and brood growth differed among treatments. Varroa mites and viruses showed no differences between treatments. Pollen and wax samples were taken during the middle of each pollination period, and subjected to a screening of 199 active ingredient residues or metabolites. We found residues from 7 insecticides, 7 miticides, 9 herbicides and 14 fungicides. Many of these residues result from labeled applications made just prior to and during bloom. Recent research by various investigators has implicated the negative impacts of several fungicides on honey bee health. Some work has shown additive or synergistic effects of certain IRAC insecticide classes when combined with FRAC fungicide groups. Our overall feeding tests have also shown bee mortality. Because of the many residues found in hives used for blueberry pollination, detailed studies on the impact of these materials, and current pest management practices have on colony health are justified.

Comparison of the relative rate of vectoring microbes by a primary and secondary stored product pest, after varying dispersal periods: Which is the greater threat?

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Abstract: Generally, few studies have assessed how stored product insects and stored product microbes interact after harvest. As a result, the relative frequency with which primary and secondary stored product insect species vector microbes has not been extensively studied. Knowing the relative risk posed by each type of insect is important for knowing how likely it is that microbes are to be introduced to postharvest commodities after the immigration of insects to novel food patches at food facilities from the landscape. Thus, the aim of the current study was to evaluate and compare the microbial growth in surrogate food patches after 3 or 5 d of foraging by Sitophilus oryzae (a primary pest) and Lasioderma serricorne (a secondary pest). Prior to entry to the food patch, insects were either given no dispersal period, or a dispersal period of 24 or 72 h in a sterilized environment. Increasing dispersal time resulted in multiple-fold reduced microbial contamination in novel food patches by L. serricorne, and S. oryzae. This was likely attributable to mechanically moving spores after emigration from each food patch. Our data suggests that there an equal and persistent risk of microbial contamination by both species, which has repercussions for food safety at food facilities.

Experiments, simulations, and modelling to assess with how many diets a population is made

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Abstract: While habitat quality early in life has long-lasting consequences to current and future generation' individual fitness, population dynamics and evolutionary trajectories, measuring the degree of heterogeneity in developmental habitat quality from population data can be cumbersome. As a result, heterogeneity in developmental habitat quality is often measured through phenotypic markers (e.g., maternal factors) or the population is assumed to be homogenous with respect to developmental habitats. Here, we provide a mixture-model framework which allows or a refined ecological estimate of habitat-specific population dynamic processes when developmental habitat qualities are unobserved. Combined a fully-factorial experiment with in silico population assembly, we firstly showed that nutrition conspecific density of the developmental habitat can strongly modulate individual fitness and population growth of the polyphagous fruit fly Bactrocera tryoni. We then used a mixture-model approach to infer the range of potential habitats mixtures which compose populations solely from population growth data. Thus, the mixture-model framework can be used to estimate heterogeneity in developmental habitat quality from field data where direct measurement of developmental habitat quality is impractical or unavailable, thereby providing an additional statistical modelling tool to better understand habitat-specific population dynamics in population ecology.

New Methods of rearing Queensland Fruit Fly (Bactrocera tryoni) for sterile insect releases; Gel diets, X-Rays and new strains

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Abstract: Bactrocera tryoni (Queensland Fruit Fly (QFF)) is the major Fruit Fly pest in Australia and over the past decade has spread to southern New South Wales (NSW) and Victoria into areas previously though unsuitable for its establishment. South Australia (SA), Tasmania and Western Australia remain free of QFF mainly due to stringent internal quarantine and interstate trade requirements. While QFF was the first Tephritid to be managed using SIT in Australia, for eradication of an outbreak in Western Australia, the program has only been serviced by a pilot facility in NSW with flies either used for research or by SA for eradication purposes. In 2013 a decision was made by PIRSA/Biosecurity SA and Horticulture Innovation Australia to build a new facility at Pt Augusta in South Australia, this led to a consortium (SITplus) including Macquarie University, CSIRO, Plant and Food Australia being established to complete the project. To achieve the desired production levels within budget limitations innovations were required within the production system and due to community resistance and the costs associated with Gamma cell irradiators' alternate irradiation systems were investigated. In addition to the facility design and development a research program to develop a Genetic Sexing Strain using genetic techniques such as CRISPR was established to improve the efficiency of the facility and efficacy of releases. An agar based diet gel was developed by Macquarie University that has allowed greater pupae production per unit of floor space and greatly reduced volume of waste. Rearing equipment at the facility has been developed to complement the gel diet and best suit the facility operations. The diet currently produces approximately 15,000 pupae per litre, at a cost of A$2.83 compared to 5-6000 from the long used chaff diet.

Two RadSource X-Ray irradiators have been purchased for sterilisation of pupae, extensive sterility and DNA damage evaluation demonstrate that the relative sterility achieved at a range of doses corresponds to that recorded using a Gamma cell irradiation source. This also provided an opportunity to test the sensitivity and accuracy of a kit developed, as a joint SARDI/Macquarie University project, to measure exposure to prior irradiation for SIT or phytosanitary purposes.

CRISPr was originally assessed as a suitable tool for gene editing in QFF by generating a white eye strain, which is blind, but can potentially be used as a functionally male only strain if the males can be recovered. In the absence of a known tsl gene for tephritids initial edits used the Shibire tsl 1 from Drosophilla and although a heterozygote strain was generated the change was lethal to homozygotes. The project identified a gene associated with pupal colour and a pupal colour mutant strain has been generated using CRISPr. Further strains using other targeted mutations are being developed.

Effects of nutritional status on infection at single and multi-generational levels

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Abstract: Nutrition is a key aspect of individuals' biology. While there is a growing interest on the role of nutrition in lifespan and reproduction, the implications of nutrient choice and intake to infection remain largely unexplored. This is unfortunate because in nature, individuals are exposed to a wide variety of infection challenges that can compromise their fitness and redirect the evolutionary trajectories of populations. The research of my team focuses in better understanding the network of interactions that defines the relationships between nutrition, immunity, and infection, to provide a more comprehensive understanding of the key determinants of the outcome of host–pathogen interactions. During this talk, I will harness the power of the vinegar fly Drosophila melanogaster and the fruit fly Bactrocera tryoni to investigate how nutritional status affects infection at a single and multi-generational levels, manipulating maternal and paternal diets. We performed a detailed investigation of the effects of diet composition pre-infection on host's survival and pathogen population growth after a septic bacterial infection. Nutritional responses and fitness-related traits were also measured. Together, our findings provide a better understanding of the relationship between diet, infection and transgenerational effects, and reveal an important but complex pattern whereby parental diet influences offspring responses to bacterial infections.

Protein changes the relationship between immune gene expression and immunity

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Abstract: Nutrition is vital to health and the availability of resources has long been acknowledged as a key factor in the ability to fight off parasites. However, the relationship between resources and immunity has typically been simplified to a single currency, such as ‘energy’, which masks the variablity intrinsic to the diet. Here we use a state-space modelling approach, the Geometric Framework for Nutrition (GFN), to assess how the balance and amount of nutrients affects an animal’s ability to mount an immune response to a pathogenic infection.
Spodoptera littoralis caterpillars were assigned to one of 20 diets that systematically varied in their protein:carbohydrate ratio and their calorie content. Caterpillars were then handled or injected with either live or dead Xenorhabdus nematophila bacterial cells. Gene expression was measured 20 h post immune challenge. For two of the immune genes (PPO and Lysozyme) we also measured the relevant functional immune response in the hemolymph. Gene expression and functional immune responses were then mapped against nutritional intake.
The expression of all immune genes was up-regulated by injection with dead bacteria, but only those in the IMD pathway (responds to Gram -ve bacteria) were substantially up-regulated by both dead and live bacterial challenge. The availability of protein was the most important predictor of the functional (physiological) immune responses but immune gene expression responded quite differently to dietary manipulation, such that the correlation between gene expression and the functional immune response changed with the availability of protein in the diet. Ultimately, we would caution against using gene expression as a proxy for immune investment, as it is unlikely to be reliable indicator of the functional immune response, except under specific dietary conditions.

Potential of biopesticides and optimising the use of conventional insecticides for the control of cabbage stem flea beetle (Psylliodes chrysocephala)

Authors: Pope Tom[1], Hoarau Claire[1], Chandler Dave[2], Prince Gill[4] and Campbell Heather[1], [1]Harper Adams University, United Kingdom, [2]University of Warwick, United Kingdom

Abstract: Cabbage stem flea beetle (CSFB; Psylliodes chrysocephala) is one of the most important pests of oilseed rape. Adults feed on cotyledons and first true leaves, while larvae mine petioles and stems. Yield losses due to adults and larvae typically range between 5 and 15%.

Since the ban in 2018 by the EU on the use of neonicotinoid seed treatments, the only insecticides used to control CSFB are pyrethroids. However, many CSFB populations in the UK have developed resistance against pyrethroids, rendering their use ineffective, and harmful to natural enemies and pollinators.

It is then of the utmost importance to find alternative ways to control CSFB populations. Biopesticides, such as entomopathogenic fungi, bacteria and nematodes, have been subject of many studies over the past decades and their efficacy has been demonstrated against other flea beetles species (e.g. Phylloletra cruciferae). These biopesticides include 1) fungi species of the genus Metarhizium spp. (M. anisopliae and M. brunneum) and Beauveria bassiana; 2) nematodes from the genera Steinernema spp. and Heterorhabditis spp.; 3) bacteria such as Bacillus thuringiensis; 4) plant extracts such as azadirachtin (extract of neem).

The aim of this project is to identify the most effective biopesticides, either applied alone, or combined with each other and/or with pyrethroids. The suitability of the use of these biopesticides in commercial situations will be evaluated, the ultimate goal being to find a feasible solution for oilseed rape producers impacted by this pest.

Towards integrated pest management of vine weevil (Otiorhynchus sulcatus)

Authors: Pope Tom[1], Roberts Joe[1] and Hall David[2], [1]Harper Adams University, United Kingdom, [2]University of Greenwich - Natural Resources Institute, United Kingdom

Abstract: Vine weevil, also known as black vine weevil (Otiorhynchus sulcatus), remains an economically important pest of a wide range of protected crops, including soft fruit and ornamentals. The last 30 years has seen many changes in crop protection practices, including wide-scale adoption of biological controls such as entomopathogenic nematodes in place of conventional synthetic insecticides. Despite these changes, growers continue to report significant crop losses associated with vine weevil infestation. Here we argue that more effective control will only be achieved when biological controls are used as part of an integrated pest management (IPM) programme and not simply as direct replacements for synthetic insecticides. We identify vine weevil biology, forecasting, monitoring and action thresholds as areas in which improved knowledge is required and report results from research addressing these aspects of vine weevil IPM.

Ecological traits of cabbage moth (Mamestra brassicae) in relation to IPM

Authors: Popov Sergei, Russian State Agrarian University - Moscow Timiryazev Agricultural Academy, Russia

Abstract: Cabbage moth, Mamestra brassicae (L.) (Lepidoptera: Noctuidae), is one of the main pests of cabbage in Moscow region, Russia. Different ecological traits of the pest were investigated in laboratory and cabbage fields during a period of 25 years. The aim of those studies was to find bottlenecks in the insect's ecology and, by manipulating them, to reduce the insecticide pressure in cabbage fields. Based on the economic injury level of one 5th instar per cabbage head, we calculated survival coefficients for caterpillars during different developmental age intervals, and created mathematic models (equations) of predicted critical population densities of M. brassicae. On the basis of k-factor life tables constructed for different cultivars of white cabbage, we found that the first two instars suffered the highest mortality. Virtually no biotic mortality factors were detected for those instars, leading to a recommendation to target them with insecticide applications. We also screened the effects of numerous F1 hybrids of white cabbage and broccoli on the life history traits of M. brassicae. Resistant cabbage hybrids could be detected under field conditions were established by quantifying the smallest egg clutches. Our findings allow optimizing the IPM program against cabbage moth.

Searching ants meander regularly and avoid crossing their own paths

Authors: Popp Stefan, University of Arizona, United States

Abstract: The evolution of behavioral traits is shaped by the benefits and costs to fitness they confer; therefore, measuring how these benefits and costs are shaped by the environment is a critical element in studies of evolution. Here I review both theoretical and empirical approaches and their surprising results for what fitness effects communication in social groups can have. Social insects like bees and ants have evolved particularly diverse and sophisticated means of communication, and we demonstrate that these are critically shaped by the resource environment and group size, but not always in intuitive ways. In particular, communication can reduce efficiency through opportunity costs, and reduce flexibility through decreased innovation. The talk will emphasize how models can be integrated with experiments to yield novel insights.

Combining landscape and functional trait research to build natural pest control in crops

Authors: Poppenborg Martin Emily A[3], Steffan-Dewenter Ingolf[3], Dainese Matteo[1], Alexandridis Nikos[2] and Clough Yann[2], [1]EURAC Bozen, Italy, [2]Lund University, Sweden, [3]University of Wuerzburg, Germany

Abstract: Managing agricultural landscapes to support biodiversity and natural pest control could be a key avenue towards sustainable and climate-resilient agriculture that works for farmers. However, precisely how to manage these landscapes – and how effective this will be - is unclear. In a synthesis of data from 49 studies (1,515 landscapes) across Europe, we examined how landscape composition (% semi-natural habitat and arable land) and configuration (density of edges including crop/crop and crop/non-crop boundaries) impact arthropods in fields and their margins, pest control, and yields. We show that edge density interacted with proportions of crop and non-crop habitats, and separating species according to dietary, dispersal and overwintering traits led to contrasting responses. Overall, highest total arthropod densities were reached in landscapes combining high amounts of non-crop habitat and high edge density. In landscapes with high edge density, 44% of natural enemy species, including particularly species not known to overwinter in crop fields, reached highest densities, and pest control improved 1.4-fold. Based on these results and on key combinations of species' traits, pathways to predictively assess natural pest control potential can be derived to anticipate the effects of landscape- and field-scale management, towards a workable ecological intensification of agricultural production under global change.

Two-sex Life Table Analysis and Developmental Rates for Nezara viridula (Heteroptera: Pentatomiade) reared with two artificial diets.

Authors: Portilla Maribel, USDA-ARS-Southern Insect Management Research Unit. Stoneville, MS, United States

Abstract: Two artificial diets, including the fresh yolk chicken egg based-diet (FYD) and dry yolk chicken egg based-diet (DYD) used for Lygus spp. were evaluated as an alternative food source for rearing the southern green stink bug, Nezara viridula (L.) (Heteroptera: Pentatomidae). Fresh and dry yolk diets had survival to adult stages, of 97.33% and 74.57%, respectively. The FYD had 100% survival from first through fourth instars. Adult Development was significantly shorter on the FYD (30.37 ± SE 0.30 days) versus the DYD (32.77 ± SE 0.16 days). Longer male and female longevity, higher fecundity, and larger egg mass sizes were found on the FYD. However, fertility and hatchability was higher on the DYD. A complete cohort life table incorporating both sexes and variable developmental rates among individuals was constructed and a novel rearing method for N. viridula was developed.

Mass rearing of Lygus lineolaris (Palison de Beauvois) (Hemiptera: Miridae) as a possible alternative for mass production of the egg parasitoid Anaphes iole (Giraul)

Authors: Portilla Maribel, USDA-ARS-Southern Insect Management Research Unit. Stoneville, MS, United States

Abstract: Two artificial diets developed for rearing Lygus spp., a none-autoclaved and an autoclaved yolk chicken egg-based diets were evaluated as a media to support a mass rearing system for the tarnished plant bug. This study was carried out at the USDA, ARS, SIMRU in Stoneville, MS. Lygus lineolaris Palison de Beauvois (Hemiptera: Miridae) was reared according to the method described by Portilla et al. 2011. Survival to adult, sex ratio, and first, second, and third instar nymphal mortality were not different between diets. Daily egg production was significantly greater in the none-autoclaved diet with 9806.91 ± 302 versus 5953.32 ± 316 eggs per day/ cage for the autoclaved diet. The cumulative egg production of L. lineolaris was significantly higher in the none-autoclaved diet (over 98,000 eggs produced in 10 days/cage) compared to cumulative egg production observed for the autoclaved diet (59,000 eggs/ cage). The percentage of no-embryo eggs produced per day was lower for the none-autoclaved diet, and the fertility and hatchability rates were higher than in the autoclaved diet. The greater egg production, lower fourth-fifth instar nymphal mortality, and higher hatchability rate obtained in the none-autoclaved diet resulted in a greater biomass accumulation. The none-autoclaved artificial diet was prepared in a single-step process, thereby avoiding the multi-step process for the autoclaved diet. The none-autoclaved diet is less expensive and requires less time for diet preparation than the autoclaved diet. This rearing system will be use in a near future for mass production of Anaphes iole Giraul (Hymenoptera: Mymaridae) egg parasitoid of Lygus spp.

Biological control with parasitoids: from the study of insect ecology to the optimisation of a biological control programme

Authors: Postic Estelle[1], Outreman Yannick[2] and Le Ralec Anne[2], [1]Frais'Nat, France, [2]Institut Agro Rennes-Angers

Abstract: Hymenopteran parasitoids can be mass-reared for release into greenhouse crops, where augmentative biological control is widely used. In particular, parasitoids are reared to control various species of aphid pests. However, in some cases, like in strawberry greenhouses, biological control of aphids remains inefficient. Thus, by studying aphid and parasitoid communities in the main regions of strawberry production in France, we studied the ecological and evolutionary determinants of the effectiveness of a biological control programme. The study of aphid and parasitoid communities spontaneously colonising the greenhouses allowed to identify the species most adapted to aphid regulation. Our work also shows that aphids are often infected by bacterial symbionts that can confer resistance to the released parasitoids. Finally, the analysis of genetic variability within populations of wild and commercial parasitoids revealed a genetic differentiation between these natural and mass-produced beneficials. As this differentiation is associated with a loss of genetic diversity in commercialized populations, the question of their effectiveness against aphids arises. This work led French strawberry growers to create their own parasitoid production specifically dedicated to controlling aphids in strawberry crops. This will make it possible to adapt parasitoid mass-rearing to the particular constraints related to strawberry crops.

Photonic e-traps for Lepidoptera

Authors: Potamitis Ilyas, Hellenic Mediterranean University, Greece

Abstract: Helicoverpa armigera is an insect-pest that belongs to the order of Lepidoptera. It is also known as the cotton bollworm and feeds on a wide range of plants, including many important cultivated crops such as cotton, tomatoes, maize, chickpeas, alfalfa, and tobacco. We monitor automatically their population in the field to detect the onset of the infestation and also assess the current and aftertreatment density of the pest so that we proceed timely to control measures (e.g. spraying). The electronic funnel trap (e-funnel) is an optical counter attached to typical, plastic, funnel traps to automatically count all captured Lepidoptera species with known pheromone. As an insect falls in the bucket, it interrupts a flow of infrared light, and the resulting voltage fluctuation is turned to a count. The counts as well as environmental data and GPS coordinates are transmitted using the GPRS mobile network from the field to a server that streamlines and visualizes data from all e-traps.

We will present detailed analysis of a 3-months monitoring period from 5 e-traps and we will talk about how we can use historical data to predict the future infestation load in the field.

Funded by the project 'Bioacoustics applications' 80680

Use of vibratory signals for the detection and monitoring of stored product pests

Authors: Potamitis Ilyas[1], Eliopoulos Panagiotis[2], [1]Hellenic Mediterranean University, Greece, [2]University of Thessaly, Dept. of Agriculture & Agrotechnology, Larissa, Greece

Abstract: Pest detection in grain storages is mainly achieved today by inefficient and time consuming methods such as visual inspection, sieving, Berlese funnels and trapping. Some other analytical and more sophisticated methods such as carbon dioxide measurement, uric acid measurement, near-infrared spectroscopy, and soft X-ray have demonstrated great potential in the lab. However, most of them are cost prohibitive and require complex operating procedures and calibrations. Insect pests of stored grains and pulses produce vibratory signals by moving, feeding or ovipositing inside the grain mass. These sounds can be used not only for detection purposes, but also for population density estimation. During the last decade, several published studies investigated the potential of bioacoustics as an alternative method for accurate, fast, non-destructive and automated detection of the insects' presence inside the stored grain mass. Moreover, reliability and efficacy of acoustic pest detection has been greatly increased in the last few years as a result of the development of improved acoustic devices and signal processing methods. Today, acoustic devices are commercially available for the continuous and automated detection and monitoring not only for adults but also for larval stages that are hidden inside infested kernels. The present study focuses on the advantages of acoustics in comparison with traditional detection methods (trapping, sampling, sieving etc), its potential for improvement (more sensitive sound technology, signal processing, machine learning techniques etc.), acoustic systems that are currently available in the market (probe piezoelectric sensors, amplifiers, software etc), and limitations for practical application (cost of acoustic technology, background noises, interpretation of acoustic emissions, multiple infestations, farmers' technical training etc.). Potential areas for growth in the use of acoustic technology in detecting and monitoring stored product pests are discussed on the basis of Integrated Pest Management in storage facilities.

Insect Surveillance meets IoT and Artificial Intelligence

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Abstract: Precision agriculture is about managing variations in the field to increase crop yield, raise productivity and reduce consumption of agricultural inputs. Agriculture remains greatly unpenetrated by IoT technologies, but perspectives are positive about future market trends. Especially, as far as crop protection from insect – pests is concerned, numerous automated, electronic devices have been developed, evaluated and marketed as insect monitoring traps.

In our vision a pest-detection device is not just a plastic bucket, it is a 'thing'. That means a cyber physical object. In even simpler words a bucket that can report wirelessly a parameter of interest (usually insect counts, environmental parameters but in some cases, more complex data). Therefore, they have at least a sensor and wireless communication. The trap is addressable meaning through a server you can direct yourself through the network of traps and reach any trap to see what is happening (e.g. listen to vibrations, see pictures, plot counts/per day). You can also see collective results of the network of traps on a map. Finally, telemetry can be applied: Meaning that the functioning of the traps and their internal state can be monitored to predict malfunction, automatic update of firmware etc.

Many traps together that report a small number of parameters (insect counts and environmental data) can form a network that has its own internet functionality (an Internet of Things - IoT). This network based on LoRa/WAN can expand practically to hundred of nodes if the traps are dispersed few kilometers one from another. The traps can be self-organized in networks that collectively report data usually at local and regional level but, in principle, could be expanded at global scales.

Artificial Intelligence comes in when the number of reported records scales to thousands. Then, one needs an automatic method to process the records to infer the infestation state. In this presentation, we will focus only in cases that have reached TRL 9.

The Internet of Bees (IoBee)

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Abstract: The internet of bees, or IoBee, is a project funded by the European Commission which aims to explore different technologies for the improvement of bee health. Finalising in April 2020, the project helped develop key innovations including (i) monitoring tool for foraging activity at the entrances of honeybee hives; (ii) sensing device for the density and diversity of wild pollinators in the field; (iii) optical-based identification of insects based on colour recognition; and (iv) big data collection and the processing and analysis of spatial information. A bee counter closely monitors activity at the entrance of the beehives, which gives valuable insights into its strength, dynamism, or presence of potential predators. Besides, in-field sensors identify both the density and diversity of pollinators as well as invasive insect species. Sensors can be applied in apiaries, crops and landscape features to establish sentinel networks and the generation of risk/pollination maps. Thirdly, satellite imaging provides phenology historical data and model predictions through the application of Spatial Decision Support Systems (SDSS). Finally, a platform integrating data generated by the ground sensors, coupled with satellite data for vegetation, ground temperatures and other environmental variables, as well as beekeepers' observations, can provide intelligent warning systems. These predictive tools will serve field practitioners such as beekeepers, farmers or land managers to aid management decisions concerning nectar flows, risks of infestations from pests, or pollination potential. The data has the scope to inform public bodies and governmental authorities with decisions on pollinator conservation, land management and climate change.

Feeding Ecology of the Japanese Beetle (Popillia japonica), a Biosecurity Threat to European Agriculture and Beyond

Authors: Potter Daniel, Department of Entomology University of Kentucky, United States

Abstract: The Japanese beetle (JB), among the most destructive invasive pests in North America, was first detected in continental Europe, in northern Italy, in 2014. Because of its broad host range (> 300 plant species) and propensity for its grubs and adults to be transported in commerce, JB is poised to become a major horticultural pest throughout much of temperate Europe. This talk summarizes research on adult JB feeding ecology and applications to pest management. JB are mildly attracted to constitutive volatiles from many plant species regardless of their suitability as hosts. Plant secondary chemistry drives acceptance/rejection at leaf surface. Additional JB are attracted to feeding-induced plant volatiles resulting in aggregation and rapid defoliation of preferred hosts. Most mating occurs on host plants, so induced odors serve as an indicator of others feeding on a high-quality host. JB also bite in to ripe fruits, directly damaging them and contaminating them with yeasts that elicit fermentation volatiles that attract secondary fruit-feeding pests. Applications of this research including use of pheromone-kairomone lures and host plant resistance in management of JB will be discussed.

Japanese beetles' feeding on milkweed flowers may compromise efforts to restore monarch butterfly habitat

Authors: Potter Daniel[1], Baker Adam[2], [1]Department of Entomology University of Kentucky, United States, [2]University of Kentucky, United States

Abstract: The eastern North American migratory population of monarch butterflies (Danaus plexippus) is in serious decline. Habitat restoration, including adding millions of host plants to compensate for loss of milkweed in US cropland, is a key part of the international conservation strategy to return this iconic butterfly to sustainable status. We report here that Popillia japonica, a polyphagous, invasive beetle, aggregates and feeds on flowers of Asclepias syriaca, the monarch's most important larval food plant, reducing fruiting and seed set by >90% and extensively damaging milkweed umbels in the field. The beetle's ongoing incursion into the monarch's key breeding grounds in the US Midwest is likely to limit pollination and outcrossing of wild and planted milkweeds, reducing their capacity to colonize new areas via seeds. Popillia japonica represents a previously undocumented threat to milkweeds that should be considered in models for monarch habitat restoration.

Enhancing biological control of Popillia japonica through a better understanding of parasitoid biology and behavior

Natural habitat mitigates negative pesticide effects on bee diversity in a traditional Andean crop

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Abstract: Wild bee communities provide key pollination services to achieve optimum crop yields. There is evidence that the loss of natural habitat and pesticides are two of the main factors contributing to bee declines, however, the interaction of these two stressors has not been much explored. Solanum quitoense, known as “lulo”, is an Andean fruit used for fresh consumption. Despite the economic importance of this crop for local communities, there is very little information about its pollinator dependency and the bee community-associated. In this study made in the Colombian Andes, we characterized the flower visitors and the change in abundance and richness of bees visiting lulo crops in ten farms that differed in landscape composition and pesticide use. In every farm, we calculated the landcover proportions (natural habitat, pastures, and agriculture) at 500m around the center of every crop field. We collected anthers from ten different plants in every farm to test with UHPLC for nine pesticide molecules commonly used in the area (Methomyl, Abamectin, Bifenthrin, Imidacloprid, Profenofos, Lufenuron, Cymoxanil, Difenoconazole, and Propamocarb). Bees were sampled in three events during the dry season with two observers walking for 30 minutes during warm and sunny days from 9:00 to 16:00h stopping and recording the identity and the number of bees observed visiting the flowers. We also estimated the contribution of pollinators to fruit production (Fruit set, fruit weight, and fruit diameter) in an exclusion experiment bagging inflorescences in 20 plants per farm. We recorded 650 visits from 16 bee species in 6 tribes. Tetragonisca angustula and Paratrigona opaca were two of the most frequent visitors. We found a reduction of 51% in fruit set when visitors were excluded, showing a high pollinator dependency. We also found a 39% decrease in fruit weight and 25% decrease in fruit diameter without bees demonstrating their contributions to crop yield. As the pasture area increased, bee Shannon diversity and richness decreased. We found 5 out of the 9 molecules tested in anthers. Propamocarb was found in 100% of the farms ranging from 1.3 to 399.5 ug/kg and imidacloprid in 80% of the farms ranging from 0.6 to 13063 ug/kg. We found that imidacloprid concentration in the anthers was negatively associated with bee diversity and richness. There was a significant interaction of natural habitat area and imidacloprid on bee richness and bee Shannon diversity index, suggesting that the negative effects of imidacloprid on bee diversity are attenuated by the increment in natural habitat. Our study provides evidence that landscape simplification and pesticides, in particular, imidacloprid, are threats to the bee community in lulo crops. However, the interactive effects between the proportion of natural habitat and imidacloprid concentrations showed that complex landscapes can help to mitigate the pesticide negative effects.

Landscapes of fear: How landscape composition influences the magnitude of antipredator responses in an agricultural insect pest

Authors: Poveda Katja[2], Perez-Alvarez Ricardo[3], Thaler Jennifer[1] and Tigreros Natasha[4], [1]Cornell University, United States, [2]Entomology Department, Cornell University, Ithaca, New York, United States, [3]Leibniz University of Hannover, Germany, [4]University of Arizona, United States

Abstract: Prey organisms often respond to the risk of predation by altering behavioral, physiological, and morphological traits. These antipredator responses increase prey survival, but often come at a cost of reduced feeding and/or reproduction rates, which ultimately may result in decreasing prey populations with cascading benefits for plant production. Although such antipredator responses have been relatively well studied in small scale microcosm environments, they remain largely unexplored for plant-arthropod communities living in heterogeneous agricultural landscapes. Here, we examined how variation in predator abundance across a gradient of landscape complexity influences antipredator responses of a major agricultural pest, the Colorado potato beetle (Leptinotarsa decemlineata). Within the study region (New York State, USA) pest populations were collected in 19 potato fields encompassing a 20-fold natural difference in predator abundance. For each pest population, we measured two behavioral responses to the risk of predation: leaf feeding and intra-clutch cannibalism. Using laboratory trials with stink bug predators (Podisus maculiventris) that were surgically manipulated so they could hunt but not kill, we also tested the magnitude of antipredator responses among pest populations. We showed that predator abundance was higher in agriculturally dominated landscapes (i.e., simple landscapes). Furthermore, pest populations from simple landscapes exhibited significantly higher levels of intra-clutch cannibalism and considerable reductions in plant feeding, behaviors known to reduce the likelihood of being predated. Results from the experiment with “sham predators” further confirm that antipredator responses were stronger in simple than in complex landscapes. Thus, our findings provide empirical evidence that landscape-level variation in predation risk is associated with behavioral changes among population of L. decemlineata. A greater understanding of these indirect landscape effects on pest regulation is necessary to fully explore the range of mechanisms by which biological control could be strengthened in agroecosystems.

All the better to see flowers with?: Eye morphology driven by feeding behavior in sap beetles

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Abstract: Nitidulidae, or sap beetles, are an ecologically diverse lineage of Cucujoidea. Members of this single family are reported to exhibit the majority of feeding behaviors known to occur across all Coleoptera. This immense diversity of feeding behavior can be seen both between major lineage such as subfamilies, but also between very closely related species within a genus. This diversity in feeding behavior could drive morphological variation and adaptations to capitalize on various resources, e.g., flower visiting vs. rotting fruit. One system possibly under strong selection is the visual system. Morphological measurements were taken using scanning electron micrographs and high-resolution stacked color images. A discussion of eye size, facet size, and facet density is presented in a phylogenetic context. We specifically tested for significant relationships between overall eye size and the following factors: flower-visiting, day-night activity, body coloration, body size, gender, and phylogenetic position.

Controlling the controller? The effect of microscopic fungi on the ecosystem services provided by ground beetles (Coleoptera: Carabidae)

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Abstract: Ground beetles (Coleoptera: Carabidae) are valuable biological control agents, supporting sustainable agriculture. Microscopic fungi, which themselves often provide valuable ecosystem services by infecting and killing pest species, may reduce this benefit when they act as ectoparasites or entomopathogens of carabids. To what extent this trade-off influences the delivery of ecosystem services ground beetles provide is yet unknown. Here, we gathered literature data using 421 papers from 198 journals in 15 languages on interactions occurring between ground beetles and fungi, and built an interaction network to 1) review available information and identify knowledge gaps, and 2) to assess how fungi can affect the ecosystem services carabids provide. We recorded 651 Carabidae interacting with 902 fungal species in 4528 unique connections, from 148 countries. The predominant interaction type was ectoparasitism between Laboulbeniales fungi and, mostly, Trechinae ground beetles. Entomopathogenic fungi most commonly infected the Harpalinae subfamily that have purely herbivorous or a mixed diet with a substantial amount of plant material consumed. Carabidae consuming fungal hyphae and mutualistic yeasts living in ground beetles' guts were also present in our network but these interactions were both underrecorded and poorly studied. The low number with which predatory ground beetle species were involved in interactions with entomopathogenic fungi suggests a moderate negative effect. Although ectroparasitism are very common, these relationships have subleathal effects, and they are reported to cause no or very little fitness decline. Thus, ecosystem services provided by Carabidae are unlikely to be substantially disturbed by interacting fungi. With numerical parametrization of the interaction links the model would provide a detailed insight into the trade-offs between fungi and Carabidae.

The impact of crop systems on aphid-pathogenic fungi interaction networks

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Abstract: The networks formed by the interactions between aphids and their pathogenic fungi are of high importance for an increased use of fungi in biological control. Yet, these networks are poorly known, and particularly the impact of crop systems in shaping these associations are seldom considered. We established a hypothetical interaction network between aphids and their fungal pathogens based on published data to (1) investigate the fungus-host specificity and their dependency on their habitat, and (2) assess the dissemination of aphid mycoses among nine major crop systems. Of the 1400 unique connections between these host and pathogen taxa, we identified pathogen specificity and assessed, which role the most commonly connected aphid species can play in the dynamics of fungal infection within and between crop systems. Fungi within the Entomophthoraceae had the highest number of connections to aphids. Pandora neoaphidis and Entomophthora planchoniana had the most connections to aphid species, suggesting that they are likely to play a key role in the establishment and dispersal of infections in aphid populations worldwide. From the aphids' side, Myzus persicae was the most connected to fungi in the network, followed by the cereal aphids Rhopalosiphum padi and Sitobion avenae, suggesting that these species are highly prone to fungal infections and therefore important players of the fungal dissemination between crop systems. The highest number of aphid species and fungal connections was present in orchards, followed by vegetable and cereal crops. Insights into the correlations between the aphid-fungal pathogen interaction networks and the impact of crops on these associations provide the basis for prediction of the infection pathways in real-life ecological systems.

Effects of naturally derived products on Aculops lycopersici and their effects on a beneficial mite

Authors: Pozzebon Alberto[1], Zanolli Penelope, Tirello Paola, Fabris Beatrice and Duso Carlo, [1]University of Padova - DAFNAE, Italy

Abstract: Tomato russet mite (TRM) Aculops lycopersici is one of the most important pests of tomato Lycopersicon esculentum. The decreasing availability of acaricides and restrictions in their use in several countries is promoting researches on alternatives to conventional pesticides. The efficacy of products based on entomopathogenic fungi (i.e. Beauveria bassiana, Paecilomyces fumosoroseus and Lecanicillium muscarium) or naturally substances (pyrethrins and azadirachtin A) on A. lycopersici was assessed in the laboratory. Mites were exposed to dry residues of products at their maximum rate and a water-treated control was included for comparison. Eriophyoid mite survival evaluated after 72 h was significantly reduced by B. bassiana, azadirachtin A and pyrethrins compared to the control. At 168 hours from applications, mite survival was reduced even on P. fumosoroseus treatment. Beauveria bassiana was associated with the lowest TRM survival rates. Escaping was significantly higher on azadirachtin A, pyrethrins and P. fumosoroseus treatments. The effects of these products were also evaluated on Amblyseius swirskii employed in biological control programmes in greenhouses.

Large-scale field monitoring on the distribution of Trissolcus japonicus and Trissolcus mitsukurii, two egg parasitoids of Halyomorpha halys, in Italy and Switzerland

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Abstract: In Europe and North America, the invasive alien stink bug Halyomorpha halys causes severe damage on agricultural crops, and proposed chemical and physical solutions do not guarantee an acceptable level of long-term pest control. On the other hand, classical biological control using the egg parasitoid Trissolcus japonicus has been identified as the most suitable method to sustainably reduce pest populations in the long-term. Adventive populations of T. japonicus have been discovered in the USA since 2014 and more recently in southern Switzerland (2017) and in north-western Italy (2016). A second Asian egg parasitoid, Trissolcus mitsukurii, was also detected on H. halys eggs in northern Italy in 2018. Considering the exceptional findings of both parasitoids and the perspectives for a biological control program in the two European countries, in 2019 a large-scale field survey in northern Italy and Switzerland was performed to define the abundance and distribution of the two species. A collaborative work plan was established, involving 20 research institutions and plant protection organizations from different Italian and Swiss regions. The monitoring activities were performed from May to September 2019 and focused on detecting naturally laid egg masses of H. halys and other pentatomids. Collected egg masses were reared under laboratory conditions to allow egg hatching or parasitoid emergence. Overall, more than 4,348 egg masses of H. halys and 285 egg masses of other pentatomid species were collected. Results indicate that both T. japonicus and T. mitsukurii are present in several sites in the investigated area, in all the habitat types where H. halys was recorded and southwards from the first Italian records. Both parasitoids were detected on cultivated plants and hedgerows in IPM or organically managed orchards, on tree/shrubs in urban and suburban areas, and in uncultivated landscapes. The distribution of the two parasitoids partially overlapped, and, in a few records, they occurred in the same area or even in the same egg mass. The percentage of parasitized H. halys egg masses ranged between 0.45% and 53.85% and between 0.17% and 20.20% for T. japonicus and T. mitsukurii, respectively, depending on the area of survey (regions, provinces, cantons). The parasitism rate ranged between 71.43% and 100% and between 88.59% up to 97.40% for T. japonicus and T. mitsukurii, respectively. Parasitization by these two parasitoids on egg masses other than H. halys was a rare event: T. japonicus emerged from Palomena prasina egg masses and T. mitsukurii from P. prasina, Dolycoris baccarum, Nezara viridula and from an egg mass ascribed to a pentatomid of the subfamily Asopinae. Trissolcus japonicus and T. mitsukurii displayed both the ability to establish self-sustaining populations in the Swiss-northern Italian climate with relatively high parasitization success of H. halys eggs, suggesting a high potential for the control of the pest in the near future. This study provided key data for the development of the biocontrol program in Europe with the release program of T. japonicus.

Native and exotic egg parasitoids of Halyomorpha halys in Europe

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Abstract: Since the accidental introduction of Halyomorpha halys into Europe, many studies focused to identify native natural enemies able to adapt to the new invasive species, especially considering the restrictions to the application of classical biological control. Particular attention was given to egg parasitoids, and field surveys in Switzerland and Italy were performed using sentinel egg masses (frozen or fresh) or collecting naturally laid egg masses. Until 2017, overall egg parasitism ranged from 0.5-4.4% in Switzerland to 1-21% in Italy, and the generalist egg parasitoid Anastatus bifasciatus was the predominant species. Moreover, the following other species were obtained: Trissolcus basalis, Trissolcus belenus, Trissolcus cultratus, Trissolcus kozlovi, Telenomus turesis and the hyperparasitoid Acroclisoides sinicus.

At the same time, the potential of some native egg parasitoid species was evaluated in laboratory no-choice tests. Besides A. bifasciatus, which confirmed its ability to develop in viable H. halys eggs, Ooencyrtus telenomicida showed to parasitize H. halys eggs successfully. In contrast, among the seven tested scelionid species (six Trissolcus spp. and T. turesis), all the Trissolcus spp. caused significantly higher egg mortality in comparison with unexposed eggs, but only T. kozlovi was able to produce offspring from viable H. halys eggs.

Due to its predominance in field surveys and its capability of developing in viable H. halys eggs, A. bifasciatus was selected as a potential candidate for augmentative releases. From 2016 to 2019, this egg parasitoid was released in fruit orchards in Switzerland and Italy. Results were contrasting, but usually unsatisfying for effective pest control. Recently, field surveys performed in Switzerland and Italy allowed discovering the presence of adventive populations of Trissolcus japonicus, considered the most effective egg parasitoids in China. Trissolcus japonicus was found first in Canton Ticino, Switzerland in 2017, and in Piedmont and Lombardy, Italy in 2018. Trissolcus mitsukurii is a second Asian egg parasitoid that was reported first on H. halys eggs in north-eastern Italy in 2018 but, given its spread and abundance, probably its presence dates some years before. Due to the large availability of their host in the field, the distribution and abundance of these exotic egg parasitoids are expected to expand, even in the absence of human intervention. To verify the status of the adventive populations, in 2019 an extensive monitoring was carried out jointly by many researchers to assess the presence and abundance of these two exotic parasitoids, pending the possible authorization for their release in the open field.

The Nearctic leafhopper Erasmoneura vulnerata, an emerging pest in European vineyards

Authors: Pozzebon Alberto[2], Duso Carlo[2], Prazaru Stefan Cristian[2], Rossetto Filippo[2], Carriero Carriero Francesca[2] and Tirello Paola[1], [1]DAFNAE - University of Padova, Italy, [2]University of Padova - Department of Agronomy, Food, Natural Resources, Animals and Environment, Italy

Abstract: The leafhopper Erasmoneura vulnerata is widely distributed in Northern and Central America, where wild and cultivated vines and other host plants are colonized. According to recent literature, E. vulnerata is not considered a major pest for American vineyards. This species was detected for the first time in Europe in 2004, particularly in Northern Italy, where it was mainly observed in neglected vineyards and wild vines for more than a decade. This situation changed in 2016 when the first outbreaks of E. vulnerata were reported in commercial vineyards in the Veneto region (Northern Italy). High population densities were observed despite organophosphates, suggesting that insecticide resistance was a key factor affecting this event. Interestingly, large populations in spring were associated with a decline of native leafhoppers (e.g., Empoasca vitis and Zygina rhamni). Susceptibility to pest infestation is influenced by vine variety. Therefore trials aimed at evaluating the economic thresholds of E. vulnerata gave contrasting results.

A remarkable response to leafhopper infestations by native egg parasitoids has been reported.

A tale of leafhoppers, Aster Yellows, and crops in the Canadian Prairies

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Abstract: Phytoplasmas are obligate parasites that cause several plant diseases around the world which affect crop production and reduce crop yield, such as Aster Yellows (AY) Disease. These organisms have been poorly studied due to difficulties in the establishment of in vitro cultures, which has not yet been successful, and also due to their high vector specificity. In the Canadian Prairies, Aster Yellows Disease is caused by the AY 16SrI phytoplasma group and primarily transmitted by Aster leafhoppers (Macrosteles quadrilinea tus Forbes). This disease can have a high incidence in canola fields (<90%) during outbreak years and can also affect other crops like cereals. However, disease dynamics are poorly understood. Moreover, there is no local population of Aster leafhoppers in the area, as these insects are introduced by wind currents in spring and early summer. In order to gain insight into biological aspects of these pathogens and one of the insect species that transmits them, different experiments were conducted, using crop and weed species commonly found in the Prairies. To study Aster leafhoppers´ host-choice behaviour and whether this can be affected by pathogen infection, two-choice bioassays were conducted using only infected and only uninfected leafhoppers. This was complimented with no-choice bioassays on different plant species, in order to evaluate leafhoppers´ oviposition behaviour and nymphal development, and if phytoplasmas can affect leafhoppers´ fitness. Arabidopsis thaliana was also incorporated into these experiments, given its importance as a model system and its relatedness to canola. Altogether, these results provide a better understanding of the AY epidemiology, resulting in management recommendations for local growers in Saskatchewan.

Screening of insect associated fungi for virulence to Tenebrio molitor larvae and potential biostimulation effect to maize

Authors: Praprotnik Eva[1], Lončar Jernej[1] and Razinger Jaka[1], [1]Agricultural Institute of Slovenia

Abstract: Several insect associated fungi have been shown to be effective in insect pest management. The aim of the presented study was to test different fungal isolates for their ability to infect mealworms (larvae of Tenebrio molitor, Coleoptera: Tenebrionidae) and stimulate maize growth. Seventy-one isolates of Metarhizium, Beauveria and Trichoderma species were isolated either from insect larvae of Galleria mellonella (Lepidoptera: Pyralidae) and T. molitor used as baits in soil samples, or from naturally occurring mycosed insect cadavers collected in the field. Some additional strains were obtained from serially diluted soil suspensions plated on semi-selective media. Virulence of isolates was tested by immersing mealworms in a conidial suspension at a concentration of 1 x 108 conidia ml-1 and assessing their mortality rate for 14 days. The isolates Metarhizium brunneum (1154) and Beauveria bassiana (2121) were found to be the most virulent, causing 100 % mortality of mealworms. In the virulence analysis, we also considered the origin of the fungi, the insect host, and the isolation method and found that fungi isolated from wild adult mycosed insects, mainly from the order Lepidoptera, and isolated from meadow soil, could potentially cause higher mortality in mealworms. Also, the role of insect associated fungi in fungus-plant systems is still poorly understood. Therefore, we additionally tested each of the isolates for their ability to stimulate maize growth. Maize seeds were submersed in a conidial suspension at a concentration of 1 x 108 conidia ml-1 and then planted in twice autoclaved commercial planting soil. Sprout emergence was monitored daily and root length, shoot length and dry weight of the plants were measured after three weeks. Prolongation of emergence time was observed in more than 60 % of the isolates. Maize root length was significantly increased by M. robertsii isolates (2691, 2693, and 2688) and reduced by Metarhizium robertsii isolates (2243 and 2636). Maize shoot length was significantly increased by Trichoderma atroviride (2882) and Trichoderma gamsii (2883) and reduced by B. bassiana isolate (2299). Plant dry weight was significantly increased by M. robertsii isolates (2146 and 2794) and reduced by B. bassiana isolates (2299 and 2300) and M. robertsii isolate (2011). Described method enabled identification of the M. robertsii isolate (2693), which caused the death of 73 % of T. molitor larvae and at the same time showed a positive effect to all measured growth parameters of maize.

The four way interactions among host plant-whitefly-virus-endosymbionts in insect and disease development

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Abstract: The whitefly, Bemisia tabaci (Gennadius) (Hemiptera; Aleyrodidae) is a highly polyphagous pest reported to infest over 600 plant hosts globally. About 42 genetic groups/cryptic species of B. tabaci exist in the world on different hosts. The species have variable behaviour with respect to feeding, development and transmission of viral diseases. Feeding on diverse host plants affect both whitefly development and the population of the endosymbionts harboured by the insects. Due to changes in the level of endosymbionts, the virus transmission efficiency by the vector also gets affected. We investigated these interactions on five host plants – egg plant, tomato, beans, okra and cotton - using a single whitefly species Asia 1 infected with three different bacteria Portiera, Wolbachia and Arsenophonus. The Asia 1 transmits the Tomato leaf curl Bangalore virus (ToLCBV) effectively and thus was used in the interaction studies. We found a significant impact of hosts on whitefly growth and development; eggplant was most favourable host, while okra and tomato were least favourable. Among the endosymbiotic bacteria, the titre of Wolbachia was significantly affected by feeding of B. tabaci on different host plants whereas Arsenophonus and Portiera were unaffected. When whitefly fed on ToLCBV-infected tomato plants, the Arsenophonus population was significantly increased, indicating its previously confirmed role in ToLCBV transmission. Further, screening of total proteins of B. tabaci Asia 1 genetic group interacting with ToLCBV coat protein was carried out using Y2H system. Some of the proteins found to be interacting with ToLCBV CP were HSPs 70kDa, GroEL, nucleoproteins, vitellogenins, apolipophorins, lachesins, enolase. The reported protein thus would be the potential targets for novel whitefly control strategies such as RNAi or novel insecticide target sites for sustainable whitefly management after confirmation of genuine proteins.

Bottom-up and top-down effects of changing soil fertility on herbivory in a grassland food web

Authors: Prather Rebecca[1] and Kaspari Michael[2], [1]Florida State University, United States, [2]Geographical Ecology Group University of Oklahoma, United States

Abstract: Anthropogenic nutrient deposition is rapidly increasing, producing numerous interacting effects on grassland food webs by simultaneously changing soil and plant fertility, plant and arthropod communities, and herbivory. Understanding how increased nutrient deposition will change these interactions is important for the future maintenance of grassland food webs and ecosystems. We created a 40-fold gradient of fertilization and tracked its effects through a grassland food web, measuring changes to soil and plant nutrients, plant biomass and richness, herbivore abundance, predator abundance, and the amount and type of herbivory plants experience. We sought to uncover the mechanisms driving herbivory within and across fertilizer durations and quantities. Changing soil fertility had rippling effects on the abundance and function of a prairie food web. As eutrophication transitions from an episodic to a multi-year phenomenon, we demonstrate a shifting response in the abundance and impact of prairie herbivores. The mechanisms we uncover could help predict responses to eutrophication.

Eusociality and the evolution of ageing: investigating the basis of positive fecundity-longevity associations.

Authors: Prince David[1], Bourke Andrew[1], Collins David[1], Donelan Jenny[1] and Chapman Tracey[1], [1]University of East Anglia, United Kingdom

Abstract: Eusocial insects present an apparent exception to the classical predictions of the evolutionary theory of ageing in that queens exhibit a positive fecundity-longevity association. This has led to the hypothesis that social insect queens lack the fecundity-longevity trade-off observed in other species, and therefore do not experience costs of reproduction. A recent study in eusocial bumblebees (Bombus terrestris) showed that reproductive workers exhibit a positive fecundity-longevity association, but that the fecundity-longevity association becomes negative when workers are experimentally forced to reproduce. This suggests an alternative hypothesis that reproductive workers, and by extension eusocial queens, are analogous to intrinsically high-quality individuals in non-social organisms, such that costs of reproduction are latent but not usually expressed. We have tested these two hypotheses by experimentally manipulating costs of reproduction experienced by Bombus terrestris queens, and comparing their longevities. The existing hypothesis predicts that the manipulation will not affect the longevity of the queens, as there are no costs of reproduction. The alternative hypothesis predicts that manipulated queens experiencing increased costs of reproduction will have reduced longevity. Our results help discriminate between these two hypotheses and elucidate the mechanisms governing ageing and longevity in social insects.

The Cognitive Ecology of Buzz Pollination

Authors: Pritchard David, University of Stirling, United Kingdom

Abstract: While most studies of cognitive ecology of pollination have focussed on pollinators foraging for nectar, over the past decade, there has been increasing interest in the cognitive ecology of pollen foraging. Most of these studies have focussed on plant species in which pollen is presented externally to bees and requires little effort to access. In contrast, to extract pollen from "buzz-pollinated" flowers, bees must vibrate anthers, producing accelerations over 10 times that produced during flight (Pritchard & Vallejo Marin, in review). Despite the effort required to extract pollen, buzz pollination is a relatively common behaviour, having evolved at least 45 times in bees and employed by 6% of all flowering plants. Buzz pollination offers several fruitful avenues for studying the cognitive ecology of pollination. Although, likely more costly that foraging from pollen using other methods, the impact of the cost of flower handling on decision making by foraging bees is still largely unknown. Also, while we have found that buzz pollinating bees collect more pollen with experience, the manner in which learning shapes buzz-pollination remains elusive. In this quick talk, I will present our results on the cognitive ecology of bumblebees (Bombus terrestris) foraging on a range of Solanum species, examining the costs of this behaviour, as well as our results on the role of learning in modifying how bees buzz flowers.

Phylogenomic insights into the evolution of ponerine ants

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Abstract: Among the different methods that use genomic data to study the evolutionary history of recent groups, the ultraconserved elements (UCEs) have proven to be ideal markers for such inferences at different time scales. The taxonomy and internal phylogeny of Formicidae have been extensively studied and have stabilized significantly in the last decades due to the active study of ant systematics on a macroevolutionary scale. The evolutionary history of Ponerinae, however, has never been extensively studied using molecular approaches. Thus, we will use ultraconserved elements to reconstruct the phylogeny of Ponerinae, in order to elucidate the internal relationships in the group, as well as the biogeographic patterns of the genera, and assist in the delimitation of the tribes and genera. For this, we targeted a set of 2,500 UCE loci using target enrichment and multiplexed sequencing of over 1000 species of Ponerinae. Specimens were selected to include nearly all major species groups from all terrestrial biomes, resulting in a comprehensive evolutionary tree of ponerines that will inform revisions of generic boundaries and classification. By combining phylogenetic inference methods with dating and biogeographic analysis, we will provide a phylogenetic framework for the knowledge of the evolutionary history of these ants.

Hidden cuticular microstructures revealed by application of modern microscopy techniques on the compressed fossils and amber inclusions

Authors: Prokop Jakub[1], Rosová Kateřina, Batelka Jan and Pecharová Martina, [1]Charles University, Department of Zoology, Prague, Czech Republic

Abstract: The integumental surface microstructures play a crucial role in the current morphology and taxonomy studies of extant insects / arthropods. However, their proper recognition and visualization on the fossil species often represent obstacle due to preservation of insect exoskeleton in various sedimentary rocks or amber resin. Moreover, the common uniqueness of fossil specimens requires to apply solely non-destructive microscopy techniques. By using environmental electron scanning microscopy on compressed fossils, inverted light or fluorescence microscopy, and confocal laser scanning microscopy applied on various amber inclusions we demonstrated capabilities of these tools on the larval and adult stages of selected insect groups. Our results based on case studies revealed details of the cephalic structures like mouthparts, thoracic structures like legs with specialized pretarsus, wings with sensory organs, and abdominal structures like terminalia, etc. With modern microscopy tools it is possible to enter cuticular microstructures on the Paleozoic and Mesozoic insects much more deeply and elucidate their functional significance. Hence, the efficient application of these modern techniques provides another perspective along the classical microscopy and should be more frequently applied in contemporary studies. This research is a contribution to the project of the Grant Agency of the Czech Republic (No. 21-05216S).

High diversity of the northern sawfly genus Euura (Hymenoptera, Tenthredinidae)

Authors: Prous Marko, University of Oulu, Finland

Abstract: The genus Euura (~650 described species) is the largest genus within subfamily Nematinae and second largest among sawflies (largest is Tenthredo, more than 1000 species) and it shows the strongest pattern of reversed latitudinal gradient in species richness, i.e. becoming more species rich towards higher latitudes and altitudes. Taxonomy of the genus is challenging due to large number of similar species and further complicated by often large within species variation. Frequently, males and females have been wrongly associated. Despite of about 130 new proposed synonymies, about 270 species are recognised in the West Palaearctic. Based on genetic data (at least mitochondrial COI and two nuclear genes), there are about 45 distinct lineages, which are not always clearly different from each other based on female or male morphology (but usually at least one of the sexes shows clear differences from the others). Most of these lineages contain multiple species where mitochondrial DNA barcoding does not allow species identification, while nuclear DNA usually does. Remarkably, about 10% of the specimens harbour multiple mitochondrial variants (heteroplasmy), which can be up to 9% different. Based on current data, species boundaries are entirely unclear in some cases due to remarkable morphological and genetic variation.

Landscape scale ecological networks as a mitigation measure against global insect declines

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Abstract: Mammals are globally in decline, with habitat loss a primary driver. How this activity affects functional associations of insects with large mammals, especially across transformed landscapes has received little attention. We assess how well dung beetle diversity tracks large African mammal herbivore diversity across a forestry plantation land use gradient by assessing how dung beetle richness and diversity compares to large mammal diversity and constructing a dung beetle-to-mammal interaction network. Dung beetles responded positively to an array of large mammals than to land use intensity, as they showed a strong preference for specific mammalian dung. Land use intensity categories had distinct mammal and dung beetle assemblages. Transformed areas also have conservation value, provided that there is functional connectivity between remnant vegetation within the modified landscapes. The loss of any native large mammal, especially African elephants, from transformed landscapes is likely to lead to a decline in insects. This suggests that protected areas are essential for the conservation of native insects and its interactions, while well designed and managed transformed areas have additional conservation value. African conservation managers and landowners should be encouraged to maintain a diversity of large mammals on their properties to maintain insect diversity and ultimately ecological resilience.

Complementary and protection value of a Biosphere Reserve buffer zone for increasing local representativeness of ground-living arthropods

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Abstract: Biosphere reserves (BRs) are areas of high biodiversity value that promote conservation and sustainable development. BRs consist of core, buffer, and transition zones. Buffer zones are where human and ecological activities overlap, and are key functional spaces that can have important complementarity value. We test this using ground-living arthropods in the highly biodiverse Kogelberg Biosphere Reserve in South Africa. We use generalized dissimilarity modelling to describe the compositional dissimilarity of assemblages as a function of environmental correlates between pairs of survey sites. Transformed spatial predictors were used as surrogates for biodiversity to assess complementarity. Important correlates of arthropod species turnover were related to mesoclimate, fire history, and geology. Buffer areas had important complementary value. Current habitat transformation across core and buffer zones does not change this, as results were the same when removing all transformed areas from the analyses. Important areas in buffer zones that increased local representativeness coincided with areas of increased intra-annual temperature variability. Orchards in transformed areas also influenced arthropod diversity in adjacent natural vegetation by <1 km from orchard edges. This edge effect influenced both core and buffer sites due to the lack of a continuous buffer, indicating that the buffer zone is important for protecting the core. As fire management is an important correlate of arthropod turnover here, the complementary value of the buffer zone can have a strong temporal dimension. Given the important complementary value of the buffer zone, conservation management should not be restricted to core areas only, especially when maximising local representativeness.

Benefits of memory use depend upon forage availability in bumblebees

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Abstract: Enormous variation in cognitive abilities is evident within animal populations, yet we currently understand little of the ecological selection pressures that shape the evolution of learning and memory. Here, we capitalize upon the unique tractability of a social insect system to quantify the relationship between cognitive performance and resource availability in the natural environment. We assayed the short, medium and late long-term memory of individual bees from 26 parasite-free colonies in the laboratory, using a radial arm maze (RAM) – a classical psychological apparatus used historically to assess working memory in rodents. Following cognitive testing, colonies were given unrestricted access to the surrounding environment (a university parkland campus), and the lifetime foraging efficiency of each tested worker monitored. We simultaneously surveyed floral resource availability within the bees' foraging range. Using a continuous, staggered design that encompassed the entire foraging season (early spring to late autumn), we were thus able to assess how changes in floral resources affect memory use. In contrast to our expectation that cognitive abilities might be most important when forage availability is low, we found that all bees performed poorly when forage was scant, while the benefits of memory performance emerged in weeks when forage was richest. Our preliminary results are the first to link memory performance with ecological selection pressures, opening the door to a link between environmental complexity and selection on cognitive performance that invites further exploration.

The evolutionary consequences of macronutrient intake in Drosophila melanogaster

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Abstract: The consumption of macronutrients has profound consequences for fitness and its related traits in insects. While the effects of macronutrient intake on life-history phenotype occurring within a generation are well documented in insects, studies that examine how insects respond to variations in dietary macronutrients across evolutionary time scale are scarce. In this study, we took a laboratory-based experimental evolution approach to study whether and how multiple life-history and physiological traits related to fitness would evolve in response to changes in macronutrient availability and balance in a model insect, Drosophila melanogaster. To this end, we established 36 independent replicated D. melanogaster populations, which were subjected to natural selection under one of six nutrient selection regimes representing all combinations of three yeast-to-sugar ratios (Y:S = 1:4, 1:1 or 4:1) and two yeast plus sugar concentrations (Y+S = 100 or 200 g L-1). After more than 70 generations of selection, D. melanogaster flies from each selection regime were shown to have evolved into distinct metabolic and life-history phenotypes reflecting their adaptations to imbalances in dietary macronutrient composition. Most strikingly, D. melanogaster flies selected under a condition where carbohydrate was severely limited (Y+S = 100 g L-1 with Y:S= 4:1) grew much larger and stored substantially more lipids compared to those selected under the other regimes. Such evolved improvement in energy utilization and storage might have conferred fitness advantages to those flies that had chronically faced energy shortage throughout their selection history. In stark contrast, D. melanogaster flies selected under carbohydrate-rich conditions (Y:S=1:4) had evolved into a lean phenotype, indicating their metabolic adaptation to counteract the adverse consequences of excess fat storage resulting from ingesting too much carbohydrates. To conclude, this study provides insights into the role of macronutrients in driving the evolution of life-history and physiological traits in an insect.

Early Intervention Strategy for spruce budworm: Can we contain outbreak spread?

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Abstract: Spruce budworm (Choristoneura fumiferana Clemens) (Lepidoptera: Tortricidae) is the major defoliating pest of spruce (Picea sp.) and balsam fir (Abies balsamea (L.) Mill) in northeastern North America. The recent resurgence of a budworm outbreak in northeastern North America has rekindled interest and discussion around how best to manage its potential impact across the region.

Early Intervention Strategy (EIS) is an area-wide management program aimed at containing the spread of spruce budworm in Atlantic Canada. In brief, intensive regional monitoring is used to help identify emerging ‘hot spots’ along the leading edge of outbreak, which are then treated with relatively narrow-spectrum insecticides (i.e., Btk or tebufenozide) to slow or prevent further population expansion. Our research represents a large-scale test of the efficacy of the EIS approach and has many key features, including work on population and community ecology, pest monitoring, public outreach, and citizen science (i.e., Budworm Tracker). Results from the first 6 years of this program indicate that under the right conditions the EIS approach has strong potential for containing budworm outbreaks with minimal impacts on non-target species

Spruce budworm disturbance ecology – what does this outbreak tell us?

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Abstract: Spruce budworm outbreaks cause large scale damage to Canada’s boreal forest. The current outbreak started further north compared to past outbreaks, in regions where trees have not co-evolved with this disturbance. We are measuring spruce budworm population dynamics and measuring ecosystem impacts from the outbreak foci to the expanding northern front of its range.

In addition to permanent plots that we have been sampling since 2006, we have established a transect that runs 600 km north of Baie-Comeau, the northern most parts of which extend beyond provincial aerial survey routes. In 2018, moth captures averaged over 4500 at our northern-most site (km 568), however, there were no L2s nor L4s observed on sampled branches. Defoliation was estimated to be below 10% on both spruce and fir. The southern most sites (e.g. km 237) had medium defoliation on black spruce and high defoliation on balsam fir with an average of 20 L4 per branch and 3300 moths captured in pheromone traps. Moths are dispersing significantly north, but are not yet contributing significantly to population growth nor defoliation. We are examining the processes and patterns of disturbance in this northern boreal ecosystem to better understand the impacts due to climate change.

A conceptual framework for the spruce budworm Early Intervention Strategy: can outbreaks be stopped?

Authors: Pureswaran Deepa[3], Johns Robert[5], Bowden Joe[1], Edwards Sara[7], James Patrick[10], Cooke Barry[2], Richard Brigitte[2], Norfolk Chris[6], Kneeshaw Dan[8], Quiring Dan[9], MacLean David[9], Carleton Drew[6], Owens Emily[5], Moise Eric[1], Emilson Erik[2], Mott Gordon[4], Régnière Jacques[2] and Stastny Michael[2], [1]Canadian Forest Service, Atlantic Forestry Centre, Corner Brook, Memorial University (Grenfell Campus), School of Science and Environment, Corner Br, Canada, [2]Canadian Forest Service, Canada, [3]Canadian Forest Service, Laurentian Forestry Centre, Quebec, Canada, [4]Maine, United States, [5]Natural Resources Canada, Canadian Forest Service, Fredericton, New Brunswick, Canada, [6]NB DNR, Canada, [7]Population Ecology Group, Faculty of Forestry and Environmental Management, University of New Brunswick, Fredericton, NB, Canada; Forest Protection Limited, Canada, [8]University of Montreal, Canada, [9]University of New Brunswick, Canada, [10]University of Toronto, Canada

Abstract: The spruce budworm, Choristoneura fumiferana, Clem., is the most significant defoliating pest of boreal balsam fir (Abies balsamea [L.] Mill.) and spruce (Picea sp.) in North America. Historically, spruce budworm outbreaks have been managed via a reactive, foliage protection approach focused on keeping trees alive rather than stopping the outbreak. However, recent theoretical and technical advances have renewed interest in proactive population control to reduce outbreak spread and magnitude, i.e., the Early Intervention Strategy (EIS). In essence, EIS is an area-wide management program premised on detecting and controlling rising spruce budworm populations (hotspots) along the leading edge of an outbreak. In this article, we lay out the conceptual framework for EIS, including all of the core components needed for such a program to be viable. We outline the competing hypotheses of spruce budworm population dynamics and discuss their implications for how we manage outbreaks. We also discuss the practical needs for such a program to be successful (e.g., hotspot monitoring, population control, and cost-benefit analyses), as well as the importance of proactive communications with stakeholders.

Circadian control of synaptic plasticity in the fly's visual system

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Abstract: Circadian clocks generate circadian rhythms in various processes, including synaptic plasticity in the brain. In the visual system of Drosophila melanogaster, the number of synapses and synaptic protein levels oscillate during the day and night. One type of synaptic contact, tetrad synapses, which form between the retina photoreceptor terminals and their post-synaptic partners in the first optic neuropil (lamina), increases in frequency at the beginning of both the day and night.
In the present study, we examined at high resolution the ultrastructure of tetrad presynaptic elements at different times during the day, particularly during the morning peak of locomotor activity, and during sleep at night using transmission electron microscopy (TEM). We reconstructed the cytomatrix called the T-bar and synaptic vesicles from TEM serial sections of the lamina using the TEM tomography method. The study was carried out using wild-type Canton S flies, flies with BRP170 or BRP190 mutations of the main cytomatrix scaffolding protein Bruchpilot (BRP), and cry01 null mutants that do not synthesize the CRYPTOCHROM (CRY) protein. We found that the number of synaptic vesicles, both translucent and dense, in tetrad presynaptic sites is similar during the morning peak of activity (ZT1) and during sleep (ZT16); however, the number of tetrad synapses is lower at ZT16, but their T-bar platform is larger at ZT16 than at ZT1. In brp?170 and cry01 flies, there were fewer vesicles than in Canton S at ZT1, but the same number was observed during the night (ZT16). As a result, day/night changes in the number of synaptic vesicles were larger in both mutants than in Canton S. A daily rhythm was not observed; however, in brp?190 and in the case of this mutant, the number of synaptic vesicles was similar to Canton S at ZT1. This pattern was observed for all vesicles, translucent and dense, but in the case of dense vesicles, their number was smaller or the same in Canton S relative to mutants at ZT1 and ZT16. Moreover, we found that the morphology of the T-bar changes during the day and night in Canton S, but this rhythm was not observed in all mutants studied. The obtained results also indicate that the CRY protein is crucial for maintaining the appropriate number of synaptic vesicles and morphological plasticity of the presynaptic T-bar during activity and the sleep cycle.

Pollination for oilseed rape employed by Chrysomya megacephala after cold acclimation

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Abstract: With the agricultural ecological intensification, pollination services are declining in landscapes with field and semi-natural habitats, especially in the early spring when few pollinators are available in nature. In this study, we used Chrysomya megacephala to replace honeybee to pollinate for important crop oilseed rape, Brassica napus. Firstly, we carried out the developmental cold acclimation (DCA) to offset the phenological mismatch of oilseed rape and C. megacephala, which increased significantly the cold tolerance of the flies. Fruit setting rate (FSR) was improved by employing C. megacephala treated by DCA. Secondly, field cage experiment showed that C. megacephala had a good ability to visit flowers and carry pollen in oilseed rape. Although FSR of oilseed rape employed C. megacephala was lower than that of Apis cerana cerana, there was no significant difference of pod length and seed number per pod for oilseed rape pollinated by two insect pollinators. Overall, C. megacephala has great potential to pollinate for crops and DCA improves the thermal adaptability of C. megacephala towards crops. Our results provide an effective pollinator alternative to the honeybees for pollination of facility agriculture crops as well as early spring wild crops.

Inheritance and fitness cost of triflumezopyrim resistance in the brown planthopper, Nilaparvata lugens

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Abstract: Nilaparvata lugens (Stål) (Hemiptera: Delphacidae) is an important agricultural insect pest all around the world due to its serious damage to rice plants. Triflumezopyrim, a novel commercialized mesoionic chemical insecticide, functions by inhibiting the orthosteric binding site of nAChRs and makes insects lethargic, poisoning them by competitive binding to the orthotopic site of nAChRs. Here, a laboratory triflumezopyrim-resistant strain (TR) and an isogenic susceptible strain (TS) were established to characterize the inheritance and fitness costs of triflumezopyrim resistance in N. lugens. The LC50 values from progenies (F1RS and F1SR) of reciprocal crosses between TR and TS strains suggested that triflumezopyrim resistance in N. lugens was autosomal and codominant. The chi-square analyses of self-bred and backcrossed progenies suggested that the resistance results from a polygenic effect. Compared to the TS strain, the TR strain exhibited a relative fitness of 0.62 with a significantly decreased female adult period, longevity, total fecundity, egg hatchability, intrinsic rate of increase (r), finite rate of increase (λ), net reproductive rate (R0), and prolonged pre-adult period and total preoviposition period (TPOP). The current study provides valuable information for optimizing resistance management strategies to delay triflumezopyrim resistance development and maintain sustainable control of N. lugens.

Volatile mediated tritrophic interactions determine behavioral changes in the pest mite B. yothersii (Acari: Tenuipalpidae), in presence of the predator E. concordis (Acari: Phytoseiidae), in citrus.

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Abstract: Mites of the genus Brevipalpus (Acari: Tenuipalpidae) have economic importance because they are vectors of viruses in several cultures, especially CiLV-C (Citrus leprosis virus C), transmitted by the species B. yothersi. Volatile organic compounds (VOCs) associated with arthropods seem to be involved in inducing the anti-predator response. Experiments were carried out using orange leaves, without symptoms of virus, consisting of 3 treatments: T1) Without previous exposure to any mite species (control); T2) Previous exposure to the pest mite B. yothersi for 24h; T3) Previous exposure to B. yothersi and the predatory mite Euseius concordis (Acari: Phytoseiidae) for 24h. VOCs were collected in passive mode and the profile of compounds was determined by GC-MS. The results showed that the average movement time in T3 was longer than in the 2 previous treatments. The presence of acetic acid, benzene and toluene was identified in all 3 treatments, which could be characteristic of the plant. Compounds present in treatments T2 and T3 (benzoic acid, coumarin and vanillin), were probably released by the pest or by the plant in response to the attack; and compounds present only in T3 (ethanol, N-benzylidene-dimethylammonium chloride), are likely signs of the predator's presence.

Short-term spatial niche partitioning between the larger grain borer and the maize weevil: do semiochemicals play a role?

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Abstract: Prostephanus truncatus (Horn), the larger grain borer, is endemic to southern North America and Central America, but invaded Africa with severe economic consequences for maize and cassava production. Its main competitor is the cosmopolitan Sitophilus zeamais (Motschulsky), the maize weevil. While competition between these two species has been studied extensively, there is little information on spatial partitioning in bulk storage of grain. Thus, our aims were to evaluate the short-term niche partitioning behavior of P. truncatus and S. zeamais when placed in a monolayer column of grain. The monolayers were divided into 24 equally-sized vertical and horizontal zones to track location of the insects on maize in each zone. After one and then seven days, monolayers were placed on their side, and the grain and insects from each zone were removed. We found that both species generally aggregated together and preferred the bottom of the grain mass. To determine whether semiochemicals played a role, volatiles were collected from maize with P. truncatus, S. zeamais, or both species using headspace collection and gas chromatography coupled with mass spectrometry. Then, preference was evaluated in a 4-way olfactometer among the stimuli. We found maize volatiles were important for orientation of P. truncatus, but not S. zeamais, suggesting a confluence of factors other than volatile semiochemicals may lead both species to choose the bottom of the grain column. These data may help improve targeting of pest control tactics by identifying the position of these insects in the grain mass.

Ecology of wild bee’s pollination in agricultural landscapes: a pollen DNA approach

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Abstract: Wild pollinators, play an essential role in agricultural landscapes with up to 80% of all crops being pollinator dependant. However, many insect populations face declines, and even extinction in the coming decades due to intensive agriculture and, specifically, the use of chemical pesticides. One potential solution to decrease the negative impacts of intensive agriculture is ecological intensification, which relies on ecological processes to maintain or increase crop yield. For such strategy to work, a better understanding of the functioning of crop ecosystems is needed. In this work, we aimed to describe the pollination activity of wild bees in sunflower crops in Chizé (France). Pollen grains were collected from wild bees using a washing protocol and plant DNA was amplified to prepare metabarcoding library, which was sequenced using Illumina MiSeq. Our analysis identified the most commonly visited plants families as Asteraceae and Brassicaceae. We found significant differences in relation to the type of agriculture (organic / conventional), the developmental stage of the crop (pre-flowering / flowering), bees’ body size and, also, their level of sociality. This study provides valuable information about which floral resources are needed in agroecosystems for wild bees to survive, and what parameters may influence their pollination pattern.

Management of adult and immature large pine weevil (Hylobius abietis L.) using novel local-provenance entomopathogenic fungi and nematodes on different soil types.

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Abstract: The large pine weevil (LPW) is a widespread forest pest in conifer clearfell restocking areas. Biological control agents are the best candidates to replace widely used synthetic chemicals with potential side effects on the environment and humans. Entomopathogenic nematodes (EPN) and fungi (EPF) are successful at controlling its immature stages and also present additive effects when applied together to tree stumps. We propose a new approach that also targets the adults that survived the control of immatures. Surviving emerging adults will be lured with volatiles like alpha-pinene to traps containing an EPF. A large-scale soil sampling campaign within various habitats has provided new locally sourced EPF to be used together with commercial EPN strains. High diversity of EPFs has been obtained from soil using a dual baiting method with larvae of Galleria mellonella (Lepidoptera) and Tenebrio molitor (Coleoptera). The local strains of EPF are tested for pathogenicity on LPW to select the best entomopathogenic agent for adult traps and to study their additive/synergistic effects with commercial EPN. To test the efficacy of the approach in the field, mark-recapture experiments will be conducted, which will inform the development of an efficient chemical-free method to control H. abietis on forest clearfell areas.

Conservation and augmentation of ladybeetles for management of Asian citrus psyllid vector of huanglongbing, a devastating disease if multi-billion dollar citrus industry

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Abstract: Huanglongbing (HLB) or citrus greening disease caused by the phloem-restricted bacteria Candidatus Liberibacter asiaticus (CLas), is transmitted by the Asian citrus psyllid (ACP) Diaphorina citri. Control of the ACP is critical for area-wide management of this vector-disease complex and sustainable citrus production. Ladybeetles are an important component of biological control of ACP. In experiments using 17 generations of ACP under field environment, we observed more than 90% mortality of its populations from biological control mainly ladybeetles. However, foliar sprays of insecticides particularly during growing season when biological control is common significantly reduce the populations of ladybeetles and other predator species. Insecticidal control is most effective when ACP adults are few and other life stages largely absent due to lack of foliar flush, mainly because the insect needs newly developing leaf tissues for oviposition. This opportunity occurs during winter months when trees go through dormancy and do not produce new growth which is needed by the ACP for reproduction, so overwintering adults of ACP are common waiting for the new growth to begin in spring. In large-scale field studies, we showed that limiting the use of broad-spectrum insecticides such as organophosphates and pyrethroids to dormant winter months provides significant suppression in ACP populations lasting into growing season thus effective for integrated management of ACP. Ladybeetles were common during the growing season in blocks treated or not with broad-spectrum insecticide during dormant winter months. This suggest that reduced use of insecticides during growing season help conserve populations of ladybeetles whereas their use during dormant winter months is less damaging because most beneficial insects leave groves as most mature trees go through dormancy not producing the new growth thus limiting psyllid reproduction and ultimately prey for the natural enemies. Studies using commercial predators have shown significant role of additional predator species to enhance vector control. Conservation and augmentation of ladybeetles for ACP control will be discussed.

The Farmers Application and Quality Control Analysis of Biological Control Agents Product in East Java, Indonesia

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Abstract: Biological Agents Postal Service (PPAH) is an institution that performs production and develops biological agent in small-scale farmers group in Indonesia. They are monitored and managed directly by government institution namely the Pest and Food Crops and Horticulture Observers Laboratory (LPHPTPH). Biological agents products have been developed by PPAH and distributed among farmers. However, there are reports of problems regarding the production process, quality control, and the use of biological agents on several cities in East Java, Indonesia. The feasibility of biological agent products is determined through quality control, and the quality control activities conducted by several PPAH do not have clear standards and affects the quality of biological agent products. This study aims to investigate the use of biological agents conducted by farmers and to evaluate the quality control held by PPAH and LPHPTPH, in East Java, Indonesia.

This study took place in five cities around East Java, namely Blitar, Lamongan, Madiun, Malang and Pamekasan. Four PPAH in each cities have been selected as object to review in accordance to LPHPTPH recommendation. Using a qualitative method made by observation research and interviews with respondents who were determined to obtain descriptive data, respondents were selected using non-probability sampling and snowball technique. During the observation, product sampling of biological agents were collected to Biological Control Laboratory, Plant Protection Department, Brawijaya University in order to obtain information about product description and quality of biological agent product including the density of spores, viability, and pathogenic bacteria test on quality assay as safely indicator of biological agents product. The data then were analysed descriptively, the interviews and observations data were rated and assessed accordingly.

PPAH-guided farmers have been successfully using biological agents to deal with pests and plant diseases in great measure. The type of biological agent that is widely used by farmers are varied among cities. In the use of biological agents, farmers in those five cities generally have been able to apply the biopesticide to some extent. Although in several cases, farmers have been utilizing biological agents and chemical pesticide simultaneously; 85% in Madiun, 62,5% in Blitar, 17,25% in Malang, and 16% in Lamongan.

The quality control of biological agents produced by several PPAH in East Java are varies. In Pamekasan, the value of the assesment can be classified as good, ranged at 73.3. In Malang, Blitar, and Lamongan, the assesment ranged at 54.2, 53.5, and 46,5 respectively which classified as adequately good. The assesment in Madiun however, only ranged at 38 and classified as not good. Only two types of biological agents in Pamekasan matched the product packaging label while the presence of contamination are also showing, namely Escherichia coli and Salmonella sp.

Climate change associated water stress and aphid herbivory interactively reduce faba bean yield while the insect pollination benefit is conserved

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Abstract: Extreme weather events, such as prolonged dry spells, are hampering crop production and are expected to occur more frequently and become more severe under climate change. In addition, warmer temperatures will increase herbivory due to more abundant insect pests. Consequently, crop production will be increasingly impacted by both abiotic and biotic climate change stressors. While such climate change stressors can cause extensive yield losses, crop yields also benefit from a suite of ecosystem services such as insect pollination, which might mitigate yield losses. Despite the importance of understanding how interactions among climate change associated stressors and ecosystem services affect crop yield, most examinations concern benefits of single ecosystem services in isolation under favourable plant growing conditions. We experimentally tested the single and interactive effects of water stress, insect herbivory and insect pollination on faba bean yield. To this aim, we used 24 rainout shelters that allowed us to simulate a period of precipitation deficit in line with climate change scenarios. Half of the plots were subjected to no water input for 46 days, while the other half was irrigated thrice per week replenishing losses via evapotranspiration, to sustain well-watered conditions. To create two levels of insect pollination, we supplemented half of the cages of each water treatment with buff-tailed bumble bee hives (Bombus terrestris). To create two levels of herbivory, a subset of plants in each plot was inoculated with black bean aphids. We found that water stress and aphid herbivory interactively reduced yield by 84% while insect pollination increased yield by 68% irrespective of water stress and insect herbivory. Our results suggest that water withdrawal for irrigation should be prioritised in crop fields with high levels of herbivore control.

Entomological mosquito surveillance for West Nile, Usutu virus and Dirofilaria spp. in Apulia region (Southern Italy) (2021)

Authors: Raele Donato Antonio[1], Vasco Ilaria[1], Marino Leonardo[1] and Cafiero Maria Assunta[1], [1]Istituto Zooprofilattico Sperimentale di Puglia e Basilicata

Abstract: The entomological survey is a fundamental action of the national surveillance plan of arboviruses (PNA, 2020-2025) at a level region to prevent risk of pathogen transmission by arthropods, including mosquitoes species. This work reports the results obtained in Apulia region in 2021 year. Adult mosquitoes were captured in areas at risk by CDC and BG-sentinel. After morphological/molecular identification, mosquito pools were prepared and tested for WND and Usutu virus, Dirofilaria (D.) repens, D. immitis by qPCR. A total of 4751 (4432 F, 319 M) mosquitoes from 8 genera and 15 species (Aedes albopictus, Ae.vexans, Anopheles algeriensis, An. maculipennis s.l. (= An.labranchiae), Coquillettidia richardii, Culex (Cx) modestus, Cx,pipiens, Cx. theileri, Culiseta (Cul.) annulata, Cul.longiareolata, Ochlerotatus (Ochl) caspius, Ochl. communis, Ochl. detritus, Orthopodomyia pulcripalpis, Uranotaenia unguiculata) were collected from 13 stations for a total of 488 capture sessions. All of 445 tested pools resulted negative for viruses; D. repens DNA was detected in 3 (3/445) pools from Cx. pipiens, Ochl. caspius and D. immitis DNA was identified in 5 (5/445) pools in Ochl. caspius, Ae. Albopictus and Cx. pipiens. Our results show the presence of mosquito species capable to be vectors of a variety of human pathogens and suggest to increase monitoring.

Evolution and function of tick endosymbionts

Authors: Raghavan Rahul, Portland State University, United States

Abstract: Ticks feed only on vertebrate blood. Hence, symbiotic bacteria likely provide the nutrients not present in blood—as has been observed in blood-feeding insects. Two common putative nutritional symbionts in ticks are Coxiella-like and Francisella-like endosymbionts (CLEs and FLEs). Both symbionts evolved from pathogenic ancestors and have lost the genes that likely made their ancestors virulent. Independent evolution of nutrient-provisioning endosymbionts from pathogenic bacteria in multiple lineages of ticks indicate that this process occurs efficiently in ticks. Rapid attenuation of virulence, and the ability of bacteria to invade ovaries and salivary glands that facilitate tick-to-tick transfer could contribute to this speedy transformation. Interestingly, unlike insects, most tick lineages do not form long-term symbiotic partnerships with a specific bacterium. For example, some species of Amblyomma (hard ticks) have CLEs, whereas others have FLEs as their primary endosymbionts. Similarly, even though FLEs are the primary endosymbionts in Ornithodoros moubata and Argas persicus (both soft ticks), each tick acquired their respective FLE independently from disparate sources. This apparent lack of selection pressure to maintain long-term symbionts suggest that ticks have ready access to a large pool of bacteria—probably pathogens encountered in vertebrate blood, that could easily be domesticated into nutrient-provisioning endosymbionts. Long-term bacterial endosymbionts tend to become inefficient provisioners of critical nutrients due to genome degradation caused by genetic drift. Ticks might be able to avoid this fate by frequently replacing old symbionts with new bacteria that have enhanced metabolic capabilities.

Current models of diapause and quiescence, with some examples from bark beetles

Authors: Ragland Gregory, University of Colorado-Denver, United States

Abstract: Overwintering insects use a startlingly wide array of physiological and developmental strategies to appropriately time their seasonal windows of growth and reproduction. In this talk I will provide a brief review of our current understanding of stereotypical ‘types’ of overwintering that has been refined through the liberal application of ‘omics approaches over the last decade. In addition, I will address how genetic and environmental variation influence the flexibility of these ‘types’, including some current findings from bark beetles.

Divergence between populations and strong local adaptation may limit adaptive response to climate change with cascading effects on the community

Authors: Ragland Gregory[2], Lackey Alycia[1], Hahn Dan[3], Feder Jeffery[4] and Powell Thomas[1], [1]Binghamton University, United States, [2]University of Colorado-Denver, United States, [3]University of Florida, United States, [4]University of Notre Dame, United States

Abstract: Consequences of a population’s evolutionary response to climate change are not limited to extinction or survival of the focal population. Rather, phenotypic shifts in one species can ripple out to affect coevolved species in the community. We measured the response to climate change in ecologically divergent populations of Rhagoletis pomonella and the cascading effects on their wasp parasitoids. Fly life cycles are synchronized with host fruit availability via regulation of diapause (dormancy). Adaptation to different host plants with different phenologies drives divergence between fly populations. Parasitoids of these fly populations have also diverged in kind, yielding a cascade of diversification. We experimentally tested the response to increased temperature of two sympatric, recently diverged (~150 generations) fly populations that infest different host plants (hawthorns and apples) and their associated parasitoid communities. We measured survival and phenology for fly and wasp populations in control or warmed (+3 degC) temperature treatments that matched daily, natural fluctuations of the sampling site. Our design allows us to parse three different responses: survivorship within populations, phenological synchrony across trophic levels, and changes to allochronic (temporal) isolation between divergent populations. The effects of increasing temperature differed markedly between populations. Apple flies suffered high mortality before breeding and are likely near their physiological temperature threshold for diapause development. Flies of both populations shifted their life cycles significantly earlier under warmed temperature regimes. However, parasitoid wasps did not shift their life cycles in response to temperature, which would cause asynchrony across trophic levels. Lastly, shifts in fly life cycles will increase the overlap in breeding seasons of the two populations, dramatically increasing potential gene flow and limiting further divergence. Given the wide-ranging importance of phenology and potential for strong local adaptation, high-confidence predictions of responses to climate change will require similar experiments that determine environmental thresholds.

Mapping spatial distribution, identifying risk factors and predicting the abundance of dengue vector Aedes aegypti in northeastern Thailand

Authors: Rahman MD Siddikur[1], Overgaard Hans J[2], [1]Department of Medical Microbiology, Faculty of Medicine, Khon Kaen Univeristy, Thailand, [2]Norwegian University of Life Sciences, Norway

Abstract: Aedes aegypti is the main vector of dengue globally. The variables that influence the abundance of dengue vectors are numerous and complex. To help guide and improve vector-control efforts, this study identified and predicted the ecological, social, and other environmental risk factors that affect the abundance of adult females and immature Ae. aegypti in households in urban and rural areas of northeastern Thailand.

A total of 128 cohort households were mapped and a cross-sectional entomological survey was conducted in urban and rural areas near or along the Mekong River in north-eastern Thailand between January and December 2019. Information on the socio-demographic; self-reported prior dengue infections; housing conditions; durable asset ownership; water management; characteristics of water containers; knowledge, attitudes, and practices (KAP) regarding climate change and dengue; and climate data were collected. Negative binomial generalized linear models (GLMs) were fitted to identify the risk factors associated with the abundance of adult females and immature Ae. aegypti. Five popular supervised learning models, logistic regression (LR), support vector machine (SVM), k-nearest neighbor (kNN), artificial neural network (ANN), and random forest (RF), were used to predict female adult Ae. aegypti abundance (high/low). Urban areas had a higher abundance of female adult Ae. aegypti compared to rural areas. Overall, study respondents in both urban and rural areas had inadequate KAP regarding climate change and dengue. The fitted GLM showed a higher abundance of adult female Ae. aegypti was significantly ($p < 0.05$) associated with many factors, such as a low education level of household respondents, crowded households, poor premise conditions, surrounding house density, bathrooms located indoors, unscreened windows, high numbers of wet containers, a lack of adult control, prior dengue infections, poor climate change adaptation, dengue, and vector-related practices. Among all assessed models, RF showed the best prediction performance for female adult Ae. aegypti abundance. The identified risk factors are important for the critical first step toward developing routine Aedes surveillance and reliable early warning systems for effective dengue and other mosquito-borne disease prevention and control strategies at the household and community levels in this region and similar settings elsewhere.

Cross talk of juvenile hormone, ecdysone and insulins in regulation of mosquito metabolism

Authors: Raikhel Alexander[1] and Ling Lin[1], [1]University of California Riverside, United States

Abstract: Being the principal vector for dengue, yellow fever, chikungunya virus and recently Zika virus, the mosquito Aedes aegypti is an extremely important organism for investigation. Many unique physiological features contribute to the incredible evolutionary success of mosquitoes, placing high energy demands on a reproducing female mosquito. Therefore, metabolism must be synchronized with these needs. We have shown that the developmental hormones, juvenile hormone and 20-hydroxyecdysone, acting through their respective receptors, Methoprene-tolerant (Met) and Ecdysone Receptor (EcR), function as regulatory switches for synchronization of metabolic events with the energy requirements of a female mosquito. Met controls downregulation of metabolic genes during the previtellogenic phase, while EcR - their upregulation during the post-blood meal, vitellogenic phase of the reproductive cycle. Insulin-like peptides (ILPs) are important regulators of metabolism in insects. CRISPR-Cas9 disruption of the mosquito ilp6 and ilp2 genes resulted in reduced body size and decreased lipid accumulation, while CRISPR-Cas9 ilp5 interference had the opposite effect increasing body size and significantly elevating lipid stores. JH/Met and 20E/EcR signals act antagonistically on the expression of ilp6 and ilp5. The EMSA and Chip assays have shown direct binding of Met and the 20E downstream factor, E74, to the regulatory region of ilp6 gene. Moreover, CRISPR-Cas9 assisted labeling of FOXO has permitted us to visualize the differential effect of Met and its downstream factor Kruppel homolog 1 as well as EcR/E74 on a subcellular localization of the downstream insulin pathway factor, FoxO. In turn, FoxO was involved in regulation of metabolic genes; the Chip analysis has demonstrated direct binding to its conserved motifs in promoters of these genes. Thus, ILPs interact with JH and 20E hormones coordinating metabolic genes to determine the exact status of metabolism and development. This study advances significantly our understanding of mechanisms governing a metabolic program in female mosquitoes.

Post-eclosion temperature effects on insect cuticular hydrocarbon profiles

Authors: Rajpurohit Subhash, Ahmedabad University, India

Abstract: The insect cuticle is the interface between internal homeostasis and the often harsh external environment. Cuticular hydrocarbons (CHCs) are key constituents of this hard cuticle and are associated with a variety of functions including stress response and communication. CHC production and deposition on the insect cuticle vary among natural populations and are affected by developmental temperature; however, little is known about CHC plasticity in response to the environment experienced following eclosion, during which time the insect cuticle undergoes several crucial changes. We targeted this crucial phase and studied post-eclosion temperature effects on CHC profiles in two natural populations of Drosophila melanogaster. A forty-eight hour post-eclosion exposure to three different temperatures (18, 25, & 30 °C) significantly affected CHCs in both ancestral African and more recently derived North American populations of D. melanogaster. A clear shift from shorter to longer CHCs chain-length was observed with increasing temperature, and the effects of post-eclosion temperature varied across populations and between sexes. Overall, our results demonstrate strong genetic and plasticity effects in CHC profiles in response to environmental temperatures experienced at the adult stage as well as associations with desiccation tolerance, which is crucial in understanding holometabolan responses to stress.

Emerging challenges of invasive whiteflies (Hemiptera: Aleyrodidae) in trees of India

Authors: Ramachandran Sundararaj, Forest Protection Division, Institute of Wood Science and Technology, Malleswaram, Bangalore, Karnataka, India

Abstract: The enormous increase in the volume, diversity and swiftness of movement of plant products throughout the world has led to a proliferation and dissemination of invasive species, particularly ones closely associated with plants, such as scales and whiteflies. Such biological invasions are a great concern as they have a pronounced impact on the native ecosystem, biodiversity, and the economy. More than 110 exotic insect species had been reported from India, of which, whiteflies and mealybugs constitute a major part of the invasion. Most alien species of whiteflies are accidentally introduced with their host plant due to their small size and cryptic nature of their and immature stages being attached to the host-plant. Due to these characteristics, they are one of the most commonly transported and most successful arthropod groups invading new geographical areas. Moreover, exotic whitefly pests can multiply in large proportion in a short time and with their high phenotypic plasticity and strong potential compete with native species and cause damage to economically important crop plants. The spiralling whitefly Aleurodicus dispersus Russell which invaded about 25 years back has been reported on over 320 plant species belonging to 225 genera and 73 families in India including economically important tree species. Recently there was a surge of invasion of whiteflies in India as within a span of last five years, seven species of whiteflies viz., solanum whitefly, Aleurotrachalus trachoides (Back) infesting on 37 plant species; rugose spiraling whitefly, Aleurodicus rugioperculatus Martin on 40 host plants; nesting whiteflies, Paraleurodes bondari Peracchi on 34 host plants and P. minei ?accarino on 25 host plants; legume feeding whitefly, Tetraleurodes acaciae (Quaintance) on 2 host plants; palm infesting whitefly, Aleurotrachelus atratus Hempel on 3 host plants and woolly whitefly, Aleurothrixus floccosus (Maskell) infesting guava. Extensive surveys revealed that all the invasive whiteflies of India except A.floccosus were found infesting severely on important tree species, like Acacia auriculiformis, Bauhinia variegata, Ficus spp., Leucena leucocephala, Pongamia pinnata, Magnolia champaca, Morinda citrifolia, Saraca asoca, Samanea saman, Syzygium cumini, Syzygium jambos, Tectona grandis, Terminalia arjuna, Thespesia populnea, Santalum album, Vitex altissima, etc., They are also found infesting many medicinal plants and expanding their range of distribution. This communication describes the emerging threat of invasive whiteflies on important tree species of India and the need to develop preventive measures to contain the spread of these invasive species.

Development and piloting of sustainable pest management strategies in vegetable production systems in South- and Southeast Asia

Authors: Ramasamy Srinivasan, World Vegetable Center, Taiwan

Abstract: Vegetables are cultivated in 42.44 million ha with an annual production of 0.88 billion tons in Asia, but the productivity (20.72 t/ha) is far below the North America (34.39 t/ha) and Europe (26.25 t/ha). One of the major constraints is the pests and diseases, including invasive species, which have been exacerbated by climate change. They can lead to complete crop failures if timely control measures are not initiated. In order to produce blemish-free vegetables that would fetch higher market prices and to avoid serious economic losses, farmers in Asia predominantly rely on chemical pesticides. Calendar-based application of pesticide cocktails (mixture of 3-4 pesticides) is common. Indiscriminate pesticide use escalates the production costs and poses serious threats to human and environmental health. Hence, it has become highly imperative to develop alternatives. World Vegetable Center has developed and piloted integrated pest management (IPM) packages through farmer participatory approaches for tomato, yard-long bean and leafy brassicas. The IPM packages are composed of sequential application of bio-pesticides, which were on par with Farmers' practice (calendar-based pesticide application) in reducing the pest infestations, without compromising yield. Hence, the IPM packages provide sustainable solutions for managing key pests on vegetable crops in South- and Southeast Asia.

Maintenance of flower color polymorphism in Lupinus polyphyllus and modification of pollinator mediated selection by abiotic conditions

Authors: Ramula Satu, University of Turku, Finland

Abstract: Variation in flower color within species is commonly thought to be caused by variation in pollinator-mediated selection. However, abiotic factors can modify selection caused by pollinators and contribute to the maintenance of this polymorphism in nature. Lupinus polyphyllus (Fabaceae) is a short-lived perennial outcrossing herb that has large showy racemens with multiple flowers. The species has a color polymorphism with blue, red and white flowers. Blue flowers are typically most common but the proportions of the different color morphs vary between populations. The main pollinators are bumble bees (Bombus sp.), that have species specific innate preferences for the different color morphs, but interestingly their preferences are also affected by ambient temperature in this system. Abiotic conditions thus have the potential to modify pollinator-mediated selection on flower color in L. polyphyllus. In this research we study populations along a latitudinal gradient from south of Finland to the species northern range edge in central Finland that differ substantially in temperature and early growing season light conditions. We combine data from pollinator observations, long term climatic conditions and population genetics to addresses the question of how pollinator community composition, pollinator behavior and abiotic factors synergistically affect the maintenance of color polymorphism in this species.

Association between Host Tree Chemistry and Ambrosia Beetle Host Selection Behavior

Authors: Ranger Christopher, USDA, United States

Abstract: Ambrosia beetles are among the true fungus farming insects, whereby they cultivate fungal gardens within host trees on which the larvae and adults must feed to obtain nourishment. Ethanol is emitted from trees in response to a variety of physiological stressors, and acts as a strong attractant for ambrosia beetles seeking a host tree. Despite the antimicrobial activity of ethanol, ambrosia beetles specifically select host trees tissues containing ethanol for establishing their fungal gardens and producing offspring. Our objective was to assess the influence of ethanol on the colonization success of Xylosandrus germanus and its associated fungal symbiont. Attacks were induced by X. germanus and other species by baiting healthy trees with ethanol lures, but none of the foundresses established fungal gardens or produced broods unless tree tissues contained in vivo ethanol resulting from irrigating with ethanol solutions. More X. germanus brood were also produced in a rearing substrate containing ethanol. Ambrosiella and Raffaelea fungal isolates from ethanol-responsive ambrosia beetles also exhibited higher biomass on media containing ethanol, while the growth of “weedy” fungal garden competitors (Aspergillus, Penicillium) were suppressed. Faster alcohol dehydrogenase enzymatic activity was also exhibited by Ambrosiella and Raffaelea fungal symbionts compared to fungal competitors. These results demonstrate the affinity of ambrosia beetles for ethanol is due in part because it benefits their fungus farming by promoting the growth of their fungal gardens while inhibiting the growth of “weedy” fungal competitors. The presence of ethanol within host trees also indirectly benefits ambrosia beetle colonization success because foundresses do not begin laying eggs until their fungal gardens are flourishing. The influence of ethanol on ambrosia beetle fungus farming will also be discussed in the context of non-ethanol responsive ambrosia beetles.

Spatio-temporal patterns of the habitat is a key for the conservation of beetles inhabiting tree cavities

Authors: Ranius Thomas, Swedish University of Agricultural Sciences Dept. of Ecology, Uppsala, Sweden

Abstract: In ancient trees, cavities containing wood mould are formed. Wood mould is loose material mainly consisting of dead wood. Cavities with wood mould constitute natural mesocosms. Among inhabiting invertebrates, many are specialised to wood mould, especially beetles, but also pseudoscorpions, mites, and dipterans. Since ancient trees are decreasing world-wide, many of these species are today decreasing and threatened.

Among this fauna, we have in particular studied one beetle species, Osmoderma eremita. The presence of O. eremita indicates a higher probability of presence also of other specialised beetle species. One possible explanation for this is that O. eremita seems to act as an ecosystem engineer, by increasing the amount of wood mould and its content of nutrients. We have studied the species' occurrence patterns and made direct observations of dispersals. We have also studied the dynamics of the habitat and the species' populations over time. In Sweden, most O. eremita individuals remain in the same cavity throughout their entire life-time. Occurrence patterns suggest that the species is dispersal limited; species' occupancy increases with the amount of dispersal sources within a radius of 200 m. An effect of dispersal sources in the surrounding has also been revealed for other beetle species in this community, but for most species the scale of response is larger, up to 2 km. Many beetle species occur more frequently in cavities with characteristics reflecting a warmer or more stable microclimate. The population size of O. eremita varies widely among cavities, and is correlated with the amount of wood mould. Trees with cavities may persist for decades and centuries, and thus inhabiting species may remain in the same cavity over a long time. The population fluctuations are narrow in comparison to many other insects. For metapopulation dynamics, the number of cavities and their quality are important, as well as the spatial location of the cavities. Thus, the spatio-temporal dynamics of the habitats is a key for long-term preservation of O. eremita and other species in this community.

We have created artificial mesocosms by filling boxes with artificial wood mould. They are utilized by a lot of deadwood-dependent beetles, even though some specialised species such as O. eremita, only rarely use them. When using such boxes in experiments, we have found that the decomposition of wood mould is affected by the inhabiting beetle fauna, and then especially large-bodied beetle species are important.

Why do bumble bees die after foraging on linden (Tilia sp.)?

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Abstract: Linden (Tilia spp.), also known as basswood or lime, is a profusely flowering temperate tree that provides bees with vital pollen and nectar. On occasion, however, bees foraging on linden trees in Europe and North America have been observed to fall, crawl and ultimately die. These bee deaths have been attributed, with inadequate evidence, to toxicity from mannose in nectar or starvation due to low nectar in late blooming linden. We investigated both factors by analyzing nectar from trees below which crawling bees were observed, and comparing healthy foragers and crawling bees using a biochemical approach. Our results showed that nectar did not contain mannose but alkaloids were detected. Principal component analysis of muscle metabolites produced distinct clustering of healthy and crawling bees, with significant differences ($P<0.05$) in > 30 metabolites. In the presentation, we will provide details of the study and the results, which provide an explanation for the intriguing linden-bee mortality phenomenon.

The effect of elevation gradients and phytochemical diversity on arthropod community changes

Authors: Rasmann Sergio, University of Neuchâtel, Switzerland

Abstract: Addressing species' responses to climate change in the absence of long-term time series data is a challenge that can be achieved by substituting space for time. For example, elevation gradients can be used to address communities responses to temperature and precipitation changes. To measure climatic clines in the top-down potential of predators on herbivores, we first studies community composition of arthropod herbivores and predators at low, mid and high elevations in the Alps. Next, to address the bottom-up forces driving herbivores' communities variation, we manipulated plant phytochemical diversity at each elevation site and recorded the surrounding arthropod community composition. First, we found that while overall biodiversity is greater at low-to-mid elevation, the biocontrol control potential of predators was stronger at low elevation. Second, we found that high community-level phytochemical diversity decreases the colonizing arthropod herbivore abundance, but mainly at low elevation. Our results, suggest that temperature changes can modify the top-down versus bottom-up control of herbivores in natural systems.

Plant species diversity influences tri-trophic interactions along environmental gradients

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Abstract: Theory predicts that mixed cultures are more resistant to pests than monocultures through increased top-down controls by natural enemies (i.e. associational resistance). However, whether plant diversity effects remain stable along elevation gradients has yet to be verified. Along elevation gradients, a general pattern is that herbivores and predators are abundant at low elevation and progressively diminish at higher elevations. To determine how plant species diversity influences top-down control of herbivores along such elevation gradients, we performed reciprocal transplant experiments manipulating plant species diversity and root herbivore pressure. Additionally, we measured soil nematode abundances. Without herbivores, nematode abundance was higher in mixed cultures than in monocultures. In the presence of root herbivores, nematode recruitment was higher in plant species mixtures. The magnitude of this effect was higher at low elevation sites, where nematode abundance was more important. We also explored the effect of root herbivory and plant diversity on plant root volatile profiles, using gas chromatography–mass spectrometry (GCMS). Overall, our results provides new insights into how species respond to environmental gradients, and highlight the importance of accounting for plant species diversity in trophic interactions.

Halyomorpha halys and Trissolcus mitsukurii in Friuli Venezia Giulia (Northeastern Italy)

Authors: Raso Rosario[2], Oian Barbara[2], Benvenuto Luca[3], Malossini Giorgio[4], Bernardinelli Iris[3], Roversi Pio Federico[1], Marianelli Leonardo[1] and Giovannini Lucrezia[1], [1]CREA -Research Centre for Plant Protection and Certification, Italy, [2]ERSA, [3]ERSA – Regional agency for rural development – Phytosanitary Service of Friuli Venezia Giulia, Italy, [4]Plant Health Service - ERSA - Friuli Venezia Giulia Region, Italy

Abstract: In North America and Europe Halyomorpha halys causes high damages on crops; chemical and physical solutions do not guarantee an acceptable level of long-term pest control. In the Friuli Venezia Giulia (FVG) region in North-Eastern Italy, the first detection of H. halys occurred in 2014 and in the following five years it spread over the whole region; the most damaged crops are apples, pears, peaches and kiwi. Monitoring by visual inspections and lured traps permitted to define the spreading of H. halys in the region, which is characterized by a fragmented landscape, with orchards surrounded by arable crops. A new perspective for a long-term solution for H. halys control is given by the discovery in FVG of an Asian egg parasitoid, Trissolcus mitsukurii, found in three different sites on H. halys eggs in August 2018. The egg parasitoid was detected on hedgerows and cultivated plants in IPM or organic orchards. T. mitsukurii was also found in 2019 in more than 25 sites across the region, showing its ability to disperse and establish in the northern Italian climate. Parasitization success of H. halys egg masses is relatively high. In 2019 the average parasitization rate was at least 25% of the total egg masses collected (mean of parasitized eggs/egg masses was 66%). In organic kiwifruit orchard it reached 82% of egg masses parasitized on 44 collected (mean of parasitized eggs/egg masses was 71%). In the same orchard in 2018 the parasitization rate was higher: 84% of egg masses parasitized on 19 collected (mean of parasitized eggs/egg masses was 87%). Surprisingly, starting from 2019, in the H. halys oldest infested areas (sites A) for the first year we observed a decrease of the bug populations, while in the new ones (sites B), in the southern part of the region and in the north close to the Alpine areas, the BMSB population increased considerably; these areas are also with the lower presence of T. mitsukurii. As an example, considering the total bug catches, the 42% reduction in sites A and 20% in sites B from 2018 to 2019 was observed. Considering the presence of H. halys juveniles only, the decrease was even higher (48% in sites A and 29% in sites B). This event was concomitant with the findings of T. mitsukurii in the same sites. In many areas, the decreasing trend of H. halys was observed also in 2020 and in 2021. In the part of the region where the occurrence of T. mitsukurii was low or absent, the population of H. halys at contrary continuously increased over years. Damages on fruit orchards in 2018 and 2019 were still considered high and “stay green” effect was very evident and widespread on soybean fields, while in 2020 and 2021 a general damage reduction was observed. Data collected could suggest that natural biological control of T. mitsukurii has started and should presumably develop in the coming years across the region.

Exploiting trap color to improve survey and detection of native and exotic longhorn beetles (Coleoptera, Cerambycidae)

Authors: Rassati Davide[2], Faccoli Massimo[2], Cavaletto Giacomo[2] and Marini Lorenzo[1], [1]Department of Agronomy, Food, Natural Resources, Animals and the Environment. University of Padua, Italy, [2]University of Padova, Italy

Abstract: Longhorn beetles (Coleoptera, Cerambycidae) are among the most significant groups of invasive forest insects worldwide. Hidden within live plants and wood-packaging materials, these beetles can escape routine inspections at entry points and some become major pests in the invaded environment. Traps baited with blends of pheromones and kairomones and set up in and around entry points are commonly used to improve chances of intercepting exotic species soon after their arrival. Factors able to affect longhorn beetle catches in traps have been extensively studied in the last years. Nonetheless, one aspect is still largely overlooked, that is the effect of trap color. In a trapping study carried out in 2019 at 16 forest sites in northern Italy, we investigated the response of longhorn beetles to baited traps of eight different colors (i.e., black, yellow, green, red, purple, grey, brown and blue). In total, 6,001 individuals were trapped, belonging to 56 species, 54 native and two exotic. Longhorn beetle species richness and total abundance were significantly affected by trap color; in particular, yellow traps allowed to catch a significantly greater number of species and individuals than the commonly used black traps. In addition, trap color affected the abundance of several species, but the response was mainly species specific. Color preferences of different longhorn beetle species are likely linked to either their food habit or their sexual behavior. In general, these results indicate that trap color can strongly affect longhorn beetle catches in traps and suggest that trap of different colors should be used in surveillance programs carried out at entry points.

Life-history trade-offs in variable environments

Authors: Ratikainen Irja, Norwegian University of Science and Technology, Norway

Abstract: The world is a variable place and a part of that variation is unpredictable to animals, but all animals have evolved ways to cope with such variable and uncertain environments.

I will discuss how environmental variation and unpredictability can affect different life-history trade-offs and how different life-history traits can co-evolve to deal with environmental variation.

As one example of this we have seen that the trade-off between reproduction and survival can be affected by environmental variation in unexpected ways. Classic theory suggests that variable environments result in evolution of long life, but novel theoretical and empirical work show that environmental variation can instead select for short lifespan and early reproduction. If reversibly plastic responses can evolve as well, we should expect that long life and environmental variation is not merely a context that sets the stage for lifelong plasticity but plasticity itself can select for longevity. Considering niche construction as an alternative to plasticity for achieving tolerance to environmental variation can reveal how the theoretical developments can help us understand social insects, and how social insects can help us understand life-history trade-offs in variable environments.

Effect of large scale disturbance on native cerambycid communities

Authors: Ray Annie[3], Traylor Clayton[2] and Franzen Emily[1], [1]Department of Biology, Xavier University, United States, [2]Department of Entomology, University of Georgia, United States, [3]Xavier University, Cincinnati, OH, United States

Abstract: The ecological and economic consequences of biological invasion have compelled research to identify mechanisms for resistance against the establishment of nonnative species. There is a growing body of evidence that suggests that biodiverse communities can be resistant to invasion (i.e., biotic resistance) due to either complementary niche partitioning or the likelihood of a highly competitive species being present. One example of niche partitioning is the pheromone niche hypothesis, where low levels of diversity in cerambycid communities allow “pheromone free space.” Pheromone niches are specific chemical, habitat, and temporal characteristics that each species uses for mating or aggregation attraction. Potential invaders are more likely to establish if they possess a pheromone niche that is free, because cross-attraction between invasive and native species will not occur. Furthermore, high intensity disturbances generally facilitate invasion by reducing native species richness, allowing invaders to establish. Most previous studies investigating these mechanisms have focused on grassland or algal communities; very few have concentrated on insects. Because of the economic importance of exotic and potentially invasive longhorn beetles, we investigated the effects of intense tree removal on cerambycid diversity in Clermont Co., OH, at a forested site inside of the Asian Longhorned Beetle eradication zone. Cerambycids were collected from April to September of 2017-2020, and abundance and diversity was compared to a similar site outside of the eradication zone. To date, we’ve found limited differences in species composition between sites, suggesting that the disturbance has not substantially altered the cerambycid community. It is possible that it is too soon to detect the impacts of large-scale disturbance on cerambycid communities and additional research is needed over a longer time period to detect community changes.

Enneothrips n. sp. (Thysanoptera: Thripidae): unraveling the real identity of the South American peanut thrips?

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Abstract: The peanut thrips is the key pest of peanut (Arachis hypogaea) in South America, where it can cause yield losses of up to 85%. So far, the species was recognized as Enneothrips flavens, but access to the holotype of this species and freshly collected material from Brazil and Paraguay revealed that specimens commonly collected on peanut crops have consistent morphological differences when compared with E. flavens. The objective of this work is to report evidences that the name currently applied to the peanut thrips is not appropriate and propose the description of a new species to this taxon. Specimens of the peanut thrips have been collected in the states of Acre and São Paulo, Brazil, and in Asunción, Paraguay. Also, specimens to which the name E. flavens could be morphologically applied were collected from different hosts in the states of São Paulo and Minas Gerais, Brazil, areas close to the type locality of the species. All the specimens were prepared in permanent microscope slides (Canada Balsam) and are deposited in the Coleção de História Natural da UFPI, Floriano, Piauí State, Brazil. In addition, to assure a correct identification, type material of all Enneothrips species currently known have been examined from California Academy of Sciences (San Francisco, CA, USA) and Smithsonian’s National Museum of Natural History (Washington, D.C., USA). Direct comparison of the peanut thrips slides with the holotype of Enneothrips flavens allowed to observe morphological differences between these two taxa, namely: (i) absence of internal markings in the metanotal reticles of the peanut thrips; (ii) coloration of abdominal tergites lighter and more uniform in the peanut thrips; (iii) closer sculpture lines in the mesonotum in the peanut thrips. Moreover, males collected together with females of the species to which the name E. flavens can be morphologically applied are macropterous, instead of brachypterous as in the species collected from peanut crops. Taking into account that the pest species have consistent differences in relation to E. flavens, and that it does not belong to any other species described in the genus, it is proposed that the peanut thrips should be described as a new species to science. Molecular studies are currently being carried out to further support this assumption.

Applying social evolution theory to design cheat-proof insect pathogen selection experiments

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Abstract: Cooperation and social conflict are important for the virulence of the insect pathogen Bacillus thuringiensis, especially the expression Cry proteins, their obligate virulence factors. Any selection regime aiming to increase the virulence of B. thuringiensis therefore needs to prevent the emergence of social cheats that do not produce these costly proteins.

Here we used a passage experiment to increase the virulence of Bacillus thuringinensis against a resistant population of diamondback moth, Plutella xylostella. We used two selection treatments: pooling of infected cadavers and competition between subpopulation in an insect metapopulation. We also investigated the value of increased mutation supply by using wild type bacteria and a mutator. We found that the metapopulation regime and the use of mutators both facilitated increases in virulence. However, selection in a meta-population was the most effective method for preventing the emergence of cheats, bacteria no longer produced Cry toxins. The metapopulation structure of host and pathogen is vital for ensuring that selection at the right scale can operate and provide a selective advantage for virulent mutants. Not only does this indicate how selection for pathogen virulence might occur in the field but also how we can re-model pathogen passage for social microbes.

Bioaugmentation of entomopathogenic fungi for sustainable wireworm management in maize and potatoes

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Abstract: Soil microorganisms influence biotic and abiotic stress tolerance of crops. Most interactions between plant symbiotic and non-symbiotic soil microorganisms and plants occur in the rhizosphere and are sustained through plant exudation/ rhizodeposition. Bioaugmentation, i.e., applying microbes with plant beneficial traits into the rhizosphere, specifically bioaugmentation of entomopathogenic fungi (EPF), could alter microbial rhizosphere communities towards increased ecological service provision and potentially replace environmentally unfriendly insecticides. Wireworms, the soil-burrowing larval stages of click beetles (Coleoptera: Elateridae), are major pests of crops including maize, wheat and potatoes, worldwide. They can be effectively controlled using granular organophosphates or pyrethroids, but these insecticides are already restricted in several countries and are gradually being phased out. Therefore a potential wireworm biological control strategy involving maize seed and potato tuber coating with soil EPF was investigated. The plant biostimulation potential to maize and wheat as well as virulence of several EPF isolates to Agriotes lineatus wireworms was assessed in a series of laboratory experiments. One M. brunneum strain was further evaluated in field settings to examine its ability to protect three maize cultivars from wireworm damage and promote plant growth, whereas four M. robertsii and two M. brunneum isolates were assessed in potato field trials. In-house reared wireworms were dipped for 10 s in a 1 × 108 ml-1 conidial suspension; maize and wheat seeds and potato tubers were coated with fungal conidia. Additionally, in the potato field trials, six EPF isolates were formulated on rice and applied as soil granular bioinsecticide, and their efficacy compared to ATTRACAP. Several EPF strains significantly increased wireworm mortality and colonized maize and wheat rhizoplane in laboratory settings to a varying extent. The strains tested were seldom isolated as endophytes. Maize plants originating from seeds treated with conidia of Metarhizium brunneum strain HJS 1868 showed significantly less wireworm damage at emergence resulting in significantly higher initial and final maize stand in field experiments. The mix of six EPF strains evaluated in potato field trials offered protection against wireworm drilling at par with bioinsecticide ATTRACAP, however, only when formulated on rice; soaking potato tubers in the conidial mix annulled this effect. The implications of EPF × plant interactions are discussed in the context of exploiting plant-microbe interactions for low input sustainable agriculture.

Acknowledgments
The research was financed partly by the Slovenian Research Agency (ARRS) (Next Generation Agriculture program group, grant number P4-0431 and a grant to EP, 1000-18-0401), and H2020 projects ECOBREED (grant 771367) and EXCALIBUR (grant 817946).

Wild cotton landraces as a source of host plant resistance to reduce thrips injury

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Abstract: Thrips are problematic pests of many agricultural, horticultural, and ornamental crops. Preventative insecticidal sprays are often necessary for managing thrips (Thysanoptera) on cotton (Gossypium spp.) throughout the United States. Host plant resistance could protect vulnerable cotton seedlings and reduce further development of insecticide resistance in thrips populations. Our work has investigated the potential for thrips resistance among the landrace collection maintained by the U.S. National Plant Germplasm system, which is a largely untapped source of genetic diversity. Identification of thrips-resistant landraces began with field trials using insecticide treated and untreated plots. Putatively resistant and susceptible lines underwent free-choice and no-choice tests with tobacco thrips (Frankliniella fusca Hinds). With further analyses of metabolomics and volatile analyses, we plan to identify the underlying causes of thrips resistance in cotton.

Development of Helicoverpa zea on transgenic maize expressing Bt toxins in the southeastern United States

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Abstract: The corn earworm, Helicoverpa zea (Boddie) (Lepidoptera: Noctuidae), can be managed in the United States using transgenic maize hybrids that express insecticidal proteins from the bacterium Bacillus thuringiensis (Bt). While practical resistance has developed in H. zea to a several Cry toxins, Bt traits still provide efficacy for reducing ear injury compared to non-Bt maize. Fitness costs or the effects of sublethal doses of Bt toxins are apparent by delayed development and reduced pupal weights on Bt maize hybrids. A longitudinal study from 2012-2019 characterized changes over time in the reduction in H. zea pupal weight on Bt maize in North and South Carolina. As H. zea has developed resistance to Bt toxins, the effects of Bt toxins on pupal weights have lessened over time. On-going research is aiming to identify potential fitness costs and their implications for insecticide resistance management. In addition, development of H. zea was examined in the field by measuring the instar- and tissue-specific feeding behavior of larvae in Bt and non-Bt hybrids. Concentrations of Cry1F and Cry2Ab2 toxins quantified using ELISA varied significantly with silk age and both were generally greater in the silk and tip tissue compared to kernels and husk. Hybrids with pyramided toxins lead to delayed development of H. zea and had reduced injury to the silk, tip, and kernel ear tissues, which was less clear with single Bt toxin hybrids. The pyramided hybrid expressing Vip3A had no injury to the ear tip or kernels, and only eight 1st instar larvae were found in the silk out of 520 ears. Larval age varied among tissues but not between hybrids. We did not detect differences in feeding behavior between Bt and non-Bt hybrids. Implications for resistance management strategies such as seed mixtures will be discussed.

Aphid parasitism in organic wheat systems of the US Southern Plains

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Abstract: A unique set of climatic conditions in the US Southern Plains allow conventional winter wheat producers to grow this crop as forage for cattle, for dual purpose (cattle + grain), or for grain only on over 5 million hectares. The success of this crop is directly attributable to well-established pest management programs that allow producers to significantly reduce inputs while effectively managing pests. Indeed, researchers in the region have demonstrated over the past several decades that low-input winter wheat serves as the primary winter habitat in the Southern Plains for a broad range of insect natural enemies, but more importantly, these natural enemies regularly maintain insect pests below economic injury levels, and subsequently reduce the need for curative insecticide applications. In fact, the effects of parasitoids on aphids in wheat are so predictable that they have been incorporated into sampling and management decisions. The increasing number of organic winter wheat systems in the Southern Plains should significantly benefit from the effects of aphid parasitoids because their numbers and diversity are likely to be conserved in the absence of detrimental, broad-spectrum, synthetic insecticides, which still are included occasionally in conventional production systems. We hypothesized that winter wheat fields on organic farms will provide habitat for parasitoids of aphid pests and prevent outbreaks, but also serve as sources of natural enemies for organic spring crops (vegetables, fruits, and herbs) common in the landscape of most organic farms. Based on methods from previous aphid parasitism studies, sentinel wheat plants in pots with aphids (bird cherry oat) were used to describe pest suppression by parasitoids in organic wheat fields versus nearby conventional wheat fields (paired and min 10 km away) over a range of growing conditions in Oklahoma. Pots/vegetation were retrieved and predators removed before being placed in emergence canisters to estimate parasitism rates and pest suppression. Preliminary observations reveal relatively high levels of parasitism in organic wheat fields by commonly described cereal aphid parasitoids in the region, similar to levels and species found in conventional wheat systems. Observations of parasitism in organic wheat systems suggest that producers should be able to adopt aphid-parasitoid management decisions utilized in conventional wheat systems throughout the region.

Attachment ability of the parasitoid Anastatus bifasciatus to its host eggs

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Abstract: Egg parasitoids attack eggs of many arthropod species and play an important role in biological control of pest species. During coevolution with their hosts, egg parasitoids have developed great ability to locate their host using chemical cues. A considerable amount of literature is available on this topic while nothing is known about a possible adaptation of egg parasitoids to the mechanical features of the egg surface and its shape when attaching to the host egg for oviposition.

In the present investigation, the attachment ability of adults of both sexes of the ooparasitoid Anastatus bifasciatus (Hymenoptera, Eupelmidae) to artificial and natural surfaces (eggs of Halyomorpha halys and Nezara viridula) with different roughness and wettability was measured with centrifugal force tester and traction force experiments. The parasitoid attachment devices and the egg surface were characterised under cryo-SEM, the wettability and the roughness of natural and artificial surfaces were also measured. Differences in the attachment devices and attachment ability of the two sexes have been observed. The collected data reveal a special ability of the female to attach to the eggs of the host species, thus suggesting an adaptation of the female to the mechanical features of the eggs during oviposition.

Application of entomopathogens for the management of wireworm in spring wheat

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Abstract: Wireworms are major pests of spring wheat and barley around the world. Insecticides as seed treatments only work as repellents. Environmentally friendly management strategies are needed to manage wireworms to conserve the environment. At the Golden Triangle Area of Montana, we are using entomopathogenic fungi (EPFs) and entomopathogenic nematodes (EPNs) to develop a cost-effective management strategy. Polenta, millet, and couscous were used as a nutritive carrier to increase the efficacy of EPFs by regrowth and conidiation after application. The tested EPFs were Beauveria bassiana GHA, Metarhizium robertsii DWR356, M. robertsii DWR2009, B. bassiana ERL836 and M. brunneum F52 on polenta, couscous and millet carrier. In 2017, at Valier, DWR356 and DWR2009 on a millet carrier at 22.4 kg ha-1, provided greater yield but all the treatments at the lower rate were cost-effective. In 2018, GHA and ERL836 on millet carrier obtained cost-effective results at irrigated and non-irrigated sites in 2018. Millet as carrier worked better than the other carriers. Further evaluation of the different carriers under various field conditions is required. The study with EPNs involves laboratory, indoor and field experiments to evaluate ten EPN strains against sugar beet wireworm, Limonius californicus. Steinernema carpocapsae, S. riobrave, S. rarum, and Heterorhabditis bacteriophora killed 50-60% of L. californicus larvae in the laboratory. Similarly, S. riobrave and S. carpocapsae were able to kill 50% wireworm larvae under shade house conditions. However, these EPN species were not found very effective for protecting wheat and barley plants due to wireworm damage. Also, Montana native EPN species (S. feltiae and H. bacteriophora) were observed to be virulent against L. californicus under laboratory conditions but not in shade house experiments. These results suggest that EPNs may have significant potential for protecting spring wheat crops from wireworms and need to be explored further.

In cold blood: deciphering the mechanisms underlying mosquito-frog interactions

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Abstract: Mosquitoes can feed on almost any animal, including other mosquitoes. While most research involves species that feed on humans, one species, Culex territans, specializes in feeding on ectotherms, primarily amphibians and reptiles. Although this species is fairly widespread in North America and Europe, surprisingly little is known about its biology and ecology. For this project, we are particularly interested in understanding: 1) How do the mosquitoes locate their cold-blooded host? 2) How do they manage imbibing cold and viscous blood? 3) What is their role in disease transmission? To better understand the cues Cx. territans uses to find its hosts, we performed olfactometer experiments and feeding assays coupled with thermographic imaging with green frogs and bullfrogs, two of the common hosts this mosquito feeds on in the wild. We also used SPME scent collection coupled with GC/MS to analyze the scents of these two species of frogs. Using electro-antennograms coupled with gas chromatography, we determined the compounds emitted by the frogs that the mosquito antennae detect. Antennae transcriptomic analyses allowed us to get hints in the specificity in odorant receptors this species has and overall on some of the adaptations developed by this species to feed on ectotherms. Finally, we know that Cx. territans transmits trypanosomes to amphibians, but it is unclear if they vector any other diseases. In order to understand the effects that this mosquito has on amphibian health, we screened blood fed mosquitoes from the field and from our feeding assays for trypanosomes as well as Ranaviruses using PCR and plaque assays. Together, this data is helping us to build a more complete picture of the evolution of blood-feeding on warm-blooded vertebrate hosts, including humans, in mosquitoes and to learn about the role Cx. territans plays in the decline of amphibian populations worldwide.

An overview of stink bugs (Euschistus servus and Nezara viridula) as pests of US corn

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Abstract: Previously the stink bug Euschistus servus was a major problem in corn, but primarily isolated to corn fields bordering wheat. After wheat was harvested, E. servus would disperse into and damage neighboring corn fields. During the past 10 years, the stink bugs E. servus and Nezara viridula have become the most problematic insect pest of corn, and continue to be major pests of soybean and cotton across the southern US. Also during the past 10 years, these stink bugs have been problematic in corn fields that are not associated with wheat. This presentation details past, recent, and future studies describing the ecology and management of stink bugs in corn.

A cotton tissue-based resistance monitoring procedure for Helicoverpa zea in Bt cotton

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Abstract: Current methods to identify Helicoverpa zea (Lepidoptera: Noctuidae) practical resistance to Bt cotton rely on the relationship of diet-based bioassays to field injury, measured as square or boll injury. However, these are often confounded by environmental variation in the field. We developed an experiment to identify quantifiable and reliable in-field plant injury as a supplementary resistance monitoring tool. Plant-based tissue bioassays have been used reliably in other systems, but are not available for Helicoverpa zea. In field experiments, we identified H. zea larval feeding patterns on cotton plants that could be indicative of selective feeding. Bolls were proposed as the target candidate for a plant bioassay because they are not prone to abscission under diverse environmental conditions, thus avoiding confounding the effect of insect feeding from abiotic conditions. We present our ongoing efforts to link feeding on bract tissue from bolls to correlate with Bt resistance in H. zea.

Global mechanisms of Bt resistance in a field strain of the cotton bollworm, Helicoverpa zea: the expected and unexpected

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Abstract: Evolved resistance to genetically modified crops including economically important products such as cotton, corn, soybeans and many others has become rapidly and globally widespread over the last 20 years. Numerous economically important agricultural pests of crops expressing Bt (Bacillus thuringiensis) bacterial proteins (Cry1Ac, Cry1F, Cry2Ac) have evolved resistance to these Bt-toxins. RNA-seq is a method to quantitatively measure total gene expression in an organism. This method was used to measure differences in global gene expression between a Bt-susceptible and a Bt-resistant strain of the Cotton Bollworm (Helicoverpa zea), where the differences in susceptibility to Cry1Ac +Cry1F toxin was 100-fold. Quantitative PCR was later used to confirm expression levels in the two strains of bollworm. We found gene expression differences that would be expected based on our current understanding of Bt mode of action and resistance including increased expression of proteases and reduced expression of Bt-interacting receptors in Bt-resistant bollworms. We have also found additional expression differences between the two strains of bollworm in genes that have not previously been thoroughly investigated. This suggests that there are multiple different mechanisms influencing the development of Bt-resistance in addition to potential previously unrecognized pathways of resistance in this agricultural pest species. Also important to consider is how investigation into the genetic mechanisms of Bt-resistance will aide in the understanding of how resistance in insects develops. Due to prevalence of insecticidal use, biology of insects, and other factors; resistance to any IPM technique is likely inevitable. Ideally this knowledge can then be applied to reduce the vulnerability of novel and next-generation integrated pest management technologies to evolved resistance in agricultural pest species.

Comparative Behaviors of Old and New Foes: Oviposition of the Container Aedes spp.

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Abstract: Container Aedes spp. mosquitoes are known to oviposit is a variety of natural and artificial containers. Various container factors have been explored in the literature, including size, nutrients, presence of predators, presence of conspecifics, and presence of competitors to assess preferred containers. However, there has been little work on the basic behavior that is being assumed in preference studies, that of “skip oviposition.” Here we present data comparing three container Aedes with different evolutionary history and ecological backgrounds: Aedes aegypti, Aedes albopictus, and Aedes triseriatus. We find both subtle and striking differences in their oviposition behavior and their propensity to skip oviposit. These differences have important implications for the interpretation of preference studies and the utility of autodissemination as a control strategy.

Investigating small RNA profiles of honey bee viruses in parasitic mites

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Abstract: The honey bee parasitic mite, Varroa destructor, is a major threat to beekeeping worldwide. One consequence of Varroa infestation is increased prevalence of viruses that are vectored by mites. While viruses are known to cause immune responses in honey bees, there have been few studies investigating the impact of viruses on Varroa mites themselves. The RNA interference (RNAi) pathway is a major antiviral immune pathway in insects and involves active degradation of viruses by Dicer into small RNA fragments of 21-22 nucleotides. Here, we examine the RNA interference response of Varroa mites to honey bee viruses. We performed deep sequencing of small RNA fragments in Varroa destructor to determine if mites mount an active response to viruses infecting honey bees. While honey bee RNA interference profiles display a classical Dicer-mediated response to viruses, the viral small RNA profile in Varroa is novel and distinct from the profile observed in bees. These results indicate that viruses are processed differently between bees and their mite parasites, and point to alternate viral RNAi pathways within these two Arthropod lineages. Further, active degradation of viruses in Varroa indicates that honey bee viruses elicit a host-mediated antiviral response by the Varroa immune system, suggesting these viruses may therefore be genuine mite infections.

How does vector transmission by Varroa mites influence the evolution of Deformed wing virus in honey bees?

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Abstract: Evolutionary theory predicts that the arrival of a vector alters the trade-off between virulence and transmission of pathogens. As the vector now transmits the pathogen between hosts, pathogen transmission is no longer dependant on extended host survival, allowing a pathogen to evolve towards higher virulence. The increase in the prevalence and abundance of the honeybee RNA virus Deformed wing virus (DWV) with the global spread of the ectoparasitic mite, Varroa destructor, nicely fits the pattern predicted by theory. DWV is vectored by the mite during feeding on the bees' fat bodies. Without the use of miticidies, honey bee colonies infested with V. destructor typically die within 6-24 months, and colony deaths have been largely attributed to DWV. Previous studies suggest that Varroa-mediated transmission places a selective bottleneck on DWV genotypic diversity, and potentially selects for increased virulence in DWV strains. At the same time, small isolated populations of honey bees around the world have developed tolerance to V. destructor, with colonies surviving without the use of miticides. Some studies have suggested that perceived Varroa tolerance is attributed to high DWV diversity and the absence of virulent strains within the given honey bee population. While these Varroa-tolerant honey bee populations differ both genetically and geographically, their common thread is an ability to keep Varroa numbers low. Clearly, mite numbers matter. The question is why. We hypothesised that if Varroa places selective pressure on DWV, then DWV diversity should be altered when the number of passages (e.g. bee-to-bee transmissions) increases. Conversely, increased transmission with no change in DWV diversity over time would suggest that Varroa transmission is non-propagative. Instead some viral variants may have increased fitness in honey bees, or may be better adapted to vector transmission. To determine the role the mite plays in the diversity of DWV we studied two honey bee populations in the Netherlands with equal mite numbers, One population is Varroa tolerant (and chemically untreated since 2008) and the other treated annually with miticides. We experimentally increased the number of Varroa mites within multiple colonies of both populations. We monitored the change in viral abundance and DWV diversity over a period 10 months, and evaluated what effect increased mite numbers have on DWV genotypic diversity. The results of this study will improve our understanding of the role Varroa transmission has on DWV evolution. This will have significant ecological and economic implications, both in managing honey bee health and in improving our understanding of disease emergence and virulence evolution.

Nitrogenous waste recycling mediated by gut microbes in oriental fruit flies for environmental stresses

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Abstract: Microbes are major contributors to insects coping with multiple environmental stresses, among them nitrogen stress is one of the critical challenges to herbivorous insects. The oriental fruit fly, Bactrocera dorsalis, is a polyphagous agricultural and horticultural pest of economically important across the world. The larvae are fruit-boring maggots, living in an independent and enclosed environment within the infested fruits. Up to now it is unknown upon which strategy employed by B. dorsalis to overcome nitrogen stress and develop successfully in the fruits. In this study, we analyzed microbial community diversity and expression profile across different life stages using metagenomics and metatranscriptomics sequencing technology, and investigated the potential functions of microbes in pupae, larvae and adults. Combining with verification tests in vitro, we compared pathway completeness of nitrogenous waste recycling (NWR) and biological nitrogen fixation (BNF) in B. dorsalis based on the annotation results of transcript sequences and KEGG database. The results showed that NWR could be efficiently driven by microbes including Enterobacterales, Flavobacteriales, Lactobacillales, Pseudomonadales and Rhodospirillales. Whereas BNF is ineffective due to its failure at the level of transcription. In addition, dominant microbes mediate essential amino acid biosynthesis by ammonium assimilation and transamination. Our study proposed a novel strategy regarding nitrogen sustainable recycling by gut microbes from nitrogenous waste to amino acid in tephritid fruit fly pests.

Insect odorant receptors: evidence for odorant-binding site access to the lipid bilayer of olfactory receptor neurons

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Abstract: The cryo-electron microscopy structure reported for the odorant receptor (OR) from the jumping bristletail Machilis hrabei (MhOR5) shows that the binding site for eugenol, a possible odorant ligand, is blocked from access to the surface of the receptor that faces the antennal lymph. Presumably the odorant is admitted to the ligand-binding site via a protein conformational change that opens up access. In order to explore possible opening mechanisms, we ran molecular dynamics (MD) simulations of MhOR5 and then analyzed the MD trajectories using Caver software to reveal molecular tunnels. Surprisingly, the main tunnel we observed leading out from the eugenol site does not end at the antennal lymph surface but instead connects to the lipid bilayer of the olfactory receptor neuron (ORN) membrane. This tunnel, which we call the lateral port, is located between helices 3 and 4. The MD trajectory shows that a bottleneck in the lateral port transiently opens the eugenol site to the lipid bilayer for 1 to 2 nanosecond periods over a 70 nanosecond interval. Using steered MD, we found that eugenol can dissociate from its binding site and pass through the lateral port bottleneck during transient openings to reach the lipid bilayer, with an energy input of little more than the free energy of binding. The lateral port could be an exit site for odorant deactivation. By entering the lipid bilayer, odorant molecules could become susceptible to deactivation by cytoplasmic P450 enzymes. Alternatively, the lateral port might be the odorant entrance site. The activation of ORs via the lipid bilayer would have interesting implications for the air-to-ORN transport mechanism. The delivery of water-insoluble odorants to ORs, either by odorant-binding proteins or pore tubules, would be able to access a much larger target if the odorants first enter the ORN membrane and then diffuse to the OR binding site.

Urbanization on Aedes sp. (Culicidae) performance: Bottom-up effects on larval habitats along an urbanization gradient in Puerto Rico

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Abstract: Urbanization is an important global issue that leads to environmental changes. Mosquito larval habitat bottom-up and top-down effects can change as a result of urbanization. These can in turn influence the abundance and biomass of larvae inhabiting those systems. Aedes aegypti (yellow fever mosquito) and Aedes mediovittatus (Caribbean treehole mosquito) are medically important mosquito species as the former vectors dengue, Zika, chikungunya, and yellow fever, while the later has been shown to vector dengue in Puerto Rico. The objectives of this study were to determine (1) how urbanization influences detrital inputs, nutrients (C and N), and larval competition in containers, and; (2) how these these parameters influence the species performance. Containers were sampled along an urbanization gradient in the San Juan Metropolitan Area in Puerto Rico. Detritus type, composition, and biomass were determined along with mosquito larval, adult, and water nutrients. Urbanization and environmental data was collected. Aedes aegypti and Ae. mediovittatus abundance (larvae and adult) and biomass were recorded from every container and were related to the previously mentioned variables. Twenty six containers were sampled and 1,314 fourth instar Aedes sp. larvae were collected. This study aimed to provide knowledge on how human activity e.g. urbanization, influences the first stage of these medically important mosquitoes, which affect adult population and therefore disease dynamics.

Spatial cognition in the context of foraging styles and information transfer in ants

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Abstract: Ants are good candidates for studying cognitive aspects of navigation because they are central-place foragers, always returning to a nest, which demands the ability to encode relationships between features in an environment or an individual's path through the landscape. The distribution of these cognitive responsibilities within a colony depends on the ants' foraging style. Solitary foraging and leader-scouting are the most challenging tasks in the context of ants' spatial cognition requiring exploration, learning, and memory. Solitary foraging was found in species of almost all subfamilies of ants, whereas distant homing based on leader-scouting has been discovered as yet only in the Formica rufa group of species (redwood ants). Surprisingly, these systems, although enormously different in their levels of sociality, have many common traits of individual cognitive navigation, such as the primary use of visual navigation, excellent visual landmark memories, and the subordinate role of odor orientation. However, in contrast to Cataglyphis, the modeling genus for studying cognitive navigation, in which chronological age and physiological development strongly determine their short out-nest life, redwood ants live long, and workers lack pronounced age polyethism. Numerous experiments on spatial cognition in redwood ants treat them regardless of their task-group membership. However, in the leader-scouting species, spatial cognition and abilities to transfer the information about a location dramatically differ among scouts and foragers depending on their cognitive specialization. The ability of scouting individuals to encode sequences of turns along the "binary tree" maze and share this information with foragers can be considered a specific cognitive adaptation closely connected with their searching patterns within the tree crown. Still, it is unknown how redwood ants translate the code in their communication into a trip to their destinations. There is much work to be done to understand what cognitive mechanisms underpin route planning and communication about locations in ants. Studying cognitive navigation in the context of information transfer can provide new insights into spatial cognition in social insects.

Anatomy and function of the olfactory system of malaria mosquitoes Anopheles gambiae

Authors: Riabinina Olena, Durham University, United Kingdom

Abstract: Anopheles gambiae mosquitoes are the major vector of malaria, a disease that affects more than a half of the world's population and results in more than 400.000 deaths every year (WHO report, 2018). Larval and adult mosquitoes rely on their sense of smell to find food sources and avoid repellent substances in their environment. However, the genetic tools to study and alter the function of olfactory neurons are currently very limited. In this talk I will highlight the recent insights into Anopheles olfaction that were acquired with the help of new genetic approaches.

Nesidiocoris tenuis induces type-IV glandular trichomes and acylsucrose- production: implications to control whitefly-transmitted viruses in tomato

Authors: Riahi Chaymaa[4], Urbaneja Alberto[2], Pérez-Hedo Meritxell[2], Fernández-Muñoz Rafael[1] and Moriones Enrique[3], [1]Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora", [2]Instituto Valenciano de Investigaciones Agrarias, Spain, [3]nstituto de Hortofruticultura Subtropical y Mediterránea "La Mayora", [4]Valencian Institute for Agricultural Research, Spain

Abstract: A trichome-based resistance (WF-resistance) introgressed into cultivated tomato from the wild tomato Solanum pimpinellifolium was shown to be effective to control Bemisia tabaci and Trialeurodes vaporariorum whiteflies (Hemiptera: Aleyrodidae). Protection was based on antixenosis and antibiosis against the whiteflies, associated with the presence of acylsucrose-producing type-IV glandular trichomes. Whitefly resistance was demonstrated to be effective to limit the spread of the begomovirus tomato yellow leaf curl virus (TYLCV) and the crinivirus tomato chlorosis virus (ToCV). Limited protection, however, was observed at the early developmental stages of tomato plants because of reduced acylsucrose production levels. Nevertheless, early induction of type IV glandular trichomes using methyl jasmonate (MeJA) applications helped increase resistance to whiteflies and whitefly-transmitted viruses in young plants. The predatory bug Nesidiocoris tenuis (Hemiptera: Miridae) is frequently used in biological control programs against pests including whiteflies, usually by pre-establishing populations during nursery stages. The phytophagy of N. tenuis was demonstrated to modulate jasmonic acid and salicylic acid signalling pathways in tomatoes. Interestingly, the inoculation of N. tenuis on WF-resistant tomato plants resulted in effective induction of type-IV glandular trichomes and acylsucrose-production. Thus, combining conventional breeding and biological control strategies in IPM programs may control whiteflies and whitefly-transmitted viruses in tomatoes.

The role of phytochemical diversity on multi-trophic interactions

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Abstract: Background/Question/Methods
Variation in phytochemical composition and diversity between and within plant species is an important dimension of biodiversity and mediates plant-herbivore-parasitoid interactions. Previous work comparing multiple species in the tropical genus Piper, found that phytochemical diversity is a predictor of herbivore diet breadth, diversity and parasitism. To expand on this work, we will address two main questions: 1) How does variation in phytochemical diversity between Piper species affect caterpillar immune response and thus parasitism? 2) How does abiotic factors, such as light, contribute to variation in phytochemical diversity of a single species of Piper and what are the potential implications to herbivores? To address these questions we took a holistic approach to investigate multiple aspects of phytochemical diversity by analyzing methanolic plant extracts using 1H-NMR and LC-MS. We combined immune data with chemical data to address the first question. For the second question we experimentally placed plants in varying light conditions and quantified the variation in phytochemical diversity and herbivory.

Results/Conclusions
How does variation in phytochemical diversity between Piper species affect caterpillar immune response and thus parasitism? We found that the immune function of specialist caterpillars was negatively associated with the phytochemical diversity of the Piper host plants, and rates of parasitism decreased with higher immune function.
How does abiotic factors, such as light, contribute to variation in phytochemical diversity of a single species of Piper and what are the potential implications to herbivores? We found that phytochemical diversity was inversely related to direct light transmittance. In partitioning phytochemical diversity, we found variation in compound composition and structural complexity. These differences in phytochemistry among individual plants caused by light heterogeneity significantly decreased herbivory. Feeding assays demonstrated a negative photoactive effect on generalist, but not specialist caterpillars.

Conclusion
Variation in phytochemical diversity between species and within species can structure plant-herbivore-parasitoid communities across the landscape and contribute to the maintenance of multi-trophic diversity.

Exploring the potential of gene silencing to manage forest pests: Prospects for the future

Authors: Rieske-Kinney Lynne, Department of Entomology, University of Kentucky, Lexington, KY, United States

Abstract: RNA interference (RNAi) is a highly specific cellular pathway that causes gene knockdown and can result in rapid insect mortality when essential genes are silenced. We are evaluating the use of gene silencing as a means of suppressing wood-boring forest pests. The endemic North American southern pine beetle, Dendroctonus frontalis, undergoes population eruptions and is expanding its geographic range in response to a changing climate. The exotic invasive emerald ash borer, Agrilus planipennis, is rapidly expanding its invaded range throughout North America. Both beetles are responsible for the loss of millions of trees in urban and wildland forests. We have shown that the RNAi pathway can be induced in both insects, and we can cause rapid and extensive mortality of both beetles when essential genes are silenced. Current efforts are focused on identifying optimal target gene(s), assessing effects on potential non-target organisms, and evaluating effective means of delivery. RNAi has potential as a pest management strategy. If this technology can be moved to the deployment phase it could provide an additional tool for integrated pest management against forest pests.

Sensory basis of nectar feeding in mosquitoes

Authors: Riffell Jeff, University of Washington, United States

Abstract: Mosquitoes are important vectors of disease and require sources of carbohydrates for reproduction and survival. Unlike host-related behaviors of mosquitoes, comparatively less is understood about the mechanisms involved in nectar-feeding decisions, or how this sensory information is processed in the mosquito brain. Here we examine the olfactory and visual preferences and neural bases of nectar preferences in Aedes spp. mosquitoes. Using a unique mosquito-flower mutualism, we show that Aedes spp. mosquitoes, including Aedes aegypti, are effective pollinators of the Platanthera obtusata orchid, and demonstrate this mutualism is mediated by the orchid's scent and the balance of excitation and inhibition in the mosquito's antennal lobe (AL). The P. obtusata orchid emits an attractive, nonanal-rich scent, whereas related Platanthera species—not visited by mosquitoes— emit scents dominated by lilac aldehyde. Calcium imaging experiments in the mosquito AL revealed that nonanal and lilac aldehyde each respectively activate the LC2 and AM2 glomerulus, and remarkably, the AM2 glomerulus is also sensitive to N,N-diethylmeta-toluamide (DEET), a mosquito repellent. Lateral inhibition between these 2 glomeruli reflects the level of attraction to the orchid scents. Whereas the enriched nonanal scent of P. obtusata activates the LC2 and suppresses AM2, the high level of lilac aldehyde in the other orchid scents inverts this pattern of glomerular activity, and behavioral attraction is lost. These results demonstrate the ecological importance of mosquitoes beyond operating as disease vectors and open the door toward understanding the neural basis of mosquito nectar-seeking behaviors.

Single Founding Event of an Ambrosia Beetle and Its Fungal Symbiont Threaten Entire Plant Family in North America

Authors: Riggins John[2], Chupp Adam[6], Duerr Don[7], Koch Frank[7], Bares Hannah[1], Smith Jason[5], Formby John[3], Oten Kelly[4], Hughes Marc[5], Dearing Natalie[1] and Brown Richard[1], [1]Mississippi State University, United States, [2]Mississippi State University, United States, [3]New Mexico State Forestry, United States, [4]North Carolina Forest Service, United States, [5]University of Florida, United States, [6]University of South Alabama, United States, [7]USDA Forest Service, United States

Abstract: Laurel wilt is a non-native tree disease that is affecting naïve plants of the family Lauraceae in the southeastern United States. This disease is caused by an introduced vector (Xyleborus glabratus) and a pathogenic fungal symbiont (Raffaelea lauricola). All North American shrub and tree species in the plant family Lauraceae that have been tested thus far are susceptible. We estimate that over 300 million redbay trees (Persea borbonia), or >1/3 of the pre-invasion population, succumbed to the disease within about 15 years of the invasion. We utilized phylogeographic methods to discern the number of introduction events and cold temperature ecophysiology to model the likely eventual range of the beetle. Genetic markers were used to test the hypothesis that the vector and pathogen entered North America as a single introduction, and a single X. glabratus haplotype was detected in the USA. Similarly, amplified fragment length polymorphisms indicated that 54 of 57 examined R. lauricola isolates were of a single clonal genotype; only minor variation was detected in three polymorphic isolates. These data suggest that a single founding event and subsequent anthropogenic terrestrial movement are responsible for the laurel wilt epidemic in the United States. Cold temperature ecophysiology of X. glabratus indicates that less than 1% of sassafras trees in North America occur in a climate cold enough to limit the beetles' eventual range. With such minor limitations on the spread of LWD, trophic cascades in the wake of this devastating invasion are possible. To document this, we compiled a literature-based catalogue of imperiled arthropod herbivores of North American Lauraceae, which yielded a list of 178 associated species, at least 24 of which may suffer substantial declines alongside their lauraceous hosts. Overall, the lack of effective control options and a vector with biology well-suited to invading new territory have enabled LWD to become one of the most destructive plant diseases on record.

Sublethal effects of neurotoxic insecticides in non-model insect pollinators: a new approach to studying acute and chronic neurophysiological effects in living animals

Authors: Rigosi Elisa[1], Nagloo Nicolas[1] and O'Carroll David[1], [1]Lund University, Sweden

Abstract: Insect pollinators are important for natural ecosystems and the human economy, yet are threatened by common agrochemicals in both rural and urban environments. Most insecticides act as neurotoxins in the insect nervous system, however, their more subtle modulation of neural activity at sublethal concentrations are often overlooked. While navigating through the environment, flying insects rely mainly on visual information. Yet how the processing of this information is affected by neurotoxic insecticides is an open question. The majority of studies on this topic have focused on bees despite recent literature showing large variability in insecticide sensitivity across species. This highlights the importance of extending the analysis of sublethal insecticide effects to non-model organisms. Here, we introduce the pollinator fly Eristalis tenax as a new model to study sublethal neurophysiological effects in living individuals stimulated by relevant sensory stimuli for natural behaviour. We developed a new system to orally expose flies and then assess visually sensitive neurons in whole, living animals, viewing computer generated visual scenes. We performed electrophysiological recordings from visual neurons involved in motion detection and flight stabilisation. We compared their physiological responses in chronically exposed animals (and controls) in vivo at different timepoints after exposure. Our data show how the visual neuropils of Eristalis are physiologically resilient to field relevant, chronic exposure of imidacloprid, a widely used cholinergic pesticide. Our techniques could reveal new insights into the neurophysiological impact of virtually any neurotoxic pesticides and open the door for employing the same experimental approach to other insect species.

Invasion of Brown Marmorated Stink Bug in California Crops: What are the Risks to the Almond and other Crop Industries

Authors: Rijal Jhalendra[1], Zalom Frank[2] and Fisher Joanna[2], [1]University of California Agriculture and Natural Resources, United States, [2]University of California Davis, United States

Abstract: Brown marmorated stink bug (Halyomorpha halys) (BMSB) is an invasive insect species from Asia first detected in the United States in the late 1990s and currently spread to over 43 U.S. states, several Canada provinces, and several other countries in Europe. Both adults and nymphs (2nd-5th instars) actively feed on the fruiting structure of the host plants that includes more than 170 species of ornamental and landscape trees, field, vegetable, and tree crops. In California, a large population in the Central Valley region since 2013 in residential areas. BMSB has been spread and established in 16 California counties. We reported the established BMSB population in commercial orchards (peach in 2016; almond in 2017) in the San Joaquin Valley as the first report of crop infestation by BMSB in California. In 2017 and 2018, we conducted monitoring of BMSB in several peach and almond orchards using two types of traps (black pyramid, and sticky panel), baited with BMSB lures. Both BMSB adults and nymphs were captured in several peach and almond orchards in both years indicating the spread of BMSB to a wider area than previously known. California almond is >5 billion USD industry. California is home to over 500, 000 ha of almond production which is accounted for >80% of the world's production. The risk associated with the BMSB infestation in this high-value crop is tremendous. In this presentation, we will report the current status of BMSB invasion and establishment in California agriculture, and associated risks to the whole industry.

Context-dependent selection of sampling plans for Tuta absoluta: dealing with economic uncertainty and risk aversion

Authors: Rincon Diego F.[1], Sánchez-Vivas Diego F.[1] and Borrero-Echeverry Felipe[1], [1]Unit of Biological Control, Tibaitata Research Center, Colombian corporation for agricultural research - AGROSAVIA

Abstract: Decision-making for pest management in agriculture is often assisted by sampling plans that guide users in classifying pest populations and in determining the need for an intervention. Effective procedures that help farmers make informed decisions on pest management favor intrinsic system controls over corrective interventions and reduce costs and detriments to the environment and health. Even though Tuta absoluta is easily recognizable by most tomato growers and that several sampling plans have been developed, adoption of decision-making systems for this pest is still incipient, particularly in developing countries. Two potential reasons are the high start-up investment (greenhouse facility) that makes tomato farmers particularly risk-averse, and the difficulty to estimate economic thresholds because of tomato market price uncertainty. Both, market uncertainty and risk aversion could be dealt with by using sampling plans that allow farmers to plan interventions according to reliable estimations of pest densities and easily adjustable economic thresholds, based on real-time, up-to-date market information. In this study, we developed five different sampling plans and evaluated them using computer simulations and field trials. We compared the efficiency and the ability of each plan to both estimate the actual mean number of larvae per plant and to classify pest populations according to a predefined economic threshold. We also analyzed the time spent, distance walked, and plants examined by human subjects applying each plan on a tomato crop with a T. absoluta infestation slightly over a predefined economic threshold. We show that, even though all sampling plans were originally developed for classifying pest populations, those that deliver the most precise classifications, are poorest in delivering pest density estimations and vice versa. Our findings are consistent for both human subjects and computer simulations. However, the sampling effort as measured by the average number of samples by simulations does not reflect the effort and time spent by human subjects sampling real plants, especially when it comes to binomial sampling, since the ability of humans to detect infested plants increases with experience. Our results show that variable-intensity, as opposed to sequential, plans can provide reliable information on a current level of T. absoluta infestation which can be used by farmers to decide on the level of reaction required to prevent the pest from reaching the economic injury level. We stressed on the benefits of plans that promote an increase in the distance walked within crops, especially for systems that regularly require intensive labor and are exposed to a wide diversity of pests and diseases, such as greenhouse tomato. The adoption and applicability of the developed sampling plans are assessed in light of crop size and phenology, presence of other sanitary problems and farmer´s willingness to reduce risk by collecting additional data.

Tsetse microbiota: Why where matters

Authors: Rio Rita, West Virginia University, United States

Abstract: Convergent evolution is exemplified by digestive tract microbiota that enable animal survival on restricted diets. Although the proclivity of these microbiota towards providing essential nutrients is similar, the specific metabolites provisioned are largely shaped by host dietary ecology. The strictly hematophagous tsetse fly (Diptera: Glossinidae), the sole vector of lethal African trypanosomes, contains a naturally simple microbiota with members exhibiting relations spanning from mutualism to parasitism. Various sequencing platforms coupled with targeted experimental assays support interdependence between tsetse and its microbiota towards metabolic provisioning, tsetse fitness, immunological priming and vector competence. Here, we detail tsetse global metabolomics obtained through nuclear magnetic resonance (NMR)-based spectrometry. Principal component analyses indicate significant metabolic differentiation between the tsetse bacteriome (the organ that exclusively harbors the ancient mutualist Wigglesworthia glossinidia) and the midgut (predominantly housing the facultative Sodalis glossinidius). Symbiont removal via antibiotic administration significantly alters the abundance of the majority of amino acids (i.e. 14 of 21) within the gut. Simultaneously, significantly higher levels of citrate (a TCA cycle intermediate) and uridine indicate impacts towards tsetse energy expenditure upon symbiont loss. Lastly, we discuss distinctions in Wigglesworthia activity following host species co-diversification. Despite only minor genome differences between Wigglesworthia isolates, transcriptional profiles within different tsetse species were significantly different in Clusters of Orthologous Groups of proteins (COGs) involved in carbohydrate, amino acid and lipid transport and metabolism. These results support symbiont functional differences arising from co-speciation. Manipulation of tsetse-microbiota metabolic coordination offers novel control strategies towards vector population control.

Grapevine cultivar affects insect vector fitness and feeding behavior

Authors: Ripamonti Matteo, Galetto Luciana, Marzachì Cristina, Cornara Daniele, Fereres Alberto, Rossi Marika and Bosco Domenico

Abstract: Scaphoideus titanus is the main vector of the Flavescence dorée (FD) phytoplasma, a wall-less bacteria associated with the FD disease of grapevine. This disease is causing severe losses to European viticulture and is continuously spreading year after year. The main preventive measures rely on insecticide treatments against the vector in the vineyard, removal of feral host grapevines outside the field, and use of healthy plant material. For a more sustainable viticulture, effective and environment friendly measures are needed. One of the possibilities to fulfil this objective is represented by plant resistance against the insect vector or the disease. After having defined a susceptibility range to FD among several grapevine cultivars, three of them were selected at the extremes of the range to describe S. titanus fitness and feeding behavior: Barbera as extremely susceptible to FD, Brachetto and Moscato as (partially) resistant to FD. Some preliminary results suggested the possibility that Moscato may resist to FD by indirectly acting against the leafhopper vector. To test this hypothesis, leafhopper fitness parameters were measured on the three cultivars, as well as feeding behaviors. Fitness was estimated by measuring nymphal developmental time, nymphal mortality, adult longevity, and female prolificacy. Feeding behavior was described using the electropenetrography (EPG) technique. In all the experiments, significant differences in fitness and feeding behavior were found among the grapevine varieties. Nymphal developmental time and mortality were significantly higher on Moscato and Brachetto, compared to Barbera. On the former two varieties, adult longevity and female prolificacy, measured as number of mature eggs per female and vitellogenin gene expression, were reduced. S. titanus feeding behavior was heavily affected by the cultivar, in particular after the first phloem contact. On Barbera, the leafhopper was able to sustain longer phloem phases with less frequent salivations, compared to Brachetto and especially Moscato. In this latter cultivar, S. titanus showed the most disturbed behavior, with less, shorter and more interrupted phloem phases. These results suggests that Moscato and Brachetto are less preferred than Barbera for S. titanus. We suggest that the impaired fitness of S. titanus on Moscato, may be due to antibiosis. while the impaired feeding behavior may be due to antixenosis mechanisms acting against the leafhopper. These two resistance mechanisms could represent a viable and successful way to counteract the spread of S. titanus and of FD phytoplasmas.

Variability of a cooperative defense behavior in social pine sawflies

Authors: Ritter Raphael[2], Wutke Saskia[1], Helanterä Heikki[4], Tynkkynen Riikka[3] and Lindstedt-Kareksela Carita[2], [1]University of Eastern Finland, [2]University of Helsinki, [3]University of Jyväskylä, [4]University of Oulu

Abstract: To determine the evolutionary potential of cooperative traits, we need to identify the genetic and environmental sources of their phenotypic variation upon which selection acts. In addition to collecting phenotypic data from wild and lab-reared populations, this also requires using quantitative genetic and molecular methods. By doing so, we studied the sources of variation in a cooperative behavior using the socially behaving pine sawflies Diprion pini and Neodiprion sertifer. During the larval stage both species feed and defend gregariously in groups of 20-100 individuals. They are specialized on pines from which they sequester defensive compounds for their defense. When attacked, the larvae raise their head and regurgitate a resinous fluid in concert which makes them less profitable for predators and parasitoid wasps. The advantage of this system is that there is natural variation in the benefits and costs of cooperation as well as in the expression of this behavior. We can also quantify the individual contribution to cooperation. This gives us the possibility to measure correlations between investment into cooperation and other life-history traits and to identify potential phenotypic and genetic constraints. We discuss how these results will increase our understanding of the mechanisms shaping cooperative behaviors.

Use of I Imaging Mass Spectrometry to Assess the Distribution of Pesticides in Insects

Authors: Riveron Miranda Jacob[2], Milnes Phillip[1], Hawkins Joe[1] and Johnson Stephen[1], [1]Syngenta, [2]Syngenta, United Kingdom

Abstract: Developing new eco-friendly pesticides, able to break the resistance of agricultural pest, is critical to secure food production. However, it is not an easy task. In many early-stage development projects, the compound's in vitro activity and the compound's in vivo efficacy do not correlate as expected. This lack of translation between in vitro and in vivo activity leads to investigating aspects of the bio-delivery pathway and its associated ADME processes. The analysis of the location of xenobiotics compounds, once it goes into the organism, gives useful information to understand the factors that limit the compound's in vivo activity. However, the study of the location of compounds in arthropod pests presents a big challenge. These include: the arthropod's small size, the difficulties in dissecting organs, the use of unlabelled compounds and low sub-lethal dosages. In collaboration with the National Physical Laboratory, Syngenta has explored the uses of new spectrometry imaging to measure compound uptake, distribution within the insect, and most importantly, if it is reaching the target site. Our results show that, although it is a promising technique, when applied in environmentally relevant doses, improving the methods for the sample preparation as well as the sensitivity of the techniques is necessary.

Chemical Ecology of Belowground Plant-Herbivore Interactions

Authors: Robert Christelle[1], Ali Jared[2], [1]Institute of Plant Sciences, University of Bern, Switzerland, [2]Multi-trophic Interactions & Chemical Ecology, Pennsylvania State University, United States

Abstract: While recognized as crucial drivers of many ecological processes, belowground interactions remain overlooked. This session aims at gathering the state-of-the-art knowledge on the infochemical pathways shaping interactions between plants, herbivores and soil-dwelling communities. Upon herbivory, plants dynamically reallocate their resources through changes in primary and secondary metabolisms affecting their above and belowground systems. These changes can result in the production of toxic secondary metabolites as well as in the release of exudate and volatile compounds. Yet, it is becoming increasingly evident that some belowground specialist herbivores have evolved the ability to utilize secondary metabolites for their own benefit, including feeding site selection, nutrition and protection against natural enemies. The role of herbivore gut microbiome in such adaptations will be highlighted and may lead to the development of further efficient pest management strategies. On the other hand, the production and release of exudates and volatiles in the rhizosphere has been reported as an efficient indirect defense strategy, attracting the predators of the herbivores. However, these signals may alter the behavior and performance of the herbivores themselves, as well as of neighbouring plants. The consequences of root signals for plants and herbivores will be discussed. The root metabolism, and its reconfiguration upon herbivory, shapes the physical, chemical and biological properties of the surrounding rhizosphere. For instance, soil-dwelling microbial communities are affected by these changes and can in turn alter the plant defense against herbivores. Because belowground interactions depend on the soil properties, they also depend on the soil history, location and use. Soil feedbacks and plant diversity are two examples that will be presented during the session. Overall, our understanding of belowground chemical interactions has been rapidly advancing. This symposium aims at consolidating the knowledge of leading research in the field, while stimulating future directions.

Understanding Environmental Risk Assessment for GE Crops and What it Means for Current and Future Pest Protection

Authors: Roberts Andrew, Agriculture & Food Systems Institute, United States

Abstract: The earliest regulatory frameworks for genetically engineered (GE) organisms were conceived in the mid 1980s, and the first commercial applications for GE crops arrived less than a decade later. These were accompanied by the development of environmental risk assessment frameworks that were informed by prior experience primarily from two sources: chemical risk assessment and biological risk assessments associated with sanitary and phytosanitary regulations. The resulting paradigm, refined over more than 30 years, has proven to be effective in ensuring that GE crops released for use in agriculture don't have unacceptable harmful impacts on the environment. Understanding this paradigm, and the principles behind it, now recognized internationally and applied by nearly every regulatory system in the world that addresses GE plants, offers some insight into how future technologies may be regulated.

Characterizing the Role and Transmission of Endosymbionts of the Spotted Lanternfly

Authors: Roberts Dana, Pennsylvania State University, United States

Abstract: While many insects are known to harbor obligate bacterial endosymbionts, members of the Hemipteran suborder Auchenorrhyncha (the lineage comprising planthoppers, and their sister lineage, Cicadomorpha, comprising tree+leafhoppers, cicadas, and spittlebugs) represent an extreme in that they exhibit a "hunger for symbionts". Spotted Lanternfly (and other Fulgoridae) harbor three obligate endosymbionts: Sulcia muelleri, Vidania fulgoroideae, and a newly described Gammaproteobacterium. Results of genome sequencing of these three endosymbionts will be presented, as these reveal the roles each endosymbiont plays in Spotted Lanternfly biology. Results will also be presented that characterize the stages of female reproductive development in which organs housing each endosymbiont (bacteriomes) change in morphology and position in order to facilitate transmission of bacteria to developing eggs.

Planthopper Endosymbionts: What we currently know about transmission, function, and diversity within Fulgoroidea

Authors: Roberts Dana, Pennsylvania State University, United States

Abstract: The planthopper superfamily, Fulgoroidea, is a speciose lineage of hemipteroid insects that relies upon bacterial and fungal symbionts with which they have co-evolved for tens of millions of years. Although other sap-feeding hemipteroids also harbor symbionts, planthoppers are unique in the way they house these symbionts. Endosymbionts are housed in organs or bacteriomes that vary considerably in their position and morphology across the 21 planthopper families. This variation in bacteriomes has implications for how these insects manage endosymbiont function and transmission. It may also contribute to the remarkable turnover and replacement of endosymbiont "species" observed throughout the superfamily. This presentation will present data from surveys of bacterial symbionts sampled from planthoppers representing 18 of the 21 planthopper families to summarize known endosymbionts and replacement events across the planthopper phylogeny. It will also present data on the function of the three endosymbionts of the invasive spotted lanternfly, Lycorma delicatula (Hemiptera: Fulgoridae) as inferred through endosymbiont genome sequencing. Data will also be presented on the phenology of female spotted lanternfly development that identifies key stages in the transmission of endosymbionts from bacteriomes to ovarioles. Comparison will be made to the rice pest Nilaparvata lugens (Hemiptera: Delphacidae) to identify key similarities and distinctions of symbiont dynamics in this distantly related pestiferous planthopper.

Using chemical ecology to enhance biocontrol of aphids

Authors: Roberts Joe[3], Bruce Toby[4], Ali Jamin[4], Pickett John[2], Birkett Michael[1], Woodcock Christine[6], Martin Janet[6], Smart Lesley[6], Wadhams Lester[6] and Jacobson Rob[5], [1]Biointeractions and Crop Protection Department, Rothamsted Research, United Kingdom, [2]Cardiff University, United Kingdom, [3]Harper Adams University, United Kingdom, [4]Keele University, United Kingdom, [5]Rob Jacobson Consultancy, United Kingdom, [6]Rothamsted Research, United Kingdom

Abstract: Chemical ecology explores the chemicals involved in ecological interactions between living organisms. Natural enemies of aphids have evolved intricate ways of efficiently detecting and locating their prey. They respond to signals associated with herbivore damaged plants and can “eavesdrop” on pheromones of their prey and use them as foraging cues. If we could enhance and manipulate such cues and signals in agricultural ecosystems, perhaps we could improve biocontrol of aphids?

There are a number of possible strategies for using chemical ecology to enhance biocontrol of aphids:
1. Activation of plant defence e.g. with cis-jasmone. A plant defence activator may make plants more attractive to natural enemies.
2. Improving plant signalling – this strategy uses aphid responsive crop varieties that release induced volatiles to attract natural enemies when they are attacked by aphids. Induced indirect defence may be amplified if there is plant-plant communication where plants are sensitive to aphid induced stress signals from their neighbours or if there are warning signals conducted through mycorrhizal connections between plants.
3. Attraction of natural enemies to dispensers (or engineered plants) releasing aphid pheromones such as alarm pheromone, (E)-ß-farnesene or aphid sex pheromone, nepetalactone.
4. Lure and reward – attracting natural enemies to supplementary food sources. This may reinforce behavioural responses to infochemicals through positive associative learning (honest signalling), as well as providing nutritional resources to sustain natural enemy populations when prey populations are low.
5. Lure and kill – this is a different strategy and deploys infochemicals attractive to the aphids themselves to lure aphids to killing agents which, in this context, would be biocontrol agents such as entomopathogenic fungi.
6. Suppression of hyperparasitoid populations – if hyperparasitism could be reduced, for example by trapping hyperparasitoids with baited traps, then the efficiency of primary aphids parasitoids would be improved.

Insect responsiveness to infochemicals can vary over time and space according to the condition of the insect and the environment. Insects process volatile signals and react differently to them according to the blend composition, the context within which they are perceived, previous experience and how the odours are released over time. For example, Aphis fabae, is attracted to a blend of host odours but repelled by the same compounds if released individually and Sitobion avenae is repelled by alarm pheromone (E)-ß-farnesene but only if exposed to a short burst and not if there is prolonged exposure. Adjusting behavioural responses gives insects the flexibility to adapt to changing environments with different host availability and by integrating many signals they get a more robust picture of their external environment. These factors need to be considered when designing control strategies based on infochemicals.

Novel delivery of phytochemicals for sustainable crop protection

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Abstract: New solutions are urgently needed for managing insect pests of crops as they evolve resistance to currently available insecticides. This project integrates chemistry, nanotechnology and entomology to provide a new way of delivering bioactive phytochemicals via nanotech complexes for use against insect pests.
Over millions of years, wild plants have evolved effective insecticidal and repellent defensive phytochemicals. However, some of these compounds have been subsequently lost from commercial crops during the breeding process, making the crops more vulnerable to insect attack and thus requiring human intervention for protection. Applying phytochemicals to crops can redress this balance. We hypothesise that this effect is bigger if phytochemicals from outside the crop metabolome are used, as pests of that crop may not have a history of exposure to them and thus may not have evolved resistance to them. However, there are multiple difficulties in using these products in a commercial setting: 1) Many are hydrophobic, and thus do not dissolve easily in water, making application difficult. This applies especially to essential oils. 2) Their volatile nature and low environmental persistence reduces any effectiveness in the field. 3) These same characteristics make storage and transport challenging.
This project uses new developments in nanotechnology to overcome these difficulties. In order to provide an environmentally friendly final product, we have developed a second-generation polymer composed solely of MHRA- and FDA-approved materials. This polymer encapsulates the active ingredient, the phytochemical. This new formulation is now hydrophilic, allowing suspension in water and therefore much easier utilisation and application. It also has modified physical properties giving greater effectiveness in the field.
In total, 32 essential oils and 20 pure compounds have been formulated and assessed for toxicity to the aphid Myzus persicae. Treatments were assessed under fumigant and ventilated conditions and for phytotoxicity, and from this several promising candidates, with good performance against the target pest (> 70% mortality and complete shutdown of aphid reproduction) but low phytotoxicity, have been selected. Promising formulations have also been successfully assessed against Western Flower Thrips, Frankliniella occidentalis.

Role of Nutrition in Resistance to Viral Challenge

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Abstract: Nutrition is critical in determining a host's ability to resist or tolerate a parasite challenge. This is due not only to a challenged host having to meet the potential associated costs of launching an immune response, but also the fact that both tolerance and resistance mechanisms may compete with other traits for finite resources.

Laboratory experiments into the outcomes of viral infection in invertebrates are often carried out in ad libitum - resource rich environments. These are not only unrealistic of interactions that would other wise be occurring in a variable natural world, but can lead to masking of any real costs associated with a defensive response or at worst misleading conclusions.

Here, I present work that highlights the importance of nutrition across a number of biological scales. From the within individual response to viral infection, to the evolution of population level immunity when evolved in the presence of a viral pathogen in a nutrition poor environment.

At an individual level, we find that the immune response is polygenetic, but the number of genes responding after viral challenge is diet specific, with individuals in a higher resource environment having a greater level of gene down-regulation. Whilst at a population level using selection experiments and whole genome re-sequencing we identify putative mechanisms of resistance that vary between nutritional environments. Genome re-sequencing of evolved hosts show that resistance mechanisms are, again, highly polygenic. It also suggests that the underlying genetic architecture may differ depending on the nutritional environment.

I also present evidence that the resource environment of a host may influence the likelihood of a viral pathogen undergoing a host shift into a novel host.

These results suggest that immune responses are not purely driven by a viral challenge, but likely to involve active modulation of immune regulation by a host, as a function of the resource availability they have. Thus, as a whole, my results emphasise the importance of nutritional resources on the outcome of host parasite interactions and the subsequent evolution of resistance.

The evolution of extreme fertility defied ancestral gonadotropin mediated brain-reproduction tradeoff

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Abstract: Gonadotropic hormones coordinate processes in diverse tissues regulating animal reproductive physiology and behavior. Juvenile hormone (JH) is the ancient and most common gonadotropin in insects, but not in advanced eusocial honey bees and ants. To probe the evolutionary basis of this change, we combined endocrine manipulations, transcriptomics, and behavioral analyses to study JH regulated processes in a bumble bee showing an intermediate level of sociliality. We found that in the fat body, more JH-regulated genes were upregulated and enriched for metabolic and biosynthetic pathways. This transcriptomic pattern is consistent with earlier evidence that JH is the major gonadotropin in the bumble bee. In the brain, most JH-regulated genes were downregulated and enriched for protein turnover pathways. Brain ribosomal protein gene expression was similarly downregulated in dominant workers, which naturally have high JH titers. In other species, similar downregulation of protein turnover is found in aging brains or under stress, and is associated with compromised long-term memory and health. These findings suggest a previously unknown gonadotropin-mediated tradeoff. We did not find a similar downregulation of protein turnover pathways in the brain of honey bees in which JH is not a gonadotropin but rather regulates division of labor. These differences between JH effets in the bumble bee and in the advanced eusocial honey bee suggest that the evolution of advanced eusociality was associated with modifications in hormonal signaling supporting extended and extremely high fertility while reducing the ancient costs of high gonadotropin titers to the brain.

Leaf-cutting ants learn from their efforts: foragers recall olfactory memories to avoid plants they previously experienced as hard to cut

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Abstract: Leaf-cutting ants reject previously-accepted plants if they prove to be unsuitable for their symbiotic fungus, a phenomenon that involves olfactory avoidance learning. We asked whether olfactory memory also underlies the avoidance of suitable plants that were previously experienced as hard to cut. Would ants associate an odor with a high cutting effort and would the odor be sufficient to recall such a negative association, leading to subsequent plant avoidance? In the laboratory, naïve workers of the leaf-cutting ant Acromyrmex lundii were initially tested for their spontaneous preferences for different odors in a binary-choice olfactometer. Then, colonies were offered pseudo-leaves (of inert material) of two different toughness, i.e., easily and hard to cut, scented with specific odors, to allow workers to gain experience with them over three days. One day later, putative experience-dependent changes in odor preferences were quantified both as individual responses using the binary-choice assay, and as a colony-wide foraging response when the two odors were offered on soft material, to reveal odor-guided preferences irrespective of the mechanical properties of the material actually cut. After their experience with the two scented materials of different toughness, single workers developed a marked learned preference for the odor associated with the soft material, and colonies foraged more material scented with the odor paired with the low cutting effort. Additional evidence for the learned avoidance of odors that are only associated with the increased cutting effort was indirectly obtained in an experiment that involved no cutting effort at all, by offering scented, yet transportable discs of tough and thin leaves over three days. Ants showed no change in their spontaneous odor preference after their foraging experience with the scented discs that required no cutting behavior to be transported, which is consistent with the idea that ant workers learn to olfactorily recognize, and to avoid, only those leaves they previously experienced as hard to cut.

Aedes and Climate Change – mechanisms, predictions and uncertainties

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Abstract: This review focuses on the latest research on the linkages between Aedes aegypti and Aedes albopictus and climate change. It synthesizes literature on the influence of changes in climate on vector-related factors, including potential changes in geographical ranges, abundance, and time trends. The importance of other drivers is also discussed. Literature on the vectoral capacity for selected Arboviruses is further synthesized and discussed with respect to the same.

The presentation further elaborates on results from studies involving predictions and projections using scenarios of future change in climate. The potential impact of climate change is looked at both in isolation and in combination with socio-economic factors, such as mobility and development. The synthesis further contrasts modelling scenarios based on different pathways for future changes in atmospheric CO2 concentration.

In the review, findings are contrasted between mechanistic and process-based models, with a discussion of the implications of associations from fitted observational data. Finally, the study concludes by highlighting knowledge gaps, and limitations of the current state-of-the-art on research of Aedes mosquitoes and climate change. It stresses the need for specific research to better understand the relationship between changes in climate, socio-economic development, and the proliferation of vectors and their respective abilities to transmit virus as a function of changes in local climate conditions.

Feeding behaviors of Yamatotettix flavovittatus Matsumura (Hemiptera: Cicadellidae) a vector of sugarcane white leaf phytoplasma using electrical penetration graphs (EPGs)

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Abstract: The leafhopper, Yamatotettix flavovittatus Matsumura (Hemiptera: Cicadellidae), is an efficient vector of sugarcane white leaf phytoplasma. Acquisition and inoculation of phytoplasma occur sometime during the process of stylet penetration into the sugarcane plant. That process is most rigorously studied via electrical penetration graph (EPG) monitoring of insect feeding. The probing behavior of the Y. flavovittatus was studied with an electrical penetration graph (EPG-DC system) technique. EPG waveforms were described based on amplitude, frequency, voltage level, and electrical origin of the observed traces during stylet penetration into sugarcane plant tissues. Additionally, through a histological study using leaf cross-sections revealing, the observed locations of the stylet tips in the plant tissue were compared to EPG probing waveforms, salivary sheath locations. This study provides part of the crucial biological meanings that define the waveforms of each new insect species recorded by EPG. The behavioral activities were also inferred based on waveform similarities in relation to other leafhoppers. By analyzing 10-h EPGs of adult females five waveforms were described: NP, A, B, C, and D. Non-penetration, NP was non-probing when the stylets did not penetrate; waveform A occurred at the beginning of stylet penetration. This waveform was detected with stylet penetration into the epidermal cells; waveform B was correlated with stylet penetration into the parenchyma and mesophyll cells; waveform C was correlated to salivation; and waveform D was correlated with ingestion, which was the longest activity observed. This detailed understanding of the stylet penetration behaviors of Y. flavovittatus is an important step toward identifying the instant of phytoplasma inoculation which, in turn, will be applied to studies of disease epidemiology and development of host plant resistance.

Community-level change in insect abundance and biomass over 50 years in a northern forest

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Abstract: Long-term community-level study of insects is rarely embedded within an ecosystem study, but this context can provide the data needed to assess drivers of change. Monitoring and experimental study of insects and birds began in 1969 at the Hubbard Brook Experimental Forest, New Hampshire, USA, and continues. Caterpillar and flying insect abundance were monitored using visual surveys and Malaise traps, respectively, from late May to early August. Results showed that caterpillar abundance fell by half, due to the loss of outbreak peaks after the 1980s. Coleoptera captured per 24-hr declined 60%, but pulsed inputs of coarse woody debris were associated with Coleoptera increases that each lasted a decade. Trichoptera and Plecoptera showed a convex pattern of change related to minimum stream flow and stream water pH. Abundance of all flying insect taxa did not decrease, largely because Diptera showed no trend and comprised on average 61% of individuals captured. Total biomass of all taxa measured at low, mid and high elevation, 1996-2018, declined significantly but only at high elevation. We will show how these dramatic changes in the structure and dynamics of the forest insect community can be linked to climate change and forest disturbance.

An Iron Fist in a Velvet Glove: Unraveling the systematics and Müllerian mysteries of the Australian Velvet ants (Hymenoptera: Mutillidae)

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Abstract: The Mutillidae (Velvet ants) is a cosmopolitan family of aposematically coloured parasitoid wasps known to form Müllerian mimicry complexes. Recent studies on the North American mutillid fauna have revealed mimicry rings, within which, multiple species that share highly discernible colour patterns are bound by discrete geographical ranges. This is concordant with the assumption that all unpalatable species within an area will adverge on an effective warning signal. Pilot studies at the Australian National Insect Collection, which assessed more than 5,000 Australian mutillid specimens (females only), identified four colouration complexes indicative of Müllerian mimicry. Unlike that of the North American system, each putative mimicry ring exhibited widespread, sympatric distributions that were not geographically delimited. If Müllerian mimicry is occurring, the high geographic overlap may be explained by a single origin of colour pattern or by convergent evolution, however, without a robust taxonomic framework, these hypotheses cannot be tested. Currently, no molecular phylogeny exists for the Australian Mutillidae and species/generic boundaries are poorly defined - a result of highly pronounced sexual dimorphism and morphological similarities. Using a comprehensive morphological and Ultra Conserved Element (UCE) dataset, this project aims to study the evolution of mutillid colouration patterns by testing the phylogenetic relatedness of all 260 described Australian species, along with 300 additional Australian morpho-types. Finding non-monophyletic mimetic taxa will negate the hypothesis that species have evolved from a common ancestor with subsequent dispersals across the Australian continent. However, finding polyphyletic taxa would do little to explain why multiple aposematic signals are being conserved in sympatric populations. One possible explanation is that niche partitioning within particular geographic regions may be maintaining the putative mimetic diversity. The present study further aims to test if mimicry rings are associated with particular habitats/microhabitats by linking environmental and ecological data with fine-scale distribution data that is mapped on to the inferred phylogeny. Via the reconstruction of the first-ever molecular phylogeny for the Australian Mutillidae, the present study will provide a framework for unraveling the evolutionary origins and relationships of this poorly studied parasitoid family. Furthermore, the study will begin to develop an understanding of the genetic basis, and mechanisms, shaping the phenotypic diversity and mimicry of Australian mutillids.

The first described pergid fossil with implications on the evolution and biogeography of Pergidae

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Abstract: The evolution of adaptive traits such as resistance to plant toxins in herbivores is often obscured by the absence of accurate phylogenetic dating mainly caused by lack of well-preserved fossil specimens. In Southern hemisphere groups, such as Pergid sawflies, this problem is exacerbated by the sparsity of the fossil record in the Southern latitudes. No Pergidae fossils had been discovered so far. Using morphological and molecular data we aim to determine the phylogenetic placement of anewly discovered Pergidae fossil from the Talbragar fossil beds, and use it for divergence time estimation of the pergid phylogeny and determine implications on the evolution of toxicity resistance in early Hymenoptera. We analysed a combined morphological and molecular dataset using a phylogenetic Bayesian framework. The phylogenetic results suggest that the fossil sawfly belongs to the clade formed by Acordulecerinae (including Phylacteophaginae) and Perginae. Within this clade it issister to Phylacteophaginae, which is an exclusively Australian group. This relationship was recovered with a low posterior probability, which impedes placing the fossil at the subfamily level. Our results suggest that spitfire sawflies (Pergidae) originated in the UpperCretaceous (ca 101 Ma) and not in the Late Jurassic, as previously proposed. This suggests that the presence of the family in South America and Australia is probably a result of both vicariance through the late break-up of Gondwana and connectivity through Antarctica. Divergence time and host plantshows that Pergidae switched to the use of Myrtaceae at least four times intependently throughout the evolutionaryhistory of the group. The first switchtook place in the Upper Cretaceous, close to 80Ma, which coincides with the origin of crow-group Myrtaceae. Other switches took place in the Eocene, closer to the age of Eucalypts. This is the first fossil Pergidae, whose discovery has implications for the historical biogeography of Pergidae and the evolution of early Hymenoptera.

Phytoplasma infection influences cranberry interactions with insect herbivores

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Abstract: Phytoplasma infection causes false blossom disease in cranberries, which is vectored by the blunt-nosed leafhopper (Limotettix vaccinii). We explored how phytoplasma infection of cranberries affects L. vaccinii and three non-vector Lepidopteran herbivores: spotted fireworm (Choristoneura parallela), Sparganothis fruitworm (Sparganothis sulfureana), and gypsy moth (Lymantria dispar). Additionally, we compared levels of nutrients, phenolics, and phytohormones, as well as volatile emissions and transcriptome profiles between infected and uninfected plants. Our oviposition data showed a preference of L. vaccinii for uninfected plants, whereas our attraction data showed no preference between infected and uninfected plants. While slower development on phytoplasma-infected cranberry plants led to larger L. vaccinii adult size, there was no evidence for any beneficial effects of infection on other performance parameters. Larvae of all three non-vector species grew 2–3 times bigger, and damaged 1.5–3.5 times more leaves, when feeding on infected plants; larval survival of one of them was also ~1.5 times higher on infected plants. Levels of ten nutrients, including nitrogen, were higher in infected plants, while levels of defensive proanthocyanidins were reduced by 20–40% compared to uninfected plants. At the molecular level, phytoplasma infection increased the expression of genes associated with nutrient metabolism, while suppressing genes associated with defensive pathways. While uninfected plants emitted higher amounts of volatiles than infected plants, we observed no effect of infection on phytohormone levels. In conclusion, phytoplasma infection through changes in phytochemistry and gene expression enhanced host-quality of cranberries to non-vector herbivores, although the benefits on its vector are less clear.

Guttation: A nutrient-rich natural food source for insects

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Abstract: Guttation is the appearance in plants of xylem drops at the tips or edges of their leaves. These fluids are usually rich in sugars and amino acids. Although guttation fluids are reported from many plant species, little is known on their effects on insects, particularly agricultural pests. In the present study, we hypothesized that guttation fluids produced by highbush blueberry (Vaccinium corymbosum; Ericaceae) provide a suitable food source for the survival of insect pests. To test this hypothesis, we determined the effects of guttation on the adult longevity of a frugivorous pest, spotted wing drosophila (Drosophila suzukii) and two beneficial insects, the wasp Aphidius ervi and the predator Chrysoperla rufilabris. Newly emerged adults were fed daily either: 1) guttation from blueberry leaves, 2) sugar solution (i.e., sucrose, as positive control), 3) protein, 4) sugar plus protein and 5) water (as negative control) under controlled laboratory conditions. Adult longevity and other fitness parameters were measured for these insects compared among the five treatments. Preliminary results indicate that insect survival is enhanced when feeding on guttation fluids. These results will be discussed in relation to the composition of the guttation fluid. This study documents for the first time the potential effects of guttation on this invasive pest and beneficial insects in an agro-ecosystem.

Developmental plasticity in spruce budworm and the importance of intraspecific variability

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Abstract: Spruce budworm (SBW) is a familiar native insect that is responsible for extensive defoliation throughout the North American boreal forest. SBW experiences cyclical population outbreaks and predicting SBW population dynamics is crucial for effective management. Much of our understanding of SBW biology was based on insects reared in the Insect Production and Quarantine facility at the Great Lakes Forestry Centre, so there are concerns that these insects may not reflect the true range of variability expressed in wild populations. We now have five colonies established from wild populations from across the range of SBW. We've documented surprising variability within the wild populations, contradicting long held assumptions of the growth and development of SBW. These traits can significantly impact our developmental models and may help explain known disconnects between predicted and observed SBW population dynamics.

Novel Textile for the Protection of Agricultural Crops

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Abstract: With an increasing world population, climate change and increased insect resistance to pesticides, a different way of thinking is needed to produce food in the future with no pesticides. Our research team has been investigating applications in the material sciences for insect and weed control and to improve plant growth even in challenging temperature conditions and water availability. We are reporting here a reusable, novel knitted textile structure, named Plant Armor, that is surprisingly open for maximum air-light-water penetration, excludes insects and weeds, and significantly increases the rate of plant growth. The technology is not based on size exclusion like typical insect barriers but creates a tortuous path. In Petri dish, choice bioassays, 50% of adult Franklinellia fusca moved across Plant Armor to a cabbage leaf in 3 h versus 10 min for Proteknet, a commercially available crop cover standard used in our studies. For similar studies with Heliocoverpa zea neonates, the time for 50% penetration for Proteknet was 2.5 h with only 10% penetration after 24 h for Plant Armor. In small cage, worst-case-scenerio bioassays where 25 H. zea neonates were applied topically to Plant Armor covered individual cabbage plants, there was no penetration after 10 days. In a separate cage, where the larvae were applied directly to the cabbage, 90% of the plant was consumed. In separate small field plots for Plant Armor versus Proteknet and where the cabbage was covered or not covered for 3 mos, there was clear phytophagy on the uncovered plants while the covered plants had no damage for both textiles. Weeds were totally excluded by both textiles. Surprisingly, the plant size based on wet and dry weight was 2-3 time greater for the cabbage covered with Plant Amor than in the other treatments where the plant weights were similar. This enhanced growth for Plant Armor covered plants was also found in green house studies with tomatoes and by independent on farm trials. Sunlight transmission was essentially 100% for Proteknet and 75% for Plant Armor. Water vapor transmission, air penetration, water penetration, Martindale abrasion, temperature and humidity for Plant Armor versus Proteknet will be presented
along with bioassay and physical research data on Plant Armor Gen II. We will also show the use of
Plant Armor in the winter in Raleigh, North Carolina (USA).

Sprayable, Mechanical Insecticides for Vector Control and Agriculture: The Future is Now

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Abstract: Research was conducted on the use of industrial minerals as a wettable powder and residual spray for adult mosquito control, use on other vector important arthropods, and use in agriculture. The work included investigating different mineral types on a variety of substrates, under different environmental conditions, under lab and field conditions, and as an alternative to chemical insecticides or in combination for dual modes of action. Our original work with amorphous silica led to the discovery of a more efficacious insecticide made from volcanic rock. In field trials in Benin, Africa in WHO approved huts and with WHO approved testing procedures, our new mechanical insecticide produced from volcanic rock was more effective and more persistent than chemical insecticides used for indoor residual sprays. Phase III field trials in Africa are in process. Field trials will also be presented for insect control in row crops. We will discuss mode of action, impact on host seeking for vector important arthropods, and its enhanced activity for insecticide resistant mosquitoes. Introduction of a new commercial product for mosquito control is planned in Africa and select countries in Central and South America by our commercial partner. Additional uses are under investigation.

WholeGarment® Knitting of Military Clothing with Bite Protection against Mosquitoes and Other Arthropods

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Abstract: In the current work, we are undertaking a research and development effort that demonstrates the benefits and capabilities of applying Wholegarment® knitting technologies to the production of bite-resistant U.S. Army knitted garments for both non-combat and combat wear.

Vector-borne diseases have had a devastating impact on the readiness of combat troops. Due to their increased exposure through training and operations outdoors, deployed military personnel are often at greater risk of receiving arthropod bites than common populations. Presently, the military uses chemical treatments (primarily permethrin) to prevent exposure to vector-borne diseases. The chemical bonding on knitted fabric is not as successful as with wovens and under normal operational conditions, these measures often result in incomplete protection. Mosquito resistance to existing pyrethroid chemistries is problematic in some areas of military operations. In addition, military personnel are concerned that exposure to pyrethroid treatments have adverse effects on their health or that of their family members. Therefore, vector control and personal protection strategies are still of critical importance in ensuring the operational readiness of armed forces. There is an urgent need to develop an alternative effective bite-resistant system, which is more effective against insecticide-resistant mosquitoes and other arthropods, reducing the potential hazard for human health. This technology is also transferable to the private sector.

Conventional approaches to creating a textile barrier to human-vector contact rely on creating impenetrable fabric structures that have reduced air and moisture permeability, and therefore, negatively impact thermophysiological comfort. As such, their applications are quite limited in practical garments. In previous NSRDEC funded research, we developed comfortable and insecticide-free bite-resistant spacer fabrics for incorporation into a military clothing system. We use multilayer spacer fabrics that are designed to minimize thermal burden while providing bite protection. One example contains 3 main constituents: 1) a bottom layer that provides tactile comfort and moisture-wicking; 2) a top layer that is open enough for breathability (air, moisture, heat transfer) and includes our patent-pending bite-resistant structure; and 3) a middle layer that provides appropriate separation of the bottom and top layers and provides additional resistance to biting.

Physical exclusion as a cultural management practice for SWD: effects on fruit infestation, yield, and microclimate conditions

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Abstract: Small-scale, diversified and organic growers depend on cultural pest management tools to preserve crop yield and quality and to meet consumer demand for reduced pesticide residues. Growers in the U.S. are increasingly using controlled environment and high tunnel production to expand the growing season and for crop protection. Physical exclusion is one of the few cultural management practices that can effectively reduce fruit infestation by SWD, allowing for a reduction in pesticide application. In the Midwest U.S., primocane-bearing raspberries are particularly susceptible to SWD infestation due to berry physiology and phenology. Fine mesh netting is required in order to effectively exclude SWD. Use of this netting in poly-covered tunnels can impact the microclimate of tunnels and exclude pollinators, consequently affecting berry yield and quality. This presentation will highlight data collected over a four-year period (2016-2019) on the effects of physical exclusion on fruit infestation, microclimate conditions, and berry yield and quality from primocane-bearing raspberries in Minnesota. Our results show that if used early in the growing season, fine mesh netting can effectively be used to protect fruit from SWD infestation. This is primarily due to the effects of physical exclusion itself and not mediated by microclimate effects. If flies successfully colonize tunnels, these habitats can become protective to flies and infestation can rapidly build within the tunnel environment. The tunnel environment typically results in higher raspberry fruit yield and quality compared to open field plots. Additionally, our results indicate that introducing bumblebee pollinators in our tunnels does not impact raspberry yield or quality and deploying baited traps for adults within tunnels has no impact on fruit infestation by SWD.

How And Why Herbivores Should Respond To Concentrated Resources

Authors: Roitberg Bernard, Simon Fraser University, Canada

Abstract: The resource concentration hypothesis posits that sites with denser plantings will harbour more herbivores per plant. This hypothesis has been the basis of many experimental tests and theoretical explorations. Here, I take a slightly different tact and ask how the rate of accumulation changes as a function of (i) the evolutionary history of the herbivore in question with regard to its historical host plant landscapes and (ii) the focal experimental landscape. I use conditional semivariograms or structure functions (Mangel and Adler 1994; Roitberg and Gillespie 2014) to describe the world of the herbivore from its point of view to explain why it might remain or move within or among plants or clusters of host plants in order to maximize lifetime reproductive success, in different environments (e.g. various planting densities). This approach marries, life history theory, landscape ecology and plant herbivore theory. I discuss implications for agriculture.

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Are Insects Declining?

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Abstract: The Rothamsted Insect Survey (RIS) has been monitoring insects since 1964 using a network of suction traps and light traps; the former collects medium-sized migrating insects at a height of 12.2 m and the latter is designed to catch moths of all sizes using a tungsten filament bulb. These two networks represent the most comprehensive standardised long-term terrestrial data on insects in the World. A RIS study of insect biomass, led by Shortall et al (2009) found that declines in biomass had occurred at one of four sites investigated but this downward trend was primarily driven by a decline in abundance of a relatively heavy fever fly. Aphids on the other hand, were shown to have shown little sign of change in annual totals over the last 50 years despite significant changes to their phenology which was shown to be driven by climate and adaptions in life cycle traits (Bell et al. 2015). Conversely, moths have seen some dramatic declines in numbers alongside a shift in their phenology. Kelvin Conrad and colleagues flagged up two-thirds of the 337 species studied declined over the 35 yr study and 21% of the species declined more than 30% 10 yr-1. But, moth declines were worse in southern Britain, with a 40% decrease in total abundance, while there was no overall change in northern Britain which has been offset by increases. These and other studies highlight that standardised long term data is best placed to answer questions concerning declines that are often nuanced in their support of trends. However, combining long term data from many sources and studies, it is unquestionable that some insects are declining at a rapid rate and changes in policy and conservation practice are needed.

Genetic structure of cereal aphids in England using genomic approaches

Authors: Romanowski Hannah[1], Morales-Hojas Ramiro[1], Greenslade Alex[1], Alvira Fernando[1], Alderson Lynda[1], Hall Mike[1] and Kruger Tracey[1], [1]Rothamsted Research, United Kingdom

Abstract: Cereal aphids are among the most economically relevant pest species in the UK. They can reduce crop yield by direct feeding but are also vectors of the barley yellow dwarf virus (BYDV). Their abundance has been monitored in the UK for over 50 years by the Rothamsted Insect Survey, which holds the longest running dataset of insect populations. Analyses of this dataset shows a long-term stability of aphid population size despite climate change. However, little is known about their population dynamics from the genetic perspective. Studying the population genetics of these pests is fundamental to determine the geographic distribution of the genetic diversity, the patterns of gene flow and dispersal, and identify potential barriers to their movement. Here, we present results of population genetic analyses of two cereal aphids in England using genome-wide molecular markers. We compare the structure of Rhopalosiphum padi and Sitobion avenae and investigate the gene flow patterns across England to understand their dispersal and discuss the potential natural barriers to their long-distance migration. We have also investigated the temporal evolution of R. padi populations and the gene flow patterns by examining the genetic differentiation in historic times using Rothamsted Insect Survey's archive of samples. We also present an improved genome of R. padi assembled using a hybrid approach with long reads obtained with ONT MinION.

The effect of land-use type on long-term trends of British moths

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Abstract: The Rothamsted Insect Survey is the most extensive, standardised long-term terrestrial insect dataset in the world. A network of light-traps across the UK has been running since the 1960s to the present day and has recorded over 700 species of macro-moths. The total abundance of moths in the network has been in decline since records began, with the most severe declines occurring in the south-east of the country and to species which feed on shrubs and low-growing plants. Habitat loss through agricultural intensification is widely thought to be the main driver of decline but strong evidence for this is lacking. Using data from over 500 trapping locations from 1968 to 2016, we show that, contrary to expectations, declines in moth populations have been most severe in the least agriculturally intensified areas, especially broadleaf woodlands, and the lowest rate of decline has occurred in arable land and improved grassland. Moth abundance in woodlands and other semi-natural habitats was much higher than in agricultural settings at the beginning of the time series, so the relative decline in abundance is more dramatic in semi-natural areas than in agricultural areas where abundance was relatively low to begin with. The mechanisms behind these findings are unclear, but it is evident that drivers other than agricultural intensification need to be more seriously considered.

Understanding the origins and spread of resistant-breaking biotypes in aphids

Authors: Romanowski Hannah[1], Morales-Hojas Ramiro[1], Garrett Dion[1], Teakle Graham[2] and Collier Rosemary[2], [1]Rothamsted Research, United Kingdom, [2]University of Warwick, United Kingdom

Abstract: Climate change is driving the phenology of aphids earlier, compromising crop production because younger plants are being targeted earlier in the season. During colonisation and subsequent feeding, young plants are more susceptible to virus transmission and high levels of infestation can cause stunted growth, leading to supermarket rejections.

The currant-lettuce aphid, Nasonovia ribisnigri, is the most damaging species of aphid on outdoor lettuce and is responsible for large economic losses. The use of insecticides and host-resistant lettuce cultivars were previously the best method to reduce aphid outbreaks. However, insecticide-resistant biotypes and others that break host-plant resistance (resistant-breaking (Rb)) have recently been found in the UK. In the absence of lettuce cultivars with a new resistance mechanism, N. ribisnigri infestations will likely escalate. It is known that the resistant lettuce cultivar is underpinned by one gene (Nasonovia-resistant gene – Nr), yet little is known about how the aphid can overcome this single gene resistance in the host.

This sequencing project used N. ribisnigri, as a model to examine and explore potential insect resistance mechanisms to the Nr¬¬-gene resistance in the host plant. The first reference genome of N. ribisnigri has been constructed using Illumina (PE 150) and MinION sequence data obtained from both susceptible and resistance-breaking (Rb) biotypes. Whole genome analysis has been conducted to obtain gene model predictions, genome comparisons of other closely related species and produce gene phylogenies.

In addition, by obtaining near-complete genomes of both susceptible and resistance-breaking biotypes of N. ribisnigri, it is hoped that potential candidate regions which confer resistance could be identified. This in turn can be used to study the evolution and spread of resistance throughout the UK and infer migration distances using the Rothamsted Research Insect Survey suction trap network archive over the past 15 years. It is envisaged that this research could be applied to other species models and act as platform to investigate alternative control strategies such as the development of other resistant cultivars.

Gene drive technology (aka scary mutant insects) in the media

Authors: Ronai Isobel, The university of Sydney, Australia

Abstract: Science communication is vital for new technologies as it can inform the community about current developments, risk assessments and regulations. The newest genetic engineering technology for insects is gene drive (uses gene editing to trick the typical rules of inheritance). Gene drive research is progressing at a rapid pace, for example, the Target Malaria research consortium is currently testing a mosquito gene drive under field realistic conditions in the laboratory. This technology is of huge public interest and will never be permitted to be deployed in the field without community support. I recently contributed to a 'Position Statement on the Importance of Continued Innovation in Gene Drive Technology' for the Entomological Society of America. This policy statement details how and why continued research into gene drives is of the utmost importance. To publicise the findings of the Position Statement to a wider audience, such as community stakeholders and lawmakers, I proposed to write an article for the online media outlet The Conversation (over 38 million article views per month). The article titled 'Gene drives in insects hold lots of promise' has thousands of more readers than the original Position Statement, which is linked in the article. I outline the process for publishing an article in The Conversation. Overall, I reflect on my experiences of effectively partnering with the media to communicate my own research to a wider audience, which is particularly helpful for early career researchers.

Aversion of the invasive Asian longhorned tick to the white-footed mouse, the dominant reservoir of tick-borne pathogens in the United States

Authors: Ronai Isobel[2], M. Tufts Danielle[1] and A. Diuk-Wasser Maria[1], [1]Columbia University, United States, [2]University of Sydney, Australia,

Abstract: The Asian longhorned tick (Haemaphysalis longicornis) was reported for the first time in the United States of America in 2017 and has now spread across 12 states. The potential of this invasive tick vector to transmit pathogens will be determined through its association to native hosts, such as the white-footed mouse (Peromyscus leucopus) which is the primary reservoir for the causative agent of Lyme disease (Borrelia burgdorferi) and other zoonotic pathogens. We placed larval H. longicornis on P. leucopus, 65% of the larvae (n = 40) moved off the host within a short period of time and none engorged. In contrast, larval black-legged ticks (Ixodes scapularis) did not move from where they were placed in the ear of the mouse. We then conducted a laboratory behavioural assay to assess the interaction of H. longicornis with the hair of potential mammalian host species in the United States of America. H. longicornis larvae were less likely to enter the hair zone of P. leucopus and humans compared to the hair of domestic cats, domestic dogs, and white-tailed deer. Our study identifies a tick-host hair interaction behaviour, which can be quantified in a laboratory assay to predict tick-host associations and provides insights into how ticks select a host.

The effect of caging and banking on queen ovaries

Authors: Ronai Isobel[3], Aamidor Sarah E[1], Oldroyd Benjamin[3], Antonio Mendes Cardoso Júnior Carlos[2], Evenhuis Christian[4] and Cole Louise[4], [1]Behavior and Genetics of Social Insects Laboratory, The University of Sydney, Australia, [2]Department of Cell and Molecular Biology and Biopathogenic Agents, Ribeirão Preto School of Medicine, University of São Paulo, Brazil, [3]University of Sydney, Australia, [4]University of Technology Sydney, Australia

Abstract: In the honey bee (Apis mellifera), queen and worker casts originate from identical genetic template but develop into uniquely different phenotypes. A mature queen lays up to 2000 eggs per day continuously throughout her life in contrast to the non-reproductive workers that are sterile in the presence of the queen. However, periodically queens stop laying eggs, for example during swarming and winter. Although facultative sterility in workers has been widely investigated not much is known about the mechanism by which queens can stop laying. Commercial bee keeping requires the transportation of queens for sale by shipment of individual queens transported in cages for up to 10 days. During this time queens do not lay eggs until reintroduction to the new colony. Here we investigated the mechanism by which queens cease to lay eggs by testing whether genes related to programed cell death are involved in the regulation of queen reproductive physiology and the morphological changes during this time. In this study we used confocal microscopy to investigate the structural changes occurring when a queen is prevented to lay. We show that already after 4 days of caging queen ovaries start to deteriorate along the ovarioles, ovariole length decreases and mature eggs are compressed at the oviduct. We show for the first time a clear morphological response occurring as a result of this environmental constraint. These observations have commercial implications for agriculture and a better understanding of honey bee health.

Stranger things in honey bees (Apis mellifera): gynandromorphy and androgenesis

Authors: Ronai Isobel[2], Aamidor Sarah E[1], Oldroyd Benjamin[2] and Yagound Boris[1], [1]Behavior and Genetics of Social Insects Laboratory, The University of Sydney, Australia, [2]University of Sydney, Australia

Abstract: Hymenoptera (bees, ants and wasps) are haplodiploid: females are diploid while males are haploid. The cytogenetic mechanisms underlying haplodiploidy enables peculiar phenomena such as thelytoky (female cloning), androgenesis (male cloning) and gynandromorphs (sex mosaics). We sampled 11 sister gynandromorph honey bee (Apis mellifera) workers and assessed parentage and sex of various tissue. Most bees were gynandromorphs with up to three paternal origins. Remarkably, one was phenotypically female, but with no maternal alleles. It was created from the fusion of two sperm nuclei (i.e. androgenesis). This is the first reported case in Hymenoptera of sperm fusion resulting in a female. We also found queen-like characteristics in some gynandromorphs indicating a breakdown in the pathways of caste determination. Overall, our results show that when gynandromorphy occurs, unusual biological phenomena can also arise. These phenomena shed light on the evolution of some of the more bizarre social systems and cast differentiation.

The potato psyllid, Bactericera cockerelli (Sulc): history and evolution of management strategies in western United States

Authors: Rondon Silvia I, Oregon State University, Hermiston Agricultural Research and Extension Center, Hermiston, OR USA, United States

Abstract: The potato psyllid, Bactericera cockerelli (Sulc) (Hemiptera: Triozidae) is a major pest of solanaceous crops that causes damage to crop plants by direct feeding (‘causing “psyllid yellows’) and by transmitting the bacterial pathogen Candidatus Liberibacter psyllaurous (a.k.a. Ca. L. solanacearum) that causes ‘Zebra Chip’. In the western United States (US), where close to 54% of the total US production of potatoes is produced, zebra chip was reported for the first time in 2011. Our industry was unprepared for such arrival. Since then, many studies have been conducted to understand vector and pathogen geographical distribution, prediction models, basic biology and ecological studies, and management control. Studies in the past 8-years have documented substantial genetic variability in this invasive species, including several haplotypes of the vector and bio-types of the bacterium, overwintering capability in non potato plants and weeds, population dynamics and timing of potato psyllids arrival in commercial fields that has helped us tailored better control options. This presentation seeks to provide a comprehensive update to B. cockerelli life history, relationship to the pathogen, and the current status of management strategies against B. cockerelli in the U.S.

Candidate chemosensory genes identified in antennae of Harmonia axyridis (Coleoptera: Coccinellidae)

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Abstract: The harlequin ladybird, Harmonia axyridis (Pallas) (Coleoptera: Coccinellidae) is an important natural enemy of several herbivore pests, but at the same time, due to its very invasive behaviour, it may negatively affect other predatory species through, e.g., intraguild predation and indirect competition. Like other ladybirds, H. axyridis uses antennae to detect chemical cues relevant for courtship, mating and for locating food sources and suitable oviposition habitats. Understanding the molecular basis of chemosensory reception in H. axyridis could provide relevant information for field application, e.g., to increase its ability to suppress herbivore pests or, conversely, to reduce its populations whenever the ladybird is recognized as a threat to local biodiversity. Using NextSeq 550 Illumina sequencing, we assembled the antennal transcriptome of Harmonia axyridis males and females and described the expressed chemosensory genes. We annotated candidate chemosensory sequences encoding 26 odorant receptors (ORs) (including the coreceptor, Orco), 17 gustatory receptors (GRs), 27 ionotropic receptors (IRs), 31 odorant-binding proteins (OBPs), 12 chemosensory proteins (CSPs), and 4 sensory neuron membrane proteins (SNMPs). Phylogenetic analyses with sequences of other beetle species allowed to assign candidate H. axyridis chemosensory genes to known groups already described for Coleoptera. Differential expression analysis revealed low variability between males and females, potentially mirroring the absence of relevant sexual dimorphism in antennal morphology. However, significant differences were detected in the expression of three chemosensory genes, namely two male-biased odorant-binding proteins and one male-biased odorant receptor, suggesting their possible involvement in pheromone detection.

Effect of microplastics on the oviposition behaviour of a herbivorous pest in a soil-plant system

Authors: Rondoni Gabriele[2], Agnelli Alberto[1], Chierici Elena[2], Conti Eric[3] and Massaccesi Luisa[1], [1]Department of Agricultural Food and Environmental Sciences - University of Perugia, Italy, [2]DSA3, University of Perugia, Italy, [3]University of Perugia, Italy

Abstract: Pollution by microplastics, i.e. 1 µm - 5 mm plastic particles, is recognized as an emerging issue of global interest. To date, most of the research on microplastics has focused on the evaluation of health risks associated with contaminated food and seafood, or on the environmental effects in aquatic ecosystems. Recent investigations revealed that remarkable levels of microplastics can be found also in natural and cultivated soils. Concerning agricultural soils, major incomes are represented by the deposition and infiltration of particles from the surrounding environment or by direct contamination from particles derived from mulching films or irrigation tubes. Microplastics may negatively interfere with the soil microorganism and invertebrate biodiversity and with the related biological processes. Notably, it has been demonstrated that microplastics can also affect plant's development, e.g. reducing aboveground and belowground biomass. Surprisingly, there is a poor understanding of how microplastics can influence the interactions between members of the different trophic levels.

Here, we aimed at investigating whether high-density polyethylene (HDPE) microplastics in the substrate affects the emission of volatile compounds from a soil-plant system, thus possibly interfering with the oviposition behaviour of a herbivorous insect. As a model system, we used economically important crop pests, i.e. fungus gnats (Diptera: Sciaridae), and lentil (Lens culinaris) as the host plant. Fungus gnats use olfaction to identify odours from the environment and to locate a suitable habitat for oviposition.

Using one-way olfactometer, we recorded the female's residence time (the time spent in the sector closer to the stimulus) when exposed to odours from plants subjected to different combinations of the following treatments: 1) 0% and 5% of HDPE soil concentration; 2) well-watered or moderate water-stressed plants; 3) 1-day or 7-day duration of the plants' treatments.

Females were similarly attracted by plants maintained 1 day in the presence or absence of microplastics. Conversely, females' attraction was significantly reduced when exposed to plants maintained 7 days with 5% HDPE compared to 0% HDPE. Moderate water stress in 5% HDPE plants did not significantly affect the attractiveness to females compared to well-watered 5% HDPE plants. Conversely, water stress reduced the attractiveness of 0% HDPE plants to a level similar to 5% HDPE plants.

We demonstrated that the presence of microplastics induced changes in the volatile emission from the soil-plant system. These changes might interfere with the plant-herbivore infochemical communication and the effect is similar to that induced by moderate water stress. The possible mechanisms involved are under investigations and include changes of the soil physical properties and soil microbial activity.

Evolution of gall wasps: a phylogenomic analysis

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Abstract: The phylogeny of gall wasps (Cynipidae) and their parasitic relatives has attracted considerable attention in recent years. The family is now widely recognized to fall into twelve natural lineages, designated tribes, but the relationships among them have remained elusive. This has stymied any progress in understanding how cynipid gall inducers evolved from insect parasitoids, and what role inquilines (species that develop inside the galls of other species) might have played in this transition. A recent analysis of ultraconserved elements (UCEs) represents the first attempt at resolving these questions using phylogenomics. Here, we present the first analysis of gall-wasp relationships based on protein-coding sequences from genome and transcriptome assemblies. To address potential problems due to model misfit, we focus on models that accommodate site-specific amino-acid profiles and that are less sensitive to long-branch attraction than standard models. Our results show that the Cynipidae as previously circumscribed are not monophyletic. Specifically, the Paraulacini and a clade formed by Diplolepidini + Pediaspidini both fall outside of a core clade (Cynipidae sensu stricto), which is more closely related to Figitidae. This result is robust to the exclusion of long-branch taxa that could potentially mislead the analysis, and it is consistent with the previous UCE analysis. Given this, we propose that the Cynipidae be divided into three families: the Paraulacidae, Diplolepididae and Cynipidae (s. str.). Our results suggest that the Eschatocerini are the sister group of the remaining Cynipidae (s. str.). Within Cynipidae s. str., our results are consistent with the UCE analysis but place two additional tribes: (1) the Aylacini (s. str.), which are more closely related to the oak gall wasps (Cynipini) and some of their inquilines (Ceroptresini) than to the other herb gallers (Aulacideini and Phanacidini); and (2) the Qwaqwaiini, which are likely the sister group to Synergini (s. str.) + Rhoophilini. Many alternative scenarios for the evolution of cynipid life histories are compatible with the relationships suggested by our analysis, but all of them display an astonishing level of complexity with multiple shifts between parasitoids, inquilines and gall inducers. Linking the different types of life-history transitions to specific genomic signatures may be one of the best ways of differentiating among these alternative scenarios. Our study represents the first step towards enabling such analyses.

From Inquilines to Gall Inducers: Genomic Signature of a Life-style Transition in Synergus Gall Wasps

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Abstract: Gall wasps (Hymenoptera, family Cynipidae) induce impressively complex galls on oaks, roses and other plants, but the mechanism of gall induction is still unknown. Here we take a comparative genomic approach to revealing the genetic basis of gall induction. We focus on a clade of cynipids, the genus Synergus, whose members are inquilines, which cause the development of nutritive tissues inside galls initiated by other species, but cannot initiate galls themselves. Recently, it has been shown that one Synergus species, S. itoensis, has evolved the ability to induce its own gall from an inquiline ancestry. We compared the genome of S. itoensis to that of three related Synergus inquilines to identify genomic changes associated with the origin of de novo gall induction. We used a novel Bayesian selection analysis, which accounts for branch-specific and gene-specific selection effects, to search for signatures of selection in 7,600 single-copy orthologous genes shared by the four Synergus species. We found that the terminal branch leading to S. itoensis had more genes (Positive Signature Genes, PSGs) showing a signature of positive selection, as identified by a significantly elevated dN/dS ratio, than the other terminal branches in the tree. Similarly, the S. itoensis branch also had more genes with lower dN/dS ratio (Negative Signature Genes, NSGs). Gene set enrichment analysis showed that the PSG set of S. itoensis, unlike the PSG sets for the inquiline Synergus species, is enriched in several types of biological process Gene Ontology terms, the most prominent of which is “Ovarian Follicle Cell Development” (GO:0030707). Our results indicate that the origin of gall induction is associated with distinct genomic changes, and provide a good starting point for further characterization of the genes involved.

Optimizing amplicon-based metabarcoding in inventorying insect communities

Authors: Ronquist Fredrik[3], Iwaszkiewicz-Eggebrecht Elzbieta[3], Miraldo Andreia[1], Marquina Daniel[2], [1]Department of Bioinformatics and Genetics Swedish Museum of Natural History Stockholm, Sweden, [2]Department of Bioinformatics and Genetics, Swedish Museum of Natural History Stockholm, Sweden, [3]Natural History Museum Stockholm, Sweden

Abstract: Genetic methods are bound to revolutionize studies of insect communities but these approaches are still in their infancy. Results obtained so far need to be interpreted with caution, accounting for biases and errors, and further method refinement is a priority. As part of an ambitious comparative study of the insect faunas of Sweden and Madagascar and their associated microbiomes, the Insect Biome Atlas project, our lab has recently been testing and optimizing several aspects of amplicon-based metabarcoding protocols for sampling insect communities. We summarize our findings with respect to optimal markers and primers, and compare communities detected in Malaise trap samples and soil samples from the same locality. We also analyze the differences between the signal retrieved from preservative ethanol versus tissue homogenate from the same Malaise trap sample. Finally, we compare the effectiveness of mild lysis protocols versus tissue homogenization in retrieving the species diversity and abundance in mock communities and in real Malaise trap samples.

Can we expect to use a single generic trap deployed at potential ports-of-entry for early detection of exotic cerambycids, bark and ambrosia beetles, and buprestids?

Authors: Roques Alain, INRAE, Zoologie Forestière Orléans, France

Abstract: Globalization is leading to an exponential increase in the introduction of non-native insects into other continents without any saturation being observed. Most of these species are phytophagous insects associated with woody plants, probably in connection with the explosion of the global ornamental trade. A growing number of the newcomers are said to be emerging because previously unknown as invaders elsewhere, or considered harmless in their areas of origin. As such, these species were not regulated before their arrival in Europe, The definition of tools allowing an early, generic detection at arrival is therefore essential. Because pheromone components are often conserved at world level among related species in Cerambycidae, successive tests in France allowed to design a blend involving 8 pheromone components as a lure with generic attractiveness, allowing to detect "unkown" species arriving from other continents. In 2018 and 2019 black multifunnel traps baited with this blend, complemented with ethanol and a-pinene, captured a total of 126 native cerambycid species in French forests, which represented 52% of the country's fauna. At potential points-of-entry, captures with the same trapping design concerned 38 cerambycid species including 8 non-native ones, two of which having never been reported in Europe, yet. These trapping designs also allowed to detect non-native bark and ambrosia beetles (Xylosandrus spp.) and platypodids (Euplatypus spp.) in forests and ports. However, these black traps caught very few buprestids whereas such species may also constitute serious threats to forests. Therefore, we compared the attractiveness of green and black multifunnel traps baited with the same 8-component blend complemented with ethanol and [-] a-pinene. The green traps effectively captured 25 species of buprestids of which 15 Agrilus spp. but the number of cerambycid species, as well as the number of individuals, significantly decreased with regard to the trappings by black traps. We would probably need to deploy traps of different colours, and baited with different lure combinations to detect both cerambycids, bark and ambrosia beetles and buprestids at ports of entry.

Using multi-pheromone blends as a tool for early detection of non-native cerambycid species at arrival on other continents: results of a worldwide trapping program

Authors: Roques Alain[2], Ren Lily[1], Auger-Rozenberg Marie-Anne[3], Yuan Yuan[1], Shi Juan[1] and Sun Jiang-Hua[4], [1]BFU & IFOPE, [2]INRAE, [3]INRAE, URZF, Orleans, France, [4]IOZ- CAS

Abstract: Globalization is resulting in an exponential increase in the introduction of non-native insects into other continents, of which a growing proportion are emerging species, yet never found outside their native range. Being capable of detecting such species at arrival at ports of entry before they establish in non-native countries is an urgent challenge. Large progresses in cerambycid pheromone chemistry revealed that sex- and aggregation-sex pheromones are rather well conserved at world level. A blend combining 8 pheromones showed a large generic attractiveness in France, with 130 cerambycid species of different subfamilies trapped. These results led to propose the development during 2019- 2021 of a joint trapping program between Europe and China using this multi-pheromone blend with the rationale: if a species is trapped in numbers in its native continent, higher is the probability of catching it at arrival on a non-native continent. The trappings were carried out in 13 European countries and 13 provinces of China. They allowed to catch 75 species at least in China and 173 in Europe, including 9 species trapped in both regions of which invaders in Europe. Attempts to generalize at world level such trappings using the same generic blend are in progress.

Specific problems of IPM in the case of maize leaf weevil (Tanymecus dilaticollis Gyll.) In Romania, ways and methods of limiting the economic impact on farmers

Authors: Rosca Ioan[1], Chiriloaie Andrei[1] and Fatu Viorel[1], [1]Research Development Institute for Plant Protection, Romania

Abstract: From 2014 to 2022, Romania granted exemptions for the use of neonicotinoids in seed treatment, because there are no effective technical alternatives to control the Tanymecus dilaticollis Gyll. which is considered the most important pest of corn, causing considerable damage and on sunflower and in the area of corn cultivation, in Romania especially in the south, east and southeast, being a limiting factor of these crops in the southeast of Romania, the favorable biological requirements of the pest, corresponding entirely to this area, there are no viable alternatives for replacing the seed treatment with other methods of pest control within the IPM. The main causes that contribute to this situation are presented, including the implications of the fact that the EFSA did not require the PLH Committee to provide standards for assessing the effectiveness of a pesticide specific to maize corn leaf beetle (this is done by "similar" standards to completely different pests by biology and mode of attack). Being proposed and justified the study of the value of the pressure of water vapor deficit in the atmosphere (VPD) calculated using the equations developed by Syswin Solutions company for assessing the risk of pest attack in maize and sunflower crops.

Does increasing field size worsen pest problems? A test in commercial citrus production

Authors: Rosenheim Jay[1] and Cass Bodil[1], [1]University of California, Davis, United States

Abstract: Agroecology theory suggests that the loss of diversity associated with crop monocultures worsens pest problems, and that the larger the monocultures, the worse the problems. This is, however, difficult to test experimentally, because most research farms are too small to replicate different field size treatments at spatial scales that are meaningful for commercial agricultural production. Here we use a database of pest densities in commercial citrus production in California's San Joaquin Valley to look for associations between field size and pest densities. We use data gathered by independent pest management consultants, who monitor a community of arthropod pests, including herbivorous mites and insects (including the citrus thrips, fork-tailed bush katydid, citrus red mite, California red scale, citricola scale, cottony cushion scale), as well as a single beneficial mite, Euseius. Although different species reveal different relationships between field size and mean pest density, we find no broad support for the idea that larger monocultures are associated with worse pest problems. We discuss the implications for agroecology theory.

Introduction to the round table "How to work on lever combination to control pests"

Authors: Rosiès Blandine, INRAE (French National Research Institute for Agriculture, Food and Environment), France

Abstract: This talk is an introduction to the round table we propose in the second hour of this symposium. The theme addressed by the round table is "How to work on lever combination to control pests". In the frame of the API-Tree project we have been working on single levers of action as well as on the design of combinations of practices alternative to chemicals to control apple pests.
Three proposals presenting different options to work on lever combinations will be briefly (3-5') developed in the following hour. Between each argument an open discussion with the room will be proposed. This round table will be concluded by an invited testimony, who will share his/her feedback and the message that's he/she is bringing home.
First proposal offers the system approach as the optimal to work on lever combinations, and argues for experimental evaluation between the levers to assess interactions, overlap and compatibility between levers of action against pests.
Second proposal proposes modelling can better capture the complexities and identify knowledge gaps.
Third proposal is that the design of such integrated systems and their dissemination require various types of knowledge, from basic, to applied and empirical knowledge, thus involving a range of stakeholders in a participatory approach to tailor agroecological orchards.

Insights into morphological disparity of Palaeodictyopterida from the late Carboniferous of Piesberg

Authors: Rosová Kateřina[2] and Prokop Jakub[1], [2]Faculty of Science, Charles University, Czech Republic, [1]Czech Republic

Abstract: New palaeodictyopterid insects from the famous Moscovian (Pennsylvanian) locality of Piesberg quarry near Osnabrück (Lower Saxony, Germany) reveal spectacular disparity in the patterns of the wing venation. So far, the still active site provided over 1400 specimens of insects giving us an exceptional view of the insect diversity in the Moscovian, in some instances with exceptional preservation uncovering microstructural details. Significant part of the insect diversity at Piesberg belongs to the superorder Palaeodictyopterida, with so far recorded 10 families and 15 genera known from this locality. Our findings extended the enormous morphological disparity in the wing venation of orders Diaphanopterodea, Megasecoptera and Palaeodictyoptera during this time section and also provided links to other Pennsylvanian deposits in Europe and North America.

K.R. gratefully acknowledges the support of her research by the project "Grant Schemes at CU" (reg. no. CZ.02.2.69/0.0/0.0/19_073/0016935).

An overview of how phylogenomics changed our view of the lepidopteran tree of life and which sections of the tree remain unresolved

Authors: Rota Jadranka, Biological Museum, Department of Biology, Lund University, Sweden

Abstract: In this presentation I provide an overview of the advances made in our understanding of the lepidopteran tree of life and which parts of the tree remain unresolved.

The unresolved phylogenomic tree of butterflies and moths (Lepidoptera): Assessing the potential causes and consequences

Authors: Rota Jadranka, Biological Museum, Department of Biology, Lund University, Sweden

Abstract: Next-generation sequencing technologies have revolutionized the field of molecular phylogenetics and we are now in the era of phylogenomics. Lepidoptera – butterflies and moths – are one of the largest animal groups on the planet and they represent the largest radiation of herbivorous insects. In the past decade a number of phylogenomics studies focusing on the order Lepidoptera have been published, advancing our efforts to resolve the lepidopteran tree of life. In this presentation, I will provide an overview of how our understanding of the lepidopteran phylogenetic relationships has changed because of the wealth of data coming from transcriptomes and genomes, which parts of the tree remain unresolved, and the potential reasons for difficulties in resolving the relationships among the lepidopteran superfamilies.

The Spotted Lanternfly (Lycorma delicatula): A Highly Under-rated but Predictable Global Invasive Threat?

Authors: Roush Richard, Department of Entomology College of Agricultural Sciences Pennsylvania State University, United States

Abstract: The rapid expansion of the Spotted Lanternfly (SLF) across Korea (from 2006) and the northeastern USA, its impact on grape vineyards, and difficulty of management highlight its threat to other countries. Nymphs and adults feed on a wide range of host plants. Adult females routinely lay eggs in rocks and dead wood. The first record in the USA was in September 2014, about 100 km NW of Philadelphia, arriving on stone imports and/or their wood packaging materials from China. The SLF is now widely distributed across southeastern Pennsylvania and into at least 3 neighboring states (New Jersey, Delaware and Virginia). Despite intensive and costly management efforts, at least one vineyard has already been killed by SLF feeding, and others have been unable to yield crops. The financial impact on industries such as nurseries, Christmas tree growers and hardwood producers and especially vineyards already exceeds US$50 million annually in Pennsylvania alone. Expansion across Pennsylvania is predicted to cost at least $325 million in damages and 2,800 jobs. The US and Pennsylvania Departments of Agriculture have already spent more than $30 million attempting to suppress SLF populations and contain their spread. The preferred host of SLF, Ailanthus altissima, which has been a key factor in its rapid expansion, is reputed to be a noxious/invasive weed in Australia, New Zealand, South Africa, many countries of central, eastern and southern Europe, and also introduced to Argentina, suggesting that all of these regions are at risk from this insect. Despite intensive research, no effective pheromones or feeding attractants have been found. The public has been heavily engaged to take advantage of one of the SLF's few weaknesses, its distinctive appearance, to help identify and map infestations. Public reports of SLF by phone or website have exceeded 90,000 in 2019 alone, with 640 outside the initial quarantine zone. Novel control and detection strategies are being tested in Pennsylvania, including the use of insecticidal nets on tall objects, which are very attractive to SLF, and sniffer dogs. Dispersal of adults is greater than expected from observations in Korea. To protect grape vineyards, control must apparently be applied against nymphs for at least 500 meters from the vineyard.

Gene regulatory elements and networks provide an insight into direct and indirect negative regulation by the ecdysone cascade

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Abstract: Introduction: Hematophagous female Aedes aegypti mosquitoes transmit pathogens for devastating viral diseases like Dengue, Yellow fever, and Zika, while blood-feeding. Being anautogenous, these mosquitoes require a blood meal for vitellogenesis - the process of yolk formation, during the maturation of eggs. Upon blood feeding, a steroid hormone, 20-hydroxyecdysone (20E), turns on the reproductive program during which thousands of genes are differentially expressed. Using transcriptomic data, we have previously detected four distinct and sequential gene expression patterns along with major regulators for each pattern, in the post blood meal (PBM), reproductive period. Pathways related to 20E-mediated gene activation are well known. However, the mechanism of repressive action by this hormone remains poorly understood.

Method: Bioinformatics combined with molecular biology techniques helped us identify the mechanisms of 20E-dependent direct and indirect transcriptional repression by the ecdysone receptor (EcR). To decipher how complex transcription networks, govern differentially expressed genes, during the vitellogenic period, we used genomics and bioinformatics tools to search for the promoters of co-regulated gene sets. Identified putative transcription factor binding sites (TFBSs) and their corresponding transcription factors (TFs), were used to build putative regulatory networks. RNAi-mediated depletion of selected TFs, ChIP, luciferase assays, and qRT-PCR of the target genes, were used for evaluation of the functionality of some of these putative TFs within the networks.

Results: Eighty-nine putative transcription factor binding sites (TFBSs) on the cis-regulatory regions of more than 1,400 differentially expressed genes, were identified. Putative transcription factors that may bind to these TFBSs were identified and used for the construction of temporally coordinated regulatory networks. Molecular biology techniques helped us uncover mechanisms of direct and indirect negative transcriptional regulation by the steroid hormone 20-hydroxyecdysone (20E) through the ecdysone receptor (EcR). Genes within the two groups - early genes and late mid-genes, with distinctly different expression profiles show lower expression at the high titers of 20E. Transcriptional repression of early genes is indirect and involves the classic 20E pathway with ecdysone-induced protein E74 functioning as a repressor. On the other hand, Late mid-genes are repressed directly by EcR, which recognizes and binds a previously unreported DNA element (EcREr), different from those utilized in the 20E-mediated gene activation, within the regulatory regions of its target genes and initiates chromatin condensation by recruiting a corepressor, Mi2.

Discussion: We have characterized two negative regulatory pathways for the liganded EcR, during the 20E-driven reproduction of the female Ae. aegypti, which advances our understanding of the 20E-EcR mediated complex repression mechanisms and could lead to improved vector control approaches.

Fire – to the rescue! Dry heathland burning has positive impact on Orthoptera diversity.

Authors: Rozenfelde Rūta, University of Latvia, Latvia

Abstract: European dry heaths have unfavourable conservation status in European boreal region and is at risk of disappearing regionally. In Latvia dry heathlands can only exist in areas where continuous disturbance is present. Since 2009 controlled burning has been applied as a habitat management practice to preserve the heathlands of protected landscape area „Ādaži". It is necessary to estimate the contribution this practice has on maintaining and improving the diversity of habitat-characteristic and rare species. The goal of this study was to learn how controlled burning influence Orthoptera species diversity. Respectively, quantitative Orthoptera occurrence data was obtained from both burned and unburned heathlands, using pitfall traps exposed in 20 sample sites over a period of one month. Projective vegetation, litter and bare ground cover was estimated, and vegetation height was measured for interpretation. We found that heathland burning had positive effect on Orthoptera species composition and diversity. Majority of the Orthoptera species were characteristic to heathlands. The diversity and occurrence of Orthoptera was positively correlated with vegetation diversity, bare ground and grass cover, and negatively with the cover of heath Calluna vulgaris. From the findings we conclude that controlled burning in dry heathlands is an effective method for Orthoptera conservation.

Effect of constant temperatures on Culicoides sonorensis midge physiology and vesicular stomatitis virus infection

Authors: Rozo Lopez Paula[1], Barbara Drolet[2], Park Yoonseong[1], [1]Kansas State University, [2]United States Department of Agriculture

Abstract: Culicoides biting midges are nuisance pests of livestock and well-known vectors of veterinary arboviruses, such as vesicular stomatitis virus (VSV). Female midges ingest viruses when feeding on blood to obtain protein for egg-laying. After ingesting a VSV-infected blood meal, the environmental temperature of the resting location mediates the rates at which blood is digested, eggs are laid, and virus particles are replicated inside the midge. VSV transmission will occur if the timing of virus amplification aligns with the next feeding–egg-laying cycle. We evaluated the impact of constant environmental temperatures on midge physiology (lifespan and reproduction), vector competence for VSV (infection and dissemination), and thermal resting preference. Our results indicate that after ingesting a blood meal, most midges prefer to rest in areas that fall within their preferred physiological range regardless of the temperatures at which they were being maintained. These preferred temperatures maximized their survival, the number of egg-laying cycles, and the likelihood of VSV transmission. Our temperature approach shows that in the Culicoides–VSV system, the preferred resting temperature selected by blood-fed midges is beneficial for both insect and virus transmission.

Venereal transmission of a Culicoides-borne arbovirus: Vesicular stomatitis virus

Authors: Rozo Lopez Paula[1], Drolet Barbara[2], [1]Kansas State University, [2]United States Department of Agriculture, Agricultural Research Service, Arthropod-Borne Animal Diseases Research Unit, Manhattan, KS, United States

Abstract: Culicoides sonorensis biting midges are well-known agricultural pests and arbovirus vectors in the USA. Natural reservoir questions remain for arboviruses that persist between vector seasons in the absence of infected animals. One such arbovirus is the rhabdovirus, vesicular stomatitis virus (VSV). This virus has a complex epidemiology with a broad range of vertebrate hosts, multiple routes of transmission, and an extensive diversity of suspected and incriminated vector species. Examining potential non-conventional routes for vector transmission, such as venereal transmission between midges, might help explain viral maintenance during inter-epidemic periods and times of adverse conditions for horizontal (bite) transmission. Under laboratory conditions, venereal transmission was demonstrated by plaque assay and real time qRT-PCR from infected females to uninfected males, and from infected males to uninfected females. Relevant anatomical sites for virus location resulting in transmission through copulation were identified by immunohistochemical staining. Our research results indicate C. sonorensis midges are capable of efficient venereal VSV transmission which may inform ecological, temporal, and spatial aspects of inter-epidemic arbovirus epidemiology.

A story on how milkweed plants defend against seed predators

Authors: Rubiano-Buitrago Paola[1], Pradhan Shrikant[1], Paetz Christian[1] and Rowland Hannah[1], [1]Max Planck Institute for Chemical Ecology, Germany

Abstract: Plants in the genus Asclepias produce cardenolides as a defence against herbivory. Cardenolides are a diverse group of compounds derived from triterpenoids and have a specific physiological target, the transmembrane protein Na+, K+–ATPase (NKA). Cardenolides are toxic because they bind to the extracellular surface of the NKA and disable passage of Na+ and K+ across the membrane. This disrupts electrochemical gradients causing many physiological systems to become dysregulated. Although the NKA is highly conserved among animals, independent evolution of NKA insensitivity to cardenolides has occurred in six taxonomic orders of insects and Asclepias are host plants for numerous insect species which in turn use cardenolides as their own chemical defence against their predators, e.g. milkweed bugs (family Lygeadeae), monarch butterflies (Danaus plexippus), aphids (Aphis nerii), and others. In this talk I present results of the isolation and identification of cardenolides from seeds of Asclepias curassavica, including the description of four new cardenolides, and the toxicity of individual cardenolides to the specialist herbivore the large milkweed bug Oncopeltus fasciatus. I describe the concentration and diversity cardenolides in seeds and the comparative inhibitory activity of the major cardenolides to three organisms, a sensitive vertebrate (Sus domesticus), a non-adapted insect (Drosophila melanogaster) and the specialist herbivore O. fasciatus. My results add to the understanding of how plants respond to specialist herbivores and opens the door to understanding how the arms race between plants and herbivores results in chemical diversity.

Can nanopore sequencing provide a cost- and time-effective solution for identifying quarantine-actionable arthropods?

Authors: Rugman-Jones Paul, University of California Riverside, United States

Abstract: Each year, thousands of arthropod specimens are found in cargo shipments and personal baggage entering or leaving the U.S. Many cannot be easily identified to species using morphological techniques and the relevant authorities typically adopt a “guilty unless proven innocent” attitude. This can trigger a host of possible quarantine measures, many of which may have been avoided had an accurate species level identification been available. DNA sequencing offers a fast and precise alternative for species identification, but until very recently, equipment costs and logistical requirements for laboratory space made it an impracticable option. However, the recent introduction of a highly portable and highly affordable DNA-sequencer, Oxford Nanopore Technologies’ MinION®, has renewed interest in the use of DNA sequences to provide a quick, accurate, cost-effective means of identifying difficult taxa to species. As a test of the MinION’s potential, I will present findings from a “proof-of-concept” project that focuses on a critical need to increase the speed, accuracy, and precision, of mite identification, to safeguard the citrus, stone fruit, and avocado industries in California.

Plant growth promoting bacteria (PGPBs) as bioinsecticides

Authors: Ruiu Luca, Dipartimento di Agraria University of Sassari, Italy

Abstract: The industrial interest in plant growth promoting bacteria (PGPBs) is significantly growing as a result of the discovery of new properties of certain microbes in benefiting agricultural crops. While several rhizobial species have been widely exploited for their ability to optimizing plant use of environmental resources, now the focus is shifted to species that are additionally capable of improving plant health and conferring resistance to abiotic stress and deleterious biotic agents. In some cases, PGPB species may directly act against plant pathogens and parasites through a variety of mechanisms including competition, protective biofilm formation, and the release of bioactive compounds. The use of this type of bacteria is in line with the principles of eco-sustainability and integrated pest management, including the reduction of employing chemical pesticides. Several strains of Bacillus, Paenibacillus, Brevibacillus, Pseudomonas, Serratia, Burkholderia, and Streptomyces species have been the subject of specific studies in this direction, and under evaluation for further development for their use in biological control. Accordingly, specific case studies are presented and discussed, including the entomopathogenic bacteria Brevibacillus laterosporus and Pseudomonas protegens.

Ability of recombinant Bacillus subtilis 26DCryChS line to induce defensive response of wheat to greenbug aphid Schizaphis graminum and bird cherry-oat aphid Rhopalosiphum padi feeding.

Authors: Rumyantsev Sergey[1], Blagova Daria[1], Burkhanova Guzel[1], Maksimov Igor[1], Veselova Svetlana[1] and Alekseev Valentin[1], [1]Institute of Biochemistry and Genetics of the Ufa Federal Research Center of the Russian Academy of Sciences, Russia

Abstract: Obtaining of biological control agents based on recombinant lines of endophytic bacteria of the genus Bacillus which combine fungicidal and insecticidal activities is one of the most effective technique in protecting plants from pests and diseases.

In our laboratory, we obtained the new recombinant line Bacillus subtilis 26DCryChS containing the Btcry1Ia gene from Bacillus thuringiensis B-5351. It retained endophyticity and the ability to synthesize lipopeptide surfactin, and also acquired the ability to produce Cry1Ia protein. We observed insecticidal effect against Schizaphis graminum Rond. and bird cherry-oat Rhopalosiphum padi L. aphids of lipopeptide rich fraction of the culture filtrate of B. subtilis 26D strain and B. subtilis 26DCryChS line. The introduction of the Btcry1Ia gene into the genome of the B. subtilis 26D strain increase the aphicidal activity of B. subtilis 26DCryChS line. It was found that in wheat plants which were colonized by S. graminum and R. padi, bacterial strains under investigation triggered induced systemic resistance (ISR). ISR was characterized by an increase in the content of hydrogen peroxide, a decrease in activity of catalase, and an increase in activity of peroxidases and proteinase inhibitors in wheat plants occupied by aphids.

The advantage of the B. subtilis 26DCryChS recombinant line was stimulation of the transcriptional activity of both salicylate (SA) and jasmonate (JA) - dependent genes, while the source strain B. subtilis 26D activated genes which are regulated via SA pathways, and the donor strain B. thuringiensis B-5351 activated JA dependent genes. The recombinant B. subtilis 26DCryChS line can be proposed as a solution for the development of modern biocontrol agents.

Inheritance and fitness cost of clothianidin resistance in the brown planthopper, Nilaparvata lugens

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Abstract: The brown planthopper (BPH), Nilaparvata lugens (Stål), one of the most important pests on rice crops and has developed resistance to many insecticides including clothianidin, a kind of neonicotinoid insecticides. Here, a laboratory selected clothianidin resistant strain and a susceptible strain were used to investigate the genetic basis and the fitness cost of clothianidin resistance in N. lugens. The clothianidin resistant N. lugens strain with 173.36-fold resistance was selected in laboratory. Data from the F1 reciprocal crosses between clothianidin-resistant and -susceptible strains indicated that resistance might be autosomal and incompletely dominance. Chi-square analyses of self-bred and backcross progenies suggested the resistance was controlled by multi-gene. The resistant strain had a relative fitness of 0.78 with the increased adult pre-oviposition period and the decreased total fecundity. The mRNA expression level of NlVg in the resistant strain was significantly downregulated compared to the susceptible strain. Clothianidin resistance in N. lugens was shown to have an autosomal and incompletely dominance mode of inheritance. The development of resistance may have a significant fitness cost for the resistant population including the decreased fecundity. Downregulation of NlVg may contributed to the reduced fecundity in the resistance. Current study provides valuable information for the establishment of resistance management strategies to delay the resistance of clothianidin in N. lugens in the field.

Predator biomass distribution and biological pest control services in agricultural landscapes

Authors: Rusch Adrien, INRA, UMR SAVE - Villenave d’Ornon, France

Abstract: Biological control of pests by their natural enemies is a crucial ecosystem service supporting agricultural production. It has been demonstrated that landscape heterogeneity or organic farming promote biological pest control services but the relationship between predator community composition and predation rates of pests remains poorly investigated.. A deeper understanding of the processes shaping interaction strength in agroecosystems is therefore needed if we are to accurately predict biological pest control services. The large body of literature studying the relationships between biodiversity and ecosystem functioning indicates that there is a positive non-linear relationship between taxonomic richness of a given community and ecosystem functioning. However, recent studies have demonstrated that other aspects of community structure such as community composition or functional diversity are important providing major insights on processes shaping emergent functions from species assemblages. If all species contribute equally to a given ecosystem function, the overall numerical abundance of individuals might best explain the level of functioning than any other characteristics of the community incorporating evenness of species distribution or functional traits. However, if a trait is strongly related to an ecosystem function then the moments of trait-abundance distribution (i.e., mean, variance, skewness and kurtosis) in the community might best explain ecosystem functioning while shedding light on the ecological mechanisms explaining these relationships (e.g., sampling effect, complementarity, asymmetric competition). Here, using large empirical datasets replicated at landscape scales, we examined how predator abundance, taxonomic richness as well as the mean, variance, skewness and kurtosis of predator biomass distribution affect pest predation rates in an agroecosystems. We particularly hypothesized that landscape heterogeneity and organic farming would enhance abundance and taxonomic diversity of predators but that parameters describing predator biomass distribution would better explain biological pest control services than metrics only based on abundance or taxonomic diversity. Our results supported our hypothesis and we demonstrated that predator biomass distribution is a key trait to explain the level of biological control. We found that the skewness of biomass distribution of predators was the most important parameter positively affecting the level of pest predation. Indeed, when the proportion of large biomass predator increases in the community, the level of pest predation decreases suggesting negative interactions between predators such as intraguild predation or behavioural interactions. This study demonstrated that considering functional trait composition of communities provides a mechanistic understanding of the processes shaping the strength of trophic interactions in terrestrial ecosystems.

Black soldier fly (Hermetia illucens L.) reared on coffee by-products enriched with microalgae

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Abstract: Nine billion people are expected on Earth by 2050 with an increase in global feed and food demand. Furthermore, a rise in waste and by-products are also expected. Insects reared on by-products represent a good example of bio-converting organisms for the production of feed and food in a circular economy view. In addition, farming of insects is sustainable in terms of land use, water consumption and CO2 production. Among several insect species, the black soldier fly, Hermetia illucens, has a promising role for both bioconversion and aquafeed production. The aim of the present study was to compare the influence of different rearing substrates on H. illucens larvae fed on a by-product of the coffee industry (coffee silverskin) enriched with different inclusions of two microalgae: Schizochytrium sp. and Isochrysis galbana. At this purpose, eight different diets based on coffee silverskin enriched with 5, 10, 20 and 25% of Schizochytrium sp. and I. galbana respectively, and a control diet composed by 100% coffee silverskin were tested. Larval mortality rate, larval development time and prepupal weights were recorded for each diet treatment. Moreover, the growth rate, the efficiency of conversion of digested food, the feed conversion rate, the efficiency of conversion of ingested food, and the waste reduction index were determined. No significant differences among diets were recorded for the larval mortality rate. Whereas, the larval development time and the prepupal weight were strongly affected by dietary treatment: higher inclusions of both microalgae resulted in shorter larval development time; and higher inclusions of Schizochytrium sp. resulted in higher prepupal weights. Moreover, the higher growth rates were recorded for larvae fed on higher inclusions of Schizochytrium sp.. Better values of the efficiency of conversion of digested food, feed conversion rate, and efficiency of conversion of ingested food, were recorded on higher inclusions of both microalgae. Finally, the waste reduction index showed significantly higher value on diet enriched with 10% of Schizochytrium sp. In conclusion, this study showed that higher inclusion of Schizochytrium sp. in the diet resulted in the best larval performances.

This research was supported by Fondazione Cariverona, Ricerca Scientifica 2017, project NUTRIFISH, code n. 2017.0571.

Sound emitted by honey bees as non-invasive monitoring methods in a beehive

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Abstract: Honey bees are very useful insects since they are able to produce honey, beeswax, royal jelly and propolis and, most important, they play a key role in the service of pollination allowing the proliferation of both cultivated and spontaneous flora. In the last decades, an increasing of bee mortality has been recorded, with ecological and economic consequences. The causes can be found in the Colony Collapse Disorder which is a situation characterized by a sudden disappearance of honeybees from the hive. Actually, the decline of honey bee colonies is the result of multiple source of stress, that act independently, in combination, or synergistically to impact the honey bees health. In this scenario, it is clear the necessity of an intensive monitoring activity in order to better understand the problems which are seriously affecting the health of honey bees. Nowadays, different monitoring methods are studied to try to solve the problem. Among them, the sound emitted inside a beehive could be one of the key parameters for a non-invasive monitoring able to determine the family condition. Sound signal modulates many colony behaviors. There is a strict correlation between the frequencies and the amplitudes of honey bee hive sounds and the prevision of events. Different sounds are used by the honey bees to communicate within the colony, in order to give notice of the presence/absence of the queen, the presence of a young queen, the swarming, the presence of smoke in the environment, and of other events. The sound is generated through vibro-acoustic signal production. Honey bees produce these sounds by gross body movements, wing movements, high-frequency muscle contractions without wing movements, and pressure of the thorax against the substrates or against another bee. Therefore, an accurate interpretation of these sounds could help to identify specific situations within the hive. In this work, a multi-sensor platform capable of real-time monitoring beehives condition has been used. The system has been developed to record the sounds emitted by the bees in the hives, and to measure parameters such as temperature, humidity, CO2, weight and weather conditions. Moreover, we applied advanced digital signal processing techniques to recognize different states in a beehive using as input audio data of beehives collected from the NU-Hive project. The proposed work aims at analyzing the bees sound introducing new advanced algorithms to determine and identify several situations, like swarming period, the absence of queen bee, and presence of smoke in the environment. Taking into consideration a real scenario, several experiments have been performed focusing on particular events to highlight the potentiality of the proposed approach. Several experimental results have been collected from a real field deployment, proving the effectiveness of the proposed approach in identifying specific situations.

Precibarial valve of Cicadella viridis (Hemiptera: Cicadellidae): a potential vector of Xylella fastidiosa

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Abstract: Xylella fastidiosa is a xylem-inhabiting, vector borne, gram-negative bacterium that infects numerous plant species. This pathogen is transmitted by xylem sap-feeding insects of the order Hemiptera, sub-order Auchenorrhyncha. These insects have a sucking mouthparts with which they are able to reach the xylem of their host plants. After the acquisition from the xylem of the source plants, the bacterium attaches to the precibarium and multiplies in it without circulation in the hemolymph. With the exception of Philaenus spumarius L. (Aphrophoridae), identified as a vector of X. fastidiosa in California and in Apulia, the American vector species are absent in Europe. In America the most important vectors of X. fastidiosa are insects belonging to the family of Cicadellidae, subfamily Cicadellinae, but in Europe only a few species of sharpshooters are present, among which Cicadella viridis (L.) (Cicadellidae). This leafhopper is widespread in the Europe, and it is considered a X. fastidiosa putative vector. There is a good amount of available knowledge on the ecology and phenology of C. viridis, but some morphological information on its feeding structures are lacking. The precibarial valve plays an important role in sap ingestion. Therefore, considering the importance of this structure in the transmission of the bacterium, we used light and electron microscopy to study the morphology of the precibarial valve of C. viridis. Up to now, the valve of Cicadellidae was described as a bulbous tip attached to the proximal side of a pit, that when opens fits into a groove at the anterior end of the basin. The use of cross-sections, compared to images taken with the electron microscope, allows us to describe a different structure. In our observations, the precibarial valve of C. viridis appears as a complex structure, with a bell-like invagination located in the middle of the epipharynx, linked to a flap-like structure that pivot on it, attached to a muscle originating on the clypellus. This structure is similar of what we observed in our previous work on P. spumarius, in which the valve opens by dilator muscles and closes through cuticular and fluid tensions, the latter leading to morphological changes to the plane of the valve based on sap flow. X. fastidiosa presents little species specificity within xylem-feeding specialists. This characteristic suggest that foregut morphological traits determine the efficiency of bacterial transmission. For this reason, the morphological similarity to P. spumarius together with its wide distribution, and its polyphagia supports the hypothesis that C. viridis can be seriously considered a potential vector of X. fastidiosa.

Rearing mealworm larvae on substrates contaminated by foodborn pathogens

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Abstract: Tenebrio molitor larvae were reared on organic wheat middling, spiked with Escherichia coli and Staphylococcus aureus at three contamination levels (1, 5, and 7 Log colony forming units per gram).

Chemical control of hala scale, Thysanococcus pandani, and its current geographic distribution on the Hawaiian Islands.

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Abstract: The hala scale, Thysanococcus pandani, was first detected in Hana, Maui in 1995. The primary host plant for T. pandani is the hala tree, Pandanus tectorius, which is found in coastal areas of the Hawaiian Islands and frequently planted as a landscape tree. P. tectorius trees are very significant to Hawaiian culture as they were part of the original canoe plants brought by Polynesian voyagers across the Pacific. Since its initial introduction in Maui, it is now widespread on Maui and Molokai, and is established on limited locations on Oahu. In April and May 2021, a statewide survey was conducted to evaluate its current distribution with an emphasis on Kauai, Hawaii Island, and Lanai. The Lanai population that was previously detected has been eradicated. There was no hala scale detected on Kauai and Hawaii Island at the available survey sites. Chemical control methods were also evaluated to determine if any treatments could be effective for reducing or eliminating hala scale in landscape settings. An open-field potted plant experiment was conducted testing the efficacy of various foliar insecticides on T. pandani infested plants. Our results so far indicate that flupyradifurone and buprofezin reduced the overall infestation levels and improved the visual appearance of the infested plants. This research provides potential control methods against hala scale, and the latest distribution of the pest statewide.

Effects of fungicide on Bombus vosnesenskii microcolony performance and microbiome composition

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Abstract: Introduction and Methods
The bacterial microbiome of bees is responsible for numerous nutritional and immune-related functions, but whether the fungi that inhabit bees and their colonies influence bee health is poorly understood. Among bees, bumble bees exhibit particularly well-characterized associations with fungi. Queens often host fungal propagules during overwintering, and worker attraction to yeast volatiles has been documented in multiple floral systems. To test the hypothesis that fungi in the microbiome are important to worker survival and health, we performed an experiment using a native bumble bee species (Bombus vosnesenskii). Fungicide was used to reduce fungal growth and to determine the importance of fungi to bee health. We exposed microcolonies of worker bumble bees to the fungicide propiconazole in their nectar supply and then gave them the opportunity to regain fungi by allowing them to feed on nectar containing fungi isolated from B. vosnesenskii queens, in a factorial design. We measured bee survival, foraging preference, nectar consumption, and microbiome composition.

Results and Discussion
We found no differences in worker foraging preferences, but bees exposed to fungicide consumed more fungi-rich nectar than bees not previously exposed to fungicide. Bee survival was negatively affected by fungicide exposure, but if bees subsequently fed on fungi-rich nectar, survival did not differ from bees in the control group which was not exposed to fungicide. Amplicon sequencing will examine changes in the fungal and bacterial composition of worker microbiomes. These results suggest that the fungal microbiome of bees influences survival, and that workers may reacquire microbes from the environment under some conditions. More research is required to elucidate the mechanisms, but these results suggest that agricultural application of fungicides may have direct negative consequences on bumble bee health and fitness.

A novel insecticidal molecule extracted from Alpinia galanga to control a pest insect, Spodoptera frugiperda

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Abstract: Spodoptera frugiperda, a highly polyphagous insect pest from America, has recently invaded and widely spread throughout Africa and Asia. Effective and environmentally safe tools are needed for successful pest management of this invasive species. Natural molecules extracted from plants offer this possibility. Our study aimed to determine the insecticidal efficacy of a new molecule extracted from Alpinia galanga rhizome, the 1'S-1'-Acetoxychavicol acetate (ACA). The toxicity of ACA was assessed by topical application on early third-instar larvae of S. frugiperda. Results showed that ACA caused significant larval growth inhibition and larval developmental abnormalities. In order to further explore the effects of this molecule, experiments have been performed at the cellular level using Sf9 model cells. ACA exhibited higher toxicity on Sf9 cells as compared to azadirachtin and was 38-fold less toxic on HepG2 cells. Inhibition of cell proliferation was observed at sublethal concentrations of ACA and was associated with cellular morphological changes and nuclear condensation. In addition, ACA induced caspase-3 activity. RT-qPCR experiments reveal that ACA induces the expression of several caspase genes. This first study on the effects of ACA on S. frugiperda larvae and cells provides evidence that ACA may have potential as a botanical insecticide for the control of S. frugiperda.

The evolution of bite force in insects

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Abstract: In vertebrates, bite force can be correlated to the ecological demands of animals but is often phylogenetically structured as well. In insects, bite force data is extremely scarce and it is unknown if similar patterns of bite force evolution occur in this megadiverse clade. Here, we present an analysis of bite force values and bite curve progression shapes of individual bites of more than 600 insect species across 111 families and 13 orders. We found an allometric relationship between bite force and head volume (both log10-transformed: $R^2 = 0.67$, $p < 0.001$). Blomberg's K indicated no phylogenetic structuring of size-corrected maximum bite force in insects ($p = 0.18$), but Pagel's lambda implied that the evolution of bite force follows phylogeny to some extent ($\lambda = 0.66$, $p < 0.001$). The variation of bite force across insects was also only weakly explained by feeding mode and general head phenotype (both $R^2 < 0.1$), while flight ability had no effect. We also found weak phylogenetic signal in models describing the bite curve shapes ($K = 0.091$, $p = 0.02$; $\lambda = 0.34$, $p < 0.001$), but statistical parametric mapping of the bite curve shapes revealed well-defined differences between hemimetabolous and holometabolous orders.

Silicon integrates into phytohormonal signalling to enable targeted plant defence against insect herbivores

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Abstract: Plants and herbivorous insects are amongst the most abundance multicellular organisms on the planet. Moreover, the two have been locked in an evolutionary arms race for over 300 million years. Plants deploy an array of defences which deter feeding or otherwise cause harm to herbivores and herbivores, in turn, develop counter-adaptations to evade their effects. Many plants, especially the grasses, acquire large amounts of silicon (Si) which can be used for herbivore defence. Silicification of plant tissues makes them physically stronger, more difficult manipulate and reduces the nutritional quality of foliage. It is unclear how Si-based defences relate to other anti-herbivore defences. Most anti-herbivore defences are under the control of the jasmonic acid (JA) pathway which is triggered following herbivore attack. Using the model grass Brachypodium distachyon, we demonstrate that chewing herbivores induce Si uptake. Similar results using methyl jasmonate suggest that induction of the JA pathway drives Si uptake. Chewers were negatively affected when feeding on plants with Si (+Si plants) which also possessed higher densities of leaf macro-hairs. Removal of these macro-hairs restored chewer performance. Crucially, attack by chewing herbivores triggered a much weaker JA response in +Si plants compared to plants without Si. Sap-feeding herbivores, in contrast, did not induce Si uptake or trigger the JA pathway and were unaffected by Si. We hypothesise that certain grasses use Si physical defences constitutively or in response to either chewing herbivory or triggering of the JA pathway, in lieu of other metabolically costly secondary metabolites. Dampened JA responses may be sufficient to stimulate Si uptake and deposition, which is irreversible, without requiring levels of JA activity needed for continued synthesis of secondary metabolites.

New insights into chromosome and genome evolution in mosquitoes revealed by improved genome assembly of the West Nile virus Culex quinquefasciatus

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Abstract: Mosquitoes of two subfamilies Anophelinae and Culicinae have different genome sizes and chromosome arrangements. However, the details of these differences are not completely understood. In this study, chromosome and genome evolution in mosquitoes was investigated using chromosome-scale assemblies for four species from the major branches of the mosquito evolution, including recently reported Cx. quinquefasciatus genome. The quality of this genome was improved using advanced genome technologies. In addition to the previously detected chromosomal rearrangements, a pericentric inversion in sex-determining homomorphic chromosome 1 between the two species was identified. Comparison of the rate of the chromosomal evolution in different species indicated that the sex-determining chromosome 1 has significantly higher rate of evolution in Cx. quinquefasciatus but not in Ae. aegypti. Our study supports the previous observations that genome evolution in Culicinae mosquitoes is associated with significant expansion of transposable elements in their genome. Concentrated only in the pericentromeric and some internal regions in the genomes of Anopheles species, they spread along the arms toward the telomeres in Cx. quinquefasciatus and became evenly distributed in the Ae. aegypti genome. We thank Culex quinquefasciatus genome consortium for providing an improved version of the genome and NIH for funding (R21 AI156280).

Quantifying insect biodiversity using distributed optical sensors

Authors: Rydhmer Klas, Copenhagen University, Sweden

Abstract: We have developed a method to quantify the biodiversity of a optically recorded dataset and correlated it with ground truthing methods. Using newly developed optical sensors, recording the back-scattered signal from any insects that flies trough its measurement volume we have recorded labelled data from ca 100 insect species. Using this dataset, we have developed a biodiversity index, to be used as a proxy for the species richness in conventional monitoring methods. The method is based on applying a clustering algorithm on a low-dimensional representation and counting the number of found clusters. In order to validate our method, we have collected field data from 5 locations from March to November.

Winners and losers of a boreal pollinator community reflect climate and land use changes

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Abstract: Changes in pollinator assemblages have been reported widely, raising the concern of potential reductions of pollination services. Much of the current knowledge is based on well-studied pollinator groups in temperate, agriculture-dominated regions. Thus, we largely lack the understanding of the generalisability of this knowledge to different geographic regions and taxonomic groups. Here, we present how species traits affect the occupancy trends of 28 bumblebees, 108 solitary bees, 145 hoverflies, and 19 longhorn beetles across a 1100-km latitudinal gradient across the boreal zone in Finland. Time series (1980-2019; except for wild bees 1930-2019) analysed with occupancy models consist of museum and distributional records. The occupancy of bumblebees and longhorn beetles changed more often than that of solitary bees and hoverflies. Among bumblebees, the numbers of decreasing species were higher than those of increasing species. In other taxonomic groups, the proportions of decreasing and increasing species varied more between different time periods. Southern distribution was related to increasing occupancy in all pollinator groups, while none of the northern species increased. Other traits associated with occupancy trends varied among taxonomic groups and time periods. The changes of boreal pollinator community reflect the expected outcomes of changes in climate and habitat availability.

Adaptations of olfactory circuits in the honeybee – function and evolution

Authors: Rössler Wolfgang, Department of Behavioural Physiology and Sociobiology (Zoology II), Biozentrum, University of Wuerzburg, Germany

Abstract: Honeybees, like many other social Hymenoptera, heavily rely on olfaction mediated by thousands of olfactory sensory neurons housed in various types of olfactory sensilla on the antenna. How the diverse world of odorants is encoded in the brain to finally result in adaptive behavior is a highly active area of research across many species of insects and vertebrates. I will focus on adaptations at three processing levels of the honeybee olfactory system – from the antennal sensilla to olfactory glomeruli, the odor processing units in the antennal lobe, to memory circuits in high-order integration centers in the mushroom bodies and their output to the protocerebrum. One striking feature of the honeybee olfactory system is a dual (medial and lateral) pathway of projection neurons connecting two distinct layers of antennal-lobe glomeruli with many thousands of large input synapses in the mushroom-body calyx. I will highlight the odorant coding properties and high potential of this dual pathway for processing complex odorant mixtures and discuss the evolution of this highly sophisticated olfactory circuitry within the Hymenoptera.

Developmental and adult neuronal plasticity of olfactory and visual synaptic microcircuits in the mushroom-body calyx of social Hymenoptera

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Abstract: Mushroom bodies (MBs) are prominent neuropils in the insect brain that perform high-level sensory integration and the organization of complex behaviors involving learning, the formation of associative memories, and spatial orientation. In social Hymenoptera, the MBs receive multimodal (olfactory and visual) input from cholinergic projection neurons (PNs) relayed to numerous MB intrinsic neurons (Kenyon cells, KCs) within morphologically elaborate (doubled and cup-shaped) MB calyxes. PNs synapse on KCs forming large identifiable synaptic complexes called microglomeruli (MG). The talk will first highlight a remarkable structural plasticity of MG associated with postembryonic brood care during pupal development in nectar-feeding ants and honeybees. We investigated that thermoregulatory rhythmic nursing behavior mediated by Camponotus mus workers on the developing pupae leads to an increase in MG density and total MG numbers in the olfactory lip region of the young adult MB calyx. Similar results were found in honeybee workers where the synaptic organization in the young adult olfactory lip is affected by slight deviations within and beyond the natural range of a constant pupal rearing temperature experienced in the brood area. The difference across the two species indicates that the favorable temperature range and the optimal temperature regime are species-specific within social Hymenoptera. The brood-temperature mediated differences in initial MG numbers in the MB calyx may have important consequences for behavior at later stages of adulthood. The second part of the talk will highlight aspects of cellular and subcellular processes that shape olfactory and visual MG in the calyx during adult maturation in Camponotus rufipes ants and honeybees. During the natural transition from nursing to foraging an overall reduction of MG is accompanied by a significant increase in postsynaptic contacts of KC dendritic spines. As a result, we infer that dendritic spines are key candidates to the reorganization of MG that occur during the age-related transition between nurse and forager. Our results suggest that the different levels of structural neuronal plasticity in olfactory and visual microcircuits play important roles in the regulation of social organization in Hymenopteran societies.

Distributed plasticity in ant visual pathways following associative and non-associative visual experiences

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Abstract: Camponotus ants possess a highly plastic visual system that comprises both “experience-independent” and “experience-dependent” components (Yilmaz et al., 2016). Our findings on plasticity in retinal opsin gene expression and optic centers suggest two independent processes—an age-related and light-induced neuronal plasticity. We suggest that both sources of plasticity in the visual system represent important components promoting optimal timing of the interior–forager transition and flexibility of age-related division of labor: the peripheral and central neuronal system must cope with new challenges such as visual orientation, long distance navigation, and learning and memory of the visual information to locate rich food sources.

Recently, we showed that C. blandus workers are able to learn the association of color information and a reward, independent of intensity differences, and form complex color memories based upon experience (Yilmaz et al., 2017). This enabled us to link associative color learning performance with structural neuronal plasticity in defined neuropils – the optic lobes (OLs), mushroom body (MB) input (collar) and output (vertical lobe) regions, central complex (CX) and anterior optic tubercle (AOTU) – aiming at identifying whether associative colour experiences are reflected in plasticity of underlying neuronal circuits. The result clearly showed that the OLs, AOTU, and CX respond with plastic changes after colour learning and long-term memory formation, suggesting a complex neuronal network in color processing (Yilmaz et al., 2019). Such a colour-processing network probably represents an efficient design promoting fast and accurate decisions during orientation and navigation.

Insights into genetics of Trissolcus japonicus populations accidentally introduced into North America and Europe

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Abstract: Adventive populations of the Asian egg parasitoid Trissolcus japonicus (Ashmead) (Hymenoptera: Scelionidae), the most promising agent for classical biological control of Halyomorpha halys, were first detected in the northeastern USA in 2014 and in the northwestern USA in 2015, and have since been reported in a total of 12 states. Although the actual pathway of entry for T. japonicus in North America remains unknown, it is presumed to have entered with parasitized host egg masses or as hitchhiking adult wasps. More recently, adventive populations were found in northern Italy and southern Switzerland in 2017 and 2018 and in British Columbia, Canada, in 2018. In northern Italy the spread of H. halys has also provided an invasion opportunity for another egg parasitoid, Trissolcus mitsukurii (Ashmead) (Hymenoptera: Scelionidae). Results from a phylogeographic study based on the mitochondrial barcoding region of the cytochrome oxidase subunit 1 revealed that all adventive populations of T. japonicus found to date belong to the same maternal T. japoncus lineage that is widely distributed in China, Japan and South Korea. The T. mitsukurii specimens recovered in Italy harbored one unique barcode haplotype which does not match any of the haplotypes evidenced so far in Asia. We developed a panel of 24 polymorphic microsatellites based on representative T. japonicus populations throughout the native range, and we used a population genetics approach to study the genetic structure and the differentiation of T. japonicus populations and to understand the origin(s) and dynamics of the spread of the adventive populations. The detection of additional genetic structure within this maternal lineage shows that these microsatellites can detect differentiation at a local scale. Our analyses indicated the existence of three genetically differentiated population clusters in the USA and one in Europe. Preliminary analysis supports the scenario of multiple invasions in USA, most likely from China, but also shows that the rapid population expansion observed in the USA retains genetic diversity within the US populations of T. japonicus, in contrast to the quarantine laboratory colonies of T. japonicus which have been maintained in the U.S. for host range evaluation. Although our comparative analyses are ongoing, the results to date provide the first clues about mechanisms contributing to adaptation and success of these adventive T. japonicus populations.

The use of Long-Lasting Insecticide-treated Nets to control the Japanese beetle Popillia japonica: a laboratory and field evaluation

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Abstract: The Japanese beetle Popillia japonica Newman is a quarantine insect pest that recently invaded northern Italy, between Piedmont and Lombardy regions. This was the first record of this pest in mainland Europe. From its discovery on, the invaded territory is getting wider, reaching in 2019 more than 6,000 square Km in Italy. In the meanwhile, findings of adults of P. japonica occurred also in Switzerland in 2017. Due to its high polyphagy and the ability to rapidly spread into new areas, this insect is considered a serious threat to agriculture. Confirming the foregoing, it is noteworthy that the new EU regulations have inserted the Japanese beetle within the EU list of priority pests. In the last decades, several trials on biological control of the Japanese beetle by entomopathogenic nematodes and fungi have been carried out with variable efficacy. However, the necessity of an integrated pest management approach to improve its control has arisen. Long-lasting insecticide-treated nets (LLINs) are a technology recently evaluated for the control of other agricultural pests with an attract-and-kill strategy. Here, we present results from laboratory evaluation of two different LLINs, Storanet (BASFTM) and ZeroFly (VestergaardTM), against P. japonica adults. Both were effective in killing the beetles; however, some differences emerged if different exposure times were compared: ZeroFly always gave 100% mortality in tests from 5-sec to 30-min exposure; Storanet showed 100% mortality only with 30-min exposure and going down to 99%–89% mortality for 15-min to 5-sec exposure. Furthermore, in order to define the possibility of the field use of such LLINs, we present the result of field experimentation in which attract-and-kill devices made by LLIN with a pheromone were left exposed outside for the entire flight period of P. japonica, which is roughly from June to September. Results showed that the full effectiveness of the LLIN is maintained for first-month exposure. After that time, the effectiveness appears to progressively decline. However, increasing natural mortality of Japanese beetles late in the growing season may compensate for decreased effectiveness of the LLIN in August and September. In conclusion, the utility of LLINs for the control of the Japanese beetle is discussed.

Trissolcus japonicus in Italy: physiological host range and egg morphology analysis provide a predictive approach to risk analysis

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Abstract: Halyomorpha halys is an invasive Asian species, causing severe damage to field crops, vegetables and fruits. This species is currently widespread in Italy and in many other countries worldwide. To date, pest control is realized by chemicals, but for a long-term solution classical biological control will be fundamental in pest managing. Trissolcus japonicus is an Asian egg parasitoid wasp considered to be the most important natural enemy of H. halys. However, its potential introduction to new regions for classical biological programs requires that non-target risk assessment studies be conducted.

The aim of this study was to evaluate the reproductive success (physiological host range) of five day old T. japonicus females in short (2h) and long (24h) exposure time in no-choice tests, using a single hemipteran egg as the test unit (instead an egg mass) of H. halys (the target species) and of other 15 native non-target Hemipterans: Raphigaster nebulosa, Palomena prasina, Acrosternum heegeri, Carpocoris purpureipennis, Carpocoris mediterraneus, Piezodorus lituratus, Dolycoris baccarum, Staria lunata, Eurydema ventralis, Peribalus strictus, Nezara viridula, Sciocoris sideritis, Coreus marginatus, Gonocerus juniperii, Rhynocoris iracundus. Moreover, we also tried to identify the possible association between morphological features of host eggs and parasitization success of T. japonicus to produce a predictive model of attack success. In addition, to verify the effect on female fecundity developed in different host species, the egg load in the ovaries of females emerged from H. halys and D. baccarum were assessed.

Our results showed that H. halys, Ra. nebulosa and Pa. prasina were the species with the highest percentages of parasitization success: 100%, 97% and 96% respectively. Lesser accepted species were Ca. purpuripennis, A. heegeri, Ca. mediterraneus, and D. baccarum (58%, 52% 46%, 11% respectively), while Pi. lituratus and Pe. strictus had low parasitization rates (3%, 5% respectively). The other species tested, i.e. Sc. sidertis, E. ventralis, St. lunata, N. viridula, the two coreids Co. marginatus and G. juniperi and the reduviid Rh. iracundus were never parasitized.

We provided evidence that using single eggs in short time exposure tests is a valid alternative in the first step of a non-target analysis, thus saving considerable time and resources. Moreover, this new approach can be also useful with rare species or those with a low rearing success in the lab. Analysis of egg morphology and parasitization success revealed that the shape and the volume of the pentatomid host eggs are features correlated with the host acceptance rate: Pa. prasina and Ra. nebulosa have eggs similar in shape and size to H. halys and displayed similar parasitization rates. Egg size also influenced the development of T. japonicus, since smaller females obtained from D. baccarum exhibited a lower egg load in the ovaries while the females from H. halys had a higher egg load

Prey DNA digestion data and their implications for carabid trophic networks and biocontrol potential

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Abstract: Molecular analysis has been a major step in lifting the veil on the structure of food webs and in gaining insights on biocontrol potential of predators. However, one substantial flaw of molecular analysis is their qualitative nature. Indeed, differential digestive rates bias both the estimate of the relative frequency of prey in a predator diet, but also the relative contribution of different predators in the consumption of a prey. To correct for this bias, the detection time of the prey DNA in the predator gut must be considered. The purpose of our study was to assess the differential digestive rates for different prey items in the diet of a range of carabid species occurring in agroecosystems. In a previous study, diet of several carabid species was assessed through a multiplex PCR diagnostic. Feeding experiments were carried out on the same carabid species. Detection times for prey DNA were assessed using the same multiplex at several time intervals after feeding. Detection times varied depending on prey group and carabid size. Finally, we applied a detection time-based weighting to the dietary data obtained in the field and observed the resulting changes in the prediction of carabid community diets and their biocontrol potential.

A single principle for male sex determination in major agricultural pests (Tephritidae): Maleness-on-the-Y (MoY), its evolutionary conservation and its usage for future genetic control.

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Abstract: The dipteran Tephritidae family includes dozens of major agricultural pest species, including the mediterranean fruitfly Ceratitis capitata (medfly), in which genetic control of sex determination has been previously studied using Drosophila melanogaster as reference to clone orthologous genes. New generation sequencing technologies and development of novel bioinformatic tools made possible to isolate novel genes of medfly on the basis of their sex-linked location and sex-specific embryonic expression. The identification of the Y-linked male determining gene of medfly, Maleness-on-the-Y (MoY), led to discover that it is widely conserved in many other species of this family, spanning 100 million of years of evolution. This evolutionary stability of a sex determining primary signal is shared for example with Drosophilidae species in which X-signaling system is widely conserved but contrast with the rapid evolvability of other sex primary signals observed even with the same species, such as the case of Musca domestica. Present challenges and on-going work are understanding MoY molecular mechanism of action in repressing the downstream female determining transformer gene and MoY biotech usage to harness innovative genetic control strategies for Tephritidae invasive species, such as the oriental fruitfly pest Bactrocera dorsalis which recently started to be sporadically detected in south Italy and poses new risks for European countries.

Plasticity of olfactory circuits in Drosophila

Authors: Sachse Silke, Dept Evol Neuroethol Max Planck Inst Chem Ecol Jena, Germany

Abstract: Most animals rely on their olfactory system to accomplish behavioral tasks that guarantee their survival and reproduction. Since the odor space consists of an enormous, nearly infinite number of possible stimuli, olfactory systems require special strategies to perceive, identify and evaluate the highly diverse odor information from the environment. The vinegar fly Drosophila melanogaster represents a premier model system for studying olfactory processing mechanisms since it exhibits a stereotyped architecture which is similar to its mammalian counterpart, but is less complex and highly tractable as well as susceptible to genetic manipulations. By exploiting these genetic techniques and linking them to neurophysiological, molecular and behavioral methods, my group is dissecting the neural circuits that are involved in coding, processing and perception of odors.

The structure and function of the olfactory system of Drosophila is well characterized. However, little is known about whether and to which extent individual experience is modulating the olfactory circuitry. We therefore aim at elucidating plastic changes at the morphological, functional and behavioral level. Our previous studies have shown that the first olfactory neuropil, the antennal lobe, reveals a unique connectivity of input and output neurons for each individual glomerulus, which is correlated to behavioral relevance. Using tracing methods, neuronal reconstructions, functional two-photon calcium imaging and behavioral assays to monitor odor-guided behavior, we investigate the influence of experience and learning to specific odors after long-term exposure. The talk will summarize our recent insight into the plastic changes of the olfactory circuitry.

Oranges and apples? Plant responses to insect herbivores of distinct feeding guilds

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Abstract: Plants face a diversity of biotic challenges in the field, including a broad range of arthropod herbivores. To understand plant responses to multiple herbivory challenges, chemical and molecular ecologists generally focus only on their proximate mechanisms, employing arbitrary herbivore loads in factorial presence-absence treatments of two species, or additive density designs. These experiments do not disentangle specific responses of plants to herbivore species from responses to the overall herbivore pressures that they experience.

We suggest a conceptual methodological approach for determining functionally equivalent loads of each herbivore species, exerting on the plant similar herbivore pressures, which can be measured using a common currency (e.g. a proxy for plant fitness or yield). We present an example, calibrating equivalent loads of leaf-chewing caterpillars and phloem-sucking aphids for similar damage to cabbage seedlings, coupled with the quantification of plant hormone and volatile responses.

Seedling vegetative growth decreased linearly with the loads of each herbivore species, producing a one-to-one equivalence mapping between herbivore loads. This mapping covered all of the implemented range of caterpillar loads, and most of the implemented aphid loads. Consequently, across these ranges, differences between plant chemical responses to the herbivores could be attributed to the identities of the herbivore species.

This calibration approach offers to remove the common confound of unstandardized herbivore pressures in multiple herbivory experiments, and can foster a more refined understanding of plant responses to the diversity of herbivores encountered in nature.

Impervious Surface Enhances Winter Survival of Evergreen Bagworm

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Abstract: Extreme cold weather events, not average temperatures limit winter survival of the evergreen bagworm (Thyridopteryx ephemeraeformis Haworth) (Lepidoptera: Psychidae), a generalist defoliator that causes extensive defoliation of urban landscapes. We sought to determine if microclimate warming associated with impervious landscape surfaces could act as a buffer and protect these insects during periods of cold weather. Northern Indiana is near the northern limit of bagworm distribution and routinely experiences temperatures that are cold enough (-18.1 °C for 24 h) to kill bagworms. During the winters of 2018 and 2019 we identified sites in Northern Indiana with latitudes ranging from 39.93 N to 41.47 N whose coldest day in the winter had a maximum temperature that ranged between -22.2 and -17.2 °C. We tested the hypothesis that impervious surface within 20 m of each host plant could keep bagworms warm enough during cold periods to improve bagworm survival. A total of 1303 bagworms were collected from 72 sites whose warmest temperature in on the coldest day in 2018 ranged between -20 and -17.2 °C. Similarly, we collected 952 bagworms from and 47 sites whose warmest temperature on the coldest day of 2019 ranged between – 22.2 and -17.2 °C. The percentage of impervious surface within a 20 m radius of each host tree was estimated by pace to plant technique. During both years, the survival of eggs and larval hatch was positively correlated increased with impervious surface area around the host trees. We conclude that in urban areas impervious surfaces around host trees can create a buffer zone where marginally hardy species like bagworm can easily survive regional temperatures that can kill bagworms. Limits of this effect have yet to be determined.

Biological Control of Weeds in Thailand: 1974 - 2014

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Abstract: A short historical and global overview of biological control of weeds was provided and a review was made to cover the activities and accomplishments on both augmentative and classical biological control of weeds in Thailand from 1974 to 2014 covering a period of approximately 40 years. It covered pertinent and relevant details on eight target weed species on their origin and resident endemic natural enemies employed in augmentative biological control programs, and nine target weed species on their origin and exotic natural enemies introduced from countries of weed original habitats employed in classical biological control programs. The successes were qualitatively evaluated as being partial, substantial and complete. The utilization of some biological control agents from Thailand in the Southeast Asian region and elsewhere was also given.

Chemical interactions between the phytophagous ladybird Chnootriba elaterii (Coleoptera, Coccinellidae) and Cucurbitaceae

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Abstract: Among Coccinellidae, Epilachninae are phytophagous ladybirds feeding on various plants species and representing serious pests for Cucurbitaceae, Fabaceae and Solanaceae crops. Research focusing on chemical ecology in phytophagous ladybird beetles is still scanty, especially regarding the interaction with Cucurbitaceae. The aim of the present work is to describe for the first time the olfactory sensilla on the antennae of the phytophagous ladybird Chnootriba elaterii (Chevrolat) under scanning electron microscopy, and to evaluate the antennal response to volatiles through electroantennographycal investigations using VOCs from Cucurbitaceae crops (Citrullus lanatus, Cucumis melo, Cucumis sativus, Cucurbita pepo, Cucurbita moschata, Lagenaria siceraria, Luffa cylindrical) and wild species (Ecballium elaterium). Moreover, two-choice feeding tests (evaluation of damaged leaf area) were performed to understand the insect preference among the same plant species. The suitability of the plant species to the ladybird was determined evaluating the development time of larvae and pupae and the total damaged leaf area during the development on the different host plants. The present research can be considered a first step in developing sustainable semiochemical-based control strategies for melon ladybirds in crops.

Pollination by sucking insects reproducing on inflorescences in Macaranga spp. (Euphorbiaceae)

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Abstract: Nearly 90 % of flowering plants have been estimated to be pollinated by animals. Since the reproductive success of animal-pollinated plants depends on the number of visitors, plants have evolved various floral traits to attract pollinators. On the other hand, a few plant groups have adopted a strategy to attract small numbers of visitors and breed them on inflorescence to increase pollen dispersal. The most studied example is Ficus spp. (Moraceae), in which daughters of the founder female fig-wasp disperse pollen. It is different from other similar systems such as yucca-yucca moth in that the flower or inflorescence phenology is precisely tuned so that the emergence of offspring matches with the timing of pollen release of the inflorescence.

The dioecious tree genus Macaranga (Euphorbiaceae) is distributed in tropical to subtropical regions. Some Macaranga species are pollinated by sucking insects (thrips or flower bugs) reproducing on the inflorescences. The pollinator insects feed on both nectar and small insects on the host plants.

In this study, we investigate if the reproduction of the pollinators benefits the host plant in Macaranga tanaius on Amami Island, Japan. We found that many larvae of the pollinator Orius atratus (Anthocoridae) on male and female inflorescences before anthesis. Both larvae and adults significantly increased their numbers towards the peak of flowering, especially on male trees. Both dry weights and stable isotope ratio of nitrogen also increased with time.

The results indicate that the reproduction of O. atratus increases the number of pollinators and enhances pollen dispersal. Though many plant groups are known to provide breeding sites to pollinators as a reword, pollinator offspring emerged from flowers or inflorescence well after the anthesis and rarely contribute pollination. M. tanarius, on the other hand, start attracting and breeding pollinators well before anthesis and use offspring to disperse their pollen effectively. On the other hand, it is not clear why pollinator flower bugs have to move between plants though the host plant provides them with food and breeding sites.

A previous study based on a molecular phylogeny indicates that brood-site pollination has evolved more than once in Macaranga. In these plants, bugs (Hemiptera) and thrips (Thysanoptera) have been reported as pollinators. Nectar is packed in the ball- or hair-shaped nectary on the bracteoles, so nectar may be only accessible to piercing-sucking insects. It is an important research topic for future studies what was the key characteristics that have caused the repeated evolution of this unique pollination system.

Trap and release of pollinators in Aristrochia spp. mediated by morphological changes of epidermal cells

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Abstract: Recent studies have highlighted the importance of the traits of the flower epidermal cells in plant-pollinator interactions. However, temporal changes of the cells during flowering and its ecological significance largely remain unexplored. Here, we report morphological change of the epidermal cells in the protogynous trap flower of Aristolochia spp. (Aristolochiaceae). In the plant species, the inner surface of the calyx tube has the papillate microstructure at the initial female phase, while it disappears during the following male phase. To evaluate the correlation between the change and the trap function of the flower, we collected the flowers at different phases and counted the number of trapped pollinators. Furthermore, to examine if the presence or absence of the papillate microstructure affect the behavior of pollinators, a pollinator was introduced into calyx tubes with the nectary part had been cut off, and we checked if the pollinator could escape from the calyx tube. The results suggest that the microstructure controls the trap and release of the pollinators, and the morphological change of the epidermal cells plays a primary role in the trap pollination of the plant species.

Dissecting the molecular mechanism of taste sensation of blood in Aedes aeypgti

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Abstract: Exploring the molecular mechanism of blood sucking behavior of female mosquitoes is one of the critical steps to fight against vector-borne diseases such as dengue and malaria, since pathogens are transmitted when mosquitoes are gorging on blood. Especially, it is important to reveal the molecular mechanism of taste sensation of blood, since female mosquitoes need to discriminate blood from sugar to deliver each to the destination after sucking them by using the identical proboscis. It has been known that adenine nucleotides in blood serve as phagostimulants for blood sucking. Besides, the presence of chemoreceptive cells is suggested in labral apical sensilla and sensilla in cibarium (pre-oral mouth cavity). However, the molecular nature of chemoreceptors and corresponding primary neurons remains to be examined. To identify molecules regulating the taste sensation of blood, we employed two approaches. First, we focused on the gustatory receptor 5 (Gr5) of dengue and zika virus-vector mosquito (Aedes aegypti) that was already reported to be expressed higher in female labella than that of males. We generated Gr5 deficient mosquitoes by using CRISPR/Cas9 system. Deletion of Gr5 did not affect attraction to host, but affected the initiation of blood sucking, suggesting that Gr5 may contribute to the taste sensation of blood. Second, we performed RNAseq analysis and compared the expression pattern of genes in brains between pre- and post-blood/ATP suction. The expression level of innate immunity-related signaling molecules, chaperons, and microRNAs was changed immediately after engorgement. In addition, the expression level of transient receptor potential like (TRPL) whose function in taste sensation was reported in Drosophila was increased after taking either blood or ATP, suggesting that TRPL might be involved in taste sensation of blood. Furthermore, we identified a plant derived molecule that negatively affects blood sucking in Aedes mosquito: mosquitoes quit sucking ATP when this molecule was present, although they were still attracted to the target and performed probing. These results may provide not only new insights into the taste sensation of blood, but also intriguing ways for identifying molecules that control blood sucking behavior of mosquitoes.

Study of The effects of three Botanical Oils on Management of Onion Thrips, Thrips tabaci (Lind) (Thysanoptera: Thripidae) and Some ecological aspects, Gezira state, Sudan

Authors: Salah Faiza, U. of Gezira, Sudan

Abstract: Onion thrips (Thrips tabaci (Lindeman) is the most serious insect pest causing damage to the crop. This study aimed to evaluate the effects of some botanical oils including cotton, castor bean and bitter cucumber oils on thrips infesting onion. Field experiments were conducted at Gezira state during two winter seasons (2015/16-2016/17). Two experiments were conducted in the first season (2015/16) at the experimental farm of the University of Gezira and in the Gezira research Station Farm (GRSF) of the Agricultural Research Corporation (ARC). The third experiment was conducted in the second season (2016/17) for confirmatory studies at the (GRSF) in (ARC) and observation plot of 20 X 40 m2 was used to study the population dynamics of the thrips and natural enemies. The design of the experiments was randomized complete bloc(RCBD) with four replications. Cotton oil, castor bean oil and bitter cucumber oil were applied at a concentration of 2.5% in the first season (2015/16). In the second season 50% upper and lower concentration of castor oil and bitter cucumber oil were applied at the rates of (1.25%, 2.5% and 3.75%). The onion variety used was Saggai. The results indicated that all oil treatments were effective against the onion thrips compared to the untreated control. Significant differences at $P < 0.01$ in the mean number of insects were found. This study show that the bitter cucumber oil was the most effective in reducing the number of thrips compared to the other two oils as well as the control treatment. Large number of natural enemies of thrips were found in the (GRSF) of (ARC), while, Orius bug and jumbing spider were most available and by the end of the season these natural enemies had a role to decrease the number of onion thrips. No significant difference was observed between treatments in yield. This study recommends that, bitter cucumber crude oil at 1.25% concentrations can be used to reduce the number of onion thriups. .

The EU Bee Partnership

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Abstract: The EU Bee Health Partnership, officially established in 2018, is a collaborative stakeholder group dynamized by the European Food Safety Authority (EFSA). It includes representatives from the beekeeping and farming sectors, NGOs, veterinarians, academia and industry. After a continuous collaboration, the partnership has concluded on the need to improve efforts for bee and pollinator data standardization and communication. To achieve data standardization, the EU Bee partnership and the Apimondia BeeXML working group are working to conclude the required standards for bee and pollinator data under the Extensible Markup Language (XML) language. On the other hand, working to further materialize data sharing and integration, BeeLife European Beekeeping Coordination is leading the development of an integrative tool for the analysis, visualization and communication of pollinator-related data, The Bee Hub. In the frame of the fast-track-to-innovation project, the Internet of Bees, a Proof of Concept of the Bee Hub is under initial construction. It aims to achieve a European (and potentially worldwide) open platform that includes any relevant data linked to pollinators, especially bees (but not necessarily restricted to bees). The objective is to build a communicative tool on the status of pollinators and pollination, both essential for food security and biodiversity. Throughout the collaborations established in the EU Bee Partnership, efforts to develop data standardization, integration and communication continue to advance. The final objective is to transform data into accessible and relevant information for stakeholders and authorities.

Did the climate changes and/or the mountains impacted the diversification process of an Andean Genus of Ladybird beetles (Coleoptera: Coccinellidae)?

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Abstract: The development of mountain belts favored a rise in biodiversity, as a result of high speciation and low extinction rates, and can be considered as species pumps that feed the rest of the continent. In South America, the Andes are a good example of interactions between mountain building and diversification processes that decisively affected present biodiversity patterns. Pleistocene glaciations are recognized as important promoters of population divergence and ultimately speciation. However, the role of these recent glaciations in speciation has also been largely debated and various studies demonstrated that several lineages diversified earlier during the Mio-Pliocene intense uplift period. The aim of the study is to test the respective contributions of Mio-Pliocene intense uplift period and Pleistocene glacial cycles on the diversification of the South American ladybird beetles Eriopis Mulsant. Mitogenomes were obtained by genome skimming approach from 35 dry specimens deposited in natural history collections and with collection data 1882-2005. These taxa were chosen to cover the whole geographical distribution of the genus. The 13 protein-coding genes and two ribosomal RNA genes were used to infer the phylogenetic tree using a Bayesian method. We established a dated phylogeny of the group using Relaxed-Clock Method.

How to find a missing gene: the case of IMD in Rhodnius prolixus

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Abstract: The immune deficiency pathway (IMD) is a major component of the innate immune system in arthropods. This pathway mediates the recognition, elimination, and tolerance of pathogens and symbionts. In the kissing bug Rhodnius prolixus, which transmit the human parasite Trypanosoma cruzi, many of the genes of the IMD pathway were not found in its genome; this pathway was therefore described as absent and nonfunctional. Subsequent characterization, however, revealed it was indeed functional towards pathogen infections. Most of the missing elements of the pathway were also described except for the IMD and Kenny genes. We present the methods and parameters we apply to find candidate orthologs and present a new candidate for the IMD gene. We used a combination of reciprocal BLAST searches, HMM protein profile searches, domains architecture, phylogenetic trees, and RNA-seq-driven gene annotation. The ultimate proof to validate candidate genes is their functional characterization. Our results highlight the use of multiple approaches to discover genes in non-model organism using information from taxonomically distant species.

Endogenous viral elements and their role in mosquito antiviral immunity

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Abstract: Endogenous viral elements (EVEs) are full or partial viral sequences integrated in host genomes. A large number of EVEs was bioinformatically identified in Aedes mosquito genomes, supporting the hypothesis that mosquito EVEs contribute to control exogenous infections by closely related viruses in nature. To experimentally test this hypothesis, we investigated the role of an EVE naturally found in Aedes aegypti populations and related to the widespread insect-specific virus cell-fusing agent virus (CFAV). Deep sequencing revealed that CFAV-EVE produced primary piRNAs in antisense orientation and targeted CFAV RNA in the naturally infected mosquitoes. Using CRISPR/Cas9 genome editing, we created an Ae. aegypti line lacking the CFAV-EVE. The absence of EVE resulted in increased CFAV replication in ovaries, possibly modulating vertical transmission of the virus. Viral replication was controlled by the interplay between viral and EVE RNAs via the piRNA pathway. Our results provide evidence that antiviral piRNAs are produced in the presence of a naturally occurring EVE and its cognate virus, demonstrating a functional link between EVEs and antiviral immunity in a natural insect-virus interaction.

Minimal fermentative metabolism fuels extracellular symbiont in leaf beetles

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Abstract: While genome erosion is extensively studied in intracellular symbionts, the metabolic implications of reductive evolution in microbes subsisting extracellularly remain poorly understood. Stammera capleta—an extracellular symbiont in leaf beetles—possesses an extremely reduced genome (0.27 Mb), enabling the study of drastic reductive evolution in the absence of intracellularity. Here, we outline the genomic and transcriptomic profiles of Stammera and its host to elucidate host-symbiont metabolic interactions. Given the symbiont's substantial demands for nutrients and membrane components, the host's symbiotic organ shows repurposing of internal resources by upregulating nutrient transporters and cuticle-processing genes targeting epithelial chitin. The turn-over of foregut- lining chitin is a common process in insects and releases several nutrients such as N-acetylglucosamines that serve as precursors for microbial membrane biosynthesis, which is eroded in Stammera. Facilitated by this supplementation and its localization, Stammera exhibits a highly streamlined gene expression profile and a fermentation pathway for energy conversion, sharply contrasting the respiratory metabolism retained by most intracellular symbionts. Lactate fermentation has been discussed in the context of parasitic eukaryotes, but is unknown in insect symbionts with reduced genomes, likely because lactate accumulation would result in toxicity within host cells. In the case of Stammera, however, the extracellular localization supports the erosion to a sole fermentative metabolism by minimizing acid stress. Our results provide insights into a tightly regulated and metabolically integrated extracellular symbiosis, expanding our understanding of the minimal metabolism required to sustain life outside of a host cell.

Predation capacity and some biological features of Simosyrphus aegyptius (Wiedemann), 1830 (Diptera: Syrphidae) on Mealy plum aphid [Hyalopterus pruni (Geoffroy) (Hemiptera: Aphididae)

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Abstract: Syrphids flies, also known as hover flies or flower flies, have two important ecological roles. When adults feed on nectar or pollen, many larvae are the most important predators of aphids and other pest species. Simosyrphus aegyptius (Wiedemann), 1830 (Diptera: Syrphidae), commonly found in aphid colonies, is common in subtropical and tropical regions of the world. In this study, predation capacity and life table of S. aegyptius on Mealy plum aphid [Hyalopterus pruni (Geoffroy) (Hemiptera: Aphididae)] were investgated. The study was carried out in 2017 in a climate room with 25 °C temperature, 60 ± 10 % relative humidity and 16: 8 hours of light: dark conditions. The raw data were analyzed based on the age-stage, two-sex life table. The preadult period of S. aegyptius was found 23.13 days and life table parameters were as follows: The intrinsic rate of increase (r), the finite rate of increase (?), the net reproduction rate (R0), and the mean generation time (T) of S. aegyptius were 0.103 day-1, 1.108 day-1, 15.00 eggs/generation and 26.37 days, respectively. Pre-adult predation rate was found as 820.21 preys/predator. The highest predation rate was observed in the 3rd larval stage as 545.64 preys/predator. This predation capacity is very high than many other aphid predators.

The eradication of the tsetse fly Glossina palpalis gambiensis from the Niayes of Senegal using an area-wide integrated pest management approach that includes the release of sterile males

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Abstract: The “Projet de lutte contre la mouche tsé-tsé et la trypanosomose dans les Niayes” targets a total area of 7,350 km2, of which 1,375 km2 were infested with Glossina palpalis gambiensis (Diptera: Glossinidae) which were solely responsible for the cyclical transmission of trypanosomes, the causative agents of African animal trypanosomosis (AAT). The tsetse population in the Niayes was completely isolated from the main tsetse belt in the south eastern part of the country, which prompted the Government of Senegal to select an eradication strategy of the vector and the disease, as the risk of re-invasion would be minimal or non-existing. The project was implemented in different phases, i.e. following a phased conditional approach, which consisted of (1) training and commitment of all stakeholders, (2) baseline data collection (BLDC) and feasibility studies, (3) pre-operational activities, and (4) operational activities. During the BLDC, entomological, parasitological, environmental and socio economic data were collected to assess tsetse distribution, population dynamics, trypanosomosis prevalence and distribution, potential environmental impact, and anticipated benefit-cost ratios. Activities during the pre-operational phase included the establishment of a colony of tsetse originating from the target area in Senegal, competiveness studies between the sterile flies and those from the target area, development of transport methods for long distance shipments of sterile male pupae, competitiveness of the sterile male flies after release in the target area, development of aerial release methods, including a new chilled adult release system, and development of a Maxent-based distribution model to guide the suppression, sterile male releases and the monitoring of the campaign. During the operational phase, the fly populations were suppressed using insecticide-impregnated traps (~3000), insecticide-treated cattle (~10,000 heads) and insecticide-impregnated fences around pig pens (~300 m). During the eradication phase, more than 5,000,000 sterile male tsetse flies have so far been released from the ground or by air. An extensive entomological monitoring system implemented in the 3 operational blocks indicated the following: no wild fly catches since August 2012 in block 1, while in block 2 et 3 the densities of the wild tsetse populations have been reduced by > 99% at the time of writing. SIT is still on going in those 2 blocks up to end of 2020 in order to ensure the eradication of tsetse in the area. Monitoring data of sentinel herds located inside and outside the tsetse-infested area indicated already a significant reduction of the AAT prevalence. The environmental monitoring demonstrated a very low impact of the project on non-target species, and the socio-economic study showed a high cost-effectiveness of the project.

The implementation approach of this project could serve as a model for future potential tsetse eradication campaigns in sub-Saharan Africa

Identification and Functional Characterization of Toxoneuron nigriceps Ovarian Proteins Involved in the Early Suppression of Host Immune Response

Authors: Salvia Rosanna[1], Scieuzo Carmen and Falabella Patrizia, [1]University of Basilicata, Italy

Abstract: Toxoneuron nigriceps (Viereck) (Hymenoptera, Braconidae) is an endophagous parasitoid of the larval stages of Heliothis virescens (Fabricius) (Lepidoptera, Noctuidae). During oviposition, T. nigriceps injects into the host body the egg, the venom, the calyx fluid, which contains a Polydnavirus (T. nigriceps BracoVirus: TnBV), and the Ovarian Proteins (OPs). OPs, originating from the ovarian calyx cells, are involved in the induction of precocious symptoms in the host immune system alteration. To functionally characterize the OPs, we carried out two approaches. Firstly, incubating hemocytes with OPs in toto, detecting several alterations on host cells: the OP injection induced an extensive oxidative stress and a disorganization of actin cytoskeleton. These alterations can explain the loss of haemocyte functionality (the reduction in encapsulation ability by the host) and the high-level of haemocyte mortality. Then, we evaluated the effect of HPLC fractions deriving from in toto OPs. Among the 28 analyzed fractions, two fractions caused a reduction in hemocyte viability and were tested to detect changes in hemocyte morphology and functionality. In accordance with previous results, obtained with in toto OPs, the two fractions caused severe oxidative stress, actin cytoskeleton disruption, loss of hemocyte encapsulation ability and high mortality rate. Moreover, a transcriptome and proteomic approach was applied to identify the proteins of the two fractions: eight proteins that might be involved in the observed host hemocyte changes were detected. Our findings will contribute to a better understanding of the ovarian components and their role in parasitic wasp strategy to escape the host immune responses.

Insects an innovative source of chitosan: possible applications

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Abstract: The polysaccharide chitin is one of the most abundant natural polymers and it is the major structural component of the arthropod exoskeleton and the cell wall of fungi and yeasts. Due to their properties, like biodegradability, bio-compatibility, non-toxicity, adsorption and antimicrobial activity, chitin and its main deacetylated derivative, chitosan, have a great economic value and they are molecules of great interest as new functional biomaterials, finding many applications in the industrial and biomedical field. The main commercial source of chitin and chitosan is crustaceans' exoskeleton. The extraction of chitin from insects, a promising alternative source, has received relatively little attention. Among insects, Hermetia illucens is a promising source of chitin. This insect is the subject of increasing research in the scientific world thanks to its ability to convert organic waste into larval biomass rich in proteins and lipids of high biological value.

Currently, the chitin contained in the exoskeleton of last instar larvae, pupae and adult flies constitutes a by-product of the bioconversion process aimed at the production of animal feed. All the available protocols for chitin and chitosan extraction from insects involve the use of chemicals, mainly acids for minerals removal, bases for both proteins hydrolyzation and chitin deacetylation, and various reagents for depigmentation. The present study focuses on chitin extraction, and its deacetylation into chitosan, from the exoskeleton of H. illucens at different developmental stages, in order to make the most of a resource not yet fully exploited. The obtained product will be investigated for different possible applications.

New insights into the main components of the venom of Torymus sinensis by a transcriptomic and proteomic approach

Authors: Salvia Rosanna[3], Falabella Patrizia[3], Scieuzo Carmen[3], Cozzolino Flora[2], Maria Monti[2], Heiko Vogel[1], Chiara Ferracini[4] and Alberto Alma[4], [1]Max Planck Institute for Chemical Ecology, [2]University Federico II of Napoli, [3]University of Basilicata, [4]University of Torino

Abstract: Venomics, the study of the entire pool of peptides and proteins of one specific venom, has acquired increasing importance as source of new bioactive molecules relevant in several fields, including agriculture, since they could constitute a weapon in the biological fight against parasitic crop species. In nature these harmful insects are kept under control by parasitoids. Torymus sinensis, the parasitoid of the chestnut gallogenic Cinipid Dryocosmus kuriphilus is the only effective means of Cinipid biological control. The knowledge of venom protein composition is extremely useful to identify new molecules that can be used as bioinsecticides in integrated pest management. We identified T. sinensis main venom components through a transcriptomic and proteomic approach. Transcriptomic data (high-throughput nucleic acid sequencing) provided an overall picture of the putative proteins in the venom gland and information on molecular functions, biological processes and putative cellular compartments. The proteomic analysis was carried out on venom components fractionated by SDS-PAGE and analyzed by mass spectrometry. Combination of proteomic and transcriptomic data allowed us to identify 185 putative proteins of T. sinensis venom. The characterization of these molecules will be essential to understand the role of venom in induction and regulation of the pathological syndrome in parasitized hosts.

Study of Chemoreception in Capnodis tenebrionis L. (Coleoptera, Buprestidae) as an innovative tool in biological control

Authors: Salvia Rosanna[1], Falabella Patrizia[1], Franco Antonio[1] and Scieuzo Carmen[1], [1]University of Basilicata

Abstract: Insects use chemoreception to interact with the environment through the perception of volatile organic compounds (VOCs) that is essential for their survival. Capnodis tenebrionis (Coleoptera, Buprestidae), a pest of Rosaceae family, is attracted by chemical signals emitted by plants. The control of this pest lacks monitoring strategies such as information on insect chemical ecology. The composition of perceived VOCs play an important role in determining the signal specificity for C. tenebrionis repulsion or attraction. To improve the understanding of how VOCs are perceived, putative soluble olfactory proteins involved in chemoreception have been identified from de novo transcriptomes of antennae and whole bodies of C. tenebrionis adult males and females. Transcriptome analysis led to the identification of a putative odorant binding protein (OBP) named CtenOBP7, similar in terms of amino acid sequence to Agrillus mali (Coleoptera: Buprestidae) OBP3, already functionally characterized. CtenOBP7 was cloned, expressed and purified. Interaction of recombinant CtenOBP7 with different plant VOCs was measured by fluorescence spectroscopy. This approach offers guidelines to understand the mechanisms involved in the interaction between plants and insects, in order to define new strategies to control the proliferation of this pest, starting from the study of insect olfactory perception at the molecular level.

Latitudinal pattern in predation, herbivore performance and herbivory in hostile and enemy free space

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Abstract: It is well recognized that predators can enhance plant growth by reducing herbivore abundance. Yet the strength of such trophic cascades has been found to be quite variable both within and between communities. Moreover, effects of various taxa were usually summed within the effect of “predators” thus it remains unclear which predators and where might control trophic cascades. We hypothesise that birds, bats and ants are important predators of arthropods, which further affect plant growth. However, their relative importance may differ along large (latitudinal) gradients due to changes in their richness and abundance and productivity of the environment. For similar reasons, we also expect that the importance of predators differs in forest canopies and understories, as productivity and trophic levels are predicted to be higher in the canopies. To find out where top-down forces control food webs, we conducted predator exclosure experiments along latitudinal and vertical gradient(s). We excluded ants, birds, and/or bats separately and in combinations from saplings and from branches in forest canopies. We protect saplings by nets (against birds and/or bats) and by tangle foot (against ants). We manipulate the cages daily to separate the effect of birds and bats. We survey the effect of such treatment on insect communities and herbivorous damage every four months. We further analyse various plant defences, which are inevitably shaping the interactions via bottom up control. Finally, we run a global search for similar studies during which predators were excluded. We conducted a meta-analysis on them and compared the results with our field-based data. At several of our study sites, bats and ants do not seem to affect arthropod communities significantly. Birds seem to be the most important predators at many of our study sites. Their exclusion led to more than eight times higher herbivory. The results of meta-analysis provide somewhat different results, with ants being very important predators. We discuss potential problems with meta-analysis vs. our data and we argue that the strength of the top down control can’t be considered without the bottom up control. We conclude that stable arthropod populations are maintained by natural enemies of various importance along gradients. In some study systems, mesopredators (spiders) were released, lowering the effect of exclusion of the focal predator. Disruption of communities of natural enemies result into significantly increased abundances of insect, increased herbivorous damage and into changes in leaf traits.

Effect of landscape structure on the abundance and diversity of pollinators in pear crops

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Abstract: Pollinators have suffered from the intensification of agricultural, especially because of the destruction of habitat. The structure of the environment, at both the landscape and plot scale, may influence the abundance and diversity of pollinating insects. The main objective of this work was to determine if wild vegetation and landscape fragmentation affected the biodiversity of pollinators in pear orchards. For this, 27 pear orchards surrounded by land with different levels of landscape fragmentation and surface of wild vegetation were selected. The structure of the landscape surrounding each orchard was characterized by quantifying the surface of semi-natural habitats (hedges, forests, thickets, etc.) within a diameter of 1,000 meters using geographic information systems. Moreover, a fragmentation index was calculated, considering: the number of fragments of natural vegetation, within the 1,000-meter buffer, and their surface area. For the sampling of pollinators, two 15-minute transects were carried in two consecutive weeks in each plantation during the flowering period of the crop in 2019. A total of 2,191 pollinating insects were observed visiting the pear flowers, of which 54% were bees (Apis mellifera and wild bees), 20% dipterans (Syrphidae and other Diptera), and 9% Coleoptera. No significant influence of the landscape fragmentation on the abundances of the different groups of pollinators was registered. However, there was a significant influence of the surface of wild vegetation on the abundances of the Syrphidae, Diptera and Coleoptera; all were more abundant with the highest vegetation densities. In contrast, although bees were more abundant in the plantations with the highest surface of surrounding wild vegetation, the effect of vegetation was found to be non-significant.

How cover crops influence the biodiversity of ground arthropods in pear orchards

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Abstract: The intensification of agriculture has led to the reduction of the diversity of arthropods in agroecosystems. This is also the case for soil arthropods due the intensive ploughing, the use of insecticides and the elimination of ground vegetation, among other factors. The aim of this work was to evaluate the effect of restoring cover crops in comparison with the conventional management. The work was carried out in a 6 ha pear orchard that was divided in three blocks where two plots of 1,600 m2 (5 rows of 100 trees) each were established at random; two treatments were assayed (i.e., restored cover and conventional management) in each block. A mix of seeds of 10 plant species was sown in the restored cover plots. Soil arthropods were sampled using pitfall traps (500 ml plastic containers, 8 cm in diameter) filled with water and propylene glycol during five different weeks in 2019. The percentage of cover was estimated for each sampling date. Cover crops had a great impact on the abundance and diversity of arthropods. Several families of spiders (Linyphiidae, Lycosidae), beetles (Carabidae, Scarabaeidae, Staphylinidae) and hymenopterans (Scelionidae) were significantly more abundant in the plots with the restored cover than in the conventional plots. In contrast, ants (Formicidae) and collembola had a significantly higher abundance in the conventional plots. Other families of spiders (Gnaphosidae, Zoradiidae), beetles (Tenebrionidae) true bugs (Lygaeidae) were not found to be significantly affected by the ground cover.

The risks and advantages of using predators that also feed on plants as biological pest control agents

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Abstract: IOmnivorous mirids (Hemiptera: Miridae) is one of the most controversial generalist predators because they feed both on prey and plants. They are particular as biological pest control agents and a thorough knowledge of their feeding behaviour and the development of management strategies are needed to minimise the negative aspects of their phytophagous character while exploiting their predatory side. In this presentation we review the worldwide importance, risks, and management strategies of omnivorous mirids. The modelling of the zoophytophagous behaviour and population dynamics are some of the tools discussed to enhance biological pest control and to reduce environmental risks. Additionally, the phytophagous character of these insects offers an interesting opportunity to enhance pest control by managing plant diversity in agroecosystems. Nonetheless, the worldwide commercialization of mirids as biological pest control agents, especially when the species is exotic to the area, entrails environmental risks that have to be taken into account. Mirids released in crops may colonize natural habitats and produce a double negative environmental impact. By one hand, exotic mirids may get established and damage wild plants; by the other, they may interfere with the communities of native arthropods.

Deep into the south, the evolutionary history of a widely distributed leaf-cutting ant

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Abstract: The southern cone of South America has gone through a great number of complex geoclimatic events that triggered diverse evolutionary process. Leaf-cutting ants, belonging to the genera Acromyrmex, Amoimyrmex and Atta, characterize by using freshly cut fragments of leaves and flowers as substrate for the growing of fungus of which they feed. The southern black ant, Acromyrmex lobicornis, an economically important leaf-cutting ant species pest in vineyards and forest plantations, is widely distributed in this region. Distribution analyses reveal that this species has two main occurrence areas: one goes through the Arid diagonal of the Monte desert ecoregion in Argentina until Bolivia, and the other goes from central Uruguay up to Rio Grande do Sul state, in Brazil. Both areas are connected by isolated populations distributed along central section of the Espinal ecoregion in Argentina. In this study we analyze the evolutionary history of this ant in a phylogeographic context, using mitochondrial and nuclear markers, in order to determine its historical demographic and dispersion processes. In contrast to previous hypotheses, this study suggests that A. lobicornis would have been originated in the northernmost section of Monte desert in La Rioja province (putative origin center harboring the highest genetic diversity) in Argentina, then spread into south and north along the Arid diagonal, and into the east through the Espinal until savannas in central Uruguay and southern Brazil. Interestingly, the nesting behavior changes in the more arid regions from nest with big domes to nest without it. The Espinal would have played an important role as bridge that maintains genetic flow between eastern and western populations of this ant. Understanding the evolutionary history of the southern black ant will provide insights into the evolutionary history of leaf-cutting ants in southern South America and the role of historical geoclimatic processes in their diversification.

Exploring the Role of Relish on Antimicrobial Peptide Expressions (AMPs) Upon Nematode-Bacteria Complex Challenge in the Nipa Palm Hispid Beetle, Octodonta nipae Maulik (Coleoptera: Chrysomelidae

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Abstract: The humoral immune responses of the nipa palm hispid beetle Octodonta nipae involves the inducible expression of the genes coding for antimicrobial peptides (AMPs) which are mediated by immune deficiency signaling pathways. In insects, the nuclear factor-kB (NF-kB) transcription factor, Relish, has been shown to regulate AMP gene expressions upon microbial infections. Here, we dissect the expression patterns of some AMPs in O. nipae during infections by entomopathogenic nematodes (EPNs) and their symbionts, before and after Relish knock down. Our results indicate that, prior to gene silencing, the AMPs attacin C1, attacin C2, and defensin 2B were especially expressed to great extents in the insects challenged with the nematodes Steinernema carpocapsae and Heterorhabditis bacteriophora as well as with their respective symbionts Xenorhabdus nematophila and Photorhabdus luminescens. The study also established the partial sequence of OnRelish/NF-kB p110 subunit in O. nipae, with an open reading frame coding for a protein with 102 amino acid residues. A typical Death domain-containing protein was detected (as seen in Drosophila) at the C-terminus of the protein. Phylogenetic analysis revealed that in O. nipae, Relish is clustered with registered Relish/NF-kB p110 proteins from other species of insect especially Leptinotarsa decemlineata from the same order Coleoptera. Injection of OnRelish dsRNA remarkably brought down the expression of OnRelish and also reduced the magnitude of transcription of attacin C1 and defensin 2B upon S. carpocapsae and H. bacteriophora and their symbionts infections. Altogether, our data unveil the expression pattern of OnRelish as well as that of some AMP genes it influences during immune responses of O. nipae against EPNs and their symbionts.

#SciComm in the classroom: practicum of public engagement with science

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Abstract: Quality entomological outreach requires both knowledge of the topic and engagement of the public. We partnered these two goals through a collegiate level experiential course to lead entomology students to find effective communication strategies for a range of audiences. Through our outreach and science communication course, we provided entomology students opportunities to (1) devise lessons plans for outreach events, (2) give and receive peer feedback about their materials and methods, (3) present outreach to different audiences, and (4) reflect on what worked and could be improved. The design and implementation of the course 'Public Engagement of Science' provided lessons for both instructors and student leaders.

Complementary interactions of native and introduced natural enemies of codling moth in New Zealand

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Abstract: Codling moth (Cydia pomonella) (CM) is a key pest of pipfruit in New Zealand. Cooler areas of New Zealand, have one generation of CM each year, while they go through two generations in warmer areas. Only two native predators are recorded and no native parasitoids of CM are found in New Zealand. Five parasitoid species introduced during the last ten decades have established in some regions, contributing to reducing CM populations. The establishment of CM parasitoid species was monitored in four main apple growing regions in New Zealand (Hawke's Bay, Nelson, Central Otago and Waikato) using corrugated cardboard bands (10-cm wide empty bands to trap wild CM larvae and 2-cm wide bands with sentinel CM larvae). Liotryphon caudatus (Hymenoptera: Ichneumonidae, released in 1906) was found in Hawke's Bay and Waikato, not in the South Island regions. Ascogaster quadridentata (Hymenoptera: Braconidae, released in the 1930s), Glabridorsum stokesii (Hymenoptera: Ichneumonidae, released in 1967), Dibrachys microgastri (Hymenoptera: Chalcidoidea: Pteromalidae, an accidental arrival) and Mastrus ridens (Hymenoptera: Ichneumonidae, released in 2012–2016) were found in both the North and South islands. The relative proportions of parasitoid species caught in different regions indicate the success of their establishment and interactions between the natural enemies of CM.

Hyperparasitoids drive host-parasitoid dynamics and structure

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Abstract: Hyperparasitoids are often seen covering a single fourth trophic level in plant-aphid -parasitoid-hyperparasitoid networks and have been predicted to either reduce the efficiency of primary parasitoids controlling aphid population or stabilise host-parasitoids dynamics and increase long term aphid top-down control. Here we show that hyperparasitoids span at least two trophic levels and that some species are extremely efficient in using their resource allowing for cryptic higher trophic levels. We further demonstrate that hyperparasitism rate increases over the season for a group of very generalist hyperparasitoid species while a more specialised group peaks earlier because they are attacked by the generalists. Experimental and long-term food web data show that hyperparasitoids reduce the control of aphid populations through primary parasitoids and can lead to the functional extinction of primary parasitoids. This places hyperparasitoids in a key position driving the structure and dynamics of host- parasitoids networks.

Spatio-temporal dynamics of Drosophila suzukii populations: A landscape perspective

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Abstract: Landscape processes play a fundamental role in pest population dynamics. In particular, natural and semi-natural habitats, despite delivering important ecosystem services, can also support insect pest populations by providing refuge during pesticide applications, suitable overwintering sites and availability of alternative host plants. This work aimed at investigating the relationship between the distribution and damage of Drosophila suzukii, an invasive polyphagous pest, and landscape processes at multiple spatial scales. D. suzukii recently invaded Europe causing considerable economic damage on several thin-skinned fruits. The management of this pest is particularly complex due to its high dispersal potential, mobility and polyphagy. First, we studied the influence of landscape complexity on D. suzukii distribution and crop damage. During the growing season, semi-natural habitats enhanced population density and damage in cherry orchards. In particular, orchards within forested-dominated landscape appeared to be more susceptible to D. suzukii attacks. Second, we examined at large geographical scale the temporal dynamics and synchronization of D. suzukii activity along steep elevational gradients in Alpine environments. Due to the high dispersal potential and mobility, the insect revealed an extremely high synchronization of population fluctuations across different locations and elevations. Considering the emerging problems linked to the invasion of D. suzukii across several temperate countries, our work emphasized the need to incorporate landscape processes to understand the spatio-temporal dynamics of pest populations across complex landscapes

Phylogenomics and diversification of Ichneumonidae

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Abstract: Ichneumonid parasitic wasps comprise one of the largest insect lineages, but the lack of a comprehensive phylogeny currently hinders our understanding of their diversification process. In a collaborative, multi-institutional effort, we generated UCE data for 800+ species from all ichneumonid subfamilies. This enabled us to obtain a powerful phylogenetic framework for the family as a whole, as well as to pursue fine-scale investigations within specific ichneumonid taxa. In spite of this massive dataset, uncertainties remain and the placement of some groups is contingent on specific dataset formatting. Even with this limitation, our phylogeny allowed for the reconstruction of biological traits and unprecedented insight on the diversification process of this hyperdiverse wasp family.

Whole genome sequencing and the phylogenetic distribution of viral domestication events in ichneumonid parasitic wasps

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Abstract: One of the most staggering adaptations associated with parasitism is the use of endogenous viruses by parasitoid wasps. Until recently, our poor understanding of ichneumonid genomes prevented the investigation of the mechanistic and evolutionary aspects of this wasp-virus interaction. In this talk, we will discuss how recent advances in whole genome sequencing are allowing the mapping of endogenous viral elements found in wasps of the family Ichneumonidae, both in terms of the genomic architecture of this integration and the phylogenetic distribution of viral domestication events across various lineages. These advances have been accomplished both through complete assemblies with long scaffold sizes and by low coverage genome sequencing. We will present the results of a broad-scale screening of the family Ichneumonidae for endogenous viral elements and what these results reveal about the evolutionary pathways that led to viral domestication in ichneumonid wasps.

Broad-complex expression in the post-embryonic development of Apis mellifera

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Abstract: Insects development is regulated by conserved pathways that were rewired in the course of evolution. Juvenile hormone (JH) and ecdysteroids (20E) are the main hormonal players in the morphogenetic events that direct the correct development. Although these pathways have been extensively studied, some of its molecular mechanisms are still unknown. Broad-complex (Br-C) is a transcriptional factor co-regulated by both JH and 20E. It is mainly related with pupal morphogenesis in holometabolous insects and with wing pad growth and development in hemimetabolous. Here I investigated the expression of Br-C during the post-embryonic development of the honey bee, Apis mellifera, and its possible role in the caste determination. The levels of Br-C varied during the development, with transcripts being detected in the fat body, head and imaginal discs of the fourth and early fifth instar larvae. The identified isoforms of Br-C presented differential expression among the tissues and ages analyzed. Considering the variation of JH hormones titers during caste development, and the well-known interaction of its direct response gene, Kr-h1, with Br-C in other insects, the relationship between these two transcription factors will be also be explored. Some remarks will be presented about a possible broader function of Br-C in development.

Financial Support: Department of General Biology, Federal University of Viçosa.

Detection of DNA modifications in eusocial bees

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Abstract: Different castes of a eusocial bee species share identical genomes. Yet castes display marked differences in morphology, behaviour, longevity, and reproductive phenotypes.

These differences are generally driven by environmental signals and thought to be mediated by epigenetic mechanisms, including DNA methylation.

While nutrition, particularly during development, is a key signal that can shift developmental trajectories, other environmental exposures, including pesticides may also influence the epigenetic landscape and caste phenotypes. Recent evidence suggests that DNA methylation is not as responsible for the link between environment and gene expression as previously thought. That is, gene body methylation patterns are colony-specific and not driven by social or environmental factors but rather inherited.

Nevertheless, DNA methylation appears to be a vital process for development and caste determination. We aim to further elucidate the distribution of DNA methylation patterns within different caste genomes in eusocial bees using a variety of different approaches, including Oxford Nanopore sequencing. Here we report on procedures and preliminary results of our effort to map and catalogue different types of DNA modifications in brain and flight muscle of honeybees and bumblebees. Ultimately, this work will allow us to elucidate how environmental and anthropogenic stressors may impact epigenetic programming of these bees.

The transmission of Candidatus Liberibacter solanacearum by the carrot psyllid is mediated by cellular actin filaments

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Abstract: Candidatus Liberibacter solanacearum (CLso) is associated with carrot yellowing disease in Israel and is transmitted by the carrot psyllid, Bactericera trigonica. Understanding the molecular interactions between CLso and its psyllid vector is imperative for disrupting CLso transmission. Intracellular pathogens often exploit the host cellular mechanisms to facilitate their entry, replication, survival, and transmission. The host cell cytoskeleton, in particular, is a well-known target exploited by vector-borne pathogenic bacteria and viruses, for inter and intracellular trafficking within the insect. Furthermore, many insect pathogens use actin-based assembly and polymerization to promote their invasion, enabling cellular infection, colonization, and translocation from the gut lumen to the hemolymph. However, hijacking the actin cytoskeleton requires the pathogens to deploy proteins that interact with actin or mimic proteins that regulate or mediate its polymerization. In this study, we analyzed the Arp2/3 complex in the carrot psyllid, which mediates actin polymerization and elucidated its role in liberibacter propagation and transmission. A recent transcriptomic study on the carrot psyllid upon CLso infection showed upregulation of ArpC2 and ArpC5 (components of the Arp2/3 complex) along with RhoGAP21 and Cdc42, all of which are involved in cell invasion and vesicular trafficking. FISH and co-immunolocalization experiments revealed the co-localization of CLso with the ArpC2 protein along the actin filaments throughout the psyllid midgut. Silencing ArpC2, by feeding psyllids with dsRNA delivered through plants, drastically reduced the F-actin formation, disrupted the usual localization pattern of CLso and increased its accumulation in the midgut. Transmission tests conducted with psyllids after ArpC2 silencing resulted in a 78% decrease in the disease transmission as compared to the control. The silencing of additional proteins involved in the regulation of F-actin formation such as Arp5, RhoGAP21, and Cdc42 resulted in similar results after ArpC2 silencing, suggesting that Liberibacter pathogenesis and transmission is Arp2/3 complex-dependent. These results further suggest that silencing those actin-related proteins significantly reduce CLso translocation from the midgut to the hemolymph and subsequently reduce pathogen transmission to plants.

Diet and dietary experience alters biocontrol potential of native transverse ladybird beetle for tomato potato psyllid in Australia

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Abstract: Tomato potato psyllid (TPP) is a major threat to Solanaceae crops worldwide. Impact is due to feeding activity and the transmission of the bacterium that causes the zebra chip disease in potato. TPP was first found in Australia in 2017. In identify suitable candidate organisms for biocontrol of TPP, we evaluated the effects of diet and dietary experience on Coccinella transversalis (transverse ladybird beetle). To evaluate the effect of diet, an age-stage, two-sex life table was used to calculate the ladybird's development and reproduction on invasive TPP. The impact of previous experience with the prey species on the ladybird's predation on TPP was assessed. Results showed that C. transversalis could successfully develop and reproduce when feeding on TPP. Early life experience of C. transversalis with TPP as a prey species improved preference and switching activity toward TPP. This was presumably due to altered prey recognition when offered combinations of prey. This may lead to more immediate control of the target pest in the field. This study provides the basis for developing an augmentative release strategy of C. transversalis for management of invasive TPP in Australia.

Mid-Summer Peach and Apple Fruits are the Better Food Sources for the Development and Fecundity of Grapholita molesta (Lepidoptera: Tortricidae)

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Abstract: Host plants are an important factor that determines the population dynamics of herbivorous insects. The phenology of host plants may affect the performance of Grapholita molesta (Busck) in the development and the fecundity that have rarely been examined. Previously, we evaluated diet suitability of immature peach, plum, and apple fruits collected in early-summer (2.3, 2.7, and 3.4 cm in diameter, respectively) and found that immature plum and apple fruits are better food source for G. molesta. In this study, we evaluated immature fruits of peach, plum, and apple fruits collected in mid-summer (3.1, 4.1, and 3.9 cm in diameter, respectively). Higher choice rate of first instar larva was found in peach (66.7%) compare to plum (16.7%) or apple (16.7%). However, pupal weight was less in peach (12.4 mg) and plum (10.8) than in apple (14.7 mg) although fecundity was higher in peach (202.0) than plum (144.0). Peach fruit had highest sugar content and was 1.64 and 1.53 times harder than plum and apple, respectively. The intrinsic rate of increase was 1.3 times higher on peach and apple than plum. Therefore, peach and apple fruit would be better food source for G. molesta than plum during mid-summer.

Rearing Method of Tyrophagus putrescentiae (Sarcoptiformes: Acaridae)

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Abstract: Tyrophagus putrescentiae (Schrank) is a pest of stored products, but a good prey source for various predaceous mites. The purpose of this study was to develop easy and economical mass rearing method of T. putrescentiae for being used as prey source to rear predaceous mites. We designed plastic jar (800 ml) of which opening is covered with filter paper filled with rice bran as an inexpensive food source and rice husk for aeration. First, proportion of rice bran and rice husk was determined. The maximum yield was obtained in the mixture of 400 ml rice bran mixed with 600 ml rice husk in plastic jar showing 83-fold increase in number after 56 days. In addition, the highest production was obtained when 76.9% RH was used by showing 60-fold increase in number after 35 days and when 25.0 ºC temperature was used by showing25-fold increase in number after 35 days. In conclusion T. putrescentiae can be mass reared in the mixture of 400 ml rice bran mixed with 600 ml rice husk in plastic jar at 25.0 ºC and 76.9% RH environment conditions.

Population genetic structure of the common bed bug in Europe and the USA

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Abstract: Bed bugs are obligate hematophagous ectoparasites, infesting shelters mainly of bats and birds. Two species are major human parasites: the common bed bug (Cimex lectularius L.) and the tropical bedbug (C. hemipterus F.). After being nearly eradicated after World War II, both are showing a comeback in the last few decades. The resurgence is attributed to various mechanisms of insecticide resistance and changes in human behavior such as an increase in international travel. Using ddRAD sequencing, we studied the population structure of C. lectularius across Europe and the USA. Our research disentangles the history and causes of the population expansion, assessing the relative importance of different dispersal routes, local demography, and rise and fixation of resistance-associated mutations. The population dynamics is also studied on a temporal scale, using extensive sampling started in 2009 and continuing to the present time. The preliminary results suggest a strikingly homogenous population across Europe, with a small proportion of outliers showing weak geographic patterns. The population also appears to be very stable on the scale of 10 years. In addition to that, our sampling effort revealed a presumably established population of C. hemipterus in central Europe, quite distant from its original range in tropical regions.

Pulsed stress hypothesis revisited – A case study of Metopolophium dirhodum and spring wheat

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Abstract: The pulsed stress hypothesis predicts that fluid-feeding insects benefit from feeding on plants that are intermittently stressed by drought due to the increased nutrient availability and restored cell turgor, but support for this hypothesis is ambiguous. We test this hypothesis by using a system consisting of young spring wheat (Triticum aestivum L.) and the rose-grain aphid Metopolophium dirhodum (Walker) by following the age-stage, two-sex life table theory. We applied periods of drought stress (soil water capacity, SWC = 40) on four occasions relative to the population development of the aphid and compared those treatments with well-watered (SWC = 70) and continuous stress conditions (SWC = 40). The timing of the stresses appeared to be important in determining its effect on aphid performance. Even though we found some improvement in fecundity when the stress occurred before the aphids were placed on the plants, the overall effect of the early-timed pulsed stress treatments on the rate of increase was negative compared to the well-watered control, which was mainly due to prolonged nymph development. The drought pulse that was timed late, during the second week of aphid reproduction, did not show any effect relative to the well-watered control. This study, therefore, provides no clear support for the validity of the pulsed stress hypothesis. We further illustrate the risk of drawing false conclusions based on incomplete data or single parameters, such as fecundity or population size, after a limited period of time.

Reconstructing Evolutionary Dynamics of Phenomes: Integrating Phylogenetic Models and Ontologies

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Abstract: Inferring historical patterns and processes driving phenotypic trait changes across the Tree of life have been major goals of evolutionary biologists. In this regard, ancestral character state reconstruction is one of the most extensively used tools for gaining insights into the evolution of individual traits. However, organismal anatomy (=phenome) is not a random assembly of individual parts. It is a structured system of anatomical entities resulting from ontogeny and phylogeny, thus producing dependencies among traits. One approach to represent knowledge about trait dependencies is by using ontologies—structured controlled vocabularies formalizing relationships and concepts. Recent advances on phylogenetic methods allowed integrating knowledge from ontologies to perform ancestral state reconstructions for entire phenomes or particular body regions: Phylogenetic Ancestral Reconstruction of Anatomy by Mapping Ontologies (PARAMO). Here we describe three developments of PARAMO: new models for reconstructing evolutionary rate shifts of entire phenomes across lineages and time; tools for assessing evolutionary rates at different levels of the anatomical hierarchy; and reconstructing the dynamics of morphospace through time. We evaluated our new methods with a large dataset for the Hymenoptera. Our results support a complex evolutionary dynamic, with particularly high evolutionary rates inferred for traits along the branches leading to the Apocrita.

Amblydromalus limonicus (Acari: Phytoseiidae) for biological of Bemia tabaci (Hemiptera: Aleyrodidae) in gerbera field

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Abstract: The whitefly, Bemisia tabaci (Genn.) (Hemiptera: Aleyrodidae) is a cosmopolitan pest that attacks several crops, causing direct damage during feeding and indirect damage due to the transmission of viruses. The two-spotted spider mite, Tetranychus urticae Koch (Acari: Tetranychidae), is a key pest for gerbera and several other ornamental plants. Amblydromalus limonicus (Garman & McGregor) (Acari: Phytoseiidae) is an omnivorous predatory mite that feeds on several types of prey, including thrips, whiteflies, psyllids, and tetranychid mites. The purpose of this study was to evaluate the performance of A. limonicus for the control of B. tabaci in commercial gerbera fields, under greenhouse conditions. The effect of the release of A. limonicus in field was also evaluated for spider mite infestation. The experiment was carried out in Holambra County, State of São Paulo, Brazil. The experiment consisted of two treatments: 1) gerbera beds with release of A. limonicus; 2) gerbera beds without the release of predators (farmer standard). Each plot (gerbera bed) was of 4.4 m^2 (4m x 1.1m). Between the beds with release of A. limonicus and the beds without release of the predatory mite, there was a bed (without release of predators) separating the different treatments. The releases of A. limonicus were performed at a rate of 34 predatory mites per m^2. Releases were performed every two weeks. The experimental design was completely randomized with two treatments and six repetitions. Samples of 10 gerbera leaves were collected from each plot, every two weeks, during five months. To evaluate the population densities of the whitefly and spider mite, an area of 16 cm^2 was removed from the central region of each leaf and observed under stereomicroscope, under laboratory conditions. There was a downward trend in whitefly and spider mite population densities, with a significant reduction in the number of eggs of both species since the first evaluation after the start of A. limonicus releases. The maximum population reductions for B. tabaci and T. urticae were above 95%. The release of the predatory mite contributed for the reduction in the damages caused by B. tabaci and T. urticae to gerbera plants.

Prey-tracking behaviour and prey preferences in a tree-climbing firefly

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Abstract: Certain specialist predators utilise prey-tracking strategies to trace olfactory or visual signals left behind by their prey. For example, snail-eating predators search for prey using mucus trails of land snails and olfactory cues. Prey-tracking behaviour has been well studied in invertebrates and vertebrates, but less is known about predator preferences for specific prey traces. Here, we focused on the tree-climbing behaviour of Pyrocoelia atripennis, a snail-eating firefly endemic on the Yaeyama Islands in Japan, and hypothesised that tree-climbing behaviour is a predation strategy adapted to preferred prey preferences. Choice experiments showed that P. atripennis larvae prefer mucus trails of land snails over distilled water trails or no-trail, indicating that P. atripennis larvae have the mucus-tracking strategy. Prey preference tests showed that larvae preferred arboreal and semi-arboreal land snails over terrestrial snails. This preference is likely to relate to different defense traits among land snail species. For example, ground-dwelling species have a closed shell aperture and protective lid, which make them difficult prey items for firefly larvae. However, semi-arboreal and arboreal snails without shell lids are relatively easy prey items for firefly larvae. Thus, the tree-climbing behaviour of the firefly larvae is likely to be linked to a prey-foraging strategy. The mucus trails left by semi-arboreal land snails on plant stems may help larvae track their preferred prey on plants.

Okaramine B, a natural product lead for insect pest and vector control: studies using target-based and phenotypic screening

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Abstract: Indole alkaloid okaramines are isolated from the fermentation products of Penicillium simplicissimum (strain AK40) grown on okara, an insoluble component of soybean that remains after pureed soybeans are filtered during the production of soy milk and tofu. Hayashi and colleagues showed that okaramines A and B were insecticidal, when assayed on larvae of a lepidopteran insect, the silkworm, Bombyx mori. Only much later was evidence obtained on okaramine mode of action. Okaramine actions on larvae were rapid and since many fast-acting insecticides target ion channels, studies were pursued on ion channels of silkworm larval neurons using patch-clamp electrophysiology. Okaramine B, the most active compound of the series, induced inward currents which reversed close to the chloride equilibrium potential and were blocked by fipronil. Thus it was tested on a silkworm RDL (resistant-to-dieldrin) ?-aminobutyric-acid-gated chloride channel (GABACl) and a silkworm L-glutamate-gated chloride channel (GluCl) expressed in Xenopus laevis oocytes. Okaramine B activated GluCl, but not RDL. GluCl activation by several closely related okaramines correlated with their insecticidal activity, suggesting that their actions on GluCls accounts for their insecticidal actions. A novel L-glutamate-gated anion channel (IscaGluCl1) has been cloned from the black-legged tick, Ixodes scapularis, which transmits multiple pathogens including the agents of Lyme disease and human granulocytic anaplasmosis. Functional expression in IscaGluCl1 in Xenopus laevis oocytes was demonstrated and okaramine B activated this tick GluCl. Using a high-throughput invertebrate automated phenotyping platform (INVAPP) and the algorithm Vectorgon, we have shown that larvae of the mosquito Aedes aegypti, an important vector of tropical diseases including yellow fever, dengue and zika, are immobilised by okaramine B. Unlike ivermectin, okaramine B was inactive at 10 µM on human a1ß2?2 GABACl and a1ß glycine-gated chloride channels and may provide a new lead compound for the development of novel, insect control chemicals.

Reducing pesticides and increasing crop diversification conserve natural enemies and offer economic benefits for farmers – A case study in Cambodian rice fields

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Abstract: With the intensification of rice production, landscape heterogeneity decreased due to land transformation, leading to high external inputs of synthetic pesticides to reduce potential yield loss by insect pests. Although, it is well understood that outbreaks of insect pests can be induced by pesticides, farmers still use them abundantly. Ecological engineering is a landscape-based approach with the aim to reduce pesticide applications and to promote insect natural enemies with food resources. However, its ecological and socioeconomic benefits are still poorly understood.

Here, we implement ecological engineering in rice agroecosystems in Cambodia. We introduce bund plants, after surveying which plants are preferred given economic and nutritional benefits for farmers; and test whether ecological engineering promotes biological control by enhancing the abundance of beneficial arthropods. Over dry and wet rice cropping seasons, we identified and compared arthropod communities among ecologically engineered rice fields, fields farmed with conventional methods and control fields that had no bund plants present and were not treated with pesticides. We then compared the costs and benefits of each treatment for the farmers.

We found significantly higher numbers of beneficial arthropods in ecological engineered and control rice fields than in conventional ones, despite no differences in rice yield among fields. We found no significant differences in natural enemy abundance among ecologically engineered and control fields. Our results highlight that pesticide applications are the main drivers causing depauperated arthropod communities of natural enemies.

Bund plants surrounding the rice fields have manifold benefits including higher landscape heterogeneity and additional yields for farmers. Furthermore, our results revealed that withholding pesticides (implementing ecological engineering) did not negatively affect rice yield but led to lower overall costs for farmers.

Synthesis and applications. Our results highlight the negative impact of pesticides on arthropod communities in rice fields and points at the manifold possibilities provided by ecological engineering. The choice of bund plants should integrate information about farmers' choice to increase potential adoption by farmers. Proper implementation of ecological engineering in combination with farmers' choice of crops is a promising solution towards sustainable rice production.

Updates to EPA Registration and Efficacy Testing of Vector Control Products Under PRIA 4

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Abstract: EPA-registered pesticide products are an important part of pest management programs to accomplish control of invertebrate pests. The Agency registers a wide range of vector control products, including wide-area mosquito adulticides and larvicides, skin-applied repellents, pesticide-impregnated clothing and nets, and modified mosquitoes. Product efficacy data for public health pests are required to be submitted to support a pesticide registration. The Agency has a number of guidelines intended to assist in the development of appropriate protocols to test product efficacy in support of pesticide registration. The Pesticide Registration Improvement Act (PRIA 4) mandated that EPA revise and implement four of its current efficacy guidelines by 2021, including EPA Product Performance Test Guideline 810.3500 Premises Treatments, originally published in March 1998. To increase clarity and consistency in efficacy testing and to include current scientific standards, in 2019 the Agency published a revised version of the guideline which now contains recommended test methodologies for a wide range of products intended to kill, control, flush, and/or knock down invertebrate premises pests, such as cockroaches, ticks, mosquitoes, flies, and wasps. The guideline also includes field testing methods for outdoor misting systems, flying-stinging Hymenoptera nest treatments, and outdoor residual foggers.

Strip cropping and natural enemies, a case study in cabbage – faba bean system

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Abstract: Strip cropping is an agricultural practice aiming at regulating agroecosystem functions such as nutrient and water dynamics, while reducing pest damage and guaranteeing high yield. However, its influence on beneficial arthropods is mostly unknown. Over two years, we experimented on an organic cabbage (Brassica oleracea) – faba bean (Vicia faba) strip cropping system with three treatments: faba bean and cabbage monocrops, and alternating strips of the two. Three groups of generalist predators were sampled, namely carabid beetles (Coleoptera: Carabidae), staphylinids (Coleoptera: Staphylinidae), and spiders (Areneae) with pitfall traps for three one-week collection periods per year. Further, naturally occurring parasitoids targeting the diamond back moth were monitored by parasitism exposure experiment. We investigated strip cropping effect on the natural enemy abundances and the carabid beetle diversity. Our results showed that strip-cropping effect varies with year, sampling time and natural enemy group. Indeed, intercropping enhanced carabid activity-density and diversity and to some extent spider abundance, but reduced staphylinids abundance and parasitism rate of diamondback moth larva. Our results highlight that crop diversification through strip-cropping does not enhance abundance of all beneficial fauna in a homogenous manner and is not stable through time. Further studies are required to unravel the mechanisms at play.

Ozonolysis of Drosophila Cuticular Hydrocarbons

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Abstract: Our research sought to characterize any sub-lethal effects that ozone might have on insects. We have currently found that D. suzukii exposure to high concentrations of ozone will result in ozonolysis of its cuticular hydrocarbons. The process of ozonolysis cleaves unsaturated alkenes, which are known to regulate mating behaviors in many drosophilan species. Data supports that mating behavior is significantly reduced after D. suzukii has undergone controlled ozone exposure. Current research seeks to understand these interactions further and develop methodology for determining drosophila speciation in terms of cuticular hydrocarbon chemical constituents.

Diet, life history traits and stress: Does the effect of dietary restriction on life history trade-offs depend on injury and infection?

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Abstract: Dietary restriction (DR), limiting certain nutrients or the overall calorie content of food, extends lifespan in diverse taxa. This is thought to result from diet mediated changes in the resolution of the trade-off between lifespan and reproduction. Although the response to DR is considered to be evolutionarily conserved, some studies have suggested genetic and environmental variation in the response. In fact, a recent evolutionary theory suggests DR will not extend lifespan under more stressful conditions. By adding stressors, such as injury and infection, to the usual benign laboratory environments we test this prediction.

To test whether the DR response remains with injury and infection stress, we reared an outbred population of adult Drosophila melanogaster on 10 diets varying in protein content. We infected a subset of flies with a low dose of bacterial pathogen (Pseudomonas entomophila), injured a subset with a sterile pin prick and had a control subset. We monitored the flies for the key life history traits of lifespan and fecundity.

Next, to test how the host and pathogen responses varied on different diets, we repeated the injury and infection treatments on a low and intermediate protein diet and measured both bacterial growth and the relative expression of antimicrobial peptides (AMPs) genes at three time points post infection in the flies.

DR extended lifespan and reduced reproduction even when flies were challenged with injury and infection. However, when infected, flies on lower protein diets had particularly poor survival compared to the control or injury treatments. Across diets, bacterial growth did not differ in the flies, however some AMP gene expression levels differed at 24 hours post infection.

These results provide novel information on how infection stress together with dietary restriction affects variation in life history traits and the resolution of their trade-offs.

Halyomorpha halys egg parasitoids and early detection of Trissolcus mitsukurii in northern Italy

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Abstract: Brown marmorated stink bug, Halyomorpha halys (Stål) (Hemiptera: Pentatomidae) is an invasive pest species native to eastern Asia that is causing dramatic outbreaks in Veneto region (northern Italy). In a 3-year survey (2016 – 2018) carried out across different sites in this region, egg parasitoids of H. halys were studied by collecting naturally laid egg masses in orchards and vineyards. Emerged insects were identified morphologically, and barcoding with mitochondrial cytochrome c oxidase I (COI) was used to assess genetic relationships with other parasitoids populations. We recorded parasitoids/hyperparasitoids from three Hymenoptera families, i.e. Scelionidae (Trissolcus basalis (Wollaston), Trissolcus kozlovi Rjachovskij, and Trissolcus mitsukurii (Ashmead)), Eupelmidae (Anastatus bifasciatus (Geoffroy)), and Pteromalidae (the hyperparasitoid Acroclisoides sinicus (Huang & Liao)). Parasitoid presence varied between species, and the most common egg parasitoid was T. mitsukurii, which emerged from H. halys egg masses collected in all three years of the survey. The 'parasitoid impact' (i.e. number of parasitized eggs over the total number of field-collected eggs) was the highest for T. mitsukurii, followed by A. bifasciatus. Here we report the earliest known occurrence of T. mitsukurii in Europe, which emerged from H. halys egg masses two years earlier than previously published records. The phylogenetic tree for T. mitsukurii inferred from COI distinguished two clades, one covering samples from Italy, Japan and China, while the other from South Korea.

Seasonal population dynamics and damage potential of Halyomorpha halys on grapevine in Italy

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Abstract: The brown marmorated stink bug, Halyomorpha halys (Stål) (Hemiptera: Pentatomidae) is an invasive polyphagous pest native of Asia that is frequently observed in vineyards in Italy, and the impact of this pest on grapevine production is not fully understood. Field observations were performed to assess seasonal dynamics in population abundance in vineyards. In a cage experiment, we evaluated the damage on grape clusters induced by different infestation densities and considered different infestation period on different grapevine cultivars. In a field experiment, we studied the association between H. halys infestation and the occurrence of grey mold and sour rot by applying a factorial experiment with treatments defined by the combination of insecticide and fungicide applications. Field observation showed cultivar effect in seasonal dynamics of this pest. Halyomorpha halys infestations caused damage on berries, showing a higher susceptibility in red varieties, in particular, Cabernet Franc, and following 50% of grape cluster veraison. In the cage experiment, the infestation by Halyomorpha halys induced an increase in Botrytis cinerea incidence. In the field experiment, the proportion of cluster damaged by grey mould and sour rot were observed on treatments with higher Halyomorpha halys infestations density. The association between H. halys infestation and the incidence of grey mould and sour rot represent the main issue related to H. halys infestation in vineyards in Italy and this aspect should be carefully considered in the definition of IPM programs on grapevine.

Assessing the regulation of nitrogen homeostasis in Aedes aegypti females

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Abstract: Female mosquitoes cause almost five hundred thousand deaths worldwide each year because of their ability to transmit pathogens through blood-feeding. Ammonia, one of the metabolic by-products of blood meal digestion, cannot be stored inside cells, and therefore nitrogen balance must be regulated to prevent ammonia toxicity. Unlike mammals that can detoxify ammonia using the urea cycle, mosquitoes lack a urea cycle. They must either directly excrete ammonia or metabolize it efficiently through specific pathways that were not thought to be present in mosquitoes. To better understand how blood-fed Aedes aegypti females regulate nitrogen metabolism, we have analyzed the impact of silencing ornithine decarboxylase (ODC) by reverse genetics on sugar- and blood-fed Ae. aegypti females. Our data indicate that RNAi-mediated knockdown of ODC significantly decreases survival, delays serine protease expression, disrupts midgut proteolysis, alters uric acid and heme excretion, and impairs reproduction in females. Moreover, in tissues of sugar- and blood-fed dsRNA-injected Ae. females, we found that ODC deficiency induces a differential transcription of genes encoding proteins involved in multiple pathways, including arigininolysis, glucose and ammonia metabolism, ammonia transporters and oxidative stress response. Our findings provide evidence that ODC is essential to maintain nitrogen homeostasis in Ae. aegypti female mosquitoes.

Nutritional mutualism of Wolbachia with the common bed bug, Cimex lectularius

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Abstract: The common bed bug, Cimex lectularius, harbors the endosymbiotic microorganism, Wolbachia, in a gonad-associated bacteriome. Wolbachia is an obligate nutritional mutualist. In exchange for protection, nutrients and vertical transmission, Wolbachia provides the bed bugs B-vitamins that are usually deficient in vertebrate blood. The obligatory nature of this association would suggest that all individuals in C. lectularius populations should be infected with Wolbachia. Yet, studies have reported variation in both infection frequency and relative abundance of Wolbachia in field-collected bed bugs. Quantification of Wolbachia over the life cycle of C. lectularius revealed highly dynamic changes in Wolbachia abundance during bed bug development, changing relative to life stage, intermolt stage, and blood-fed status. Findings suggest that disparities in Wolbachia infections may be due to low abundance during certain developmental stages of the bed bug.

Using a Wolbachia-free bed bug model, we address two questions in the Wolbachia-bed bug mutualism:

(1) Bed bugs, unlike other hemotaphagous arthropods, have not been linked to any human pathogen or disease. We investigated the effect of Wolbachia on virus replication of a model pathogen, feline calicivirus, in C. lectularius. There was no difference in virus titer between the Wolbachia-positive and Wolbachia-free groups, suggesting that Wolbachia is not involved in virus suppression within bed bugs.

(2) We investigated the contribution of Wolbachia to bed bug fitness by supplementing host blood with various vitamin mixes. Specific vitamins influenced bed bug development and fecundity.

The link between habitat preference and performance in pit-building predators

Authors: Scharf Inon, Tel Aviv University, Israel

Abstract: Pit-building insects are sit-and-wait predators that construct pit-traps in loose soil. Wormlion larvae are such predators, common in Mediterranean cities under man-made shelters. Together with pit-building antlions, they present a fine example of convergent evolution. The goal was to examine which habitats wormlions prefer and whether they perform better in their preferred habitats. I first demonstrated that wormlions prefer dry over wet sand, deep over shallow sand and fine over coarse sand. I then detected a match between habitat preference and performance: wormlions construct larger pits and hunt more successfully in the preferred habitats. My second goal was to examine what makes wormlions so successful in urban habitats and whether those from urban and more natural habitats differ in their behavior. Wormlions are probably so abundant in the city due to a more favorable arthropod composition in the city that provides plenty of suitable prey, compared to a less favorable arthropod composition in the countryside. Furthermore, urban wormlions construct larger pits, respond faster to prey and are choosier regarding their preferred microhabitat, suggesting that the city provides better opportunities for wormlions. Finally, I will discuss how disturbance affects pit relocation in wormlions and compare my findings to other trap-building predators (spiders and antlions).

Investigating a novel surface insecticide treatments for control of dermestids

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Abstract: Recently there has been and increasing interest and concern in the stored product industry regarding dermestid species in processed grain products, warehouses, and processing facilities. Trogoderma inclusum LeConte, larger cabinet beetle, and T. variabile Ballion, warehouse beetle, are two highly destructive dermestids that infest a variety of food products and are often captured in insect traps. T. variabile is capable of moving across multiple floors of a facility. Recent advances on surface treatment applications have been reported for other species of stored product insects, but there is no data regarding efficacy against Trogoderma spp. Therefore, we investigated efficacy of two formulations of insecticide (methoprene + deltamethrin and methoprene + deltamethrin + piperonyl butoxide synergist, PBO), applied to concrete or metal surfaces, on adult and larvae of T. variabile and T. inclusum. Results for both species, regardless of life stage, show minimal positive effect of the PBO when added to the standard methoprene + deltamethrin formulation. The application of both insecticides was more effective on the metal surface compared to the concrete surface. Though adult mortality was <100% on both treated surfaces, the methoprene portion of the insecticide was highly effective and prevented exposed larvae from developing to the adult stage. These insecticides can be highly effective on population control of Trogoderma spp. in warehouses, storage facilities, or grain bins which all have different substrates. By controlling populations of stored product insects, it will in turn provide extended production of stored grain products.

Halloween genes spook, shadow and shade determine oocyte length in the desert locust, Schistocerca gregaria

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Abstract: Ecdysteroids are widely investigated for their role during the molting cascade in insects. However, they are also involved in the development of the female reproductive system. Ecdysteroids are synthesized from cholesterol, which is further converted into the main molting hormone, 20-hydoxyecdysone. This biosynthetic conversion process heavily relies on the activity of cytochrome P450 hydroxylases, which are encoded by the Halloween genes. Five Halloween genes, spook (spo), phantom (phm), disembodied (dib), shadow (sad) and shade (shd) were identified and their spatiotemporal expression profiles were characterized in the desert locust, Schistocerca gregaria. Here, we investigated the possible role(s) of these genes during oocyte maturation using RNA-interference mediated knockdown experiments. Our results showed that depleting the expression of SchgrSpo, SchgrSad and SchgrShd had a significant impact on oocyte development, oviposition and hatching of the eggs. Moreover, the shape of the growing oocytes, as well as the deposited eggs, was very drastically altered by the experimental treatments. Consequently, it can be proposed that these three enzymes play an important role during oocyte maturation.

We are very grateful to the Special Research Fund of KU Leuven, the European Union's Horizon 2020 Research and Innovation program, and the Research Foundation of Flanders for their financial support.

Engineering the white pupae phenotype for sustainable pest control

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Abstract: Mass releases of sterilized male insects, in the frame of sterile insect technique (SIT) programs, have helped suppress insect pest populations since the 1950s in a sustainable and species-specific way, which additionally is immune to resistance development. In several major horticultural pests a key phenotype, white pupae (wp), has been used for decades to selectively remove females before sterile male releases, yet the gene responsible remained unknown. We used classical and modern genetic approaches to identify and functionally characterize causal wp– mutations in these fruit fly species. We found that the wp phenotype is produced by parallel mutations in a single, conserved gene. CRISPR/Cas9-mediated knockout of the wp gene leads to the rapid generation of white pupae strains in C. capitata and B. tryoni. The conserved phenotype and independent nature of wp– mutations suggest this technique can provide a generic approach to produce sexing strains in other major medical and agricultural insect pests, allowing the application of the environmentally friendly SIT method to novel pest species.

Global data access, data visbility, and data citation in entomology

Authors: Schigel Dmitry, Global Biodiversity Information Facility (GBIF), Secretariat, Denmark

Abstract: GBIF—the Global Biodiversity Information Facility—is an international network and research infrastructure funded by the governments and providing anyone, anywhere, free and open access to data about all types of life on Earth, including data on insects. Coordinated through its Secretariat in Copenhagen, the GBIF network of countries and organizations, working through participant nodes, provides organizations around the world with data standards and tools to enable sharing primary data on the species occurrences in space and time. The GBIF network links together data from diverse sources such as museum collections, field surveys and citizen scientists' observations—more than 2.1 billion species occurrence records in total in April 2022. More than 1,800 institutions around the worldwide publish datasets under the machine-readable Creative Commons licenses. Data openness, together with DOI-based credit and provenance mechanisms, support the use and applications by researchers, scientists and others users in peer-reviewed publications as well as assessment and policy papers. These studies only take place at such scale and taxonomic coverage because of the integrated, freely and quickly accessible integrated biodiversity data.

GBIF.org is a central access and discovery point for biodiversity data worldwide, and is the largest collection of spatiotemporal biodiversity evidence in the world. Heterogeneity, complexity and diversity of the data publishers and data sources leads to the biases in taxonomic, spatial and temporal coverage. Open biodiversity data require educated data use and management, dealing with the outliers and uncertainties, and taking other steps to optimize data fitness for use in research and practice. Adequate data use is, of course, only possible if data content is centrally and digitally available and data indexing enables filtering and search. Commonly, users access data by searching by taxon name, locality, date and a few others parameters. Data from resources shared through GBIF.org can be downloaded or accessed through GBIF API, and every data download is issued with a unique DOI that provides a registry of the data sources that contributed to the download, as well as a mechanism that enables both machine- and human-readable data citations.

By April 2022, insect data in GBIF are represented by 154.5 million occurrence records and over 1.1 million names (Fig.1), dominated by human observations and preserved specimens. The number of records by higher taxa is largely controlled by the observation and sampling effort, and the popularity of the taxa among non-professional, but not the species numbers, functional importance or other biodiversity drivers. The presentation will cover the status and future plans of this work and highlight individual, organisational and national benefits of integrated data approach in entomology. Fig. 1. Taxonomic distribution of insect occurrences in GBIF https://www.gbif.org/species/216 by 19 April 2022.

A regulatory mechanism for thermotolerance in kissing bugs, and its consequences for geographical distribution

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Abstract: Temperature affects practically all the physiological processes of organisms, and is the most important abiotic factor in the geographic distribution of insects. The thermal tolerance range is given by the minimum critical temperature (CTmin) and the maximum critical temperature (CTmax). I will present results showing how the geographical distribution of seven species of triatomines, vectors of Chagas disease, can be explained, in part, by their thermo-tolerance range. Briefly, we analyzed the relationship between the ecological niche and the limits of the physiological thermal niche in seven species of triatomines. For this, we combined two methodological approaches: species distribution models, and physiological tolerances. In triatomines, thermo-tolerance range increases with increasing latitude mainly due to better cold tolerances, and we also found positive effects of acclimation on thermotolerance, especially on the CTmin. For one of the seven species studied, i.e., Rhodnius prolixus, a model organism in insect physiology, and an important vector of Chagas disease, we demonstrated, by thermolimit respirometry and video thermo-imaging, a significant decrease of body-temperature and extension of its upper limits of temperature tolerance (CTmax) by evaporative cooling. Studying the relationship between the physiological mechanisms that allow modulating the effects of high temperatures and geographical distribution is of great importance especially when analyzing invasive insects, pests or vectors of diseases such as triatomines.

Modulation of thermal tolerance by heat or cold hardening in the hematophagous insect Rhodnius prolixus: the role of heat shock proteins

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Abstract: Temperature is an important abiotic factor affecting many physiological processes in ectotherms, including insects. The thermal stress produced by extreme temperatures can have deleterious effects on insects. So, there are many mechanisms to withstand it including the production of heat shock proteins (HSPs). We investigated the effect of a moderate heat or cold shock on thermotolerance of the hematophagous insect Rhodnius prolixus, as well as the role of HSPs. For that, groups of insects were exposed 1 h to two hardening temperatures (10 or 37°C) or keep at 25°C (control group), and thereafter standard thermotolerance tests, such as, critical thermal maxima (CTmax) and critical thermal minimum (CTmin) were performed. Results showed that heat hardening (37°C) increase thermotolerance by affecting both, CTmax and CTmin. In the same way, cold hardening (10°C) increased tolerance to high and low temperatures, which strongly suggest that both, heat and cold hardening could induce a thermotolerance improvement. In addition, HSP70/HSP90 RNAi knockdown insects showed lower resistance to low and high temperatures compared with their controls. These results provide further insight into the physiological adaptations of hematophagous insects to harsh environmental conditions.

A high-quality genome of bark beetle Ips typographus by PacBio sequencing: major milestones completed and first comparison to other Coleopteran herbivores

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Abstract: For Ips typographus, a major pest of Picea spp in the Palearctic, we have generated a high-quality genome sequencing database as the best possible foundation for analysis of specific genes in our own research (chemosensation, detoxification, immune response), and other current European research, as well as the bark beetle scientific community in general.

Workflow: We have created a highly inbred line (sibling-mating single beetle pairs for 10 generations) to allow sequencing with Pacific Biosystems technology. The inbreeding reduced heterozygosity, i.e. reduce the amount of natural sequence variation due to allelic variation, which is very detrimental when working with PB. The resultant assembly is of extraordinary quality, with a total size of ~239 MB present in 279 contigs. From the assembly the longest contig was 16 million bp, while the mtDNA exists as a single 28 kbp contig.

Stranded RNA-Seq data from multiple life stages and tissues previously generated by the CULS group was aligned to the genome assembly. State-of-the art software and workflow (RepeatModeler, Repbase, RepeatMasker MAKER3, HiSat12 etc) analysis of genome and transcriptome sequences supporting gave “automated” gene model predictions, allowing inter alia an comparison to other high-quality beetle genomes.

There are a total of 23,937 genes predicted with at least some form of supporting evidence and missing only 38 (2.3%) of the BOSCO insect orthologs. This is comparable with the Asian longhorn beetle (22,035 genes). Genes number for chemosensation, detoxification, and pesticide resistance was similar or higher compared to 11 Coleoptera genomes.

Outlook: The sequence data and first analysis is prepared for submission. Direct use of data will follow during 2020 and onwards, including manual annotation for chemosensation and detoxification genes, for the downstream de-orphanisation of olfactory receptors, insect-tree RNA-Seq transcriptomics, and for gene knockout and -knockdown experiments. In the longer term, the result will be an annotated, very high-quality genome, that we hope will be useful not only for study of evolution, ecology, and, management in Ips spp, but also for other Ipini and Scolytinae.

Moving from univariate biodiversity to community responses to agricultural environments

Authors: Schmidt Jason, University of Georgia, United States

Abstract: Here using a data from a variety of agricultural systems collected over the past five years, we explore challenges, similarities and differences in understanding the structure of communities and associated trophic interactions determined through molecular gut content analysis.

Anatomy of male and female genitalia of Acanthoscelides obtectus (Chrysomelidae: Bruchinae) in interaction

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Abstract: The membraneous endophallus of male A.obtectus is armed with spicules. We checked if these spicules penetrate the wall of the female bursa copulatrix during copulation. Other than in Callosobruchus maculatus, these spicules leave no traces of penetration, as revealed by microscopical investigations. Identification of the exact relative position of male and female copulatory organs while mated by means of MicroCT confirmed that the spicules do not cause wounds in the bursa wall. During copulation, only the tip of the median lobe of the aedeagus is inserted into the female genital opening. The everted endophallus extends over the full length of the ovipositor, and the spermatophore is placed in the bursa. Females hinder mounting of the males by kicking them off by vehement movements of their hind legs. Copulation is generally terminated by the females who push off the males with their hind legs.

Diverse or simple: (non-)volatile chemical cues that predict bee foraging choices.

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Abstract: Bees, like most herbivores, often face a considerable diversity of chemical cues and thus complex information pattern when foraging, but have to make quick decisions on whether or not a resource is appropriate.
We wanted to better understand how social bees master this challenge, whether e.g. they select and focus on meaningful cues, rely on colony feedback or learn entire chemical profiles of preferred resources. We therefore studied the role of chemical information for pollen collection in bumblebees (Apidae: Bombus terrestris) and resin collection in stingless bees (Apidae: Tetragonula carbonaria), combining different behavioral assays and chemical analyses of resources.
We found that cue perception differs with the type of resource collected. For instance, stingless bees learn the entire complex volatile profiles of preferred resin sources and specifically target these resins, while bumblebees appear to prioritize lipid perception when assessing pollen appropriateness and generally select pollen of comparatively lower fat content. In both cases, decisions appear to ultimately affect colony fitness. Resins specifically targeted by stingless bees show comparatively high bioactivity (e.g. antimicrobial, predator repellent); and fatty pollen severely decreases survival of bumblebees.

Evidence for a chemical arms race: Lections from the chemical mimicry system of a cuckoo wasp

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Abstract: Brood parasites can exert strong selection on their hosts by exploiting their hosts' parental care. This can lead to coevolutionary processes in which adaptations by the parasites face counter-adaptations by the hosts. We studied interactions between 1) digger wasps, 2) the digger wasps' prey and 3) the digger wasps' brood parasites. We found evidence for a coevolutionary arms race between hosts and their brood parasites, which mimic the cuticular hydrocarbon (CHC) profiles of their hosts. Digger wasps of the genera Cerceris and Philanthus hunt either Coleoptera or Hymenoptera. It was previously shown that these wasps preserve only Hymenoptera prey against fungal infestation by applying a specific hydrocarbon mixture identical to their own (i.e., the predator's) body surface CHC profile. The hydrocarbon profile of Hymenoptera-hunting, but notably not of Coleoptera-hunting species, thus needs to retain its anti-fungal properties which limits the CHC profile diversification. We hypothesized that Coleoptera-hunting digger wasps benefit from relaxed selection on their CHC profile in order to escape from chemical mimicry by their parasites. We found: 1) less overlap in the CHC profiles of Coleoptera-hunters and their parasites, compared to that of Hymenoptera-hunters and their brood parasites: 2) that CHC profiles of Coleoptera-hunters are more diversified in females than in males; and 3) that female cuckoo wasps of Coleoptera-hunters "follow" the chemical space of their female hosts. We conclude that species preying on Coleoptera have diversified their CHC profile as an adaptation to escape chemical mimicry from their brood parasites. This strategy cannot be adopted by Hymenoptera-hunters, which must maintain a specific CHC profile for prey preservation.

Spatiotemporal genomic analyses and insights into pest evolution

Authors: Schoville Sean, Dept. of Entomology University of Wisconsin, United States

Abstract: Agricultural pests are extraordinarily successful in responding to environmental and human-imposed selection pressures. The ability of agricultural pests to overcome these challenges threatens food security and the development of sustainable agricultural practices. A growing body of research demonstrates that rapid phenotypic evolution is prevalent in agricultural pests, but questions remain about the molecular mechanisms that underlie rapid evolutionary change. I discuss the strengths of population genomic studies that stratify population samples both in space and in time, leveraging a hypothesis-testing framework in order to investigate how pests evolve. These genome-scale data provide a broad framework to investigate evolutionary mechanisms, understand the genetic basis of pest phenotypes, and to improve management outcomes in agroecosystems. Focusing on my own study system, the Colorado potato beetle, Leptinotarsa decemlineata, I demonstrate how underlying standing genetic variation and polygenic trait architecture contributes to the beetle's ability to rapidly evolve to insecticide resistance. Comparative genomic data of related species further support the role of high standing variation and elevated rates of positive selection in driving rapid evolution in this pest lineage. Comparing these results to other recent studies suggests that certain species-specific traits may contribute to rapid evolution, though there remain a number of challenges to interpreting spatiotemporal genomic data.

The genetic basis of color variation in Nebria ingens complex in alpine habitats of the Sierra Nevada

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Abstract: Understanding how microevolution results in species' diversity and natural selection is one of the primary goals of evolutionary biology. Knowledge of the genetic basis of morphological and physiological traits is increasingly important in documenting evidence of organismal adaptation to the environment. To detect the genes that underlie complex phenotypic traits, one can employ association mapping approaches to identify the genetic markers that have conspicuously high statistical association with the focal phenotype. These approaches are rarely applied in non-model organisms due to cost and demanding experimental designs, however natural hybrid zones offer a powerful context to effectively apply these methods. In this study, we focus on several morphological traits including metallic color of carabid beetles, by applying association mapping to the Nebria ingens complex in the Sierra Nevada Mountains of California. Two subspecies, N. i. ingens and N. i. riversi, as well as many hybrid populations were sampled for phenotypic variation and genotyped using low-coverage whole genome sequencing. Reads were mapped to a reference genome assembled from long read PacBio sequencing. Our preliminary results provide the first identification of metallic color pattern genes in beetles.

Population genetic structure supports local persistence in multiple glacial refugia in the montane net-winged midge Liponeura cinerascens cinerascens LOEW 1844 (Diptera: Blephariceridae)

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Abstract: Populations of stream organisms exhibit varying levels of isolation, depending on where they have their preferred habitat within the dendritic network and how well they can – and actually do – disperse in aquatic or terrestrial life stages. Net-winged midges generally prefer microhabitats with boulders and strong current that naturally occur in isolated stream sections, often across distinct mountain ranges. Here we study the population genetic structure of the net-winged midge L. c. cinerascens based on range-wide microsatellite genotyping and COI sequencing of individuals from the Pyrenees, Jura Mountains, Bavarian Forest and Carpathians. Our results indicate distinct genetic differentiation between mountain ranges, coupled with near panmictic gene flow across distances exceeding 100km within each studied mountain range. These results suggest that adult and larval mobility allow L. c. cinerascens to disperse between watercourses in highly structured mountain ranges. Lowland regions, however, pose a significant dispersal barrier, possibly because high gradient stretches with boulders are rare in such landscapes. Distinct COI lineages, microsatellite population genetic structure and high levels of regionally private alleles provide evidence that mountain range populations have been evolving independently from each other for several million years. We posit 1) that each of the studied mountain regions represents an independent Pleistocene glacial refuge, and 2) that L. c. cinerascens was able to persist glacial cycles in extra-Mediterranean periglacial refugia in the Jura Mountains, Bavarian Forest and Carpathians.

Investigating grain aphid insecticide resistance and BYDV transmission in post-Neonicotinoid Ireland

Authors: Schughart Maximilian, Teagasc, Ireland

Abstract: The grain aphid Sitobion avenae is a major agricultural pest in Europe. It damages crops by feeding on the grain and transmitting barley yellow dwarf viruses (BYDV), which can result in high yield losses. In recent years, aphid control for farmers has become more challenging due to the EU-ban on Neonicotinoids, as well as the emergence of resistance to Pyrethroids in a clonal lineage of S. avenae, caused by a mutation (knock-down resistance; kdr) in the insecticide target membrane molecule. Therefore, with the loss of Neonicotinoids and Pyrethroids remaining the primary control option, it has been hypothesized that the incidence of Pyrethroid resistant grain aphids will rise, due to the favourable selection after spray application. In order to investigate the incidence of kdr- and BYDV- carrying grain aphids in post-Neonicotinoid Ireland, a two year field survey has been carried out in 50 fields in crop growing regions across the country. Our results indicate that both kdr and BYDV are widely present in Irish grain aphid populations, underlining potential future difficulties in controlling S. avenae, and subsequently BYDV, in years where weather conditions are favourable for aphid flight and where chemical control options are limited.

Alien vs. Herbivore: Ant-mediated plant defense as an option for biological control of leafcutter ants

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Abstract: Leafcutter ants are a major pest in vineyards in Argentina, but biological control methods have not been successful so far. The Argentine ant Linepithema humile (Mayr) is a common invader of vineyards worldwide and has a strong preference for carbohydrates. Sugary rewards can trigger ants to act as plant bodyguards against a wide range of herbivores. In a first 10-week field experiment, we attracted L. humile ants to a group of vines using sugar feeders, while empty feeders were used for a second group. Ant-excluded control plants were also deployed. We found that the leafcutter ant Amoimyrmex bruchi caused >90% leaf area reductions in vines without L. humile, while plants with L. humile were rarely attacked. In a second short field experiment, we evaluated the impact of L. humile on A. bruchi foraging behaviour. The presence of L. humile decreased A. bruchi's foraging activity and the amount of material transported by it. The development of biological control strategies that include the ecological services of ants as natural enemies of herbivorous pests could become a useful tool in sustainable viticulture and horticulture.

The insect Hermetia illucens: a sustainable source of molecules of high biological and economic value

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Abstract: The worldwide growing protein demand for farm animals breeding can no longer be satisfied by the intensive farms and the intensive use of agricultural land. Insect proteins can play an important role in the progressive substitution of proteins commonly used to feed animals, and prospectively in the progressive integration as novel food. Some insect species, such as the Diptera Hermetia illucens (BSF), can be reared on different types of organic waste, obtaining valuable secondary products: larvae/meal rich in protein and lipid, for aquaculture, poultry and pigs; chitin, exploitable in biomedical, pharmaceutical and agri-food fields; larval frass usable for crop fertilization. To study the effect of different substrates on insect growth, larval component and substrate reduction, 10000 larvae were reared on three byproducts from the agri-food chain (strawberry, tangerine, orange) and on a standard diet. The results highlight that BSF can successfully feed on all the tested substrates, although development time, growth rate, final larval biomass and larval components are affected by different substrates. The bioconversion process of agrifood by-products by BSF is a valid means for their valorization and for the sustainable production of alternative animal proteins and molecules of high biological and economic value, with a circular economy view.

Olfactory perception of Hermetia illucens: a source of inspiration for the development of new biosensors for the monitoring of agrifood products shelf life

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Abstract: Insect physiology study at the molecular level and innovative technology implementation allows the development of applications useful to human. An example is the olfactory perception of Hermetia illucens, a saprophagous Diptera that has aroused interest for organic waste bioconversion. Females oviposit on decaying organic matter and larvae feed on it. Through RNAseq, de novo assembly and annotation of larval, male/female adult transcriptomes, we identified H. illucens Odorant Binding Proteins (OBPs) that mediate chemoreception of volatile organic compounds (VOCs) found in decaying substrates. We detected 15 HillOBPs expressed both in larvae and adults. The use of OBPs specific for organic decomposition VOCs are proposed as sensing layers of innovative Quartz-Crystal- Microbalances (QCMs) sensors, for monitoring food product preservation and shelf-life, in a new approach to food logistics. Affinities with 57 identified VOCs, emitted by different decomposing substrates colonized by H.illucens larvae, were calculated by molecular docking technique and were confirmed for 4 cloned, expressed and purified HillOBPs immobilized on a gold-layer of QCMs. These experiments provided useful information about biosensor selectivity, as the ability to discriminate ligands of different nature. Four compounds indicative of lipidic decomposition were detected with high affinity in a pool of VOCs, known to be spoilage markers.

Conditional female transformation for enhanced genetic control of New World screwworm and Australian sheep blowfly

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Abstract: The New World screwworm and the Australian sheep blowfly are major pests of livestock. Screwworm and blowfly females lay their eggs in an open wound and the hatched larvae eat the animal alive. In addition to being a major animal welfare issue, economic losses from screwworm in South America were estimated in 2005 to be almost $4 billion annually. The goal of this project is to develop screwworm and blowfly strains for efficient suppression of screwworm populations in Uruguay through downregulation of the transformer (tra) gene. tra is essential for female development in screwworm and blowfly. An unidentified Y-linked male-determining gene (M) switches off tra in males. In females, tra switches the doublesex and fruitless genes into their “female-mode”, which leads to female development and behavior. Injection of double-stranded RNA into pre-blastoderm embryos led to females developing male characteristics. The conditional transformation strains carry two gene constructs. A driver expresses the tTA transcription factor. The effector is “tetO-traIR”, carries two copies of approx. 500-700bp region of the tra genes in inverted orientation. The transcribed RNA is self-complementary and forms a 500-700bp dsRNA. In the absence of tetracycline, tTA activates expression traIR, producing dsRNA that leads to degradation of tra mRNA and consequently females develop as males. An advantage of this approach compared to female-killing strategies, is that all eggs produced in a mass rearing facility develop as males.

Development and evaluation of modified strains of Drosophila suzukii for genetic suppression

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Abstract: Drosophila suzukii larvae are capable of infesting a wide range of host fruit but appear to be most significant pests in stone fruits (peach, cherry, and plum) and berries (caneberries, blueberries, and strawberries). As a compliment to existing approaches, we have been developing genetically modified strains of D. suzukii for population suppression. Several fs-RIDL strains have been made and evaluated. The strains are all based on the tetracycline transactivator (tTA), which binds very specifically to the tet operator sequence from bacteria. Binding is disrupted by the addition of tetracycline to the diet. The fs-RIDL strains produce only males on standard diet but females are fully viable and fertile on diet supplemented with tetracycline. We are currently evaluating the potential of the strains for population suppression in small cage experiments in containment.

Several Cas9-based genetic strategies have recently been proposed that could be more efficient, and thus less costly, than fs-RIDL. As a first step towards development of Cas9-based strains for population suppression, we have made transgenic strains that express Cas9 in the male and female germlines. The strains were evaluated by crossing to transgenic strains that express gRNAs that target the white and Sex lethal (Sxl) genes. The most active Cas9 lines produced a high proportion of white-eyed offspring after crossing with a white gRNA line. Crosses with Sxl gRNA lines produced female offspring that were sterile. This suggested a conserved role for Sxl in the female germline. The Cas9 strains could be used to evaluate homing gene drive constructs that target genes required for female development or fertility.

Opportunities and challenges for innovation in Aedes surveillance, control and disease prevention in a globally changing climate

Authors: Scott Thomas, University of California, Davis, CA, United States

Abstract: Although vector control is well documented as an effective strategy for prevention of mosquito-borne disease, the burden of several Aedes-transmitted diseases is increasing. It is reasonable to ask why vector control for those viral infections not been effective more often? Unsuccessful programs are often attributed to a lack of resources, lack of political will or ineffective implementation. Also responsible, however, are deficiencies in understanding vector ecology and pathogen transmission, methods for assessing and responding to risk, failure to use existing knowledge and surveillance for control decisions, and a changing global climate. In brief, concepts in disease prevention remain incompletely defined and underutilized. Current dengue prevention emphasizes universal surveillance and control, which has stifled development of a conceptual and factual foundation for adaptive disease management. There is an urgent need for a new framework for surveillance and intervention that (1) better defines relationships between measures of risk and human infection and (2) uses that information to direct public health measures that prevent disease. In this talk I will explore enhancing Aedes-transmitted disease prevention with locally adaptable tools and strategies that account for heterogeneities in transmission.

High Quality Genomic Resources for Stored Product Insects to Improve Integrated Pest Management Tactics

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Abstract: Stored product insects threaten global food security by causing millions of dollars of losses post-harvest around the globe. Although tactics, such as mating disruption, fumigation, and sanitation provide successful control of these insects in many environments, resistance to insecticides and fumigants and tolerance to cold to mating disruption have been observed in field populations, necessitating the development and diversification of integrated pest management tactics in this system. Until recently, the only genome assembly available for this diverse group of insects was Tribolium castaneum (red flour beetle) and challenges including cost, heterozygosity, and DNA input impeded the advancement of these resources for species. However, long-read assemblies generated from low DNA input on the PacBio instrument for six different families of stored product insects through USDA's AgPest100 initiative are allowing us to release resources for this important group of insects at an unprecedented scale and obtain a glimpse into the genetic factors that enable these pests to adapt to management tactics and survive inhospitable conditions, including cold temperatures and lack of food resources. Overall, these resources will allow us to look for common resistance tactics among this diverse group of insects and also common genetic features that could be used to manage many species of stored product insects simultaneously.

Generation of genomics resources for the meadow spittlebug Philaenus spumarius

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Abstract: Philaenus spumarius (Linnaeus, 1758) and other spittlebug species (order Hemiptera) are xylem-feeding insects that vector the bacterial pathogen Xylella fastidiosa, which has caused dramatic declines of a wide variety of plant species and most recently destroyed the olive production industry in southern Italy. Spittlebugs were not considered major threats to agriculture in Europe before the discovery that they are able to transmit X. fastidiosa. P. spumarius is native to the Palearctic regions, and was unintentionally introduced in other regions, e.g. USA and New Zealand. The insect quickly adapts to new environments, and may be considered invasive. As a first step to improve our knowledge of the evolution and genomics of this species, we generated a draft assembly of the 2.7 Gb genome of P. spumarius. The assembly has a scaffold N50 length of 120Kb with the longest scaffold of ~4 Mb and a high (2.3%) heterozygosity level. Annotation of the genome revealed a highly repetitive genome and presence of 97% of conserved genes among arthropods suggesting a complete genome assembly. The assembly of the genome of a second froghopper species, Aphrophora salicina, revealed a genome size of 2.3 Gb. This assembly had a scaffold N50 length of 625Kb with the longest scaffold of ~5 Mb and a lower (0.7%) heterozygosity level.

We started to generate genome assemblies of other 16 potential vector of X. fastidiosa as well. In the future these will form the basis of comparative genome analyses to assess differences between phloem and xylem feedings insects within Hemiptera. They will also allow assessing the population structure and putative dispersal of these species between host plants. This research is part of a larger UK-government funded collaborative project (named BRIGIT; https://www.jic.ac.uk/brigit) and all genome sequence data and annotations generated in this project will be made freely available via http://sapfeederhub.jic.ac.uk/.

Male-biased sex-ratio of the meadow spittlebug, Philaenus spumarius (Hemiptera: Aphrophoridae) detected in forest populations of Turkey.

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Abstract: Recent data obtained from some natural populations of Turkey for Philaenus spumarius are presented here. Preliminary results showed that the adult proportions of males were extremely high, compared to females particularly in autumn samples. The percentage of males in some samples increased up to 90%, and has usually been around 80%. This is a quite the reverse situation to many European and North American populations where the frequency of males are in highest early in the season due to slightly earlier average emergence in adult form and that they slowly decline as a proportion of populations toward and into fall. Mechanisms playing role on this male-biased sex-ratio need to be investigated in future studies, namely the effects of temperature on differential hatching and development between male and females; or the presence of endoparasites or endosymbionts, which are known to affect population sex ratio, although most usually they cause a female-biased ratio. Also, the impact of this sex-ratio distortion on the population dynamics should be addressed. Understanding this system may provide important data to incorporate in risk assessment models for the transmission of the plant pathogen Xylella fastidiosa by this known insect vector in Europe.

Identification of novel RNAi targets to control brown marmorated stink bugs (Halyomorpha halys) using proteomics

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Abstract: Originally from East Asia, and now established in Europe and North America, brown marmorated stink bugs (Halyomorpha halys; BMSB) are an invasive pest that causes severe damage to an extensive number of crops. While generalist chemical controls are failing to meet growers' needs, RNA interference (RNAi) has shown remarkable potential in killing most of the treated individuals by disrupting the expression of specific target genes. Further development of dsRNA to target multiple genes can allow the rotation of treatments in the field, and avoid building resistance in the BMSB populations, thus insuring a potential long-term usage of RNAi to control BMSB. To do so, we have analysed the proteins present in all the different BMSB life stages (from eggs to adult, both males and females) using a Tims TOFF mass spectrometer and the MaxQuant program. We present here the results of our data analysis on the differences in protein profiles between stages, and highlight which pathways are especially enriched. Furthermore, we discuss novel potential targets for RNAi, which could affect most stages, and that we are planning to validated in vivo. This research is the first step to support the development of an efficient, multi-target RNAi control for BMSB.

Species-selective agonists of juvenile hormone receptor signaling

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Abstract: Diverse synthetic compounds mimic juvenile hormone (JH) effects and are used to disrupt insect development as pesticides of the insect growth regulator (IGR) class. Juvenoid IGRs are agonists of the JH receptor (JHR). However, current IGRs have poor selectivity towards target pest species. To discover selective JHR agonists, we performed automated, high-throughput chemical screening, initially in a Drosophila cell line carrying a JHR-dependent transcriptional reporter. Primary hits were validated through follow-up assays including ligand-receptor binding, dimerization of the JHR subunits, and effects on developing insects. This campaign uncovered novel compounds with JHR agonist activities exceeding those of a reference juvenoid methoprene. To identify species-selective juvenoids, we devised cell-based reporter systems utilizing JHR proteins from several target insects. Hits from high-throughput chemical screens were further diversified, yielding potent agonists, some of which preferentially activated JHRs of particular insects. When tested in vivo, the discovered compounds blocked metamorphosis of target species. These results demonstrate feasibility of our approach toward discovery of novel and selective JHR agonists for potential use as research tools and eco-friendly means of pest control.

Supported by grant 20-05151X (Czech Science Foundation) and project LM2018130 (MEYS) to the National Infrastructure for Chemical Biology CZ-OPENSCREEN.

Lessons learned: Biological control of eastern spruce budworm in Canada

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Abstract: The eastern spruce budworm (SBW) Choristoneura fumiferana (Lepidoptera: Tortricidae) is the most important forest defoliator in eastern North America. Because of the important economic losses to the forest industry, many attempts to decrease SBW population levels or to protect trees from defoliation during outbreaks have been undertaken, using various methods such as chemical and biological insecticides, mating disruption or biological control.

Most of the attempts of biological control were intentional introductions of natural enemies, also called classical biological control (CBC), using mainly species from Europe but also parasitoids from C. occidentalis from western Canada (relocations). However, none of the CBC attempts against SBW are regarded as successful. Augmentation of native species as biological control agents has been attempted with a few natural enemies such as the egg parasitoid Trichogramma minutum (Hymenoptera: Trichogrammatidae) being by far the most prominent and successful example. Several other augmentative programs have been attempted although they remain hidden in the gray literature. As with many pests, conservation biological control is often mentioned by authors but has received very little attention in practice, and the same is true for integrative pest management (IPM) approaches.

The review of biological control attempts against SBW in Canada has many valuable lessons to teach us about the applicability of this pest management approach against outbreaking defoliators. For example, it highlights the relative lack of success that CBC has had against indigenous pests, in contrast to the augmentation of native natural enemies where there has been some measure of effective control. Opportunities for the future of SBW management can also be identified in review. With new ecological insights (e.g. density-dependence of parasitism of T. minutum) and new techniques (e.g. UAVs and rearing techniques), the efficacy of biological control could be increased and overall costs decreased. Given the recent focus on early intervention strategies, IPM approaches that include biological control as a management option should be considered.

Potential impact of climate change on an important parasitoid of a North American outbreaking forest defoliator

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Abstract: Choristoneura fumiferana (Lepidoptera: Tortricidea), the spruce budworm (SBW), is the most important outbreaking defoliator in conifer forests of northeastern North America. The SBW food-web has five trophic levels including almost 100 species of parasitoids. Different species of natural enemies have different abundances and impacts depending on the outbreak phase. For example, the multivoltine Tranosema rostrale (Hymenoptera: Ichneumonidae) is the most important species during the extended period between outbreaks while other univoltine species such as Glypta fumiferanae (Hymenoptera: Ichneumonidae) and Apanteles fumiferanae (Hymenoptera: Braconidae) are more important during the rise in population density.

Models predict that climate change will impact the distribution and severity of SBW outbreaks. However, its impact on the interaction between the budworm and its natural enemies is not clear. A research project on T. rostrale showed that its overall performance was greatly reduced at high temperatures. Further experiments have shown that the underlying mechanisms involve both a downregulation of the parasitoid's polydnavirus gene transcription and an enhancement of host immunity gene transcription. Physiological experiments confirmed an increased encapsulation activity in SBW larvae at high temperature. In accordance with these results, a temperature-dependent individual-based model predicts that regions of higher T. rostrale performance shift northwards under a climate warming scenario.

What makes a good natural enemy for classical biological control of arthropods?

Authors: Seehausen Lukas

Abstract: Criteria that are used to select parasitoids and predators for classical biological control are mainly based on two characteristics: their ability to control the pest in the area of origin or in other areas of introduction and their host or prey specificity to prevent non-target effects. Beyond this, selection criteria are traditionally focused on particular biological traits of natural enemies that are thought to favour establishment of the agent and target control. But statistical analyses show that few of these traits actually influence the outcome of classical biological control. Therefore, the criteria should also focus on target traits and more consideration is needed for issues such as climate suitability, the composition of the natural enemy complex in the region of introduction, and the occurrence of sibling species or biotypes with specific attributes. The increasing use of integrative characterization of insects, i.e. the combination of morphological and genetic taxonomic tools with biological and ecological studies to investigate inter- and intra-specific differences of insects, has become an important tool to select better biological control agents. However, to validate these criteria and improve risk assessments, it is paramount to conduct post-release studies, which are unfortunately still rather uncommon in insect biological control.

Arthropod decline in grasslands and forests is associated with landscape-level drivers

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Abstract: Recent reports of local extinctions of arthropod species1, and of massive declines in arthropod biomass, point to land-use intensification as a major driver of decreasing biodiversity. However, to our knowledge, there are no multisite time series of arthropod occurrences across gradients of land-use intensity with which to confirm causal relationships. Moreover, it remains unclear which land-use types and arthropod groups are affected, and whether the observed declines in biomass and diversity are linked to one another. Here we analyse data from more than 1 million individual

arthropods (about 2,700 species), from standardized inventories taken between 2008 and 2017 at 150 grassland and 140 forest sites in 3 regions of Germany. Overall gamma diversity in grasslands and forests decreased over time, indicating loss of species across sites and regions. In annually sampled grasslands, biomass, abundance and number of species declined by 67%, 78% and 34%, respectively. The decline was consistent across trophic levels and mainly affected rare species; its magnitude was

independent of local land-use intensity. However, sites embedded in landscapes with a higher cover of agricultural land showed a stronger temporal decline. In 30 forest sites with annual inventories, biomass and species number—but not abundance—decreased by 41% and 36%, respectively. This was supported by analyses of all forest sites sampled in three-year intervals. The decline affected rare and abundant species, and trends differed across trophic levels. Our results show that there are widespread declines in arthropod biomass, abundance and the number of species across trophic levels. Arthropod declines in forests demonstrate that loss is not restricted to open habitats. Our results suggest that major drivers of arthropod decline act at larger spatial scales, and are (at least for grasslands) associated with agriculture at the landscape level. This

implies that policies need to address the landscape scale to mitigate the negative effects of land-use practices.

Diplurans, the forgotten soil-cave-organisms

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Abstract: Diplurans are basal terrestrial hexapods equipped with tracheal system, devices for indirect transfer of spermatophores, and remnants of Malpighian tubules. They can be considered as one of the first land colonizers most likely in the Early Ordovician. Their morphology and behaviour reveal a primitive life link to cryptic subsurface habitats in soil and cave ecosystems at up to one thousand meters depth, not far from the limit of terrestrial fauna. In spite of their phylogenetic interest and importance as part of the soil and also cave community, diplurans receive little attention in research and they have been almost forgotten about in scientific literature. However, diplurans play a part in their own neglect, especially with regard to their important role in the trophic chains. Ecological studies in soil and cave environments largely ignore diplurans mainly because of taxonomic difficulties, such as the distinction of genera and species by few sophisticated characters. Fortunately, these tiny differences were masterly managed thanks to a handful of forward-thinking taxonomists (Filippo Silvestri, Bruno Condé, Jean Pagés, among others) who advanced the description of globally about 1000 species to date. Nowadays, scanning electron microscopic studies of cuticle surface or sensilla join with advances in molecular analysis help us to build a more natural phylogeny in diplurans, a necessary tool to understand the dipluran distribution areas and resolve biogeographical and paleobiogeographical questions. Diplurans display many more trophic levels than other groups of soil arthropods and include herbivores (Parajapygidae, Octostigmatidae), zoophages (Projapygidae, Campodeidae), detritivores (Campodeidae) and also top carnivores (Japygidae, Heterojapygidae). Six of seven dipluran species live in unconsolidated materials in soils from O to C horizons. Although having little capacity to excavate, diplurans are able to move through small spaces left behind by roots or holes made by other soil animals. But diplurans, mainly Campodeids flourish in cave ecosystems, in all kind of caves in limestone to volcanic rocks. Turning to the fields of anatomy and biological studies, great advances have been made in aspects such as internal and external morphology including sensorial equipment and glands involved in the moulting process, growth and reproduction cycles (Camille Bareth among others). The prospects for future research in all fields are exciting, potentially including genetics for phylogenetic studies to better understand the amazing tiny anatomical structures involved in the survival of these primitive terrestrial animals in the subsurface of the Earth.

DNA metabarcoding revealed expected but also some exceptional prey species in the diet of carabid beetles in Mediterranean agriculture

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Abstract: Carabids are mainly predatory beetles but still certain proportion of them are omnivores and herbivores. Since they feed on pest insects and weeds and being abundant among the soil-active arthropods capable of consuming close to their body mass of food daily, carabids are considered important within the agroecosystem food webs. The DNA metabarcoding as one of the state-of-the-art methods for depicting trophic interactions were used to evaluate the ecosystem services of carabids within Mediterranean vineyards and olive orchards in Croatia, under Integrated Pest Management (IPM) and Ecological Pest Management (EPM). Carabids were collected at five sites including unmanaged site, and subdued to the molecular gut content analyses using NGS. After dissection, DNA from the gut content was extracted and amplified using general and newly designed carbide-exclusion primers within COI gene, and successfully sequenced. Here we present the results of trophic interactions in respect of carabids potential to feed on agricultural pests but also on overall diversity that was discovered by eDNA. High diversity of invertebrates within their gut content, intraguild predation and plant DNA were revealed. The results support the use of agricultural measures to promote higher biodiversity in the Mediterranean, and to sustain natural enemies of crop pests.

From bee hives to farm lands: promoting pollinator health and sustainability

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Abstract: Pollinator populations have been facing several debilitating challenges for several decades now. These challenges include intensification of agricultural practices, habitat degradation, increased need for migratory honey bee colonies, indiscriminate use of agrochemicals, and pests and diseases. Simple but effective management practices including reinstating habitat diversity around farmlands, integrated hive management, minimizing and using agrochemicals appropriately while increasing nutritional diversity for pollinators have played a significant role in improving pollinator health and sustainability. Farm management practices promoting pollinator diversity and abundance include planting pollinator habitats along margins of fields growing herbicide tolerant crops, incorporating pollinator-friendly forbs into cover crop mixes and retiring sensitive farmland from agricultural practices and restoring them into natural habitats. Urban areas considered as bee diversity hotspots can foster native pollinator populations through the actions of interested citizens enthusiastic to promote and protect bee-friendly habitats. Lastly, improving the health of honey bees, the most efficient of pollinators, happens by improving the overall nutritional status, which is a product of the availability of important dietary resources in the environment and the physiological capacity of bees to harvest these resources. Migratory beekeeping, where honey bee colonies are placed in fields needing pollination for successful fruit production has placed a lot of strain on honey bees as they are exposed to pollen and nectar from a single crop for a brief period before moving onto a different crop field. Hives are likely to experience shortages of certain nutrients or exposure to certain potentially toxic phytochemicals, depending on the crop they are pollinating. Developing targeted solutions towards the betterment of colony nutrition even as hives are pollinating crops ensures healthy colonies for continued pollination services to the farming community. This is also important for other commercial pollinators including bumblebees and leaf-cutter bees. Results from our ongoing research on these topics will be presented and the implications of our findings on pollinator health and sustainability will be discussed.

Potential role of radiation hormesis in augmenting biorational pest suppression approaches against a serious polyphagous pest, Spodoptera litura (Fabr.) [Lepidoptera: Noctuidae]

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Abstract: Radiation hormesis is a phenomenon using very low level of ionizing radiation for stimulating the various behavioural and physiological activities of organisms. This property of radiation hormesis can be exploited in various biorational approaches of insect pest control. Biological responses to ionizing radiation often conform to a 'linear-no-threshold' (LNT) model, which predicts that the degree of damage scales linearly with the irradiation dose. Generally, the radiation exposure is well documented to have a range of negative effects on cellular, developmental and behavioral traits. However, a considerable evidence supports an alternative model known as hormesis, in which low-level stress (radiation) exposures can have beneficial or stimulatory effects on biological performance even though the higher levels are inhibitory. Although the hormetic dose–response relationships have been documented across broad phylogenies (bacteria to mammals), radiation hormesis has rarely been studied in a life history framework of insects. Understanding the fitness-related influence of radiation may be important in augmenting certain biological based insect control tactics. Radiation hormesis using gamma radiation from Co-60 Teletherapy unit was studied in various pre-imaginal stages of a tropical pest, Spodoptera litura (Fabr.) in order to stimulate the insect's physiological system. In the initial phase, low doses, 0.25-1.25Gy, were evaluated on 0-1 day old eggs, third instar larval stage (L3) and 2-3 day old pupa in terms of growth index and adult behaviour (survival and mating success), with an aim to rearing the quality moths. The results indicated the potential hormetic gamma doses as 0.75 Gy and 1.0 Gy for egg, 1.0 Gy for L3 and 1.0 Gy for pupa. These hormetic doses enhanced the longevity of moths and increased their mating success. In the next phase, the irradiated adults derived from preimaginal ontogenic stages, having absorbed hormetic radiation, were examined to show better survival and more insemination rate at the sub-sterilizing dose (130 Gy) proposed for the F1 sterility technique. Further, the study on influence of the hormetic radiation (given in juvenile development) on the reproductive fitness and the expression of certain physiologically vital genes (associated with survival, antioxidant defense and reproduction) related to substerile male parents and their F1 progeny is in progress.

Also, the low gamma dose range of 1.25 -1.5 Gy administered to the dauers of entomopathogenic nematodes (EPNs), Steinernema glaseri and S. thermophilum against host larvae of S.litura induced faster host mortality and enhanced parasitoid proliferation.

The radiation hormesis may play a positive role in augmenting radiation mediated F1 sterility technique (parabiological tactic) and classical biological control methods. Further, the multifaceted role of radiation hormesis is discussed in augmenting various biorational pest suppression approaches and improving the quality of useful insects.

Creation of new industrial sericulture using genetically modified silkworms

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Abstract: Recently, a new industrial sericulture has been developing using genetically modified silkworms (transgenic silkworms). An innovative method for generating transgenic silkworms was established in 2000, and since the epoch-making technological development, long-standing efforts have succeeded in developing novel silks that enable the manufacture of new textile materials or regenerative medical uses. Furthermore, a new system of recombinant protein production has been developed successfully. As a novel silk, the fluorescent silk has been developed by fusing the fibroin with the fluorescent protein. Using the fluorescent silk, some trial products, such as a silk dress, have been made. Another modified silk, spider silk, has been developed incorporating a gene from a spider species encoding a dragline protein. A silk for improving the adhesive abilities or the growth of cells was also constructed. Using the silks, an artificial blood vessel and the sponge sheet has been made. In a system for producing recombinant proteins in the sericin layer of the silk, transgenic silkworms have been shown to produce a wide variety of biologically active proteins, including antibodies, enzymes and so on for cosmetic, pharmaceutical and medical applications. Some of these recombinant proteins for cosmetic products and diagnostic pharmaceuticals have been in commercial use since 2011. Moreover, a clinical trial of antibody drug will be performed in the next few years. For the mass production of new the new silks or recombinant proteins using transgenic silkworms, the regulations for the handling of genetically modified organisms should be followed. In Japan, rearing with prevention of the dispersal of transgenic silkworms (type 2 use) and rearing without preventing their dispersal (type 1 use) are both in use. Rearing by the measure of type 2 use is already established for the practical production of recombinant proteins by several companies. For the establishment of the protocol of type 1 use, several transgenic silkworm strains producing recombinant silk has been reared in a limited area to assess its impact on the biodiversity. In 2017, a silk-raising farmer Japan began rearing transgenic silkworms that produce green fluorescent silks, according to the protocol of type 1 use. In addition, a company developed a new mass rearing apparatus for transgenic silkworms. Another company completed a large-scale year-round aseptic sericulture plant. Thus, a new industrial sericulture using transgenic silkworms has already begun.

Thermal tolerance mediates predator-prey interactions to determine elevation distributions of mayflies

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Abstract: Temperature is often implicated as a primary mechanism driving species turnover across elevation gradients. The modified climate variability hypothesis proposed by Janzen (1967), posits that the seasonal temperature variation experienced across temperate mountains should favor the evolution of species with broad thermal tolerances, greater dispersal ability, and wider elevation range sizes. On the other hand, tropical mountain species should evolve narrower thermal tolerances in response to stable temperatures, restricted dispersal across elevation, and narrower range limits. Previously, we demonstrated that tropical aquatic insects from the Ecuadorian Andes have narrower thermal breadths (CTmax – CTmin) and lowered acclimation ability compared to their temperate relatives from the Colorado Rocky Mountains. However, thermal breadth alone does not adequately explain the abrupt cessation of one species' occurrence and the beginning of another's in certain streams sites. We therefore propose that important biotic interactions, such as predation, mediated by temperature, may play a role in determining mayfly elevation range limits, and explain the observed pattern of species turnover. We tested this hypothesis in the temperate and tropical systems by artificially simulating range expansions of low elevation mayflies to high elevation streams and high elevation mayflies to low elevation streams, in a lab setting. "Transplanted" mayflies were exposed to suboptimal temperatures in the presence of native stonefly predators. Survival of transplanted mayflies was measured after 24h and compared to that of native mayflies in the same testing arena. We predicted that transplanted mayflies would be preyed upon more heavily than native mayflies because lowered performance in response to suboptimal temperatures would exacerbate their susceptibility to the predators. We also predicted that this effect would be stronger in the tropical Andean species where thermal breadths are even narrower. Temperatures are rising at an unprecedented rate in mountain streams, which are some of the most biodiverse ecosystems in the world. The effects of warming may be especially bad in tropical mountain systems where species are more thermally sensitive. To better predict how aquatic species will respond to changing temperature, it is imperative for us to gain a mechanistic understanding of how temperature affects distributions of resident taxa, and how tolerance to temperature shapes the outcome of interactions among species in freshwater communities.

Use of DNA Barcodes to identify invasive Spodoptera frugiperda (Noctuidae: Lepidoptera) species in Pakistan

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Abstract: Spodoptera frugiperda (Noctuidae: Lepidoptera) is the most damaging agricultural pest which has invaded Asian countries in recent years. The current investigation confirms the occurrence of fall armyworm in Pakistan and discusses its phylogenetic relationship with S. litura and S. exigua. The cytochrome c oxidase subunit I (COI) gene, ‘‘a universal barcoding region’’ of FAW having 650 bp, was isolated using specific primers. Maximum likelihood phylogenetic analysis of S. frugiperda, S. exigua, S. litura, and many others revealed significant variations among the sequences. S. frugiperda showed intraspecific disparities with reference to different geographical locations. Multiple sequence alignment presented similarities and differences found between the barcodes of the three pest species. The study proves the utility of the COI barcoding region for the identification and discusses phylogenetic interrelations existing between the pest species.

Characterization of CYP18A1 a key steroid hormone inactivation, is essential for metamorphosis in Chilo suppressalis.

Authors: Shahzad Muhammad Faisal, Gomal University

Abstract: Juvenile and ecdysteroids hormones are key regulators in insects development and metamorphosis. Regulatory processes must be precisly timed in insects development to ensure appropriate cell growth and differentiation at each defined life-stage. Major developmental transition are triggered by steroid hormones for coordination molting and metamorphosis. In contrast, less is known in ecdysteroids inactivation in in the lepidopteran species. Here we reported the ecdysteroid agonist-responsive cytochrome P450, CYP18A1 in rice striped stem borer, Chilo suppressalis. Prompting our hypothesis it exerts ecdysteroids inactivation action those reported in other insect species. We amplified full length of Chilo suppressalis CYP18A1by rapid amplification of cDNA ends. Temporal and spatial expression pattern of CYP18A1 showed that it was predominantly expressed in the midgut during wandering and early pupal stage like other lepidopteran model insects. RNAi knockdown of CYP18A1 resulted in pupal lethality, suggesting essential role of ecdysteroid inactivation for proper pupal development. Thus our results strongly suggest that CYP18A1 is involved in steroid hormones inactivation in rice striped stem borer, Chilo suppressalis, as seen in other species.

The black soldier fly (Diptera: Stratiomyidae: Hermetia illucens) as a natural enemy reducing pest populations from agricultural wastes

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Abstract: In Israel, tons of agricultural plant wastes are produced annually, mostly handled in an environmentally inconsiderate way, becoming a source of area-wide reinfestation of pests. In this study, we investigated the ability of the BSF larvae to treat three types of agricultural wastes, and to reduce their pest populations: apples, tomatoes and mushrooms. Apples left in the orchards after picking are a source of the Mediterranean fruit fly Ceratitis capitata. Tomato plants are the provenance of Tuta absoluta infestations. Mushroom-growing wastes are the origin of the phorid fly Megaselia haltera spreading. In laboratory experiments, we compared the pest populations that emerged from wastes treated and untreated by BSF, with and without pretreatments. The results indicate that BSF larvae significantly reduced C.capitata adults' emergence from apples, as long as the fruits were cut. BSF also significantly diminished T.absoluta emergence from tomato leafs. Forid fly population on the other hand was not significantly different than control treatment. Using Drosophila fly as a model we have found that BSF larvae can reduce Drosophila population by entomophagy of eggs and larvae but not pupae. We conclude BSF, can be successful as a part of Integrated Crop Management reducing both waste biomass and pest populations.

Photochromic insecticides for spatiotemporal modulation of ion channels

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Abstract: Photopharmacological ligands provide a powerful way for optical control of the activity of a molecule, which will facilitate better understanding of toxicological mechanism. By blending of photoswitchable azobenzene or dithienylethene with nAChR agonists neonicotinoids, GABAR antagonist fipronil and RyR modulator diamides, we prepared series of photochromic ligands (PCLs) acting on insect nAChRs, GABARs or RyRs. Some PCLs showed different insecticidal activity before and after light irradiation. These PCLs were then used to optically control over the insect nAChRs (sodium channel), GABARs (chloride channel), RyRs (calcium channel), neurons and insect behavioral responses of mosquito larvae (Aedes albopictus) and cockroach (Periplaneta americana).

Using entomopathogenic nematode pheromones and group behavior to improve biocontrol

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Abstract: Entomopathogenic nematodes are used to control a wide variety of economically important insect pests. However, field efficacy can be inconsistent. The ability of a nematode to find and infect (invade) a host insect is critical to successful pathogenesis. Thus, elucidating mechanisms that enhance nematode dispersal and infectivity will lead to improved efficacy. We discovered that entomopathogenic nematodes move in groups, like a pack of wolves seeking their prey. We also discovered that the nematodes produce ascaroside-based pheromones that induce dispersal and infectivity. In laboratory and greenhouse experiments, biocontrol efficacy against target pests was substantially increased when entomopathogenic nematodes were exposed to these pheromones. New research will expand upon these findings.

Mapping of inversion breakpoints on the X chromosome in the Maculipennis subgroup of malaria mosquitoes

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Abstract: Closely related species of malaria mosquitoes often have fixed chromosomal inversions. Anopheles messeae Fall. belongs to the Palearctic Maculipennis subgroup with large areal and well-developed inversion polymorphism. An. messeae diverged from the An. maculipennis around 2 million years ago and has at least one fixed inversion in the 3R arm. However, the number and locations of fixed inversions on the X chromosome have not been determined. Here we developed 32 DNA-probes based of the An. atroparvus reference genome and hybridized them with polytene chromosomes of An. messeae. We mapped four breakpoint regions (BP) of the X chromosome inversions fixed between An. messeae and An. atroparvus/An. maculipennis, and which divided the X chromosome into five synteny blocks. LTR retrotransposons from Gypsy, BEL and Copia families were most abundant in BP. Polymorphic inversions X2 and X0 do not reuse the BP with exception of the proximal BP, which can be involved in X2. Reconstruction of the rearrangement events based on the synteny blocks order and direction using GRIMM-MGR, demonstrated that the X1 chromosome of An. messeae could have originated by two sequential inversions, one of which is nested into another one. The X1 arrangement is likely ancestral because it differs from An. maculipennis by only two inversions, which do not correspond to polymorphic inversions in An. messeae/An. daciae. Thus, studying chromosome evolution is a useful approach for understanding historic relationships among closely related species of malaria mosquitoes. The study was supported by the Russian Science Foundation grant № 21-14-00182 to I.V.S.

Unraveling the 3D genome of human malaria vectors

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Abstract: Chromosomes are hierarchically folded within cell nuclei into territories, domains and subdomains, but the functional importance and evolutionary dynamics of these hierarchies are poorly defined. Here, we comprehensively profile genome organizations of five Anopheles mosquito species and show how different levels of chromatin architecture influence each other. Patterns observed on Hi-C maps are associated with known cytological structures, epigenetic profiles, and gene expression levels. Evolutionary analysis reveals conservation of chromatin architecture within synteny blocks for tens of millions of years and enrichment of synteny breakpoints in regions with increased genomic insulation. However, in-depth analysis shows a confounding effect of gene density on both insulation and distribution of synteny breakpoints, suggesting limited causal relationship between breakpoints and regions with increased genomic insulation. At the level of individual loci, we identify specific, extremely long-ranged looping interactions, conserved for ~100 million years. We demonstrate that the mechanisms underlying these looping contacts differ from previously described Polycombdependent interactions and clustering of active chromatin.

A chromosome map of Anopheles messeae: application for physical genome mapping and population genetics

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Abstract: The development of high-quality genome assemblies requires anchoring genomic supercontigs to the precise chromosome locations. Recent studies developed chromosome maps for several malaria vectors from the Maculipennis group – Anopheles atroparvus, An. sacharovi and An. beklemishevi. The cytogenetic map for An. atroparvus helped to improve the quality of the genome assembly for this species. However, a chromosome map for An. messeae, the species with the widest distribution in Eurasia, is still missing. In this study, we developed a standard map for the chromosomes from salivary glands of An. messeae. High-quality images of orcein-stained squashed chromosomes were processed to obtain straight chromosome arms. Five DNA probes were mapped to the different chromosome arms using fluorescence in situ hybridization (FISH) to prove the robustness of the map for physical mapping. In addition, we describe chromosomal location of five polymorphic inversions. Using microdissection of polytene chromosome we developed DNA probes, overlapped the breakpoints of polymorphic inversions. These probes were applied for precise chromosome mapping of polymorphic inversion borders. Cytogenetic analysis is a robust technique for identification of chromosomal inversions in natural populations. The standard map includes the standard inversion arrangements XL1, 2R0, 3R0 and 3L0 and the standard 2L arm, which lacks the inversions. To simplify inversion identification, we also developed maps for two inversion variants of the X chromosome (XL0 and XL2) as well as 2R1, 3R1, and 3L1. Moreover, we presented images of heterozygous inversion variants for each chromosome arm. The utility of the chromosome maps was demonstrated in our analysis of inversion polymorphism in several natural populations of An. messeae.

Acknowledgments: The image processing and fluorescent in situ hybridization were supported by the Russian Science Foundation grant No. 19-14-00130 to MVS. The development of the DNA-probes for polymorphic inversions mapping was funded by Russian Foundation for Basic Research according to the research project 18-34-20106 to GNA. Mosquito collections and chromosome preparations were supported by the Russian Foundation for Basic Research 18-04-01117 to MIG.

A chromosome-based tool for identification of mosquito species Aedes behningi, Ae. excrucians, Ae. euedes and Ae. communis (Diptera: Culicidae) in Russia.

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Abstract: Mosquitos from genus Aedes represent carriers of human diseases. About 30 species from this genus were found in Tomsk region in Russia. Thus, precise identification of Aedes species is of medical importance. However, because of the absence of clear morphological differnces or molecular markers, the tools for precise species identification are still missing. In this study, the karyotypes were analyzed in 4 species from the genus Aedes: Ae. behningi, Ae. excrucians, Ae. euedes and Ae. communis. Mosquitoes were collected in Tomsk region, Russia at larval stage. 4-instar mosquito's larvae were used for the cytogenetic analysis. The mosquitos from genus Aedes have three pairs of chromosomes. In this study, chromosome lengths were measured using ImageJ program. For the analysis of the chromosome banding patterns, staining with lacto-aceto-orcein and DAPI were performed. In addition, the locations of ribosomal genes (rDNA) were identified by fluorescence in situ hybridization (FISH). The results were analyzed using light and fluorescence microscopies. Chromosomes were numbered according to the standard classification of the Aedes chromosomes, as the smallest chromosome 1, the longest chromosome 2, and the intermediate chromosome 3. The centromeric index was calculated as $Jc = p/(? + q)$, where p is the short chromosome arm and q is the long arm. The study identified that all three chromosomes in studied species are metacentric but the chromosome lengths varied between the species. Ae. excrucians has longest chromosomes, Ae. behningi has shortest chromosomes, Ae. euedes and Ae. communis have intermediate chromosome lengths. According to the analysis of the chromosome patterns we developed chromosome idiograms that reflect interspecies differences among the species Ae. behningi, Ae. excrucians, Ae. euedes and Ae. communis. Lacto-aceto-orsein staining revealed a significant difference in the position of bands in chromosome 1, DAPI bands indicate a distinction across all three pairs of chromosomes. It is known that DAPI staining detects DNA enriched with AT repeats. FISH revealed the location of rDNA loci in the chromosomes. Ae. behningi, Ae. excrucians, Ae. euedes have one rDNA locus in chromosome 1 but in Ae. communis chromosomes the rDNA locus was found in chromosome 2 suggesting that a translocation between these probably occurred in evolution of these species. Thus, this study developed a chromosome-based tools for the species identification. The chromosome length, chromosome banding pattern and location of rDNA allows to clearly distinguish 4 aedini from the genus Aedes.

A physical map of the Aedes albopictus genome

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Abstract: The Asian tiger mosquito, Aedes albopictus is an aggressive, day-time biting insect that is emerging throughout the world as a public health threat following its primary role in recent dengue (DENV) and Chikungunya (CHIKV) outbreaks. Part of its impact on human health is due to its ability to adapt to suburban and urban environments, develop egg diapause when exposed to short day length, and its opportunistic blood choice (preferring to bite humans if available). Progress in understanding the science of mosquitoes and building up the instruments to battle them has been eased back by the absence of a great genome assembly. In this study we developed a new approach using fluorescence in situ hybridization to validate and orient fifty transcripts or gene exons from twenty largest genomic supercontigs to the mitotic chromosomes of Ae. albopictus. Physical mapping allows to check for the quality of the assembled genome by confirming or dismissing assembly predictions. Our approach was based on amplification of DNA probes using cDNA instead of Bacterial Artificial Chromosome (BAC) clones because utilizing BAC clones for highly repetitive genomes such as Ae. albopictus becomes extremely challenging. In addition, we mapped 18S rDNA in the region of the secondary constriction in region 1q22. The intensity of the signal significantly varied among chromosomes suggesting variations in number of ribosomal genes. We also mapped the largest bioinformatically-identified viral integration in the assembly confirming that this viral DNA is integrated to the chromosome 2q close to the telomere end. Physical mapping of PPO genes supported the genomic data of the presence of three clusters of these genes in chromosome 2.

Advances in physical mapping of malaria mosquito genomes

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Abstract: Development of high-resolution chromosome maps is an important step in genomic studies. Anchoring genomic supercontigs to the chromosome positions is required for the development of chromosome-based genome assemblies. Cytogenetic maps are also important for identification of chromosome positions of genes, chromosome segments or chromatin proteins. Physical mapping of inversion breakpoint regions is necessary for studying chromosomal rearrangements. For example, physical mapping of the genomes of Anopheles gambiae, An. atroparvus and An. albimanus revealed near-whole arm chromosome translocation during mosquitoes evolution. Despite the development of long-read sequencing techniques, such as PacBio and Oxford Nanopore, as well as application of the Hi-C technology for scaffolding of genome assemblies, chromosome maps are still useful in guiding the genome assembling process. Malaria mosquitoes have six chromosomes in the diploid complement. Due to the small number of chromosomes and perfect-quality polytene chromosomes, about 100 chromosome maps are available for Anopheles mosquitoes. The technology of cytogenetic mapping evolved from simple drawn chromosome maps to high-resolution digital photomaps that are currently available for 10 most important malaria vectors. Some of these chromosome maps have been used for the physical mapping of the reference genomes for An. gambiae, An. stephensi, An. albimanus, An. atroparvus, and An. sinensis. Here we present a high-resolution chromosome map of An. messeae s.l., the member of the Maculipennis subgroup. This species is an important malaria vector in Europe and Russia and it occupies a large territory of Eurasia. The species has well developed inversion polymorphism located on four chromosome arms including the X chromosome. The application of region-specific microdissected DNA-probes is demonstrated as a useful approach for precise mapping of inversions breakpoints.

Geographic distribution and inversion polymorphism in natural population of cryptic species Anopheles messeae and Anopheles daciae in Eurasia

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Abstract: Anopheles messeae Falleroni is geographically widespread and genetically diverse Eurasian species, which was the major vector of malaria transmission over this territory in the past. Five highly polymorphic inversions associated with the geographical distribution have been reported in this species. A cryptic species A. daciae, Linton, Nicolescu & Harbach was first discriminated from A. messeae in 2004 by five nucleotide substitutions in ITS2. However, distribution of A. daciae in Eurasia and inversion polymorphism in this species remain poorly understood. In this study, mosquito larvae and adults were collected from eight geographically distant regions in Eurasia from Russia and Latvia. ITS2 sequences were analyzed in 1465 specimens of Anopheles, of which 993 were karyotyped. Our study supports a previous observation that among the five described nucleotide substitutions in ITS2 only two have fixed differences between A. messeae and A. daciae. We observed varying species composition among the collected samples, which ranged from the complete absence of A. messeae in Voronezh and Sevastopol (Russia) to the complete absence of A. daciae in Irkutsk (Russia). Both species were found in equal proportions in Riga (Latvia), Moscow, Ufa, and Novosibirsk (Russia). Interspecies hybrids were rare and were identified only in Tomsk and Novosibirsk. Three other species A. maculipennis, Meigen, A. atroparvus, Van Thiel, and A. beklemishevi, Stegniy, Kabanova were found in several locations. A cytogenetic comparison of A. daciae and A. messeae samples demonstrated that the two species significantly differ from each other by the frequencies of polymorphic inversions. Previously described inversion X0 fixed in A. messeae was found in this species at an extremely low frequency. Inversions X2 and X4 were found only in A. messeae. Principal Component Analysis based on the frequencies of autosomal inversions in the populations studied clearly distinguished two species and demonstrated much higher diversity between the populations of A. messeae. Average Fst value between species was 0.147 with highly significant values for the majority of inter-species population comparisons. Nested AMOVA analysis indicated that significantly more variation was accumulated between the species than between their geographical populations. Overall, our study demonstrated that A. daciae prevails in the western locations and is absent in the Eastern Siberia. This study also uncovered genetic differentiation between A. messeae and A. daciae associated with chromosomal inversions. Understanding the species composition of malaria vectors in Northern Eurasia and their genetic divergence will be instrumental for developing an adequate strategy for the vector control.

Sequencing and statistical analyses were supported by the Russian Science Foundation grant 19-14-00130 to MVS.
Karyotyping was supported by the Russian Foundation for Basic Research 20-54-04017.

Relationship of characters of the propodeal-metapectal complex and ovipositor to host use in Ichneumonidae

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Abstract: A recent hypothesis by Li et al. (2015) suggested there are four main types of propodeal-metasomal articulations in parasitoid wasps related to distinct oviposition postures adapted for different types of hosts and host habitats. Here we test this hypothesis by examining covariation among morphological features of the propodeal-metapectal complex and ovipositor along with host in extant Ichneumonidae.

Estimating the number of global insect species extrapolating data from Costa Rica: Erwin was right!

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Abstract: Employing recently generated data from reared and Malaise-trapped, barcoded specimens from Área de Conservación (ACG) in north-western Costa Rica, we generate estimates for the total number of Microgastrinae in ACG's 125,000 terrestrial hectares of dry forest, cloud forest and rain forest. This is accomplished by comparing the number of microgastrine COI BINs (Barcode Index Numbers) from reared caterpillars with those of Malaise-trapped BINs. Entire samples from dozens of Malaise-trap years have been barcoded and this allowed us to compare the relative species-richness of microgastrines with other braconids, ichneumonids, Hymenoptera, and other insects. With these estimates for ACG, we extrapolate estimates for these taxa for Costa Rica and the world. These broader estimates were generated by using the number of tree species in ACG, Costa Rica, and the world as a template. Our results indicate that Terry Erwin's (1980) estimate of 30 million insect species is a reasonable approximation.

Overcoming the taxonomic impediment: A radical solution for an intractable problem

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Abstract: The magnitude of the taxonomic impediment is outlined using data collected from decades of biodiversity research in Costa Rica. We demonstrate that, given the current rate of species descriptions, it will take thousands of years to treat all extant species. The solution proposed is a DNA (COI) barcode approach to characterize species, similar to that published in Deutsche Entomologische Zeitschrift by Meierotto et al. in 2019. Each species treatment consists of a diagnosis based on the information contained in the barcode region of the COI gene, an image of the specimen, and some details necessary to conform with the International Code of Zoological Nomenclature. An example using hundreds of new species from Costa Rica is presented. It will emphasize that these treatments are not meant to be the final step in species-level taxonomy for hyper-diverse taxa, but rather a necessary first step that will facilitate more comprehensive treatments when warranted and to be integrated with classical morphology-based descriptive taxonomy in an efficient manner.

Towards a new infrageneric structure of the genus Copelatus Erichson, 1832 using the Australasian species as an example

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Abstract: With its 454 described, mostly tropical species, Copelatus Erichson, 1832 is the largest genus in the family Dytiscidae. The genus remains poorly studied, being one of the taxonomically most challenging dytiscid clades. Creating and using a species group system for large genera has been proved to be a very useful in taxonomic studies, although such species groups are informal, artificial units. However, application of molecular analyses and more detailed investigations of morphological characters allow us to suggest natural species groups, i.e. monophyletic groups. Copelatus is traditionally divided into 15 groups, following Sharp's (1882) species group classification based on the number of elytral striae. Recently, several studies on African, Neotropical and Oriental species showed that the numbers of these striae could strongly vary and, therefore, the present infrageneric system of the genus is in need of revision. Since nine of the known Copelatus species groups include Australasian species, and the species of this region are the most poorly studied, we initiated a project on their systematics with one aim being the revision of the species group classification.

We studied in details the morphology of the species from Australia, New Guinea, and Solomon Islands. We chose shape and setation of the male genitalia as a set of key characters for the new Copelatus species group structure. Two main development tendencies of the median lobe were discovered. Using them, as well as shape and setation of paramere, we proposed 12 new species groups for more than 100 species in Australasia, approximately 90 of which are new. A weak correlation of the groups with the number of the elytral striae was noted. Results of our preliminary phylogenetic analysis based on molecular data confirmed monophyly of most of the groups. Further examination with involving of the larger species number from the different regions is planned to verify our preliminary results on the new infrageneric structure of the genus Copelatus.

BMSB Economic Impact Survey (Republic of Georgia)

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Abstract: The emergence of the Brown Marmorated Stink Bug (BMSB) in the Western part of Georgia has left visible damage across the agricultural sector. This study served to analyze and determine the economic impact of the BMSB on Georgia's hazelnut sector. In particular, this study calculated the foregone export earnings, utilizing secondary data sources, as well as descriptive statistics. In addition to calculating the foregone foreign exchange earnings, the study also analyzed the household composition, farming practices and alternative income sources of hazelnut farmers to provide a more holistic analysis. The result shows that actual yield levels in MY2016-17, MY2017-18, MY2018-19, MY2019-20, and MY2020-21 were 63%, 40%, 26%, 50% and 70% of growers' expectations, respectively. The unrealized export earnings in MY 2016-17, MY2017-18, MY2018-19. MY2019-20, and MY2020-21 amounted $US 4 million, $US 36 million, $US 74 million, $US 50 million and $US 11 million. The study found that the proportion of damaged kernels (blank, shriveled, mouldiness) has increased from 14 % in MY 2016-17 to 28 % in MY 2018/19, followed by a decline to 10% in 2020/21. Hazelnut output projection for MY2021/-22 is less positive than those during the last two years, given that reportedly plant protection measures have been implemented on a limited scale in 2020-21 and fall 2021. However, projections could be revised given intensive plant protection campaign already initiated by the MEPA/ NFA during the current production season and favorable weather conditions.

Findings and results of this study do not suggest that losses in yield and quality of hazelnut during the 2016/17-2020/21 production season were solely due to the BMSB. Rather, Georgia's reduction in hazelnut production and quality is also due to the combination of negative factors that include increased pressure from the BMSB as well as an increased presence of fungal diseases and unfavorable weather conditions. These factors, coupled with farmers' failure to adhere to proper production practices, contribute to the total foregone revenue of farmers and processors. The joint efforts made by different stakeholders (government, development agencies, local authorities, professional associations) during the last few years including awareness raising campaign on monitoring and control of BMSB may play critical role in improvement of yield levels and reduction of unrealized export earnings.

"beesofcanada.com": A resource of assisting in the conservation of bees in Canada, and the current status of our bees

Authors: Sheffield Cory S.[2] and Heron Jennifer M.[1], [1]British Columbia Ministry of Environment and Climate Change Strategy, Canada, [2]Royal Saskatchewan Museum, Canada

Abstract: In Canada, species at risk are assessed using two methods: 1) broad assessments for all species of a given taxa (e.g., all bees) at the national scale via "Wild Species: the General Status of Species in Canada" (Wild Species), and 2) at the individual species level via assessments done through the Committee on the Status of Endangered Wildlife in Canada (COSEWIC). Wild Species assessments are done every five years using NatureServe methodologies, and assessments include species that are not at risk as well as those considered potentially at risk. COSEWIC assessments for individual species use International Union for the Conservation of Nature (IUCN) Red List procedures and are only done on select candidate species. However, both methods require species data, and for the ca 900 bee species in Canada, such data is not readily available. The website "beesofcanada.com" was developed to provide users with an easy to use resource for all things bees in Canada, including a filterable species list generator for each jurisdiction, a complete catalogue with synonymies and type information, summaries of ecological information, and detailed point maps for each species. Though the website is currently being populated with data, information was recently used to assess bees for Wild Species; the results of this assessment will also be summarized.

Bacterial Communities of Artificial and Natural Mosquito Breeding Sites in Taiwan and the Search for Microbial Insecticides

Authors: Shelomi Matan, National Taiwan University, Taiwan

Abstract: This presentation covers three separate experiments done as part of a three-year project on mosquito-microbe interactions in Taiwan.

1) Container-breeding mosquitoes detect the presence of certain microbes in the water, stimulating oviposition. We hypothesized that the presence or absence of certain microbes in containers thus drives the differential attraction of different mosquito species to different container types, and that these relationships could be detected via metagenomics. We focused on Aedes aegypti and Ae. albopictus, both of which coexist in artificial containers in Southern Taiwan, and sought to see if these species' presence or absence in a container correlated with that of certain microbes.

2) Artificial containers are attractive to Aedes, but other mosquitoes prefer natural, plant-based water containers, or phylotelmata. These include large axils, tree hollows, and bamboo tubes. We sampled from such containers in Northern Taiwan, in the autumn and the spring, to compare the microbiota over time and across species, and to once again see if mosquito presence or absence correlates with microbiota.

3) We cultured many microbes during our collecting trips. Did any of these have effects on mosquitoes that could be detected in the laboratory? We present the results of our larvicidal assays on environmental microbes, as well as on known but terrestrial entomopathogenic microbes, in the hopes of finding a possible biocontrol.

Antimicrobial Peptides of the Phasmatodea

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Abstract: The Phasmatodea, or stick and leaf insects, are an understudied clade of insects whose pathology is of interest to cultivators and conservationists. Part of an insect's innate immunity are antimicrobial peptides (AMPs), which have therapeutic potential in human and veterinary medicine. We exposed stick insects to a mixture of pathogens to induce an immune response, and used RNA-Seq to identify subsequently differentially and/or highly expressed genes in Peruphasma schultei. AMPs were identified in the attacin, coleoptericin, defensin, thaumatin, and tachystatin families. We also found C- and i-lysozymes and several pattern recognition proteins [gram-negative bacteria-binding proteins and peptidoglycan recognition proteins]; as well as a large group of short, cysteine-rich, secreted peptides, many of which were highly induced and predicted to potentially have AMP activity. We also found 45 different sequences of hemolymph lipopolysaccharide-binding proteins, which is an unusually large number for insects. This is the first work to look at AMPs and immunity in stick insects, with implications for Phasmatodea conservation and pathology.

Ovarian specifically expressed genes of rice pest brown planthopper and theirs contributions for the reproduction.

Authors: Shen Yan, Zhejiang University, China

Abstract: The vast majority of insects, reproduction requires not only monitoring of internal physiological stimuli, but also depends on complex physiological responses to the external environment. We learned that most of female insects are oviparous. In a general way, ovulation is followed rapidly by fertilization and then oviposition. The regulation of insect reproduction are poorly known in insects, especially compared with knowledge of vertebrate reproduction.

The brown planthopper (BPH), Nilaparvata lugens, a phloem-feeding hemipteran insect, has emerged as a major pest of rice plants in Asian countries. Robust capacity for fecundity is one of the main causes of the serious economic losses inflicted by BPH. As there are so many genes participating in the reproductive events. We thoroughly searched and analyzed the genomes of BPH at both genomic and transcriptomic levels, and selected genes who were almost exclusively expressed in ovary of BPHs. They account for more than 1% of the total N. lugens genes encoded in the genome. We supposed these ovarian specifically expressed genes may be associated to female reproduction and even play significant roles in fecundity. To determine their functions, we conducted RNAi experiments in 0- to 2-h female adult BPHs. Here, we select three representative and interesting examples in our recent study:

1. The very first process in the reproductive success of oviparous species is the biosynthesis of vitellogenin (VTG, Vg). Here, we identi?ed a Vg and two Vg-likes from BPH. We found NlVg is a conventional insect Vg that is involved not only in reproductivity and embryogenesis, but also in nymphal development; NlVg-like1 is related to hatching; NlVg-like2 is associated with oocyte nutrition absorption.
2. A pair of healthy oviducts is important for female adults. We identi?ed a novel neuropeptide-like protein, Nl851, is specifically expressed in female's oviducts. We found more than one eggs were stuck in oviducts simultaneously during spawning. TEM showed the epithelial cells of lateral oviducts were loosely and irregularly arranged, which increasing the difficulty of female reproduction.
3. Eggs are compressed during passage down the narrow oviducts in spawning, so eggshell's elasticity facilitates oviposition. We identified an eggshell-related protein, Nl6565, who was essential for egg maturation in BPH. All oocytes appeared concavity in the middle portion with thin and rough endochorion layers after the injection of dsNl6565. Some developed oocytes had even entered the hypertrophied bursa copulatrix, causing the inability of reproduction.

Our findings help to better understanding of the ovarian specifically expressed genes in the phloem-feeding species and reveal a new angle for finding potential targets at BPH management based on RNAi technology. However, there are much still to learn about the genes associated with reproduction.

Impact of the Nagoya Protocol on biological control activities in Australia

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Abstract: Australia is a signatory, but has not ratified the Nagoya Protocol (NP) since it came into effect in 2010. There have been a number of publications explaining the implications of the NP for classical biological control activities some of which have described procedures to ensure biological control activities address the requirements of the Nagoya Protocol. While Australia undertakes a wide range of classical biological control programs against mainly weeds, vertebrate and invertebrate pests, Australian biological control research agencies have not formally developed or applied any such procedures to their practices when engaging with native range countries. Addressing the NP has largely involved understanding the implications of it for classical biological control programs and developing close working relationships within native range countries to work within the spirit of the agreement. This includes signed agreements with local research agencies including certain levels of Australian investment and paid collaboration. Obtaining all the relevant local permits for collection and shipping, being explicit about the activities being undertaken, and making sure that all the biological control activities resulting from these interactions remain within the public good not-for-profit basis under which most classical biological control programs are undertaken. The NP has certainly had an impact on the capacity to collect and ship potential biological control agents from some jurisdictions, but these jurisdictions appear to be operating under local legislation and regulatory mechanisms that go well beyond those relevant for the standard implementation of the NP. In such instances Australian research agencies do engage consular services from the relevant AU embassies to help with negotiations, but this has not always led to easier access to potential biocontrol agents. Part of the issue is the diversity of ways in which countries that have ratified the NP are implementing it within their jurisdictions and given this, the reluctance of research agencies within Australia to get bogged down in formal NP based negotiations with all native range countries Australia needs to access for fear this would grind biological control programs to a halt. Australia as far as possible continues to work within the spirit of the NP using the principles developed in the published guidelines for classical biological control activities.

Molecular characterization of pars lateralis neurons relevant to diapause control in the blow fly, Protophormia terraenovae

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Abstract: Many insects anticipate the arrival of an unfavorable season by sensing photoperiod to enter diapause. Although endocrine mechanisms underlying diapause induction have been studied in many species, neural mechanisms mediating environmental control of diapause have not been understood well. Adult females of the blow fly Protophormia terraenovae develop the ovary in long days, whereas ovarian development is inhibited via suppression of juvenile hormone (JH) biosynthesis in the corpus allatum (CA) to enter reproductive diapause in short days. Brain surgery and neuroanatomy showed that neurons with somata in the pars lateralis (PL) and fibers in the posterior lateral tract in the brain, termed PL neurons, are necessary for diapause under short days. However, PL neurons are heterogenous in their neurochemistry and in fiber projection, and it is not known which types of PL neurons are important for diapause control. Location of clock protein PERIOD-immunoreactive dorsal neurons (DNs) seems to be close to the PL in P. terraenovae. It is possible that some PL neurons may correspond to DNs themselves. In this study, we characterized PL neurons by single cell PCR and immunohistochemistry to discuss relevant neurons to diapause control. After fluorescent dye filling through the nervi corporis cardiaci, labelled PL somata were individually collected for nested-PCR to examine gene expression of neuropeptides and circadian clock proteins which had been localized either in P. terraenovae PL neurons or in Drosophila melanogaster DNs. Of 24 PL somata (females, N=6) 75 % expressed at least 3 clock genes (clock-gene expressing PL somata). Two kinds of neuropeptide genes expressed in more than 60% of the clock-gene expressing PL somata. Antibodies against these neuropeptides labeled PL neurons extending fibers in the CA, and receptor genes of both neuropeptides expressed in the CA. Quantitative PCR revealed that one of the receptor genes tended to express higher under short days than under long days in the CA. These results show a possibility that some PL neurons function as circadian clock DNs and also as neurosecretory cells releasing the neuropeptide to control the CA for diapause under short days. We are investigating effects of the candidate neuropeptide on JH production or release by the CA, and comparing activities of the PL neuron under different photoperiods in near future.

Morphological analysis of Pigment-dispersing factor immunoreactive neurons and pars lateralis neurons in the larval brain of the flesh fly Sarcophaga similis

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Abstract: Many insects in the temperate zone alter physiological states according to day or night length to develop or enter diapause, in order to survive unfavorable seasons. This response is called photoperiodism. The mechanism underlying photoperiodism consists of three components: “photoreceptors”, “photoperiodic clocks” and “endocrine systems”. Responsible organs and molecules about the photoreceptors and endocrine systems have been studied in many species, but little is known about which neurons are responsible for the photoperiodic clocks.
The flesh fly Sarcophaga similis enter pupal diapause in short days (SD), but S. similis reared under SD are destined from diapause to non-diapause pupae when they receive only 4 or 5 long days (LD) in the larval stage. Pupal diapause is caused mainly by suppression of ecdysteroids. In many lepidopteran species, prothoracicotropic hormone (PTTH) secreted from neurosecretory cells in the pars lateralis (PL) of the brain is important for synthesis of ecdysteroids. In addition, endogenous circadian clocks have been considered being involved in the photoperiodic clocks. Brain neurons expressing a neuropeptide pigment-dispersing factor (PDF) are known as circadian clock cells in several dipteran species. In this paper, to explore neural mechanisms underlying photoperiodism in S. similis, we examined projections of PDF neurons and PL neurons which have cell bodies in the PL. We hypothesized that PDF neurons may store photoperiodic information. Then additionally we examined whether PDF neurons change the morphology between SD and LD.
First, we performed immunohistochemistry using an antiserum against PDF combined with backfill staining of PL neurons using neurobiotin with the third instar larval brain. Three to 6 PDF-immunoreactive (-ir) cells were shown in a hemisphere. Fibers extended from the somata were found at dorsal protocerebrum, and many immunoreactive varicosities were found along the terminal arborizations to the PL. Furthermore, we compared the number of PDF-ir varicosities between diapause (SD) and non-diapause destined larvae (exposed to only 5 days of LD in SD). Although there was no significant difference, the number of varicosities in SD was slightly less than that in LD. By unilateral backfills from a third from the distal end of the ring gland, 6 cells in the ipsilateral PL (PL-i) and 2 cells in the contralateral PL (PL-c) were labeled. Many fine fiber branches were labeled around the neurite from PL-i and PL-c cells. Since PTTH neurons are generally 2 pairs and terminate contralateral ring gland in D. melanogaster, the PL-c neurons are probably PTTH neurons. In addition, double staining of PL and PDF-ir neurons shows that PDF-ir fibers are close to fibers of PL-i and PL-c neurons. These results suggest that PDF neurons have interaction to PTTH neurons. PDF neurons may store photoperiodic information and send it to PTTH neurons.

Nutritional niches reveal domestication tradeoffs in fungus-farming ants

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Abstract: During domestication, human farmers traded greater crop productivity under cultivation for lower yields outside these specialized conditions. We found similar domestication tradeoffs across the phylogeny of fungus-farming attine ants. We first defined the fundamental nutritional niches (FNNs) of fungal cultivars and discovered they transitioned from broad and variable in loosely domesticated fungi to narrowed and specialized across millennia of domestication. We next tested whether ant farmers strategically harvest realized nutritional niches (RNNs) of nutritionally defined substrate mulches and found that colonies strictly regulated protein harvest to target their cultivars’ FNNs. We then combined molecular inference and extensive field studies to reveal that neighboring attine colonies often farm different fungal haplotypes with different growth properties. However, ant farmers can also navigate landscapes of nutritionally variable substrates to harvest broad RNNs and target their cultivar’s specific FNN. We finally explain how this integrative approach can unify the study of diverse farming systems around ecological niche and evolutionary mutualism principles.

Import and release of invertebrate biological control agents: regulation in Brazil

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Abstract: Import and release of exotic invertebrate biological control agents are potentially extremely beneficial or harmful. Proper research and regulation may help tip the balance in favor of its benefits. We will present the current status of Brazilian regulations.

Improvement of insect nets: Red-colored nets most effectively suppress the onion thrips, Thrips tabaci (Lindeman) invasion

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Abstract: Onion thrips, Thrips tabaci Lindeman, is distributed worldwide, and caused serious damage to Welsh onion, onion (Imai et al., 1988), persimmon (Morishita and Oue, 2001) and Citrus (Tsuchiya, 2001). T. tabaci is also known as a vector of Tomato spotted wilt virus (TSWV) (Zawirska, 1976) and Iris yellow spot virus (IYSV) (Doi, et al., 2003). In Welsh onion cultivation in Japan, T. tabaci is mainly controlled by insecticides. However, the pyrethroid resistance of T. tabaci has been reported in Japan, the USA, Canada, and Australia (Morishita and Oue, 2001; Allen et al., 2005; Shelton et al., 2006; Herron and James, 2008; Morishita, 2008).

Insect net is one of the physical control methods. Although the control effects of mesh size of the net on the insect invasion have been reported, there are few reports about the effects of the net color. Oya et al. (2011) reported that the density of T. tabaci on cabbage covered with the red-colored nets was very low. However, there are lots of unclear points about the behavioral response characteristics of this species against the red-colored nets. In this study, therefore, we examined the behavioral response characteristics of T. tabaci against the red-colored nets, and the control effects by covering Welsh onion with the red-colored nets under field condition, as one of the physical control methods.

1.Behavioral response characteristics of Thrips tabaci on Welsh onion against the red-colored nets

To evaluate the control effects of the red-colored nets against T.tabaci, we investigated the invasion rates of the thrips into the nets and the number of damage spots by the thrips on Welsh onion fully covered with six types of colored nets under laboratory condition. As a result, the invasion rates of T.tabaci into the nets were significantly lower by fully covering with the red-colored nets (red-white, red-red, and red-black type) than by fully covering with the white-colored nets (white-white type). In addition, the number of damage spots by the thrips on Welsh onion fully covered with all types of the red-colored nets was suppressed from approximately one-ninth to one-third of that with the white-colored nets.

2.The control effects by covering with the red-colored nets against Thrips tabaci

The control effects by covering Welsh onion with the red-colored nets (red-red type) on the populations of T. tabaci were investigated in the commercial fields in Kyoto Prefecture, Japan. The populations of T. tabaci on the plants fully covered with the red-colored nets were reduced to approximately one-tenth of those without nets covering. Furthermore, even only surrounding the fields by the red-colored nets, T. tabaci populations on Welsh onion were suppressed to approximately one-half of that without the red-colored nets.

These results indicated that the red-colored nets are effective and economically efficient measure for controlling T. tabaci.

Seasonal adaptations of the blister beetle, Epicauta gorhami, a hypermetamorphic insect

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Abstract: The bean blister beetle, Epicauta gorhami (Coleprtera: Meloidae), is distributed in Japan. The adults are polyphagous herbivores and occur in summer to autumn. In contrast, the larvae feed only on grasshopper eggs in soil. As is common with other species in Meloidae, E. gorhami larvae undergo hypermetamorphosis, with four distinctive larval stages in the typical meloid life cycle: the planidium, first grub, coarctate (pseudopupa), and second grub stages. The pseudopupa (fifth instar in the case of E. gorhami), a form characteristic of hypermetamorphosis for meloid beetles, is a dormant stage that is adapted for diapause. First, we have found that larval development of E. gorhami is controlled by temperature and photoperiod: at 25ºC all larvae enter diapause at the fifth instar as pseudopupae under short-day conditions, whereas substantial part of larvae pupate directly from the fourth instar under long-day conditions. At lower temperatures larvae enter pseudopupal diapause, whereas at higher temperatures they pupate directly from the fourth instar under any photoperiodic conditions. We have also observed that E. gorhami larvae metamorphose precociously if they encounter food shortages during the fourth instar. These larvae pupate or pseudopupate earlier with a smaller body size (precocious metamorphosis) compared to those supplied with sufficient food. The incidence of precocious pupation is influenced by the food supply: larvae under a food shortage tend to pupate even under short-day conditions at 25ºC. Consequently, the reaction norm is modified by the feeding conditions. The post-feeding period (11-12 days) before pupation is unchanged, irrespective of feeding conditions, and thus larvae in the face of food shortages may undergo normal physiological processes. In nature, large variation of food availability may exist among individual larvae of E. gorhami because the size of grasshopper egg pods available to the first-instar larvae varies greatly depending on the grasshopper species. In the face of food shortages, larvae are unlikely to find a new food resource because those at the feeding stage (i.e. first grub) are less mobile. Under such circumstances, it appears that an adaptive response occurs, in which larvae control metamorphosis in response to food availability. Finally, we examined how the reaction norm of food-deprived E. gorhami larvae functions in nature by rearing insects outdoors in different seasons with manipulation of the food supply. The results indicated that most fully-fed larvae entered pseudopupal diapause, whereas food-deprived larvae tended to pupate precociously without entering diapause, especially early in the season. The resulting smaller adults reproduced early in the autumn and their progeny attained the pseudopupal stage before winter, indicating that the reaction norm may have an adaptive role in controlling seasonal development in the face of food shortages, producing a bivoltine life cycle.

Eating for Winter – Diet Macronutrients Affect Caterpillar Diapause

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Abstract: Surviving winter is a severe challenge for many insects. Diapause allows insects to become dormant during harsh seasonal conditions like winter, thus synchronizing their growth, development, and reproduction with favorable seasonal conditions. Diapause may last many months and is often accompanied by the cessation of feeding, representing a substantial nutrient cost. However, many insects live in nutrient limited or risky foraging environments, so may struggle to obtain the nutrients needed for diapause. How might nutrient intake affect an insect's likelihood of diapause? Furthermore, how might an insect's feeding preferences change if it is destined for the resource intensive diapause program? We are investigating these questions in the corn earworm, Helicoverpa zea, using the geometric framework for nutrition to examine the relative roles of carbohydrate and protein nutrition. Overall, diapause and nutrition are mutually linked. Our experiments lay the groundwork for future studies to test the relative importance of nutrient intake and nutrient stores, or test the extent to which nutritional differences in agricultural crops may delay diapause and affect overwintering survival in the field. Our findings may contribute to IPM recommendations in agriculture landscapes with host plants predicted to cause different diapause incidence and overwintering survival in H. zea.

Landscape-scale consequences of nutritional heterogeneity in a major agricultural insect pest, Helicoverpa zea (Lepidoptera: Noctuidae)

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Abstract: The corn earworm/cotton bollworm, Helicoverpa zea, is a major generalist crop pest in North and South America. In the United States, H. zea typically shifts from utilizing corn as a host early in the growing season to cotton where it is an important mid-late season pest. Nutrition can have profound effects on insect growth, survival, and the ability to deal with environmental stressors. Corn and cotton vary substantially as nutritional resources for developing H. zea larvae, with corn being a very carbohydrate-biased nutritional resource whereas cotton offers a slightly protein-biased ratio of the two major macronutrients. When reared on carbohydrate-biased diets mimicking corn, H. zea larvae were more susceptible to both Bt toxins and nuclear polyhedral virus (NPV) infection relative to larvae reared on protein-biased diets that reflected the macronutrient profile of cotton. These results suggest that (i) selection for resistance to transgenic and biological control strategies whose efficacy can be affected by nutrition such as Bt toxins and NPV should be stronger for larvae utilizing corn as a host earlier in the season, and (ii) cotton provides a favorable nutritional environment that further facilitates their survival later in the year.

The Potential of Fluorescence Imaging to Distinguish Insect Species

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Abstract: We demonstrate a fluorescence analysis technique for discriminating between species of insect. Fluorescence was measured using a fluorescent stereomicroscope imaging system using violet and GFP filters. The imaging system recorded the emission of fluorescence, following excitation at various wavelengths (between 405-500nm) and emission in the ranges 460-700+nm. The set-up was successfully used to photograph a suite of pest and non-pest species in laboratory conditions. Several species exhibited fluorescence, which increases the scope for their detection and identification with implications for automated pest monitoring and early detection. This set-up can easily be adapted for field use increasing the scope for early detection and identification of insects with implications for automated monitoring

Anatomical differences between leaf galls of European Diplolepis eglanteriae (Hymenoptera: Cynipidae) introduced into Canada on exotic roses and galls of the endemic Diplolepis nebulosa on wild roses

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Abstract: The accidental introduction into Ontario, Canada of the European cynipid Diplolepis eglanteriae provided an opportunity to compare the structure and development of its gall with what appears to be an identical gall of the endemic species Diplolepis nebulosa. Both galls are spherical, about the size of a small pea, single-chambered, and with a smooth surface. Not only do galls of D. eglantariae occur on the adaxial (upper) surface of rose leaves whereas those of D. nebulosa occur on the abaxial (lower) surface of rose leaves, there are differences in the site of initiation, growth patterns and structures. Galls of D. eglanteriae are initiated from palisade cells, retain an epidermis, and when mature, have larval chambers lined with a thin layer of nutritive cells and a weak sclerenchyma layer within their walls. Galls of D. nebulosa are initiated from mesophyll cells, develop without an epidermal layer, have a thick layer of nutritive cells and a prominent sclerenchyma layer with cells filled with phenolics. These findings are consistent with the generally accepted observation that each species of Diplolepis induces structurally distinct galls.

Diversity and distribution of Protura in the world

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Abstract: Protura, known also as coneheads, are soil-dwelling microarthropods, wingless, eyeless, with slender, elongate bodies ranging in size between 0.7–2 mm. Due to their minuteness and cryptic edaphic lifestyle they were discovered relatively late in the history of entomology. Since their first description in 1907 up to 835 valid species belonging to 76 genera and three orders (Acerentomata, Eosentomata and Sinentomata) have been described worldwide. The proturan fauna of the northeastern Palearctic (59 species), Africa (60 species), Australia (32 species), North America (76 species) and South America (60 species) may be assumed to be poorly known in relation to the size of these areas as well as in comparison to the species diversity of the proturan fauna of Europe (187 species), China (217 species) and Japan (89 species). Analysis of the distribution patterns of proturans only a few cosmopolitan genera: the most diverse in the world comprise the genus Eosentomon (Eosentomidae), four genera of the Acerentomidae and the genus Proturentomon (Protentomidae). The members of the order Sinentomata are distributed exclusively in the Far East (China and Japan). Among the members of the Acerentomidae practically all genera of the Nipponentominae and some genera of the Acerentominae are distributed in the eastern Palearctic and North America. Members of the Berberentulinae, which are characterized by reduction of some morphological characters, instead are distributed mainly in the Pantropical region and the western Palearctic.

Recent faunistic analysis of the Arctic region at the northernmost border of Protura distribution showed that Arctic proturans are not species-rich (23 in total) but quite diverse: in addition to the cosmopolitan genus Eosentomon they are represented by eight genera of Nipponentominae as well as five genera of Acerentominae. The occurrence of proturans in Arctica is limited to Beringia. Some genera are known from both the American Arctic and Siberia, but the majority of their species have restricted distributions, and none has been found in both the American Arctic and Siberia. The higher number of Asian-North American genera confirms the generally accepted theory that northeastern Asia was the main center of speciation of Holarctic species, with the Bering land bridge serving as the most important exchange route from west to east and vice-versa.

Carcasses as caring nurseries: carrion preservation by the burying beetles and their microbiome

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Abstract: Carrion is an ephemeral resource, which is highly nutritious but susceptible to rapid microbial degradation. Despite carrion's susceptibility to putrefy and quickly turn unpalatable, the burying beetle Nicrophorus vespilloides is seemingly immune to any ill effects of feeding on decaying carcasses. Carrion is the sole source of nutrition for the larvae, and the maintenance of its quality is important for larval survival and development. Carcasses support a wide diversity of life forms including bacteria, fungi, nematodes, and mites that can affect carcass quality as well as compete with larvae for nutrients. How do the burying beetles cope with a challenging resource such as carrion, despite burying it in the microbe-rich environment of soil?

We demonstrate that the burying beetle successfully manages the carrion microbiota by preventing microbial succession typically associated with putrefaction. Instead, beetles inoculate their own gut microbes containing specialist, symbiotic bacteria and fungi on the carrion, which prevents carrion degradation. By comparing beetle-tended carcasses with untended carcasses, we show that the beetles' gut microbes reduce concentrations of putrefactive polyamines and modify the levels of digestive enzymes. This regulation of the carcass' biochemical and microbial properties is adaptive for beetles, for when disrupted, it reduces larval growth. The study demonstrates how insects modify their habitats to enhance fitness and regulate microbial competitors on an ephemeral resource such as carrion.

From Species Delimitation to Novel Vector Surveillance Tools in Culicoides

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Abstract: A multifaceted approach to species delimitation can often add clarity to issues such as cryptic species or species complexes. In North America, the main vector species is Culicoides sonorensis which belongs to a complex of species that have both morphological and molecular similarities. Single nucleotide polymorphism (SNP) data from individual Culicoides collected across the US and Canada identified an additional two cryptic species within the existing three species of this complex. The inability to differentiate these from the vector species in the past has undoubtedly affected vector competency estimates, species distribution maps, and vector surveillance efforts. Interestingly, there was also discordance between the SNP and mitochondrial data which explains why barcoding these species has had limited success. Based on these molecular identifications, we highlight subtle morphological and overt ecological differences that support these species designations. The larval habitats within this species complex are vastly different and could be evidence of speciation through ecological niche partitioning. Finally, species-specific microsatellite markers were developed to rapidly, and economically, differentiate the non-vector species from C. sonorensis. Continued study of the speciation of closely related vector and non-vector species will produce valuable evolutionary insights into vector competency as well as improve current surveillance programs.

Evaluation of Hook-SWD for Management of Drosophila suzukii in Low Pressure Systems

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Abstract: Attract-and-kill tactics work well in low pressure systems where the population of Drosophila suzukii rarely exceeds 20 flies per trap per week. The HOOK trade name encompasses a suite of attract-and-kill products, each formulated for a specific target pest and manufactured by ISCA Technologies. The effect of attract-and-kill product HOOK SWD, containing a proprietary fruit volatile-based attractant, a red dye, and 0.25% spinosad, on D. suzukii infestation was measured in conventional and organic commercial blueberry systems in north central Florida. Treatments included: 1) HOOK® applied every 7 days + grower's standard (suite of pesticides and practices), 2) HOOK® applied every 14 days + grower's standard, and 3) grower's standard only. Adult SWD population density was measured using Scentry® traps and lures, and adult emergence was measured by allowing adults to emerge from decomposing fruit. Trap catches revealed that there was no difference in treatments for adult density. However, larval counts as a result of adult emergence was significantly different among treatments. There was also a treatment-by-week interaction indicating reduced emergence later in the season. There was no difference between Hook applied at 7 d versus 14 d. These findings support the potential use of attract-and-kill as an additional IPM tool for D. suzukii management in low pressure systems.

Integrated and novel management strategies for Drosophila suzukii

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Abstract: Spotted-wing drosophila, Drosophila suzukii, is a worldwide pest of soft-skinned, stone and small-fruit. This species is able to utilize different habitats and substrates for both nutrition and reproduction. This capacity can be attributed to a significant capacity for adaption, a topic of multiple investigations. Here we will discuss seasonal biology, overwintering survival strategies, the use of population models, cultural, behavioral and chemical management options within the context of a whole-production management system.

Practitioners affected by this insect are currently largely dependent on agrochemicals in order to maximize yields and maintain quality standards. In some cases these crops have agrochemical input costs that are 61 times higher than non-specialty crops, in part because of this damaging insect. D. suzukii management costs can comprise up to 1/6th of the production costs of fruit production. These inputs however result not only on economic costs. Additional costs include those to the environment, pesticide resistance, and secondary pest outbreaks. The introduction of new control strategies including agrochemicals can be slow and corporate consolidations have reduced the number of organizations investing in R&D, which negatively affects the availability of novel control strategies. The goal of this talk is to provide a perspective of how season-long coordinated, novel, and conventional management strategies can result in significant savings to practitioners.

Non-target effects of insecticides labelled for organic use for management of Drosohila suzukii in berry crops

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Abstract: Drosophila suzukii is an invasive pest of soft fruits in North America, South America, and Europe. This destructive pest has led to the disruption of berry IPM programs due to the increase use of insecticides to manage this pest. Thus far, only one insecticide, spinosad (Entrust®) labelled for organic use has proven effective against D. suzukii populations. As more insecticide products become available for organic growers it is important to evaluate their residual effects on key natural enemies in the system. Here, we evaluate the effects of six organic insecticides alone and in combination with three adjuvants and two phagostimulants on three common natural enemies including two predators, Orius insidiosus and Chrysoperla rufilabris, and a parasitoid wasp, Aphidius colemani in laboratory bioassays. Sabadilla alkaloids caused mortality to O. insidiosus equal to that of spinosad. All insecticides evaluated were slightly toxic to A. colemani. The adjuvant, polyether-polymethylsiloxane-copolymer polyether caused mortality that was not significantly different from spinosad. When the sublethal effects of the two predatory species were examined by measuring eggs laid and % egg hatch, minimal sublethal effects were observed in C. rufilabris. Alternatively, all insecticides resulted in a reduction in egg hatch in O. insidiosus compared with the control.

Status of Insecticide Resistance in Drosophila suzukii in the United States

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Abstract: Drosophila suzukii is an invasive pest of small and stone fruits in the United States. Females oviposit into ripe or ripening fruit and larvae feed and develop inside the fruit. Due to very low tolerance for infested fruit in the market, preventative insecticide applications are made to control this pest which is not a sustainable approach and may lead to resistance development in field populations of D. suzukii. It is therefore extremely important to monitor field populations for resistance and implement resistance management strategies proactively. This presentation will provide information on protocols developed for rapid screening of field populations and results of a survey conducted to assess status of resistance against commonly used insecticides in D. suzukii field populations in the United States.

Effects of DEHP on development, ecdysteroid pathway, and reproduction of the moth Spodoptera littoralis

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Abstract: Bis(2-ethylhexyl) phthalate (DEHP) is a widely produced plasticizer considered as an endocrine disrupting chemical in vertebrates. Indeed, many studies have shown that DEHP alters hormonal levels, reproduction and behaviour in vertebrates. Few studies have focused on the effects of DEHP on insects while DEHP is found almost everywhere in their natural habitat, in particular soils and plants. Here, we investigated the effects of DEHP on sexual behaviour and physiology of a pest insect, the noctuid moth Spodoptera littoralis. In this nocturnal species, olfaction is crucial for sexual behaviour and ecdysteroids at the antennal level have been shown to modulate sex pheromone detection by males. In the present study, larvae were fed with food containing different DEHP concentrations, then DEHP concentrations were measured in resulting adults (males and females). Hemolymphatic ecdysteroid concentrations, antennal expression of genes involved in the ecdysteroid pathway (nuclear receptors EcR, USP, E75, E78 and calmodulin) and sexual behaviour were then investigated in adult males. The success and latency of mating as well as the success of egg hatchings were also studied from couples with one DEHP male versus one uncontaminated female or couples with one DEHP female versus one uncontaminated male. We also studied the offspring obtained from couples with contaminated females to test transgenerational effect of DEHP. Our results showed a general downregulation of nuclear receptors and calmodulin gene expression for the higher concentration of DEHP, suggesting a peripheral olfactory disruption. We found some effects on male behaviour, but without alteration of their mating rate. Effects on offspring mortality and developmental rate at the N+1 generation were also found for the highest doses of DEHP. Altogether, the study shows for the first time that larval exposure to DEHP could induce delayed endocrine disruptive effects in adults of a terrestrial insect as well as effects on the next generation.

Influence of insecticides on diurnal locomotor activity of Hylobius abietis L. (Coleoptera: Curculionidae)

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Abstract: The large pine weevil, Hylobius abietis, is an economically harmful insect pest in reforestation areas in boreal coniferous forests. The adults cause damage by feeding on the tender bark of stems of young conifer plants. Various methods have been attempted to control H. abietis. The use of pesticides (synthetic pyrethroids, neonicotinoids) in critical areas for environmental and health reasons should be minimised or banned. Many alternative repellents (botanical insecticides) are implemented to protect transplants against weevils. Application of new alternative control methods and introduction of biological insecticides require profound knowledge on the ecology and behaviour of forest pest insects. Little information in known about the diurnal rhythms of locomotor activity.

The aim of current research was to determine how industrially manufactured botanical insecticide karanja oil (a.i. karanjin) and neonicotinoid insecticide Actara 25 WG (a.i. thiametoxam) influence the adult pine weevils locomotor behaviour in laboratory contitions.

The experiments were carried out in an video tracking arena. Ethovision XT 11 (Noldus, The Netherlands) was used to record and analyze the movement of insects.

The results can be summarised as follows:

- In constant laboratory conditions the locomotor activity of the adults of H. abietis began to increase prior to the beginning of experimental darkness, revealing a peak during several hours of darkness, and decreased only some time after the end of the scotophase. In daylight, the beetles were relatively inactive. These rhythms appear to be of endogenous origin.
- Lethal concentration (0.2%) of Actara 25 WG influenced strongly female and male beetles` diurnal locomotor activity. In first hours after treatment beetles had locomotor disturbance and high activity. After 4 hours locomotor activity lowered and persisted low until the end of experiment. On beetles treated with thiametoxam endogenous rhytms disappeared.
- Karanja oil (10.0%) reduced beetles locomotor activity but natural diurnal movement dynamics of insects persisted.

Lethal and mobility effects of insecticides on the beneficial Pterostichus niger Schall. (Coleoptera: Carabidae)

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Abstract: Carabid beetles (Coleoptera: Carabidae) are biological indicators in agricultural landscapes. The aim of current research was to determine the food-related effect of industrially manufactured botanical insecticides NeemAzal-T/S, neem oil (a.i. azadirachtin), karanja oil (a.i. karanjin) and neonicotinoid insecticide Actara 25 WG (a.i. thiametoxam) on the mortality and mobility of the adult carabid beetles Pterostichus niger Schall.

The results can be summarised as follows:

- Reduced concentration (0.14%) of Actara 25 WG was the most toxic, causing the death of 43% of P. niger adults within 10 days.
- As a result of a dosage 10 times smaller than the recommended concentration of Actara 25 WG (0.02%), as many (19%) of P. niger died due to this within 10 days, as due to NeemAzal-T/S (12%) and neem oil (12%).
- Considerably less (9%) of P. niger died as a result of karanja oil compared to the reduced concentrations of Actara 25 WG. The preparations of neem (NeemAzal-T/S, neem oil) had similar effect on P. niger as karanja oil.
- Reduced concentrations of Actara 25 WG (0.14% and 0.02%) influenced the mobility of P. niger – 24 h after eating, the mobility of some insects were disturbed or they became immobile. Part of the immobile and insects with limited mobility recovered within 10 days.

Future studies should explain the influences of thiamethoxam and neem preparations to predatory carabid beetles and other beneficial arthropods behaviour and mortality. So far less studied karanja oil known to have insecticidal activity needs more comprehensive studies.

Dynamic interactions between the symbiont Candidatus Erwinia dacicola and its olive fruit fly host Bactrocera oleae

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Abstract: The olive fly, Bactrocera oleae, is the most important pest of olive orchards worldwide. The ability of olive flies to utilize olives for their development appears to be rare and unique in nature and has been associated with interactions with symbiotic bacteria. In the current study we reveal critical aspects of this unique symbiotic relationship between the olive fly and bacteria of the genus Candidatus Erwinia dacicola. These new insights presented here may stand as the basis for the future development of novel olive fly control approaches targeting the symbiont, by using molecular and classical tools in smart applications.

The determination of the relative abundance of Ca. E. dacicola with real time quantitative PCR analysis during the life cycle of the olive fly revealed a significant fluctuation between different developmental stages. With the use of microscopy, the localization of the the symbiont and the morphology of the gastric caeca between different larval stages were studied. Second instar larvae appeared with distended gastric caeca, filled with the bacterial mass, while during the third instar stage they were smaller and convoluted. We showed that the bacteria reside extracellularly in the gastric caeca and during the transition to late third instar stage, they are discharged into the midgut accompanied by a change in caeca size and morphology due to the contraction of the muscles surrounding the caeca.

Furthermore, a comparative transcriptomics analysis of gastric caeca dissected out of second and third instar larvae collected from the field, in comparison to samples obtained from a laboratory strain devoid of Ca. E. dacicola was carried out. Two pairwise comparisons were set; gastric caeca from second and third instar larvae, in order to identify genes potentially involved in this developmental transition and gastric caeca from second instar larvae developing in olives and in artificial diet, in order to identify olive fly genes potentially involved in the establishment and regulation of the symbiotic relationship, since wild-type animals contain huge numbers of the symbiont while the laboratory-reared not. Significant changes in transcript expression were noted and genes associated with the developmental changes revealed by the microscopic analysis as well as responses to microorganisms were highlighted.

Entomortierella and red wood ants - candidates for a yet undescribed symbiosis?

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Abstract: Entomortierella is one of the fungal genera recently determined in the study of the Mortierellaceae phylogeny1. The etymology of the name: entomon- refers to a frequent isolation of this genus representatives from insects. However, a determination of any explicit insect-Entomortierella interaction is still missing. In our studies on the mycobiota of Formica polyctena, we have isolated species of Entomortierella from the ants' environment. Precisely, we have isolated those strains from: the ants' cadavers3, infrabuccal pellets, and mound material. Moreover, preliminary results of our study suggest Entomortierella as a characteristic taxon for the F. polyctena mound material compared with the surrounding forest litter. Finally, in our preliminary behavioral studies, we have observed F. polyctena workers feeding on E. beljakovae hyphae and a tendency of ants to prefer this hyphae over soil-borne M. alpina. A nutritional value of E. beljakovae for the ants still remains unknown, however this species produces a great abundance of enlarged cells filled with oil droplets, which could possibly work as a supplementary food source. Observed presence of Entomortierella representatives in the F. polyctena environment and ants' interest towards the fungi suggest an occurrence of a previously unknown ant-fungal interaction, which needs further research to be fully understood.

Designing pest-resilient sustainable apple orchards using simulation models

Authors: Sigsgaard Lene, University of Copenhagen Department of Plant and Environmental Sciences, Denmark

Abstract: Simulation modeling is a highly useful approach when the goal is to predict, quantify, and compare outcomes for a range of complex input variables. There are numerous examples of successful integrations of simulation modeling used to develop sustainable crop management practices and to quantify the downstream effects on pest populations. The API-Tree research team experimentally and observationally gathered data on diverse plants' effects on insect communities in European apple agroecosystems. Using these data as inputs, we use simulation models to evaluate field designs for pest resiliency. We hypothesize these simulations will result in new, location-specific hypotheses for optimal pest-resilient field designs.

Round table. Proposal 1: The system approach to work on lever combination against pests

Authors: Sigsgaard Lene, University of Copenhagen Department of Plant and Environmental Sciences, Denmark

Abstract: Pest management is complex and dynamic and must be able to accommodate changes. In a system approach to pest management, it must rely on combining and integrating pest control methods to keep pest populations below the economic threshold. In integrated pest management –IPM, preventative measures are essential and include conserving and augmenting the natural enemies in and around the crop, choosing healthy cultivars and on crop management decisions, including physical management, use of fertilizers or irrigation and any biological or chemical control. Field experiments allow us to assess, in a real field context, the effect of different levers of action including management practices and lever combinations. In experimental fields, replication of treatments and controls can provide data with less variation and guide what should be tested in more realistic on-farm trials. In on-farm trials cropping system performances can be assessed. Results from experimental fields and on-farm experiments, provide a basis for developing management and testing novel field designs, such as the introduction of intercrops or flower strips.

Proposal 3: Participatory approaches as a way to tackle complexity towards the design of agroecological orchard

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Abstract: Perennial systems such as orchards are complex agroecosystems that encompass spatial (i.e., multi-layer design) and temporal (i.e., carry-over effects across consecutive years) dimensions. The design of such systems and/or their dissemination require various types of knowledge, from basic, to applied and empirical knowledge, thus involving a range of stakeholders in a participatory approach to tailor agroecological orchards.

Beside various types of experiments and modelling approaches to evaluate combinations of levers of action against pests and explore scenarii, co-design is a powerful way to innovate and tailor solutions adapted to farmers' context. Co-design permits creativity and to collect, mobilize, organize and hybridize knowledge from various sources in the design of complex agroecosystems. Participative approaches also permit farmers to appropriate experimental systems or parts of experimental systems to design their own ones on their farm. In system experiments, the way levers of action against pests are experimented and decisional systems formulated are key-elements to produce both generic and localized knowledge to feed the agroecological transition and face uncertainties. This advocates for more and renewed interactions among farmers, advisors, researchers and other stakeholders in the foodchain to innovate in a co-design process.

Fungi are more transient than bacteria in caterpillar gut microbiome

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Abstract: Despite a massive increase of studies on caterpillar gut microbiota (Insecta: Lepidoptera), there has been an emphasis on bacteria, neglecting the fungal component. Therefore, we lack data on whether are fungal microbiotas resident or transient, and shaped by similar factors as those of bacteria. Moreover, negligible attention has been paid to the role of microbiota in determining the host specificity. We sampled nine polyphagous caterpillar species from several tree species at multiple sites to determine factors shaping leaf and gut bacterial and fungal microbiota. We also investigated to which extent caterpillars acquire their microbiota from the diet. We performed 16S and ITS2 rDNA metabarcoding of leaves and guts to determine composition and richness of the respective microbiotas. Leaf bacteria and fungi were shaped primarily by spatial variables; however, in the guts, they affected only fungi. Gut bacteria were shaped primarily by caterpillar species, with some species harboring more specific assemblages. There were significant differences between leaf and gut microbiotas; in bacteria, this difference was more pronounced. Moreover, the leaf–gut similarity of bacterial but not fungal component differed significantly among caterpillar species, suggesting that some species have more transient bacterial microbiota than others. Our results suggest that the factors shaping caterpillar gut microbiota are complex, and highlight great interspecific differences in microbiota residency within the same insect functional group.

Research was supported by the Czech Science Foundation (GA18-08803S).

Optimal habitat matching in (semi)aquatic insects: A privilege of specialists?

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Abstract: Habitat selectivity and its effects on fitness remain poorly understood, especially in relation to specialization. We studied habitat selectivity and its consequences in selected taxa of aquatic insects (Hemiptera: Notonectidae, Coleoptera: Dytiscidae). From each group, we chose one habitat generalist (Notonecta glauca, Dytiscus marginalis) and one species specialized to fishless habitats (Notonecta obliqua, Acilius sulcatus). In a series of mesocosm experiments we quantified their responses to the vegetation type (no macrophytes, only floating macrophytes, floating and littoral macrophytes) and the presence/absence of fish predator (Carassius auratus), both at population and individual levels. To verify the preference–performance relationship, we investigated the survival of two selected species (Notonectidae: Notonecta glauca, Dytiscidae: Graphoderus cinereus) under the same experimental setting. At the population level, no differences were found between specialists and generalists, but similar preferences were found within individual groups. Both species of backswimmers showed a clear preference for pools without fish with floating macrophytes, while in both species of diving beetles it was impossible to determine the preferred habitat type. In backswimmers, at the level of individuals, no differences were found between the preferences of males and females; the decisions of both species were relatively consistent, and were governed by conspecific attraction. Contrarily, the selection of diving beetles was primarily density dependent, regardless of the presence of fish or vegetation structure. Their consistency in habitat selection decisions was generally lower than in backswimmers, and sex-related differences were found; males more often opted for the same habitat type, while female choices were rather random, probably due to male harassment. The survival rate was significantly higher in fishless pools with macrophytes, which was the preferred habitat type for both studied species. Therefore, optimal habitat matching is not a privilege of specialists but is rather a result of intra- and interspecific interactions and life- history strategies. In intensive fishponds with high fish stock density and altered vegetation structure, mismatch of cues for optimal habitat selection may lead to altered structure and composition of aquatic communities. Such ponds, ubiquitous in European agricultural landscape, may either deter many insect taxa from colonization and oviposition, or act as ecological traps through fish predation.

This research was supported by the Czech Science Foundation (GA-18-24425S).

Diversity and phenology of hoverflies (Diptera: Syrphidae) in pine forests (Pinus halepensis Miller) of Algeria

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Abstract: Hoverflies are good indicators of ecosystem integrity, especially in drylands. However, the key factors explaining hoverfly diversity in North African forest ecosystems are still not addressed. The current study provides data on the diversity, structure and functional trophic groups (FTG) of the hoverfly community in Aleppo pine forests under a semi-arid climate in northeastern Algeria. Using an entomological net, hoverflies were sampled weekly during 2008–2009. Alpha and beta-diversity of hoverflies and functional trophic group (FTG) were analyzed using several parameters and indices (e.g. species composition, richness, occurrence, diversity, estimations, similarity, etc.). In total, 602 individuals of 21 species were collected with a constant species (Eupeodes corollae)

and four common species (Episyrphus balteatus, Chrysotoxum intermedium, Eristalis arbustorum and Eristalis tenax). Most species (17) occurred accidentally or very accidentally in samples. The highest diversity was recorded during spring, corresponding to the flowering season of most understory plant species. Seasonal rarefaction and extrapolation curves indicated that the expected species richness would be higher in autumn and spring compared to summer and winter. The spectrum of FTG ranked predators first with 52.4% of species, followed by saprophagous (42.8%) and then phytophagous (4.8%) species. Hoverfly communities showed high taxonomic richness and alpha-diversity all over the year, with peaks during spring that coincides with flowering period of most plant species of the forest understorey and favourable climatic conditions.

The Near infrared spectroscopy technique for surveillance of disease vectors; Lessons learnt in the past 12 years

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Abstract: Vector control programs need high throughput, rapid and cost-effective surveillance tools to estimate the impact of interventions, determine exposure risk and direct interventions to disease hotspots. Traditional surveillance tools such as those that estimate insect survival or those that detect infections in insects are either laborious, technically demanding, or costly for operational use. Our team has been assessing the applicability of the near infrared spectroscopy (NIRS) technique as an alternative surveillance tool for vector control programs. It is a non-destructive one stop shop technique that can be used to measure multiple characteristics of an insect sample such as infection, species identity and age with just a single, 3-second reading of the insect. The technique does not require reagents to operate therefore hundreds of samples can be scanned and analyzed immediately.

We have collected over 20,000 NIR spectra from insects around the world. Our main goal is to be able to use these spectra and machine learning algorithms to predict the age, species, infection status and insecticide status of disease vectors. We will present results on the development and refinement of the technique over the past decade, challenges, lessons learnt and plans underway to successfully facilitate its incorporation into surveillance programs

Chemical composition of Tenebrio molitor (Fabricius, 1798) (Coleoptera: Tenebrionidae) reared on organic waste

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Abstract: The objective of this study was to evaluate the chemical composition of insect meals from Tenebrio molitor (MT) rearing in poultry litter (PL). A total of 250 T. molitor larvae were distributed in a completely randomized design with 5 treatments and 5 replications of 50 larvae per experimental unit. The larvae were placed in plastic containers (30cm x 15cm x 10cm) and arranged in bookshelf metal. The control diet (0%) was based on chicken feed (300g), wheat bran (475g), milk powder (125g), oats (475g) and barley (125g), and the other diets were 25, 50, 75 and 100% replacement of the control diet by PL. The PL used was rice husk base. Each repetition received 300g of feed, and the rearing moisture was controlled with the use of chayote (Sechium edule), which was checked every two days and replaced when it was senescent in appearance. At the end of the experiment, the larvae were accounted for, dehydrated in a greenhouse and ground for meals production. The meals T. molitor were evaluated for their bromatological and mineral composition: Dry matter (DM), mineral matter (MM), crude protein (CP), ether extract (EE), calcium (Ca), magnesium (Mg), phosphorus (P), potassium (K), zinc. (Zn), copper (Cu), manganese (Mn) and iron (Fe). All variables analyzed were subjected to analysis of variance, SNK (Student-Newman-Keuls) test. The values of Ca (0.58e, 21.56d, 25.32c, 28.73b e 30.57a), Mg (2.07d, 6.06c, 10.23b, 9.45b, 12.17a), P (8.360c, 3.44d, 9.29b, 9.88b e 10.39a) and Zn (100.30e, 121.70d, 130.30c, 136.30b e 145.50a) presented linear increase with the addition of PL in the diet; the K (30.27c, 45.87a, 29.90c, 40.73b, 23.83d) and Fe (56.78b, 62.07a, 35.07c, 5.75d, 5.65d) obtained higher values in MT when used 25% of PL and lower with use of 100% of PL; the Cu (10.50a, 11.75a, 2.28b, 1.70b, 1.83b) had higher values for the larvae reared with 0 to 25% of PL and Mn (10.79 c, 7.05d, 15.93b, 20.57a, 3.313e) to 75%. The DM of MT (meals) increased with the addition of PL (86.71b, 86.76ab, 85.98ab, 87.69ab, 88.48a) and CP decreased (48.16a, 45.89a, 46.08a, 47.31a, 40.26b) with the addition of 100% PL. The EE values were higher in the diet with 25% of PL (31.97bc; 34.25a, 31.30c, 27.22d, 32.88b). Larval development was better for the treatment with addition of 50 and 75% of PL (1,020b, 1,009b, 1,458ab, 1,705a, 1,058b), differing from the others, showing satisfactory development of the insects created in the residue. The results indicate that the used PL can influence the meal composition of T. molitor larvae without compromising the nutritional quality and larval development of the insect.

Temporal dynamics of Bemisia tabaci (Gennadius) (Hemiptera: Aleyrodidae) in commercial soybean cultivation

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Abstract: The objective of this research was to evaluate the temporal dynamics of adults and nymphs of B. tabaci on commercial Bt soybean crops. In the 2017/2018 harvest, the planted varieties were Brasmax BônimoIPRO® and BRS 9180IPRO®, and in the 2018/2019 harvest the varieties sown were Brasmax BólioIPRO® and Brasmax ExtremaIPRO®. The area for each variety was 16,000 m2, divided into 160 sample units of 100 m², in a 10 x 10 m experimental grid. The third trefoil counting from top to bottom was used for sampling of whitefly adults and nymphs. Counting of whitefly adults was done with care to avoid agitating the insects, with the help of a mirror to reflect the leaf's abaxial surface and facilitate counting in three plants per sampling point (4 evaluations/point and 3 plants/evaluation). The number of nymphs was determined by counting the insects on the leaflet's abaxial surface with the aid of a manual magnifying glass, on four leaflets per sample point (4 evaluations/point and 4 leaflets/evaluation). The sampling of nymphs and adults of B. tabaci was carried out in all 160 points previously georeferenced, in which at each sampling point four evaluations were made, 2 m equidistant from the central point (4 repetitions/sampling point). B. tabaci adults were recorded in the crops beginning 56 and 45 days after emergence (DAE), in the varieties Brasmax BólioIPRO® and BRS 9180IPRO®, respectively. In the 2017/2018 crop, nymphs were observed on both cultivars between 70 and 73 DAE. However, it is noteworthy that there was a progressive increase in the number of whitefly adults and nymphs on both varieties evaluated according to the days after emergence, even with the application of insecticides aimed at the control of B. tabaci adults and nymphs. In the 2018/2019 harvest, the beginning of the infestation in the Brasmax BonusIPRO® variety was approximately 64 DAE for adults and nymphs. In the same harvest at around 58 DAE, the onset of infestation by adults and nymphs of B. tabaci in the Brasmax ExtremaIPRO® variety was recorded. In the 2017/2018 and 2018/2019 crops, the number of adults and nymphs of B. tabaci on the Brasmax BônimoIPRO® variety remained close to one adult/plant and one nymph/leaflet. Regarding the BRS 9180IPRO® variety, in the 2017/2018 harvest there was a population abundance of almost ten adults/plant, and about two nymphs/leaflet, at 101 DAE. In the following harvest at 92 DAE the population peak of adults and nymphs of B. tabaci on the variety Brasmax ExtremaIPRO® was observed, with about five adults/plant and four nymphs/leaflet. Considering the stages of development of the plant, in general in both seasons, the infestation started between V8 and R2 and the peak population of adults and nymphs of B. tabaci was between R5 and R7. However, it can be seen that late cycle cultivars presented a greater infestation by B. tabaci adults and nymphs.

Genomics through the lens of pest management: how reference-quality assemblies are bringing the sterile insect technique to the 21st century

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Abstract: The sterile insect technique (SIT) is a concept devised by Knipling in the 1950s for the genetic control of pestiferous insects. Through the release of sterile males, SIT provides an approach that is a species-specific with few off-target effects but relies on damaging irradiation and manual sorting for mass-release of sterile male-only agents. Through the development of novel genomic techniques, reference-quality and chromosome-scale genome assemblies are accessible to investigators of non-model systems and can now be applied to make advancements in SIT. In our research, we employ single-molecule sequencing, linked-read sequencing, HiC mapping, and linkage mapping to identify genes and loci which can be exploited to produce conditional lethal sex-specific phenotypes that will facilitate male-only releases which could cut programmatic costs of SIT in half. These results are currently being applied in CRISPR microinjection and rearing projects to create a new genetic sexing strains in tephritid fruit flies that pose a threat to specialty-crop agriculture worldwide.

CTL4 gene-knockout to block Plasmodium infection in the vector mosquito

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Abstract: The development of genetically modified (GM) mosquitoes for malaria control has gained strength through the recent advances in gene-drive technology and an increased understanding of vector-parasite interactions. While most work aiming at the development of GM malaria resistant mosquitoes, suitable for population replacement, has focused on the over-expression of anti-parasitic genes, here we have explored a strategy relying on CRISPR/Cas9-based inactivation of mosquito encoded Plasmodium agonists. During its sexual cycle inside the mosquito vector, Plasmodium engages in intimate interactions and relies in numerous Anopheles derived host factors, which act as facilitators of infection. The C-type lectin CTL4 has been identified as a Plasmodium agonist (Osta et al., 2004). In our recent work we showed that the C-type lectin-mediated protection against parasite melanization in the African vector A. gambiae is dependent on the intensity of infection, rather than the mosquito-parasite combination (Simões et al., 2017). RNA interference (RNAi)-based silencing of CTL4 resulted in melanization and reduction of live parasites, albeit RNAi results in only partial gene silencing. We hypothesized that the knockout (KO) of CTL4 would result in complete melanization of the parasites, and consequently a complete halt of P. falciparum's development inside the mosquito. We are currently using CRISPR/Cas9
technology for targeted CTL4-KO in A. gambiae. We generated gRNA overexpressing A. gambiae transgenic lines that were crossed with the Vasa::Cas9 strain, to generate CTL4-KO A. gambiae mutants. These CTL4-KO GM mosquitoes are being evaluated for parasite blocking of total Plasmodium-agonist disruption. The effects of CTL4-KO on bacterial and fungal development inside the mosquito are also being screened.

Niche conservatism and functional traits of invasive Leaf-beetles

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Abstract: Non-native invasive insects have major impacts on ecosystem function, agricultural production, and human health. To predict the geographical distributions of these species, correlative ecological niche models are typically used. Such methods rely on assumptions of niche conservatism, although there is increasing evidence that many species undergo niche shifts during invasions. However, knowledge regarding niche conservatism and functional traits related to invasion dynamics remain incipient for many insect groups, in particular to Coleoptera – largest clade of Animalia. We compiled a novel database of 66 globally invasive beetle species, tested for niche expansion, unfilling across this group, and examined if factors such as human influence, climate, feeding habits, and body size may be associated with observed niche changes. Here we present results with a special focus on the family Chrysomelidae.

Mechanisms underlying plant specialization in the pea aphid complex

Authors: Simon Jean-Christophe, INRAE

Abstract: While the vast majority of insect herbivores feed on a few host plants belonging to a single or closely related taxonomic families, the molecular mechanisms underlying plant specialization remain poorly understood. The pea aphid Acyrthosiphon pisum forms a complex of biotypes, each specialized to one or few species of cultivated or wild legumes. This system offers a unique opportunity to study the molecular basis of plant specialization in the complex and to test whether the same or independent gene set determines plant specificity. Using a genome scan approach of pooled individuals from different biotypes of A. pisum, we first revealed hotspots of genomic differentiation that contain several genes of the chemosensory system and the salivary system, two functions respectively involved in host selection and exploitation by the aphid. Using functional tools, we validated the role of specific salivary genes as effectors in the aphid-legume interactions. Finally, using a GWAS approach on a large panel of pea genotypes, we identified resistance factors that may govern the outcome of plant-aphid interactions. Identification of aphid effector targets and the molecular basis of resistance factors in legumes will provide a better understanding of the mechanisms that determine host specificity in A. pisum.

Effects of intercropping aromatic plants with apple trees on aphid control

Authors: Simon Sylvaine[1], Gautier Hélène[2], Morel Karine[3] and Gomez Laurent[2], [1]INRAE Gotheron, UERI, France, [2]INRAE Avignon, PSH, France, [3]INRAE Gotheron, UERI, France

Abstract: In fruit tree production, the development of alternatives to chemical control is a major lever for solving the problems caused by the intensive use of pesticides. Compared to a monoculture, several studies have shown the benefits of introducing companion plants (CPs) with crops to repel pests and attract their natural enemies. However, the field evaluation of candidate CPs has not been carried out in orchards, which is a bottleneck for the use of this strategy by farmers. We hypothesized that some aromatic plants (Rosmarinus officinalis, and Tagetes patula) can affect the performance of aphids favoring their biocontrol, and can promote the action of their natural enemies and improve orchard productivity. Repellent aromatic plants intercropped with apple trees have been tested in a field experiment at the INRAE Gotheron experimental station and compared to grass ground cover as control. We studied the impact of the presence of aromatic plants in orchards on the abundance of the rosy apple aphid (Dysaphis plantaginea), a major pest of apple orchards. Our analytical approach was also based on observations of the abundance of natural enemies and measures of their efficacy in the bioregulation of the pest. This agroforestry system can offer an alternative or a complementary approach to optimize apple pest management and can produce aromatic plants answering the growing demand for these products.

Multifaceted impacts of resin use by honey bees for social immunity and colony health

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Abstract: Honey bees are constantly dealing with threats from pathogens, pests, pesticides and poor nutrition. It is critically important to understand how honey bees' natural immune responses (individual immunity) and collective behavioral defenses (social immunity), can improve bee health. One form of social immunity in honey bee colonies is the formation of a propolis envelope, made up of bee-collected plant resins, within the nest that acts as an important antimicrobial layer. Previous research has indicated that honey bees (Apis mellifera) use these resins as both and indirect and direct defense against various microorganisms. Further, a resin-rich environment effects individual physiological immune responses and resin foraging behavior can be influenced by pathogen exposure. The intricate role of propolis on individual bee and colony health is further compounded by other environmental conditions including resource availability, pesticide exposure and the microbiota of the colony. A large-scale effort examining these different factors will be discussed under the context of the impact of increased resin use of colonies involved in a commercial beekeeping operation and those maintained in stationary apiaries in Minnesota and Louisiana.

Gryllus veletis: a model for insect freeze tolerance

Authors: Sinclair Brent, The University of Western Ontario, Canada

Abstract: Freeze tolerance, the ability to survive internal ice formation, was first described in insects more than 250 years ago. However, we still have only a limited understanding of the mechanisms underlying this ability, perhaps because of a paucity of suitable model systems. Here, I introduce a new model freeze tolerant species, the spring field cricket, Gryllus veletis. Gryllus veletis can be reared en masse in the laboratory, and acclimated to induce freeze tolerance. When freeze tolerant, it can survive 7 days at -8°C or 1.5 h at -12 °C. G. veletis is large enough to allow us to dissect and study individual tissues ex vivo. My lab has assembled a transcriptome, characterised the gut microbiome, are embarking on genome sequencing, and are close to developing a functional RNAi protocol for gene knockdown. There are additional untapped resources, including (likely) genetically differentiated populations from its broad geographic range. I will then give two examples of how we have already used G. veletis to show that there is a metabolic cost to recovering from freezing, and that different cryoprotectants in a multi-component system have different functions in cellular protection.

The physiology and functional genomics of invasiveness in the Asian longhorned beetle

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Abstract: For many invasive insects, the ability to survive winter can dictate success of establishment and therefore influence the risk they impose on naïve environments. To cope with low temperature stress during temperate winters, many insects enter diapause and become more stress tolerant. The Asian longhorned beetle (Anoplophora glabripennis) is an invasive species whose native range spans both subtropical and temperate climates that likely drive variation in overwintering capacity among populations. Therefore, introduced A. glabripennis could pose variable invasion risk based on their source population. The objectives of this study were to identify transcriptomic and metabolomic markers of diapause and cold tolerance using established, invasive populations of A. glabripennis from North America. Overwintering larvae from these invasive populations enter diapause, suppress their supercooling point using cryoprotectants, and are partially freeze tolerant. These phenotypic changes correlate with significant transcriptomic changes including those functioning in the heat-shock response, epigenetic modification, and insulin signalling. Ultimately, these data will be used to identify population-level differences in the genomic regulatory regions associated with variation in diapause and cold tolerance phenotypes and therefore allow us to develop genomic markers correlated with invasion risk.

Role of Heat Shock Proteins in Aedes aegypti to cope up with high temperature exposure

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Abstract: INTRODUCTION
Dengue is one of the major public health problems in India. Studies have shown that insecticides exposure also imposes stress on mosquitoes' physiology. The present study was carried out to understand the role of Heat-Shock Proteins in response to temperature exposure and the identification of new physiological markers under combined exposure of temperature and insecticides in Aedes aegypti.
METHODOLOGY
Exposure experiments were carried out in Percival Incubator. Survival and exposure experiments were ranged from 5-45°C Temp & 65-75%RH. To optimize the expression of HSPs Quantitative real-time PCR was carried out for detailed analysis. Further, 1H-NMR spectroscopy-based metabolomic analysis was carried out to determine the impact of temperature on physiology along with insecticide exposure (4% DDT/5%Malathion/0.05% Deltamethrin) following the standard procedure. For tissue extract preparation 6% PCA and D20 for spectral acquisition were used. TSP was added as a chemical shift reference.
RESULTS
The results of experiments show a decreasing trend of adult emergence with increasing temperature. The impact of temperature on survival showed that at 36°C and 38°C vector could survive for 12±3.2 and 9±0.81 days only. Enhanced up-regulation of HSP70 was evident at all exposure ranges of temperature. HSP70 & HSP26 showed a significant up-regulation of 219 and 2580 folds at 40ºC for 1-hour exposure while HSP90 up to 18259 fold at 1-hour post-exposure at 35ºC. Actin was used as a control gene. 1H-NMR spectra of Aedes aegypti under temperatures and insecticides exposure revealed the presence of aliphatic, alcohol, vinyl, carbohydrate and aromatic low/ high mol. wt metabolites. The majority of the signals were found between the 0-9ppm part of the spectra. Of identified peaks, the maximum was in the aliphatic region of the spectrum as compared to the aromatic. The generated spectra show that the metabolites composition is highly variable between control & exposed groups (Temp./Insecticide+ Temp./Insecticide). The conc. of ßHOB, Lac, Acetoacetate, Chol, Hist, and Glu were fluctuating between control & exposed groups.
DISCUSSION
The study indicates that the varying exposure of Aedes aegypti to temperature affects longevity and survival. The up-regulation of HSP70, 90 & 26 for 1-hour exposure suggests that the vector is able to withstand the extremes of temp. and reduction in their longevity will not occur as expected. Metabolite profiling revealed the presence of dynamic metabolites and changes in the concentration under stressed exposure. The presence of HSP constituent's amino acids supports the role of HSPs in coping with environmental stress. The changes in the histidine are important as they play a crucial role in enzymatic catalysis and ligand binding. The generated Aedes aegypti metabolite profile appears to be a step forward to understand the impact of temperature in different scenarios of exposure. The detailed results will follow.

Role of Collembola in recycling of nutrients: a case study of Kathara coalmine area of Jharkhand, India

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Abstract: Collembolans – soil and litter apterygotes play an important role in the carbon cycle and have role in flux of soil biotic carbon pool. An experiment was carried out in the reclaimed over burden dumps (ROBDs) of Kathara coalmine area, Jharkhand, through 2007 – 2009 (early) to analyze the pedosphere arthropod mesofauna in general and Collembola in particular. Three ROBDs along with one disturbed ecosystem system with natural succession (DESWNS) were selected for the study. Through Berlese-Tullgren funnel method field trash were shorted and analyzed in the laboratory. It was observed that from five years old reclaimed over burden dump (ROBD) 305 soil mesofauna arthropod (SMA) were collected, whereas from fifteen years old ROBD 291 SMA, from thirty years old ROBD 407 SMA and from 50 years old DWNS 364 SMA were collected. The diversity index (DI) for five years ROBD was 1.7953, fifteen years ROBD was 1.8258, for thirty years was 1.7846 and for 50 years old DESWNS was 1.8183. In all the four selected sites the percentage occurrence of Collembola was higher with higher diversity index among all other soil mesofauna - Acari, Protura, Diplura, Symphyla, Pseudoscorpion, Enchytraeids and others – collected from the four study sites. Implicitly, collembolans are hard species and thrive in adverse situations. They have succeeded over the other mesofaunal arthropods and support the decay processes for nutrient cycling via micro flora and fauna of pedosphere eventually help in above ground floral succession.
Keywords: Collembola, soil mesofaunal arthropod, Berlese-Tullgren apparatus, reclaimed, ROBDs, pedosphere.

Omnivorous wasps as mobile samplers of particulate matter

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Abstract: Insects can be used in biomonitoring as mobile samplers of airborne particulate matter (PM). However, current knowledge on their susceptibility to PM is limited to pollinators. We investigated the capability of two omnivorous wasp species (Vespula sp.) in external accumulation of coarse (PM10) and fine (PM2.5) particles. The internal accumulation of particles in wasps' gut tissues was also assessed considering heavy metals acquisition. Female individuals of V. vulgaris and V. germanica were sampled with a hand-netting near to Harjavalta Cu-Ni smelter and in the reference areas in southwestern Finland. They were analyzed with microscopy (LM, SEM, TEM) and X-ray spectroscopy (EDX) methods. Near to the smelter wasps trapped significantly more particles, which were of bigger size and which surface density was higher. V. vulgaris accumulated larger particles than V. germanica, but that wasn't associated with morphological characteristics such as size or hairiness. In both areas, accumulated surface PM carried clays and silicates. Only in polluted environments wasps consistently carried heavy metal particles (from high to moderate weight %) of Fe, Ni, Cu, and S – major pollutants emitted from the smelter. External PM contamination in wasps is suggested as a qualitative descriptor of industrial emissions.

Target Enrichment Phylogeny of Pipunculidae (Diptera)

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Abstract: Using over 1300 targets developed for Syrphidae phylogenetics, we were able to develop the first large-scale genomic phylogenetic hypothesis for big-headed flies (Diptera, Pipunculidae). We show that the syrphid targets are widely applicable beyond the target family that they were developed for and that resulting topology is similar to a 5-gene analysis published in 2021 but with higher support values. Big-headed flies are primarily parasitoids of leafhoppers and their relatives (Auchenorrhyncha) and we hope that this analysis will lead to a greater understanding of host relationship and morphological evolution while providing a robust comparative framework for future ecological questions.

Recent Advances in Auchenorrhynchan Phylogeny: Insights from Transcriptomic and Genomic Sequencing

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Abstract: The hemipteran suborder Auchenorrhyncha, comprising cicadas (Cicadoidea), planthoppers (Fulgoroidea), spittlebugs (Cercopoidea), and leafhoppers and treehoppers, (Membracoidea) is an insect group for which a stable evolutionary hypothesis has been difficult to achieve. In a previous study, we reconstructed auchenorrhynchan phylogeny using 84 auchenorrhynchans representing 27 families. Despite this extensive sampling, several regions of the tree still suffered from lack of support and several biologically important families were not represented. We used transcriptome sequencing or targeted ortholog assembly from genome skimming to obtain data from 44 additional auchenorrhynchan species, including representatives of previously missing families as well as several key lineages from regions of the tree with poor support or unexpected placements. While many of the deep relationships obtained within Auchenorrhyncha were well-supported and retained across data types and analytical methods, others remain unstable; thus, we used partitioned coalescence support scores and four-cluster likelihood mapping to explore putative sources of phylogenetic conflict in this group. Additionally, incorporation of transcriptome and targeted assembly of genomic data are shown to have utility for phylogenetic investigation of some lineages within Auchenorrhyncha, which may benefit future evolutionary and comparative studies in these groups.

Characterization of the Kenyan honey bee (Apis mellifera) gut microbiota

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Abstract: Pollinators including honey bees have a major impact on food security worldwide. Their gut microbiota plays important roles in host physiology such as digestion, protection, detoxification and development of immune responses, among others. The honey bee (Apis mellifera) has emerge as model for gut-microbiota host interaction studies due to its high conservation and simplicity. In this study we have characterized for the first time the honey bee gut microbiota in the tropics and in Africa, using 16S rRNA library sequencing. In contrast to other latitudes, we found that the most abundant genera are three bee specific bacterium: Gilliamella, Snodgrassella and Frischella but not Lactobacillus. This suggest that they might play a key role in the tropical African continent and helps to do further analysis on their potential functions in the host.

Selection of resistance in Aedes aegypti by exposure to an essential oil spatial repellent

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Abstract: Wide spread insecticide resistance has increased interest in development and use of alternative control strategies. One alternative strategy that has increasing interest is the use of spatial repellents as a means of limiting human exposure to mosquitoes by controlling their access to dwellings. Pyrethroid-based spatial repellents have been shown effective against a variety of biting insects however their popularity may contribute to the spread of resistance to permethrin, one of the most commonly used insecticides worldwide. Mosquitoes with resistant genotypes may have altered phenotypes for life history traits along with reduced mortality after exposure. Thus new products, including spatial repellents, should be investigated and adapted for mosquito control. It is unknown how rapidly resistance may develop to spatial repellents nor the consequences to other mosquito life history traits, but this information is key to effective reduction of human-mosquito contact. This study investigates the efficacy of using essential oils as spatial repellents against Aedes aegypti, with a focus on development of resistance to essential oils and subsequent effects on mosquito life history traits.

Simulated impacts on vectorial capacity from resistance and exposure to insecticides and repellents in Aedes aegypti

Authors: Smartt Chelsea[3], Lord Cynthia[1], Henneberg Austin[2], Light Jebidiah[2] and Chen Tse-Yu[2], [1]Florida Medical Entomology Lab University of Florida, United States, [2]Florida Medical Entomology Laboratory University of Florida, United States, [3]Florida Medical Entomology Laboratory University of Florida, United States

Abstract: High levels of resistance to commonly used insecticides have been documented in many populations of Aedes aegypti, resulting in increased interest and use of alternative chemicals and spatial repellents. Mosquitoes carrying resistance genes to insecticides or repellents may have other changes in their physiology, affecting fitness and vector competence for arboviruses. Exposure to chemicals, whether sub-lethal doses of insecticides or spatial repellents, may also alter physiology. Vectorial capacity, the entomological components of the basic reproduction number of a vector-borne arbovirus, is a useful way to integrate these varied effects to estimate impact on pathogen transmission. Relatively little is known about the relationships between resistance and exposure and mosquito physiology traits (survival, biting rate) and virus interaction traits (infection and transmission rates, extrinsic incubation period). Using an individual based model, we are integrating net effects on vectorial capacity under different assumptions about relationships between traits and resistance or exposure (e.g. increasing, decreasing and no effect). Individual estimates are summed for population level vectorial capacity estimates. We will compare population vectorial capacity across traits, relationships, resistance levels and exposure to assess which are most influential and where better estimates will have the strongest effect on prediction of outcomes. These results will inform mosquito control strategies in an environment of increasing resistance and use of alternative chemicals, and identify regions of parameter space where risk of transmission may increase with exposure.

Host plant based variation in virus load in white peacock caterpillars

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Abstract: Secondary metabolites in plants serve as a defense mechanism against herbivorous insects. However, some specialist species have evolved to sequester these secondary metabolites and use the compounds to their own advantage. Our study focused specifically on the role of iridoid glycosides (IGs) on virus load in Anartia jatrophae larvae infected by a Junonia coenia densovirus (JcDNV). Larvae were randomly assigned to either the novel host plant of high IG-content (P. lanceolata) or the native host plant, which lacked any IGs (B. monnieri). Quantitative PCR was used to observe viral replication by measuring virus load each day post-inoculation of three different doses. We hypothesized that IGs assist the specialist insect herbivores in fighting off pathogenic infections. Supporting this idea, our study showed a consistently lower viral load in individuals reared on P. lanceolata compared to individuals fed on B. monnieri. Other variables tested revealed a significantly greater viral load in individuals inoculated with a high dose over those given a medium or low dose, and no significant difference in viral load through days sacrificed post-inoculation. Interestingly, there was no significant interaction between host plant and dose given, suggesting that the pattern with host plant was consistent regardless of viral dose given to the larvae. There was also no significant interaction between host plant and day sacrificed. However, even though viral replication progressed consistently through the different days between the two host plants, there was a consistently lower viral load with a slightly steeper viral load decrease in larvae reared on the introduced host plant with high IG content than those reared native host plant lacking any IGs. This suggests that IGs help larvae defend against pathogens by decreasing overall load, possibly by allowing more of the virus to be suppressed or cleared. The mechanisms for how IGs benefit specialist insects still requires further investigation.

Novel immunological interactions as an overlooked aspect of global change: insights from the host range expansion of Lycaeides melissa

Authors: Smilanich Angela[1], Yoon Su'ad[1] and Forister Matthew[1], [1]University of Nevada, Reno, United States

Abstract: The emerging field of ecological immunology seeks to understand how ecological variation may contribute to immunological variation in the wild, and how these levels of variation can contribute to evolutionary processes. My dissertation research has focused on how different components of ecological variation such as novel resource use may impact the immune response of a specialist Great Basin butterfly, Lycaeides melissa, the Melissa blue butterfly. L. melissa has colonized the exotic legume Medicago sativa in the past 200 years; L. melissa frequently utilizes M. sativa throughout its range despite the fact that L. melissa larvae suffer both reduced survival and decreased adult fecundity on this host, compared to development on a common native host Astragalus canadensis. This interaction with the novel, exotic host plant represents a novel immunological interaction due to the fact that nutritional variation is tightly linked with immunological variation in plant feeding insects, an interaction which I sought to quantify in this study. Specifically, I investigated how L. melissa responds to experimental infection with a highly virulent insect pathogen, Junonia coenia densovirus (JcDNV), and whether resistance to this pathogen is affected by host plant use. I asked the following questions: (1) Does host plant quality affect the ability of Lycaeides melissa larvae to resist JcDNV infection? and (2) Will population of origin affect the ability of Lycaeides melissa larvae to resist JcDNV infection? Preliminary results show that L. melissa larvae are less able to resist JcDNV infection when feeding on the novel, exotic host plant.

Field-evolved resistance to Bt crops in Canada

Authors: Smith Jocelyn[1], Farhan Yasmine[1], Hallett Rebecca[1] and Schaafsma Art[1], [1]University of Guelph, Canada

Abstract: Since the introduction of Bt crops in North America over 25 years ago, their use has become integrated into corn production systems as standard practice, typically regardless of the levels of pest populations they were designed to control. Patterns of insect resistance to Bt corn in Canada have generally followed those of the United States; however, in recent years, novel situations have been observed in Canada, including the first instance of field-evolved resistance to Cry1F in Ostrinia nubilalis Hübner (Lepidoptera: Crambidae). This case will be highlighted along with a review of Bt corn resistance in Diabrotica spp. LeConte (Coleoptera: Chrysomelidae) and Striacosta albicosta Smith (Lepidoptera: Noctuidae) in Canada. The implications and challenges to mitigating these resistance cases will be discussed.

Bringing Back the River of Grass: Gauging Melaleuca (Melaleuca quinquenervia) Biological Control Success in Florida's Everglades

Authors: Smith Melissa[4], Allen Dray F.[3], LaRoche Francois[2], Buckingham Gary[3], Wheeler Gregory[3], Rodgers Leroy[2], Purcell Matthew[1], Rayamahji Min[3], Pratt Paul[3], Tipping Philip[3] and Center Ted[3], [1]Australian Biological Control Laboratory, Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia, [2]South Florida Water Management District, United States, [3]USDA Agricultural Research Service, United States, [4]USDA Agricultural Research Service, United States

Abstract: The southern tip of North America coalesces into one of the world's largest freshwater wetlands, the Everglades. Though this region is much like an island, home to high biodiversity and endemism, it is also the site of a century of development and landscape scale engineering to control the vast quantities of water. Melaleuca quinquenervia, a tree native to tropical Australia, was planted extensively throughout South Florida as street trees, levee stabilizers and later to reduce standing water in marshy areas. Millions of seeds and seedlings were planted during the first half of the 20th century, resulting in far ranging monocultures of melaleuca trees throughout native sawgrass and tree island habitats. The latter third of the last century saw the start and formation of a collective effort to restore the ecological integrity and function of Florida's vast Everglades, including reducing invasive species, notably melaleuca. Through extensive cooperation with the USDA's Australian Biological Control Laboratory in Brisbane, three biological control agents were released and later successfully established. To further capitalize on the efficacy of these agents, a multi-year, multi-agency areawide project was funded to determine best practices for integrating management techniques. Now fifteen years out from the start of the TAME (The Areawide Melaleuca Eradication) Project, melaleuca populations have contracted significantly from their maximum. Land managers now consider melaleuca "under control" in most areas and resources and attentions have been diverted to more immediately pressing plant invasions. Melaleuca control is an example of successful agent prioritizing and integration of biological control to produce long lasting positive impacts on an ecosystem wide invasive species.

Automatic quantification and classification of honey bee comb and its contents

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Abstract: The ecological dominance of the social insects is due, in part, to their ability to allocate tasks among workers. In honey bee colonies, task allocation is also spatial, because the organization of the nest dictates where certain tasks occur. The spatial configuration of the nest itself changes and develops during a colony's lifetime, reflecting both the current state of the colony, and its environment. Studying comb use and nest development, however, is unfortunately understudied, partly because quantifying the nest requires time-consuming manual tracing. These tedious traditional methods make it intractable for large-scale data acquisition, which limits our understanding of how nests develop. Here, we present a system for automatic, high-precision honey bee comb quantification. We built an affordable imaging box for taking high-resolution images of comb, with uniform lighting, even in field settings. Then, using a deep convolutional neural network for image segmentation (U-Net), we designed software that quickly and accurately quantifies the amount of comb, and the contents of the comb, specifically: capped brood, uncapped brood, honey, pollen, and empty comb. We tested our method in varied environmental conditions, showing that the system is robust across multiple colonies and hive designs. This new method is faster and more accurate than previous manual methods, now making it possible to understand how environmental and biological stressors impact colony health and development.

EFLa-type neuropeptide mRNA trans-splicing in hemimetabolous insects

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Abstract: EFLa-type neuropeptides are present in many arthropods, including several insect orders. Besides EFLa elusive function, the way how the mature EFLa-encoding transcripts are formed is also enigmatic, as EFLa exons spliced to exons of Proh-4 gene were found in Pyrrhocoris apterus (Heteroptera), Bemisia tabaci (Sternorrhyncha) and Locusta migratoria (Orthoptera). Presence of intergenic Proh-4/EFLa fused transcripts can be theoretically explained by canonical cis-splicing, cis-splicing of adjacent genes (cis-SAG), or even by trans-splicing, a rare molecular mechanism in insects. We focused on P. apterus, where Proh-4/EFLa transcripts represent about 1/10 of Proh-4 expression, EFLa pre-mRNAs lack in-frame translation start site, and where gene-linkage and genome analyses excluded cis-splicing and cis-SAG mechanism of Proh-4/EFLa generation. Trans-spliced Proh-4/EFLa transcripts were detected by full-length mRNA sequencing using Oxford Nanopore technology with isoform-specific resolution. In-silico analysis of 3' splice site (3'ss) strength predicted weak 3'ss of Proh-4 intron 2, permitting trans-splicing with 10-fold stronger EFLa outron 3'ss. Analogous analysis in L. migratoria found less profound Proh-4 to EFLa 3'ss strength difference, reflected in 10-fold lower Proh-4/EFLa trans-splicing, determined by quantitative real-time PCR. We conclude that although the exact trans-splicing mechanism generating Proh-4/EFLa transcripts stays elusive, it can represent conserved and sound gene expression mechanism.

Pursuing proactive approaches to identifying insecticide resistance in blood feeding arthropods (Diptera: Muscidae)

Authors: Smythe Brandon, New Mexico State University, United States

Abstract: Identification of insecticide resistant field populations of horn flies (Haematobia irritans) has historically been reactive. Initial indicators of insecticide resistance are largely based upon consumer observations of decreased efficacies or overall failure of commercial products across time. At which time, researchers can confirm the presence of resistant using available molecular or bioassay techniques. However, the confirmation of insecticide resistance in field populations following ineffective product performance does little to maximize producer profit. Currently, researchers at New Mexico State University are re-evaluating existing confirmational techniques to develop proactive solutions for cattle producers. Modifying existing techniques to provide proactive horn fly management programs will be discussed within the context of developing sustainable animal production solutions.

Phenotypic variability of life-history traits and voracity of Macrolophus pygmaeus (Hemiptera: Miridae) in two populations of Portugal: Mainland and Azores

Authors: Soares António Onofre[1], Borges Isabel, [1]University of the Azores, Portugal

Abstract: Tuta absoluta (Meyrick, 1917) (Lepidoptera: Gelechiidae) is a major pest attacking tomato that may lead to 60-100% of crop losses. This invasive pest species native to South America landed in Europe in 2006, in Spain, and 3 years later it spread to Portugal. In 2012, it was recorded for the first time in the Azores archipelago. Macrolophus pygmaeus Rambur (Hemiptera: Miridae) is a predator used as biological control agent against the tomato leaf miner. The biological characteristics of two populations of M. pygmaeus, one collected in the mainland Portugal and the other collected in the Azores Isalands (Portugal), were studied on single diets of a potential natural prey (T. absoluta eggs) and of a substitute prey (Ephestia kuehniella Zeller (Lepidoptera: Pyralidae) eggs) used for predator mass rearing in biofactories. The comparations included life history traits, including immature development and reproductive performances, population growth parameters, voracity of immature stages and ovipositing females. The most noticeable differences between the biology of populations were in the reproductive performances, in which reproductive performance of the Azorean populations were higher.

Evidence of Lumpy skin disease virus transmission from subclinically infected cattle by Stomoxys calcitrans

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Abstract: Lumpy skin disease virus (LSDV) is a vector-transmitted capripox virus that causes disease in cattle. Stomoxys calcitrans flies are considered as major vectors and were recently shown to be able to transmit virus from LSDV infected cattle showing typical clinical signs to naïve cattle. Currently no conclusive data is available whether subclinical or preclinical infected cattle play a role in virus transmission. Therefore an in vivo transmission study with 13 donor and 13 acceptor bulls was performed. S. calcitrans flies were placed either on subclinical or preclinical infected animals. Subclinical and preclinical lumpy skin disease (LSD) was characterized by the absence of nodules and detection of LSDV genome. LSDV transmission from vectors fed on subclinical donors was evidenced in 2 out of 5 acceptor animals. One of these acceptor animals developed clinical disease while the other remained subclinical. No proof of LSDV transmission from vectors fed on preclinical donors was observed in the 8 acceptor animals. Our results show that subclinical animals can contribute to virus transmission. Therefore, stamping out of only clinical diseased LSD animals seems insufficient and will possibly lead to reappearance of LSD.

Flower-insect interactions and biodiversity in the Eastern Ghats forest, India

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Abstract: Insects visit flowers for their sustenance. They use pollen as protein source and nectar as energy source. The pollen they inevitably lose in going from flower to flower is important to plants for pollination. Different insects have different pollinating abilities depending on the floral density and floral morphological and functional characteristics. The interactions between insects and flowers appear to have led to the evolution of certain traits in them for mutualistic benefits. Insects require food throughout the year. Perennial, annual and ephemeral plants play a vital role in sustaining insects. These plants flower at different times and thus provide food to insects throughout the year. Among different plants, perennials, especially trees are very important to sustain insect diversity. In return, plants receive the benefit of self or cross-pollination. Among the insects, bees, wasps and butterflies were observed on different plant species that flower at different times of the year. The field work coupled with lab work indicated that both generalist and specialist pollination syndromes exist. Certain plants use all available insects for pollination while certain other plants have specialized floral traits that are adapted to particular classes of insects. In the eastern ghats forest, dry season is very crucial for the local insects due to the dearth of forage, this is because a few tree species flower at this time and serve as keystone plant species for the structural and functional integrity of the ecosystem. Further, in the study, some self-incompatible and obligately out-crossing endemic and endangered plant species have been recorded and they are obligately dependent on certain categories of insects for their fruit/seed set. The studies indicated that insect-flower interactions are mostly mutualistic and their relationships are the basis for the continued existence of biodiversity in this forest ecosystem. Therefore, it is imperative to take measures for the conservation and management of pollinator fauna in order to ensure the sustainability of plant taxa and the pollinators dependent on them.

Wood ants prefer conifers to broadleaved trees in mixed temperate forests

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Abstract: Wood ants (species of the subgenus Formica s. str.) are one of the most important groups of insects in forest ecosystems due to their high abundance and activity. Their mutualistic interactions with tree-dwelling aphids can affect tree growth. The Białowieża Forest is widely regarded as the best example as a forest with limited anthropogenic impact in the temperate zone in Europe. We assessed the preference of host trees for Formica polyctena and Formica rufa, the two dominating wood ant species in this ecosystem. In addition, we compared coniferous and mixed stands. In 2017, we chose 15 wood ant mounds of the Formica rufa group: F. rufa (8 mounds) and F. polyctena (7 mounds) based on an earlier wood ant nest inventory, conducted in 2016 in the Białowieża Forest. In March 2017, all trees within the study plots were mapped and their species, diameter at breast height (130 cm above soil level) and distance from the ant mound were measured. In our study we used term 'host trees' and 'non-host trees" as trees foraged upon by the ants and trees not visited by the ants. Around each mound a circular study plot with a radius of 20 m was established. During 2017 and 2018, all trees on the study plots were monitored for ant activity from May to September (twice a month in 2017 and monthly in 2018). If ants were present on the tree trunk, their number was counted on a 50 cm stretch at breast height, representing a snapshot method at the time of assessment.

In mixed stands F. polyctena visited more trees per plot than F. rufa. Formica polyctena might forage a larger area due to higher population sizes, which further confirms higher foraging pressure of F. polyctena in comparison to F. rufa.

In our study area, host trees of the ant-aphid mutualism were larger in diameter than non-host trees. The ants also preferred trees situated closer to their nests. Both in mixed and coniferous stands, the most visited tree species was Norway spruce. The Białowieża Forest is experiencing a massive bark beetle outbreak. This outbreak started in 2012 and already killed approx. 1.4 million m3 of spruce. Outbreaks are likely to further increase in extent and severity in the future due to climate change. As wood ants seem to have concentrated on using spruce as a host tree, it is possible that wood ant colonies are endangered. The decline of living spruce in the Białowieża Forest may endanger their food source and impact on the vitality of ant colonies.

Invasion and control of Lycorma delicatula in the Republic of Korea

Authors: Song Myung Kyu, Chungbuk Agricultural Research and Extension Services(CBARES), South Korea

Abstract: The spotted lanternfly(SLF) or Lycorma delicatula(order Hemiptera, family Flulgoridae) is a planthopper native to China, India, and Vietnam. Although it has two pairs of wings, it jumps more than it flies. Its host plants are grapes, pines, stone fruits, and Malus spp. It was accidentally introduced in Korea in 2006.

The damage by L. delicatula : grapes(The ratio of grapes' commercial value was 19.2% with no paper bag in organic farming because of L. delicatula's nectar. And there was the sucking damage.) and other plants. The hosts of the spotted lanternfly are ailanthus, poplar, grape vine and so on. Total 41 trees are known in Korea.

The ailanthus branch and leaves were withered. The lanternfly spot the sweet dew very much on the fruit, leaves, grape's bag and all of place. The sweet dew became the sooty mold. Because of the sooty mold, the vine truck was infected secondary, the commercial value of grapes was fell down. This grape didn't be sold. The leaf photosynthesis was interrupted by the sooty mold.

In Korea, we used monitoring, spraying the chemicals, physical method to control L. delicatula. The media supported the control time and the government's managing strategy was done.

Time is required to balance the density of the newly introduced pest. Lycorma delicatula does harm to the vine. To reduce the damage of L. delicatula, the governments, Institutes, farmers and all people should strive to pest control.

Neuropeptide bursicon homodimers-induced prophylactic immunity in Tribolium castaneum

Authors: Song Qisheng[1] and Li Jingjing[1], [1]University of Missouri

Abstract: Bursicon is a cystine knot family neuropeptide, composed of bursicon (burs) and partner of bursicon (pburs) subunits. It can form heterodimers to regulate cuticle sclerotization and wing maturation in insects. Recent studies show that bursicon subunits can also form homodimers to mediate midgut stem cell proliferation and prophylactic immunity. However, the underlying molecular mechanism of bursicon homodimer-regulated immune response remains unclear. Using the red flour beetles, Tribolium castaneum, as a model organism, we have shown that burs and pburs were expressed throughout larval-adult development. Knockdown of burs or pburs decreased the expression of antimicrobial peptide (AMP) genes, including Attacin 1-2, Coleoptericin 1 and Defensin 3, in the larvae. Treating larvae with recombinant pburs (r-pburs) protein led to up-regulated expression of these AMP genes in a dose dependent manor. Bacterial infection resulted in increased expression levels of burs and pburs in the larvae. Silencing burs or pburs increased larval mortality upon bacterial infection while injection of r-pburs protein facilitated bacterial clearance. Furthermore, r-pburs protein activated the transcription factor Relish. We infer that bursicon homodimers-induced AMP gene expression is via Relish in T. castaneum.

Current Status and Control Strategies of Lanternfly in Korea

Authors: Soo Kang Wee, Crop Protection Division, National Institutes of Agricultural Science, South Korea

Abstract: Introduction: Since 2000th so many sporadic insect pests have invaded to Korea from abroad. They are Lantern fly (Lycorma delicatula, 2004, from China), citrus flatid planthopper (Metcalfa pruinosa, 2009, from USA), the Ricaniid Planthopper (Ricania shantungensis, 2010, from China) etc. And they are doing great damage to crops. Among them, Lantern fly has been shown to be incomparable with the other two species in terms of spreading rate and damage since it was first discovered in Seoul and Cheonan in 2004. Since the first inflow of L. delicatula into Korea, the area of occurrence is as follows; 1ha(‘06) ? 7ha(’07) ? 91ha(‘08) ? 2,765ha(2009) ? 8,738ha(2010) ? 7,400ha (2011) ? 6,905ha(2012) ? 3,433ha(2013) ? 1,800ha(2014) ? 1,176ha(2015) ? 2,561ha(2016) ? 2,852ha(2017) ? 2,107ha(2018) ? 1,091ha(2019), Since 2011, the occurrence area of Lantern fly has been gradually decreasing.
Methods: In Korea, various techniques have been developed and used for controlling Lantern fly. Through the development of trap plants that attract and kill Lantern fly, sticky traps, registration of various insecticides, wintering survey, early hatching nymph density survey, spawning adult survey, etc. In addition, farmers have jointly controlled joint efforts to reduce the area of occurrence and damage. Currently, a kinds of parasitoid, Anastatus sp. is imported from China and multiplyed and released in large quantity in areas with high density of Lantern fly.
Results/Conclusion: The incidence of Lantern fly invaded in 2004 has been increasing by 2011, and since then, the area has gradually decreased. The most important factor is attributed to the result of close monitoring of pest control personnel in the city and county centers and the joint efforts of the central and local governments.

What alligator weed distribution models in its native and invaded ranges tell about its invasion story and biological control

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Abstract: Biological invasions are one of the most important drivers of biodiversity losses around the world. Weed biological control has a history of more than 100 years, with good examples of success. One example is the introduction of the flea beetle Agasicles hygrophila to control alligator weed (Alternanthera philoxeroides), an amphibious aquatic plant native to Southern South America and has invaded several countries around the world, including Australia, Italy, China and USA. Other potential control agents include beetles Disonycha and Systena. In this work, occurrence records of the weed and control agents were compiled from multiple sources. Ecological niche models were made to establish the potential areas of current and future distribution. Alligator weed future scenarios show an increase in potential and climatically favorable areas towards northern South America compared to the current model. For Agasciles and the other potential agents, models did not show the same trend; on the contrary, the future scenarios are not very different from the current potential areas. Agasciles model was the best matched the most suitable areas of the current Alligator weed. This study allowed us to understand the current distributions as well to estimate future scenarios that will allow us to improve control strategies.

The Apterostigma auriculatum species group: Phylogenomic species delimitation and taxonomy

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Abstract: The fungus-farming ant genus Apterostigma, occurring in the Neotropics and the Caribbean, is divided into three species groups based on morphological and molecular data: the auriculatum group (13 spp), the pilosum group (30 spp), and the megacephala group (1 sp). Associations between Apterostigma species and their fungal cultivars are strongly correlated with phylogeny. Species in the auriculatum group cultivate agaricaceous fungi, the ancestral fungal cultivar of all fungus-farming ants. Species in the pilosum group cultivate pterulaceous fungi, presumably as a result of a transition from a leucocoprineaceous to a pterulaceous cultivar in their most recent common ancestor. Finally, the single species in the megacephala group is the only lower fungus-farming ant known to cultivate the highly modified and most recently evolved higher cultivar, cultivated by most leaf-cutter ants. To study the associations between the ants and their fungi, Apterostigma species need to be properly delimited. Our dataset includes 142 taxa (58 belonging to the auriculatum group), including eleven paratypes (5 belonging to auriculatum group), and ~2300 UCE loci. Preliminary results suggest that major clades within the auriculatum group originated very rapidly around 10–12 Ma and that the group contains at least nine new species.

Management and Insecticide Resistance of Stink Bug Populations (Hemiptera: Pentatomidae) in Commodity Crops

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Abstract: Pest management of stink bugs (Hemiptera: Pentatomidae) on soybean [Glycine max (L.) Merr.], corn (Zea mays L.), and cotton (Gossypium spp.) agroecosystems is of major concern in several countries of the Americas. Euschistus spp., Dichelops spp., Nezara viridula (F.), and Piezodorus guildinii (West.), are the most abundant species. In this presentation we will review their distribution, damaged caused, and methods used to control the most important pest species in the Americas, with emphasis on those occurring in Brazil. We will also present and discuss the implications of the trends toward decreased susceptibility of stink bug populations to insecticides, and the current difficulties to manage these pests. Currently, Euschistus heros (F.) is less susceptible to organophosphate insecticides than in the past. Reduction in E. heros susceptibility to pyrethroids and, to a lesser extent, to neonicotinoids, has also been observed. Metabolic detoxification is involved in organophosphate, neonicotinoid and pyrethroid reduced susceptibility. Use of insecticides with similar mode of action may have favored selection of resistant phenotypes in stink bug populations. Considering the restricted number of insecticides with different modes of action against stink bugs, a defined program of insect resistance management is needed. Some strategies to reach this goal are recommended, and include: 1) Avoid chemical control of overwintering populations. During overwinter, E. heros populations are in diapause and natural enemies are prevalent. Therefore, chemical application is useless to reduce populations and adds pressure to select insect resistant individuals. 2) Use selective insecticides (nucleopolyhedroviruses, Bacillus thuringiensis based products, insect growth regulators, etc.) to control caterpillars with different modes of action from the products used against stink bugs. 3) Check out on fixed times stink bug resistance rates to organophosphates, neonicotinoids, and pyrethroids, and use a proper insecticide. 4) Avoid problems with application technology. 5) Apply integrated pest management measures when action threshold is reached. 6) Do not increase the insecticide dose when control fails, but instead use a product with a different mode of action; and 7) Control weeds and volunteer plants that may host stink bugs. Monitoring and mapping areas of resistance could be useful in insecticide management of stink bug populations. Since their control relies exclusively on chemicals, actions should be taken to reduce selective pressure. Educational programs to train growers to use insecticides wisely should be implemented to improve chemical control. Although large areas (> 2,000 ha) hinder stink bug population monitoring and proper control time, growers should be aware of the consequences of inadequate management of these pests. Ideally, insecticide applications should be restricted to areas where the action threshold has been reached.

From lab to field: Biological control of the Japanese beetle (Popillia japonica) with entomopathogenic fungi

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Abstract: The Japanese beetle Popillia japonica is an invasive scarab and listed as quarantine organism. Originating from Japan, it invaded North America, the Azores and recently mainland Europe. The gregarious beetle threatens agri- and horticulture by feeding on leaves, fruits and flowers of a wide range of valuable crops and ornamental plants. Larvae feed belowground mainly on grass roots and damage golf courses, football fields and other areas covered with turf. An efficient but environmentally friendly control strategy is pending.

In Switzerland, larval populations of damaging native scarab species, such as Phyllopertha horticola or Melolontha melolontha, are controlled by applying registered products containing the entomopathogenic fungi Metarhizium brunneum or Beauveria brongniartii. The goal of our research is to adapt this control strategy to the invasive pest. In laboratory experiments and large-scale field trials, we assessed the control effects of those registered fungal strains against Japanese beetle larvae and adults.

Inoculation experiments in the laboratory showed that adult beetles are highly susceptible to fungal attack, while larvae resist infection with fungal spores applied by topical spraying. However, when injected directly into the hosts' hemolymph, the fungi were able to infect and kill the larvae. This gives evidence that the cuticle of the larvae plays a major role in the defense against entomopathogenic fungi.

In two field experiments, barley kernels colonized with M. brunneum strain BIPESCO 5 were applied to infested meadows with a no-till seeder. When applied in September, we found no effect of the fungus on the larval population, while the application in spring slightly reduced the number of larvae per square meter. Furthermore, we sprayed M. brunneum conidia dissolved in water against P. japonica adults on a soybean field with an air-supported trail sprayer. While we found an effect on beetles collected after the spray treatment, we did not detect a clear control effect on the field. Hence, a screening for more virulent strains and research on more efficient application methods might help to increase efficacy of fungal treatments against Japanese beetle adults and larvae.

Evolution of sexual conflict in scorpionflies (Mecoptera)

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Abstract: Scorpionflies (Mecoptera) are one of the oldest holometabolous insects, known since the Permian. They flourished in the Mesozoic but most of their lineages rapidly declined during the Cenozoic. Mecoptera are models in sexual conflict study as their mating practices are very diverse, including coercive behaviour and nuptial gift provisioning. The male behaviour towards the female may be coercive in such a degree that the expression 'rape' has been used in the past for describing their mating rituals. The role of palaeontology in sexual conflict studies remains negligible, namely due to the paucity of well-preserved fossils. Mecoptera were very abundant insects in the past, so their fossil evidence is abundant enough to trace the evolution of their mating behaviour. Three exceptional scorpionflies from three different Cretaceous and Eocene ambers deposits, each belonging to a distinct panorpoid lineage allow us to extrapolate trends observed among extant relatives. Fossil evidences suggest that panorpoid mecopterans had accordingly disparate mating strategies in the past. The forcing mating strategy in this group is secondary derived and did not evolve prior to the Eocene. However, extreme coercive mechanisms did not survive until today among scorpionflies. Our data provide first steps toward gaining a deep-time perspective able to inform discussions on the evolution of mating-related sexual conflict over mating among insects.

Importance of mobility of plant pests across borders

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Abstract: The increase in international trade over the recent decades has risen the number of exotic insect species that cross borders, and with this, the invasion of plant pests. Invasive species are a very important issue, they cause significant losses on agricultural production and have intense impact on the environment. The entry of these organisms produces an enormous economic expense in the public sector to be able to carry out the official management and the private sector sees it yields greatly reduced.

The group of mealybug insects are typical invasive pests due to their small size and cryptic behaviour. These population outbreaks are frequent when mealybugs are introduced into new areas without their specific natural enemies. The invasive condition of the family pseudococcidae and the difficulty to control them by chemical methods have made this group of insects a target of this problem. In recent years we have several examples in Europe, Delottococcus aberiae De Lotto species is one of them in citrus crops in eastern Spain. This species of mealybug is native to southern Africa and was recorded for the first time in Spain in 2009. It is an invasive citrus pest that cause different types of direct fruit damage, mainly protuberances around fruit calyx or size reduction. A large percentage of the distorted fruit loses completely its commercial value. At present, chemical control is the main strategy used to management the populations of this pests.

To avoid these problems, it is necessary to implement tools that make these invasions difficult. It would be very appropriate to give a globalization perspective to this type of problem. For example, well-done Pests risk analysis can be highly beneficial, can be an important tool that can limit the impact of harmful exotic species. On the other hand, mealybugs are a target of biological control strategies, for this reason, establishing agile classic biological control programs, based on the introduction and release of exotic natural enemies from the native area of the pest, seems another good management tool. It is essential to detect the mobility of plant pests and reduce the risk of invasive pests through the increasingly globalization of measures.

Diversity, transmission mode, and evolution of symbiosis in an insect community

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Abstract: Species communities are shaped by a wide diversity of ecological interactions, including symbiosis. Defined as a long-term interaction between dissimilar species, symbiotic interactions range on a continuum between costly and beneficial, depending on the host-symbiont system considered. For instance, the symbiotic bacterium Wolbachia, which is estimated to infect about 60% of all insect species, can either benefit its host in presence of pathogens, or negatively affect its host fecundity. Consequently, symbionts have been suggested to play an important role in the dynamics of the host species populations, and of their host interactions with competitors, predators or preys. Despite this, most eco-evolutionary studies of natural insect communities rarely consider the insects' symbiotic partners. Hence, we lack a comprehensive view on how important symbionts are in the ecology and evolution of natural host communities. I propose to investigate this topic using the insect community associated to the ribwort plantain (Plantago lanceolata) in the Åland islands. This system is particularly well described, and includes several species that have been studied for over 30 years (e.g. the glanville fritillary butterfly Melitaea cinxia and its associated parasitoids). I aim (i) to characterize the occurrence, abundance and distribution of symbionts in this unique insect community; (ii) to investigate the transmission modes of the symbionts within and between hosts in the field; and (iii) to study whether these different symbiotic interactions have played major roles in the evolutionary history of their insect host species. In order to address these questions, I will combine fieldwork across the Åland islands with experiments in the laboratory, and phylogenetic analyses. My research will contribute to the better understanding of various host-symbiont interactions, and unravel the important role of symbionts in shaping host species interactions in natural communities.

Storage of Trichogramma pretiosum Riley, 1879 at low temperatures and different relative humidity levels to improve Applied Biological Control programs

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Abstract: Biological control (BC) is increasingly important in Brazil as a component of Integrated Pest Management (IPM). With the increase in BC utilization, commercial companies are now selling biological control agents such as the parasitoid wasp Trichogramma pretiosum Riley (Hymenoptera: Trichogrammatidae). One problem encountered is the logistics of storing and transporting these insects, considering that they may need to be stored during periods of low usage or transport from one region to another. If the insects are stored without protocols based on their biology, they may emerge before the scheduled time, be less efficient as pest control agents, or die. The techniques currently used in Brazil have not been tested scientifically, and the low temperatures currently used can affect biological parameters of T. pretiosum and therefore the wasps' performance in the field. The present study evaluated the effect of low temperatures and relative humidity on biological characteristics of different life stages of T. pretiosum. The pupal stage proved to be the most suitable for storage. At a temperature of 10°C, pupae survived for up to 10 days with no deleterious effect on the emerged parasitoids, whereas longer storage periods reduced pupal viability in relation to a control group (insects reared at 25°C). Trichogramma pretiosum females emerged from pupae stored at 10°C showed reduced parasitism capacity after 20 days of storage. The effect of air relative humidity (RH) on T. pretiosum pupae in eggs of A. kuehniella stored at a temperature of 10°C (based on the previous study) was evaluated, using RH levels of 30, 50, 70 or 90 ± 10% and periods of 5, 10, 15 or 20 days. The optimum relative humidity for storage of T. pretiosum was 90%, for up to 20 days at 10°C; the parasitism, pupal viability and sex ratio were not affected. Parasitoids emerged from immatures kept at 10°C and RH of 90% showed a reduction of parasitism capacity just at 20 days of storage. Low RH affected the parasites' viability after 10 days of storage. These data show that pupae of T. pretiosum can be stored up to 15-20 days at 10°C and 90% RH without affecting the biology/quality of immature and adult parasitoids.

How many genes do we need, and which ones?

Authors: Spasojevic Tamara, Natural History Museum Basel, Switzerland

Abstract: Sequencing technologies advanced at great speed in the last years and have made the cost-effective assembly of very large datasets feasible even for non-model taxa. Datasets with hundreds to thousands of genes promise to resolve phylogenetic problems that have previously been deemed unsolvable. However, the allure of big data does not come without its pitfalls, mainly because analysis methodologies have not yet caught up with the growth in dataset size. We investigate how data filtering approaches can help strike a better balance between the number of genes and the rigor of the analytic approach. Filtering criteria such data completeness, evolutionary rate, clocklikness and model mismatch were tested and show differing performance in improving tree resolution. We discuss how these methods allow us to investigate the reliability of the current hypothesis of the evolution of hymenopteran families, especially with respect to the Eusymphyta hypothesis.

Challenges and potentials of total-evidence dating: a case study of hyperdiverse Darwin wasps

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Abstract: Total-evidence dating (TED) is currently the most comprehensive approach for estimating divergence times, which integrates extant and fossil taxa, and molecular and morphological information in a Bayesian framework. Along with applying TED to date Pimpliformes, one of the most diverse groups of parasitoids belonging to Darwin wasps (Hymenoptera, Ichneumonidae), we explore the impact of taxon sampling and missing morphological information on the age estimates. Based on newly compiled molecular data from ten nuclear genes and a morphological matrix that includes 222 characters, we show that age estimates become both older and less precise with the inclusion of more distant and more poorly sampled outgroups. In addition, we discover an artefact that might be detrimental for TED: "bare-branch attraction," namely high attachment probabilities of certain fossils to terminal branches for which morphological data are missing. Our analysis recovers a Jurassic origin for Pimpliformes and Darwin wasps, an older origin than previously thought but also that diversification of the crown group happened well before the Cretaceous-Paleogene boundary. Our case study demonstrates that to obtain robust age estimates, total-evidence dating studies need to be based on a thorough and balanced sampling of both extant and fossil taxa.

How old is the association between PDVs and Darwin wasps?

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Abstract: The age of the association between parasitoid wasps and their adopted viruses can provide insights into the environmental and co-evolutionary context in which it occurred. The oldest known fossil Darwin wasps (Ichneumonidae) date back to the Cretaceous (~130 Ma), but their taxonomic placement remains unclear. The oldest fossils described in Campopleginae and Banchinae – the two subfamilies currently known to harbour PDVs – only date back to the Eocene (~50 Ma). To bridge the gaps in the fossil record, we used a molecular tree of the group, combined with a new method to calibrate the molecular clock that integrates fossils directly into the analysis ("total-evidence dating"). We found that the origin of the family lies deep in the Jurassic (~180 Ma), and that Banchinae and Campopleginae split in the Cretaceous. However, more extensive taxon sampling is needed to pinpoint the more recent gains and losses of virus associations in this group, and it should be coupled with an intensified study of the Darwin wasp fossil record, which still holds many undescribed species.

Compounds without borders: quantifying scent pollution of complex odor blends

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Abstract: Bumblebees are critical pollinators whose populations have been experiencing troubling declines over the past several decades. Successful foraging improves colony fitness, thus understanding how anthropogenic influences modulate foraging behavior may aid conservation efforts. Previous work has demonstrated that pollution of a learned odor signal with the scent of non-insecticidal agrochemicals resulted in modulation of bumblebee foraging behavior. Additional work on diesel exhaust, petrol exhaust, and ozone degradation of floral blends indicates that modulation of floral-odor signals may be a pervasive issue that many pollinators contend with. However, given the vast array of potential odor pollutants, individually testing candidates is an ineffective approach. The ability to quantitatively measure how much scent-pollution of a floral-odor bumblebees can tolerate and subsequently predict responses to novel odor pollutants would represent a paradigm shift in odor-pollution studies. Existing statistical methods for analyzing complex odors have poor predictive power because statistically-derived odor-spaces are rewritten when new odors are added. This study presents an alternative method of analyzing complex odor blends based on the encoding properties of insect olfactory systems. This “Compounds Without Borders” (CWB) method vectorizes odors in a multidimensional space representing the relevant functional group and carbon characteristics of their component odorants. A single vector can be built for any scent, which allows the angular distance between any two odors to be calculated – including a learned odor and its polluted counterpart. The data presented here indicate that CWB-angles are capable of both describing and predicting bumblebee odor-discrimination behavior: odor pairs with angular distances in the 20-29° range are generalized, while odor pairs over 30 degrees are differentiated. Given that the neurophysiological properties underlying CWB-vectorization of odors are not unique to bumblebees, this method of characterizing complex scents likely has applications to other species. Indeed, CWB-angle analysis of published data on a hawkmoth supports the idea that this method may be broadly applicable.

Multicomponent interactions involving insect-transmitted plant viruses: presumed norms, deviations, and spillover effects

Authors: Srinivasan Rajagopalbabu, University of Georgia, United States

Abstract: Insect vectors transmit plants viruses in multiple modes across the transmission spectrum ranging from non-persistent to persistent-propagative fashion. In the process, these microbes (plant viruses) either directly or indirectly (plant modulation) affect the fitness of their insect vectors. The general assumption being that fitness benefits to vector insects are more robust and obvious in the case of persistent viruses as opposed to non-persistent viruses. While this assumption is based on experimental evidence, recent studies with diverse plant viral pathosystems seem to challenge such an assumption. The driving factors seem to be the susceptibility status of the plant to the microbe, the resulting phenotype, and the temporal stability of such a phenotype. Antithetical to the original assumption, the resulting interactions on insect fitness are more favorable in the case of some non-persistent viruses and less obvious in the case of some persistent viruses. At times, the effects of plant-microbe interactions on their vector herbivores are accompanied by a very high degree of fidelity and are so very specific. However, at times, there seem to be spillover effects extending to non-vectors in the same and different feeding guilds. These effects will also be discussed with multiple plant virus-based pathosystem studies. Further, the spillover effects of plant-microbe interactions on the next-trophic level on entomophagous insects with relevance to biological control is also documented. A few relevant papers published by our group are listed below; the presentation in the symposium would revolve around these studies as well as ongoing studies pertaining to impacts of plant-virus-vector interactions on biological control.

Gadhave et al. (2019) A non-persistent aphid-transmitted Potyvirus differentially alters the vector and non-vector biology through host plant quality manipulation. Scientific. Reports 9, 2503 doi:10.1038/s41598-019-39256-5.

Legarrea et al. (2015) Temporal Effects of a Begomovirus Infection and Host Plant Resistance on the Preference and Development of an Insect Vector, Bemisia tabaci, and Implications for Epidemics. PLoS ONE 10(11): e0142114. https://doi.org/10.1371/journal.pone.0142114

Shrestha, et al. (2012). Direct and indirect effects of a thrips- transmitted Tospovirus on the preference and fitness of its vector, Frankliniella fusca. Exp. Appl. 145: 260-271.

Srinivasan et al. (2006) Influence of hairy nightshade Solanum sarrachoides (Sendtner) and Potato leafroll virus (Luteoviridae: Polerovirus) on the preference of Myzus persicae (Sulzer) (Homoptera: Aphididae). Environ. Entomol. 35: 546-553.

Macro- and micro-level impacts of a plant-infecting orthotospovirus on its thysanopteran vector

Authors: Srinivasan Rajagopalbabu[1], Culbreath Albert[1], Shrestha Anita[1], Champagne Donald[1] and Abney Mark[1], [1]University of Georgia, United States

Abstract: Thrips-transmitted orthotospovirus, tomato spotted wilt virus (TSWV), affects several agriculturally important crops resulting in billions of dollars worldwide. Thrips maintain intricate interactions with orthotospoviruses such as TSWV, and transmit such viruses in a persistent and propagative manner. Using a peanut-tobacco thrips (Frankliniella fusca (Hinds))-TSWV pathosystem, we evaluated the component interactions at macro and micro levels via preference bioassays, biology studies, and next generation sequencing. Macro-level assays indicated that TSWV infection altered thrips fitness positively by enhancing egg production, and negatively by reducing survival and increasing developmental time. Next generation sequencing with three life stages of TSWV-infected and non-infected thrips revealed substantial differential gene regulation between infected and non-infected thrips. Differentially expressed contigs pertaining to thrips development, and vector-virus interactions including virus reception and multiplication, and immune responses were annotated. Small RNA sequencing also indicated the virus is being processed differently in thrips than in plant hosts, and demonstrated that there is extensive upregulation of SiRNAs pertaining directly to viral genes. These results show that though there were positive effects on thrips following virus infection (primarily induced by modulation of plant biochemistry), there also were substantial virus-induced negative fitness effects on the vector itself. TSWV is structurally akin to many animal infecting bunyavirales' members, and there seem to be similarities in vector-virus interactions between plant- and animal-infecting members of bunyavirales. All the above-stated results have been published and will be discussed in depth.

Srinivasan et al. 2017. Virus research 241, 203-212
Shrestha et al. 2017. Journal of General Virology 98, 2156-2170
Fletcher et al. 2016. Frontiers in plant science 7, 1349
Shrestha et al. 2012. Entomologia Experimentalis et Applicata 145, 260-271

Differences in transcriptomes between an orthotospovirus vector and non-vector thrips species

Authors: Srinivasan Rajagopalbabu[1], Culbreath Albert[1], Shrestha Anita[1], Champagne Donald[1] and Abney Mark[1], [1]University of Georgia, United States

Abstract: Thrips function as important pests of numerous agricultural crops Worldwide via directly feeding on them and/or indirectly by transmitting devastating plant viruses such as orthotospoviruses (Order: Bunyavirales). Even though hundreds of species have been recorded as agricultural pests, only a handful of species have been recorded as vectors of orthotospoviruses. Species within the same genus function as vectors and non-vectors of orthotopsoviruses. Thrips-transmit these important group of plant viruses in a persistent-propagative manner, likely resulting in complex and intricate interactions. It is not clear as to which transmission determinants differentiate a vector and a non-vector. To understand this phenomenon, the transriptomes of a vector thrips species (Frankliniella fusca Hinds) and that of a non-vector (Frankliniella tritici Fitch) were synthesized de novo and compared. Gene ontology-based annotations revealed several differences across the functional categories. Transcripts associated with vector-virus interactions in both species were further examined in depth. Results revealed important differences between vector and non-vector thrips. For instance, transcripts of an important ubiquitous cell surface receptor (heparan sulfate) that is known to facilitate virus entry was identified only in the vector species transcriptome, but was conspicuously absent in the non-vector transcriptome. Differences in other transmission determining factors such as virus replication inhibitors (belonging to an important enzyme superfamily known as Viperin), and various immune pathways were also observed between vector and non-vector species. Overall, the immune pathways were more robust in the non-vector as opposed to the vector. The roles of these putative molecular determinants are yet to be functionally validated. Nevertheless, differences in key molecular transmission determinants observed in this study enhance our understanding and offer plausible explanation of why some thrips alone are able to function as vectors of orthotospoviruses. The information included here has recently been published and will be discussed in depth.

Shrestha A, Champagne DE, Culbreath AK, Abney MR, Srinivasan R (2019) Comparison of transcriptomes of an orthotospovirus vector and non-vector thrips species. PLoS ONE 14(10): e0223438. https://doi.org/10.1371/journal.pone.0223438

Vector-virus interactions in non-persistently- and persistently-transmitted plant viruses

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Abstract: The vector-mediated transmission is obligatory for majority of plant viruses. We studied vector-virus interactions in two diverse pathosystems involving a non-persistent Potyvirus, Papaya ringspot virus (PRSV), and a persistent and circulative bipartite Begomovirus, Cucurbit leaf crumple virus (CuLCrV). Our findings revealed that PRSV differentially altered the vector; melon aphid (Aphis gossypii Glover) and the non-vector; silverleaf whitefly (Bemisia tabaci Gennadius) biology through host plant quality manipulation. CuLCrV transmission studies revealed that B. tabaci transmitted CuLCrV vertically and horizontally with low frequency and accumulation, and showed no transmissibility to non-infected squash plants. These interactions highlight complex and context-specific interactions between Hemipteran vectors and the viruses they transmit- each with significant implications for virus transmission and spread.

Intra-specific host associated morphometric and genetic variability in Helicoverpa armigera (Hübner) populations from India

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Abstract: The Old World Bollworm, Helicoverpa armigera (Hübner) is one of the most prominent polyphagous species of Heliothinae pest complex of worldwide occurrence, including India. In India, this pest species attacks around 96 different crops and thereby causes huge monetary losses. In addition to it, Indian populations of H. armigera occurring on different host plants and at different geographical locations also exhibit differential responses to various selection pressures, thereby rendering its management more difficult in our country. Detailed understanding of the morphometric and genetic differences in different host associated populations of H. armigera can be very useful to know about its population structure. Thus in the present study, we conducted morphological studies and DNA barcode analyses using cytochrome oxidase I (COX-1) gene, which unraveled the mystery of H. armigera breeding on different host plants. The insect cultures collected from eight major crop plants of India, namely chickpea, pigeonpea, pea, okra, tomato, chilli, wheat and cotton were maintained in laboratory on artificial diet up to two filial generations. Phenotypic traits such as body colour patterns, larval and pupal length, length of femur, fore wings and genital organs in adult moths were recorded. For molecular characterization of different host associated populations, the COX-1 gene sequences of H. armigera obtained in FASTA format were imported into the MEGA 6.0 software package and multiple sequence alignments were performed with the ClustalW algorithm using default parameters. The results revealed that populations differed significantly for most of the morphometric traits studied at larval, pupal and adult stages. Significant differences were also observed among the different host associated populations with respect to occurrence of green or brown colour morphs, pigmentation patterns on lateral band and frequency as well as intensity of black pigmentation on larval body. Besides external phenotypic traits, attributes of genital organs like aedeagus and valval length in males and length of bursa copulatrix and bursa seminalis in females also differed significantly among populations. Thirty four polymorphic sites were observed in the COX-1 gene sequences of the studied populations, showing both transitional and transversional substitutions. The pair-wise genetic distance ranged from 0.000 to 0.037 with highest evident between cotton and chilli populations. The neighbour-joining tree also showed clustering of the populations into two distinct clades. Differences based on morphometry and genetic analysis clearly indicates the possibility of existence of different host specific races in H. armigera populations of India. Such information will be very helpful for the development and deployment of appropriate integrated management strategies for this pest species in the region.

Evolution of filter-feeding in aquatic insects dates back to the middle Triassic: new evidence from fossil stemgroup mayflies (Insecta: Ephemerida)

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Abstract: Within aquatic insects, mayfly nymphs have developed a remarkable diversity of life strategies and feeding habits. However, early evolution of these strategies and the role of mayfly nymphs in freshwater palaeoecosystems remain largely unknown. We investigated fossil mayfly nymphs of the Grès à Voltzia Formation from the middle Triassic, France, which represents the oldest known outcrop including a diverse mayfly fauna. We focused on three species, namely Mesoplectopteron longipes, Vogesonympha ludovici and Triassoephemera punctata, and investigated both original type material and numerous previously unstudied specimens. As a result, we provide a new interpretation of their morphology, life histories, and systematics. The nymphs of M. longipes, V. ludovici and T. punctata were aquatic and at least the former two species undoubtedly lived in flowing water as passive filter-feeders. This finding represents the so far earliest occurrence of this feeding strategy in aquatic insects. The most obvious morphological adaptations to this lifestyle are long filtering setae arranged in rows on forelegs, analogous to some modern mayfly nymphs.

Is pomegranate a superfood for Leptoglossus zonatus? - Fall hosts and overwintering of a polyphagous insect pest in California

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Abstract: The leaffooted bug Leptoglossus zonatus (Hemiptera: Coreidae) is a key pest in many California specialty crops. Feeding causes damage in almond early in the season, followed by damage in pistachio around April to mid-May when L. zonatus moves between crops. In fall, large populations of L. zonatus have been observed on pomegranate before migration into overwintering habitats. The location of a suitable fall host for nymphal development of the third and final generation before overwintering may be a key element in developing a successful control program, which also includes improved monitoring of overwintered adults migrating into nut crops in spring.

In this study, the influence of the potentially excellent fall host pomegranate on L. zonatus population build-up is evaluated. Additionally, migration into and out of overwintering habitats is monitored.

Fall survival of caged L. zonatus nymphs and developing adults of the third generation was higher in pistachio than in pomegranate, walnut, and citrus. Surprisingly, a fourth generation was completed in pistachios and walnut, which could be added to the list of L. zonatus host plants. Migration from pomegranate into the overwintering host citrus was observed from beginning of October onwards.

The results will contribute to the development of successful IPM programs for this polyphagous pest in California.

Phylogenetic relationships of true bugs (Hemiptera: Heteroptera)

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Abstract: With ~45,000 species, the true bugs (Heteroptera: Hemiptera) are ecologically and behaviorally diverse, including diurnal and nocturnal species as well as herbivores and predators. Additionally, many heteropterans are of economic importance, as several are agricultural pests, disease vectors and beneficial biological control agents. Likely in part due to their economic importance, in recent years a large number of analyses have explored relationships among the seven infraorders. While the relationships between infraorders are largely resolved, relationships between superfamilies and families remain uncertain for many groups, and in some cases have yet to be tested. Previous phylogenetic studies have been limited in their scope primarily by low taxonomic sampling, not enough molecular data to resolve relationships, or no molecular data in some cladistic analyses of morphological characters. Using the new alignment-based sequence extraction software (ALiBaSeq) we extracted loci from a combined transcriptomic and genomic dataset, covering over 80% of heteropteran families. We used the 2395 orthologous loci set from Johnson et al. 2018 as our baits and performed reciprocal blast to test for paralogy. We then generated a phylogenetic hypothesis in IQtree and tested relationships between infraorders, superfamilies and families.

Phylogenomics of Thrips (Thysanoptera)

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Abstract: Members of the order Thysanoptera (Paraneoptera), commonly named thrips, amount to over 6,000 described species. A small number of species are responsible for extensive damage to agriculture and horticulture directly through mechanical feeding damage and indirectly through the spread of tospoviruses, a damaging plant virus group. Previous studies on the phylogenetic relationships of this order lacked the resolution of family and subfamily relationships, especially in the Thripinae subfamily which has previously been shown to be paraphyletic.

We investigated intraordinal relationships between families and used fossils to time calibrate their divergence from one another. Monophyly was tested for the suborders, families, recognized subfamilies, and proposed lineage groups. We built phylogenies using 2050 known orthologs assembled using aTRAM 2.1. We sampled 57 thysanopteran species including representatives of five of the nine families, 51 genera and all Phlaeothripinae lineage groups. The two suborders, Tubulifera and Terebrantia, are recovered as monophyletic. The two most speciose families, Thripidae and Phlaeothripidae, as well as Aeolothripidae, were also recovered as monophyletic. The inferred phylogeny has strong nodal support across the tree, clarifying relationships between families, subfamilies, and the relationships between the lineage groups within Phlaeothripidae. Further sampling is needed to test the relationships of Uzelothripidae, Stenurothripidae, and Fauriellidae; families missing from both the current analysis and previous studies.
We will show examples of how this phylogeny has already impacted thrips research and share results of two downstream studies that rely on the inferred phylogeny: cophylogenetic analysis of Tospoviruses and their Thrips vectors; and the pattern of rapid mitochondrial genome rearrangements in Thysanoptera.

Biodiversity and systematics of jumping plant-lice of the subfamily Liviinae (Hemiptera: Psylloidea: Liviidae) with particular focus on the Neotropics

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Abstract: Psyllids constitute a predominantly tropical taxon, characterised by narrow host ranges. The Neotropics house arguably the most diverse and, at the same time, the least studied psyllid fauna. Recent targeted field work in Brazil supports this claim. Only two species of Liviinae, referred to Diclidophlebia, have been reported from Brazil, while over 60 undescribed species are represented in the recent collections. For analysing the host patterns of the Brazilian species, phylogenetic analyses of the world Liviinae were performed using seven mitochondrial and nuclear gene regions (COI, cytb, 12S, 16S and 28S rRNA, wg, H3) as well as 61 morphological characters of adults and immatures. The Brazilian species belong to two new genera. Genus 1 consists of four species associated with Malvaceae. Genus 2 comprises around 60 species of which a majority is associated with Melastomataceae and Annonaceae. Within Melastomataceae, Miconia hosts the largest number of psyllids (19 spp.). The remaining species develop on Asteraceae (4 spp.), Cannabaceae (1 sp.) and Myristicaceae (4 spp.). Neither Melastomataceae nor Annonaceae are restricted to a monophyletic species group, suggesting repeated colonisations by psyllids rather than cospeciation with the psyllids. This is a general pattern known also from other psyllid taxa.

Spatio-temporal dynamics in the microbiomes of pear psyllids reveal complex interactions between host biology and its microbial associates

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Abstract: Psyllids (Hemiptera: Psylloidea) are phloem-feeding insects that can transmit plant pathogens such as phytoplasmas, intracellular bacteria causing numerous plant diseases worldwide. Using 16S rRNA gene metabarcoding, we compared the microbiomes of three sympatric psyllid species associated with pear trees in central Europe, Cacopsylla pyri, C. pyricola and C. pyrisuga, that are vectors of 'Candidatus Phytoplasma pyri', the causative agent of Pear Decline disease. Our results revealed potential relationships between insect biology and microbiome that varied during psyllid ontogeny and between generations in C. pyri and C. pyricola, and among localities in C. pyri. In contrast, no variations related to psyllid life cycle and geography were detected in C. pyrisuga. In addition to the primary endosymbiont Carsonella ruddii, we detected another highly abundant endosymbiont (unclassified Enterobacteriaceae) in C. pyri and C. pyricola which was related to endosymbionts harboured by other Psyllidae. In contrast, C. pyrisuga carried a different taxon of Enterobacteriaceae related to the genus Sodalis. Our study provides new insights into host–symbiont interactions and highlights the importance of host biology and geography in shaping the psyllid microbiome structure.

Wolbachia infection dynamics in a natural population of the pear psyllid Cacopsylla pyri (Hemiptera: Psylloidea) across its seasonal generations

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Abstract: Wolbachia is one of the most abundant intracellular symbionts of arthropods and has profound effects on host biology. Wolbachia transmission and host phenotypes depend on its density within the host, which can be affected by multiple biotic and abiotic factors. However, very few studies measured Wolbachia density in natural host populations. Here, we describe Wolbachia in the pear psyllid Cacopsylla pyri from three populations in the Czech Republic using phylogenetic analyses based on wsp and multilocus sequence typing genes. Our results demonstrate that C. pyri harbours three new Wolbachia strains from supergroup B. To obtain insights into natural Wolbachia infection dynamics, we quantified Wolbachia from C. pyri at one of the sites across an entire year, spanning several seasonal generations of the host. All tested females were infected and Wolbachia density remained stable across the entire period, suggesting highly efficient vertical transmission and no extrinsic influence from the environment and different host generations. In contrast, we observed a tendency towards reduced Wolbachia density in males, with a significant drop in Wolbachia titer in May. This may suggest gender-related differences in Wolbachia-psyllid interactions. Taken together, this study enhances our understanding of Wolbachia infection dynamics in natural host populations.

The Male Aedes Sound Trap: Field results from Central American and Pacific regions

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Abstract: Aedes aegypti and Aedes albopictus are vectors that transmit viruses such as dengue, Zika and chikungunya. Unfortunately, both mosquito species are also expanding their global distributions at alarming rates. Effective surveillance of current and emerging mosquito populations requires sensitive and affordable mosquito traps. We have developed the Male Aedes Sound Trap (MAST), an inexpensive and low maintenance mosquito trap that uses a low power sound lure and a physical design that selectively attracts male Aedes mosquitoes. The Male Aedes Sound Trap was field evaluated in Mexico, Belize, Australia, and Papua New Guinea using a variety of sound lure frequencies in Latin square experiments including BG-Sentinel traps. The Male Aedes Sound Trap captured both male Ae. aegypti and Ae. albopictus in comparable numbers to BG-Sentinel traps, but with dramatic reductions in other insect bycatch including other mosquito species. Male Culex bycatch can be further minimised, when required, by fine-tuning the sound lure frequency emitted from the trap. These results not only present the most comprehensive field studies of male Aedes attraction to various sound lure frequencies, but also support the utility of the Male Aedes Sound Trap as an effective tool for selectively monitoring male Ae. aegypti and Ae. albopictus populations in the Americas and southwest Pacific including Australia.

Environmental drivers of population fluctuations of the painted lady butterfly (Vanessa cardui) in the Western Palaearctic

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Abstract: One of the main features in the ecology of long-distance migratory insects is the extreme variability of their annual population size. These large fluctuations in numbers are most probably driven by rapid population growth in response to favourable breeding conditions (i.e. a classical ‘r-selected’ strategy) followed by substantial mortality during migration or when new generations are produced in the colonized habitats. However, a rigorous testing of this idea has remained elusive given the lack of precise information on the distribution of wintering populations but also of high quality population data from temperate regions. In this study we focused on the painted lady butterfly (Vanessa cardui), a cosmopolitan multigenerational migrant that, in the Western Palaearctic, undertakes seasonally predictable movements between Europe, North Africa and the Sahelian region. Population data were obtained from 25-yr butterfly counts in three well-established Butterfly Monitoring Schemes in the NW Mediterranean region and NW Europe. Climatic and atmospheric data covering the critical regions and periods where populations originate were extracted with GIS and used as explanatory variables to identify direct and indirect links between the generations monitored in Europe from March to September. Our results confirm that plant productivity (measured as NDVI) in African source regions is the main factor to predict the abundance of populations migrating into Western Europe, but the system is more complex and encompasses a much larger area than previously though. In particular, our results strongly suggest that winter conditions in the Sahel interact with spring conditions in the Maghreb to explain population levels as recorded in Europe in spring and summer. An analysis of migration trajectories demonstrates that it is perfectly feasible for painted ladies to have crossed the Sahara from the West Sahel region to the next potential breeding ground in the Maghreb during periods with suitable high-altitude tailwinds. In addition to conditions in African regions, the climate experienced by populations developing in Europe also explains breeding success and, ultimately, butterfly counts in this continent. Our results shed light not only on the population dynamics of this iconic migrant, but also hold much promise for predicting invasions of a range of other species.

Neither PERIOD, nor TIMELESS 1, nor CRYPTOCHROME 2 are essential components of the molecular clockwork of circadian clock neurons in the Madeira cockroach

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Abstract: Despite of conserved general schemes, molecular circadian clockworks differ between insect species. With RNA interference (RNAi) the circadian clockwork of the hemimetabolous Madeira cockroach Rhyparobia maderae was examined. With injections of double-stranded RNA (dsRNA) of cockroach period (Rm´per), cryptochrome 2 (Rm´cry2), or timeless 1 (Rm´tim1) we searched for essential components of the clock´s core feedback loop. A single injection of dsRNA of each clock gene into adult cockroaches permanently knocked down respective mRNA levels within ~two weeks, deleting daytime-dependent mRNA rhythms for all three clock genes tested. Rm´perRNAi or Rm´cry2RNAi affected both genes, while Rm´tim1 was independent of both. Unexpectedly, circadian locomotor rhythms always remained. They expressed shorter periods for Rm´cry2RNAi and Rm´tim1RNAi, and normal periods for Rm´perRNAi. We hypothesized that coupled clock cells express different periods based on core feedback loops with either PER, TIM1, or CRY2/PER complexes as negative feedback of the clockwork. [Supported by DFG grants STE531/18-1,2; STE531/26-1 to MS; “clocks” grant by the University of Kassel to MS]

Does it pay off? Fitness consequences of anti-herbivore defence priming by oviposition

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Abstract: Insect egg deposition can serve as stimuli which indicate future herbivory for the plant, as it often precedes the attack of herbivorous larvae. Various plant species improve their defence against herbivorous larvae when they previously perceived insect egg deposition as a priming signal. Defence priming is assumed to be an adaptive strategy by which the plant optimizes cost-benefit trade-offs of induced defence. Therefore, we investigated the fitness consequences of oviposition by two herbivorous insect species on the wild tobacco, Nicotiana attenuata. This plant induces more defensive phenylpropanoid-polyamine conjugates in response to feeding by lepidopteran generalist (Spodoptera exigua) and specialist (Manduca sexta) larvae when it had been previously oviposited (1,2). But only larvae of the generalist and not of the specialist are negatively affected in their performance due to this increased defence response. We determined growth parameters and the production of reproductive units such as flowers, capsules and seeds as fitness estimates. Consistent with the effects on larval performance, we found that the fitness loss due to larval feeding by S. exigua was smaller for oviposited plants in terms of seed production, while the fitness loss due to herbivory by M. sexta was not affected by prior oviposition. But, M. sexta herbivory on N. attenuata is also known to induce tolerance responses, such as transient carbon allocation to the roots that can result in a prolonged reproductive phase (3). Therefore, we exposed plants in a full-factorial setup to oviposition and larval feeding by M. sexta, followed by a total aboveground shoot removal. These experiments revealed that a previous oviposition in combination with larval feeding can increase the fitness of regrown plants. Thus, oviposition-mediated defence priming may not just be beneficial if the defence is effective against the herbivore but additionally by increasing tolerance responses to larval feeding.

(1) Banodly et al., 2015; Plant J., 83(4)
(2) Bandoly et al., 2016; Plant Cell Environ., 39(4)
(3) Schwachtje et al., 2006, PNAS, 103 (34)

Improving the use of the IOBC toxicity ratings by using a more realistic test methodology on existing populations and introducing the predator/prey or parasitoid/host ratio

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Abstract: Toxicity ratings for side-effects on beneficial organisms, from the IOBC working group ‘Pesticides and beneficial organisms’, are widely used all over the world to identify selective plant protection products, in order to enhance biological control and integrated pest management in crops all over the world. This working group had developed standard methods which are not only used for IPM purposes, but also for registration dossiers. By far the majority of these tests are done under laboratory and semi-field conditions, on fresh residue on glass, plastic or plants, and more rarely in field tests under practical conditions. Although this approach seems to work well for most products, some problems occurred in practice in the early 2000’s where insecticides that were classified as harmless, when tested under IOBC conditions, turned out to be very toxic in practice, eliminating whole populations of pollinators and released predators and parasitoids. Typical examples of this are abamectin, spinosad and indoxacarb. Conversely, some products that were mainly classified as harmful, like tau-fluvalinate, turned out to be rather safe for a number of important biological antagonists. IPM Impact therefore developed its own testing systems on existing populations, rather than on dry residue. More criticism of the IOBC ratings came when it became clear that often no distinction was made between toxicity and the removal of food, in casu the pest, certainly in the case of ‘specialists’ where no alternative food could be given during the trial. Instead, IPM Impact developed a formula to calculate the predator/prey or parasitoid/host ratio, rather than relying only on the toxicity of a product to a beneficial. To achieve this, efficacy trials are conducted for several pests. As a result, products that are moderately harmful (class 3) or even harmful (class 4) could still be used in IPM schemes If effective against the pest, which lead to a more realistic approach in practice.

A heather nectar metabolites inhibits infectivity of a bumblebee parasite through flagellum removal

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Abstract: Pollinators may medicate themselves with plant metabolites in nectar or pollen against pathogens. Declining plant diversity through anthropogenic landscape change could, however, reduce the availability of medicinal nectar plants for pollinators, exacerbating their decline. I will here address three important current limits in our understanding of pollinator medication by floral rewards: First, existing studies on the medicinal value of nectar and pollen for bees have either been restricted to few, commercially available phytochemicals, or failed to identify active principles in floral rewards with medicinal qualities. There is therefore a need for new approaches to identify key medicinal plants for pollinators. To overcome this limitation, I here present a bioactivity-guided fractionation in vitro screen of nectar metabolites from 17 important bee foraging plants that newly identifies callunene (4-(3-oxobut-1-enylidene)-3,5,5-trimethylcyclohex-2-en-1-one) from heather (Calluna vulgaris) nectar as a metabolite with strong activity against the common bumblebee gut parasite Crithidia bombi. Second, mechanistic insights into how plant metabolites may affect bee diseases are largely lacking. We therefore studied the interaction between callunene and Crithidia bombi in vivo in the bumblebee host Bombus terrestris. The location of C. bombi infections in the ileum of the host means that the parasite here is protected against the influence of callunene in vivo, as the compound is degraded in the midgut.
In contrast, bumblebees received protection against novel infections through callunene, as short-term exposure to callunene in the anterior gut (crop) of the host induced the loss of the flagellum in C. bombi, a structure that is necessary for attachment and motility in the hindgut. This provides a mechanistic basis for a prophylactic benefit from foraging on heather nectar for bumblebees against C. bombi infections. Third, it remains poorly understood if pollinators can actively chose to visit specific plants with medicinal benefits when infected or threatened with infection, a condition for true “self-medication” behaviour. I will here present novel results analysing the foraging of experimentally infected or uninfected bumblebees in a field experiment, questioning the ability of bumblebees to actively self-medicate. Medicinal benefits may rather be acquired passively through the availability of suitable foraging plants in the environment. The strong decline of a putative medicinal plant like heather (Calluna vulgaris) and plant diversity more generally could therefore affect disease dynamics in the wild.

Harnessing ecosystem services from field margins to support agroecological intensification in common beans (Phaseolus vulgaris).

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Abstract: Agroecological intensification enhances ecosystem services (ES) that have nutritional, environmental and socio-economic benefits for smallholders. Chief among these are natural pest regulation (NPR) and pollination services (PS) which both rely on non-crop habitats for food and refuge. Common beans (Phaseolus vulgaris) are a smallholder staple in East Africa provisioning protein and vitamins alongside income. Smallholders experience major yield shortfalls with beans, but these could be reduced by harnessing ES. Here we report how field margins support beneficial invertebrates in beans. We used exclusion experiments to establish the contribution of PS to yield and economic gain and fluorescent dyes to measure movement between field margins and the crop to identify which insects used field margins. We conducted farmers surveys to assess smallholders’ knowledge about PS and NPR and how farmers value field margins.
Bean yields increased from 681 Kg/Ha in self-pollinated to 1,478kg/Ha in open-pollinated beans with more pods and seeds and greater seed weight per plant. Thus, PS contributes significantly to bean yield. Marking studies demonstrated that flower-visiting insects including natural enemies and pollinators moved from field margins into crops suggesting high levels of spatial flux in the arthropod assemblage. Aphid mortality rates (parasitism levels on sentinel plants) did not differ between the field edges and centre so smallholders with small fields did not experience strong edge effects. Surprisingly few farmers understood the contribution of bees/PS to crop yield while 2% were aware of NPR. Most considered ALL insects as pests. Training programmes explaining the role of field margins supporting ES changed farmers views and behaviours regarding their maintenance. Field margins around smallholder bean fields are useful habitats to natural enemy and pollinating taxa that move to adjacent crops providing NPR sand PS thus safeguarding and augmenting ES through effective land management is vital for optimising bean production sustainably.

Natural Pest Regulation of Orphan Crop Legumes in Africa for smallholders.

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Abstract: Natural pest regulation (NPR) by wild insects in agriculture is enhanced by flowering plants in field margins that provide shelter, nectar, alternative prey, or pollen. There is little information on how these field margins influence natural enemy abundance or their pest controlling efficacy on orphan crop legumes. Many orphan crops offer climate resilient traits such as drought tolerance, an increasingly important challenge in smallholder farming systems, so support food security among marginalised farmers.

We identified Aphidius colemani as the key natural enemy of black bean aphids (Aphis fabae) a common legume pest in Kenya and Tanzania. The high genetic diversity of the population shown using cytochrome oxidase I barcoding suggested that this species originated in East Africa. In Malawi, Lysiphlebus testaceipes, a neotropical exotic parasitoid, was dominant in legumes and along with A. colemani should be a target for conservation biological control on orphan crops.

Additionally, we report that natural enemy diversity on orphan crop legumes (focusing on beans and lablab) is influenced by crop management strategies and specific field margin species. We also evaluated how NPR integrates with other pest management approaches. For example, we show that commercially available botanical insecticides work more effectively with NPR than synthetic products.

Effects of defoliation on growth and yield in rice

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Abstract: Rice plants in large field plots were mechanically defoliated at 0, 33, 66, and 100% with a weed eater at two-three leaf, early tiller, late tiller, and green ring growth stages across three planting dates. Large amounts of yield loss were observed when plants were defoliated either 66 or 100% at the green ring growth stage. A delay in heading was also observed when plants were defoliated at 66 or 100% during any growth stage, with delays ranging from 2 days for defoliation occurring at the 2-3 leaf growth stage to 28 days for defoliation occuring at the green ring growth stage. Yield loss and delays in heading were greater for the June planting date compared to the April or May planting date. This data will help form a defoliation based threshold in rice to help keep rice growers profitable.

Evaluation of alternatives to neonicotinoid seed treatments for tobacco thrips management in cotton

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Abstract: Tobacco thrips, Frankliniella fusca (Hinds), is a predictable pest of cotton production systems in the United States. Damage from these pests have the potential to delay maturity and reduce crop yields. On average, insecticide seed treatments have resulted in increases of 128 kg ha-1. Thrips management has been highly reliant on insecticide seed treatments, with thiamethoxam and imidacloprid being the two most widely used options. With the decline in efficacy of thiamethoxam, it is vital to identify alternative control measures for effective tobacco thrips control. Therefore, the objective of this study was to evaluate foliar insecticide applications at various timing intervals as an alternative management strategies for thrips control. Studies were conducted during 2015 and 2016, in Arkansas, Mississippi, Louisiana, and Tennessee using a randomized complete block design with four replications. Treatments included foliar applications of acephate at the following intervals: cotyledon, cotyledon plus two weeks post emergence, cotyledon plus two and three weeks post emergence, and only week two and week three post emergence. All treatments were compared to an untreated check and an imidacloprid seed treatment. There were no differences in cotton yield among any treatments, but early management decisions decreased the overall amount of thrips damage sustained.

Evaluation of Bt Resistance in Helicoverpa zea Strains Using Various Bt Cotton Plant Tissues

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Abstract: Current resistance monitoring methods for Bt resistance in Helicoverpa zea populations consists of populations being assayed for resistance to a single purified Bt protein. Although current monitoring methods adequately indicate if a population has developed resistance to a particular Bt protein, they fail to evaluate how that may impact performance in the field. An assay utilizing Bt cotton plant tissue diet overlays may be utilized to evaluate field performance of a resistant Helicoverpa zea population.

Potential Impact of a New Bt Protein, Cry51Aa2, on Cotton Insect Pest Management in the Southern U.S.

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Abstract: Thrips (Thysanoptera: Thripidae) and tarnished plant bug, Lygus lineolaris (Hemiptera: Miridae), are among the most important economic insect pests of cotton (Gossypium hirsutum) in the mid-southern U.S. including Arkansas, Louisiana, Mississippi, Missouri, and Tennessee. In cotton, these pests are currently managed by insecticides. However, a new Bt cotton technology under development by Bayer CropScience (Cry51Aa2, ThryvOn®) is being evaluated for control of thrips and tarnished plant bug. Field, cage and laboratory studies were conducted to evaluate the effects of this novel Bt-transgenic toxin on insect management in cotton. These data indicated protection from thrips injury to seedling cotton with the Bt trait was as good or better than an insecticide-based approach. The use of this Bt trait also resulted in reduced numbers of immature tarnished plant bugs and protection from plant bug injury. Cotton yields were increased by the use of this Bt trait compared with the non-Bt isoline when insecticides were not used. Although the Bt trait reduced the need for insecticide applications, foliar-applied insecticide applications were needed to provide adequate plant protection against tarnished plant bug. The current recommended treatment thresholds for tarnished plant bug performed similarly well for both Bt and non-Bt cotton isolines.

Interestingly, it appears much of the efficacy of Cry51Aa2 results from insect avoidance, resulting in reduced oviposition on cotton. Adult thrips avoided cotton plants expressing Cry51Aa2c in field choice tests. In a greenhouse choice test, more adult thrips and eggs were found on non-Bt cotton by approximately a 2:1 margin over Bt Cry51Aa2 cotton. In cotton that was not sprayed with insecticides, Bt Cry51Aa2 did not affect the distribution of tarnished plant bugs within the canopy, but in choice tests, adult tarnished plant bugs exhibited a non-preference for Bt-cotton expressing Cry51Aa2 compared with non-Bt cotton. The Bt-transgenic toxin Cry51Aa2 is expected to reduce the need for insecticide applications targeting thrips and tarnished plant bugs and should be a valuable addition to an overall insect management program in cotton. The behavioral response of these pests when exposed to this new Bt toxin will play an important role in the efficacy and potential resistance management strategies once this new technology is introduced commercially.

Use of HaNPV for Corn Earworm Control in Mid-Southern U. S. Soybean & Milo Production

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Abstract: Corn earworm (CEW), Helicoverpa zea (Lepidoptera: Noctuidae),is one of the most damaging pests in soybeans. On average, around 50% of southern USA soybeans are infested with corn earworm, costing farmers over $100 million per year. A key part of this cost results from half of the infested acres not being sprayed with chemical insecticides, causing yield loss from “sub-threshold” damage. Among the most used chemical control options are the diamides, which, because of their high cost (>$15 per acre), are applied at high worm thresholds (e.g. 9 per 25 sweeps for $9 per bushel soybeans).

A new approach, based on applying Helicoverpa nucleopolyhedrovirus (NPV) at a much lower threshold, has been evaluated in southern soybeans over the last 6 seasons. NPV is unique, because the virus replicates in the field, providing season-long control at a similar cost to pyrethroids. Using this new approach, farmers can effectively manage low numbers of CEW, thereby greatly reducing the damage that occurs before reaching a diamide action threshold, resulting in significant yield gains. Importantly, NPV will often eliminate the need for a subsequent insecticide application, further improving farmer’s profitability.

There are several other advantages of an NPV-based strategy. This includes resistance management for diamides, which are valuable tools during high pressure situations, and preservation of beneficial species, which provide important “behind-the-scenes” suppression of soybean pests.

The Midsouth Entomologist Group’s NPV recommendation is based on a multi-year evaluation of Heligen, a commercially available Helicoverpa NPV with over 15 years of proven performance in other markets. When applied according to recommendations, a single application of Heligen offers a cost-effective alternative for season long management of corn earworm.

Value of Foliar Insecticide Applications on Bt Cotton Cultivars Against Helicoverpa zea

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Abstract: Cotton is a high input crop for growers. Each year, the cotton bollworm (Helicoverpa zea, Bodie), infests 100% of cotton planted in Arkansas. It remains a major pest of post-bloom cotton in the Mid-South despite widespread use of transgenic Bt cotton varieties and foliar insecticides are often needed to supplement control. Kerns, et. al. conducted studies in 2017 that indicated widespread resistance to Cry1AC, the major gene associated with Bt cotton. Also, a meta-analysis of cotton data since 2007 throughout the Mid-South indicated that there has been increasing amounts of square damage in dual gene technologies. These findings led to research which established a new bollworm threshold based on damaged fruit rather than insect numbers with the new threshold being set at 6% fruit damage; and in some cases where bollworm populations get exceedingly high, such as South-east Arkansas, an egg threshold of 25% is used. This study indicates that dual gene varieties may not provide the protection needed to prevent fruit damage from bollworms and may require foliar applications. In this study, the newer triple gene cotton varieties are currently providing the control needed to maximize yield without requiring foliar applications.

Termites thrive on wood in association with species-specific ectosymbiotic bacterial communities

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Abstract: Termites have established many associations with gut symbiotic microbes, including many microbes with nutritional functions. In contrast to gut microbes, the associations between termites and ectosymbiotic microbes are known to exist but have rarely been studied. Here, we studied the bacterial communities associated with three wood-feeding termite species using 16S rRNA amplicon sequencing, and we demonstrate the ability of termites to shape the bacterial communities in their direct environment. We show that, on top of their stable association with gut microbes, termites are also associated with numerous ectosymbiotic microbes whose function remains to be determined.

How do termites and humans contribute to the soil fertility in the Congo Basin?

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Abstract: Tropical rainforests are treasures of biodiversity, and are increasingly exploited by local communities, to a degree that should alarm us about the biodiversity fate. In order to protect this biodiversity, any modifications can only be initiated by local communities that need to change their land management habits if the new techniques will help them, too. To demonstrate the positive impact of such new practices, we conducted a long-term experiment on the organic matter turnover, weighting the tropical soil incomes and outcomes, and absolute and relative contribution of particular players in this process. We set up eight plots, roughly one hectare each, at the land-use gradient, with identical geological, climatic and geographical conditions, at the North of the Congo Basin (near Mbalmayo, Cameroon). The plots were established in primary and secondary forests, in cocoa agroforestry systems and in a maize field (two plots per habitat). We studied the energy flow through the soil in the plots by using different techniques and we collected about 50 sociological questionnaires focussing at land-use practices, crops and animal stock, means of money-making and spending, in order to suggest a long-term sustainable agricultural strategy which may contribute to protecting the primary forests.

Fungal symbionts of invasive shot hole borers (Euwallacea spp.) in California can support both beetle systems on artificial media

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Abstract: The specificity of ambrosia beetle-fungus relationships is unknown for the vast majority of ambrosia symbioses, but has important implications for the success of these beetles and fungi in their surrounding environments. The polyphagous shot hole borer and the Kuroshio shot hole borer (Euwallacea spp.) are invasive ambrosia beetles that exist sympatrically in California, USA, and together with their fungi cause Fusarium Dieback in over sixty host tree species. The potential for the two beetle species to exchange symbionts is unknown, but has important ecological consequences. We performed symbiont switching experiments to determine if the polyphagous and Kuroshio shot hole borers can survive and reproduce on each other's symbiotic fungi. Aposymbiotic foundresses were assessed on their ability to reproduce on each of the beetles' primary (Fusarium spp.) and auxiliary (Graphium spp., Paracremonium pembeum) fungal symbionts, grown on sawdust-based artificial media. Offspring were collected to confirm which fungi were present in the different sexes and life stages. The ability of aposymbiotic and non-aposymbiotic foundresses to survive and reproduce on non-ambrosial Fusarium species was also tested. We found that reproduction is maximized on the beetles' primary Fusarium symbionts, regardless of whether a beetle was paired with its own Fusarium symbiont or its congener's, indicating that there is potential for symbiont switching in natural populations of these beetles. The addition of auxiliary fungi to treatments containing Fusarium spp. had no effect on overall offspring production, and females that were fed solely on auxiliary fungi produced significantly fewer offspring. Females that were fed non-ambrosial Fusarium species produced significantly fewer offspring than when reared on symbiotic Fusarium, and this was especially pronounced in aposymbiotic females. From our experiments, the putative roles of the primary versus auxiliary fungal symbionts, as well as the implications of these roles for beetle reproduction and development in their surrounding environment, are discussed.

What phenotype does Wolbachia express in ambrosia beetle hosts of the Euwallacea fornicatus species complex?

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Abstract: Wolbachia is an endosymbiotic bacterium, well-known as a reproductive parasite that influences its hosts' reproduction systems. The intracellular bacteria is typically acquired by vertical transmission from mother to offspring, and several reproductive manipulations are caused by Wolbachia which enhance its frequency in the infected population, including cytoplasmic incompatibility, male killing, feminization and parthenogenesis.

Several closely related species of ambrosia beetle, belonging to the Euwallacea fornicatus species complex, have invaded multiple countries over the last few decades. Native to southern and southeast Asia, these beetles carry with them their own food source, symbiotic fungi which are seemingly also pathogenic to many host trees in invaded areas. At least three species of this complex are commonly found in Taiwan, the tea shot hole borer (TSHB) (E. fornicatior), kuroshio shot hole borer (KSHB) (E. kuroshio) and the polyphagous shot hole borer (PSHB) (E. whitfordiodendrus). A fourth (most likely) species, currently referred to as H22, is also common. These four species are variously infected with Wolbachia. No infected populations of KSHB are known, but H22 and TSHB are 100% infected. In contrast, both infected and uninfected individuals exist of PSHB. Interestingly, PSHB is infected with the same strain of Wolbachia as H22 (based on multi locus sequence typing). However, although infection status is known, the actual effect Wolbachia has on these ambrosia beetles is unknown. We will report on our experiments to determine the costs/benefits of Wolbachia infection in these species.

Life span, foraging activity, effect of parasites and the conservation of bees

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Abstract: Recently, global decline of insects and particularly bees is proposed by scientists. Almost 10% of bees are threatened in Europe. Even worse situation with decline of bees is coming from regional red lists and studies. Currently, we know that something is happening on the level of assemblages. However, we know nearly nothing about effects of environmental factors and climatic change to life span, foraging activity, timing of the first emergence of a species in the year and some other important features on the level of individuals from various species. We present research results based on daily observation of two solitary ground nesting bees Andrena vaga (Andrenidae) and Anthophora plumipes (Apidae). We included all available environmental variables to the generalized linear model and interpreted the results. Most of our models explain more than 60% of deviance in the data. In separate analysis we also included observed A. vaga individuals parasitized by Stylops ater (Strepsiptera) endoparasites that castrate host bees and are thought to manipulate host individual behavior. The results in accordance for both species show that the relative activity (activity per life span), emergence date and amount of precipitations are the most important predictors of life span of bees. Relative activity itself is modulated by emergence date, mean foraging activity per day and amount of precipitation during active day. Temperature during active days was far the fourth important factor either for life span, or activity of bees. However, seasonal temperature was together with seasonal precipitation the most important factors for the first emergence date. The most negative effect to length of life have late emergence in season, drought, higher seasonal temperature and possibly low availability of pollen source. Species probably have some optimal temperature for activity and too low or too high temperatures can be negative. We find out that limited and only at most one quarter of bees that are actually alive can be active in a single day. Usually les than 10% from living bees are active. Inactive bees do not leave their nests whole day. We also find out that parasitized bees differ from unparasitized bees only in their emergence date. Other differences, i.e. in length of life and activity, are only effects of earlier emergence and would be the same for healthy bees when emerged early. Described results are important for variable selection in further ecological research and considered effects of climatic change.

Blood feeding initiates hemocyte proliferation through activation of the insulin signaling pathway in mosquitoes

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Abstract: Anautogenous mosquito species must feed on blood of a vertebrate host to produce eggs. Multiple cycles of blood feeding promote frequent contacts with hosts, which enhance the risk of exposure to infectious agents and disease transmission, as well as proliferation of the gut microbiota, which could put mosquitoes at risk of systemic infection. Blood feeding triggers the release of insulin-like peptides (ILPs) and ovary ecdysteroidogenic hormone (OEH) from the brain of the mosquito Aedes aegypti, which together regulate egg formation through activation of the insulin signaling pathway and ecdysteroid production. In turn, hemocytes have essential immune defense functions. Prior studies indicated that blood feeding stimulates hemocytes to increase in abundance as an anticipatory defense against potential infection. Here, we determined this increase is stimulated by select ILPs but not OEH or ecdysteroids. However, ILP-induced proliferation of hemocytes does not result in up regulation of other immune defense responses. Comparative studies further suggest ILP-induced proliferation of hemocytes after blood feeding is broadly conserved across anautogenous species but has been lost in autogenous mosquito species that no longer blood feed to produce eggs. Taken together, our results further clarify the role of the insulin signaling pathway in regulating an anticipatory immune defense response in mosquitoes that transmit vertebrate pathogens.

Regulation of immune cell proliferation in mosquitoes

Authors: Strand Michael, University of Georgia

Abstract: Most mosquito species are anautogenous, which means they must blood feed on a vertebrate host to produce eggs, while a few are autogenous and produce eggs without blood feeding. Egg formation is best understood in the anautogenous mosquito Aedes aegypti where insulin-like peptides (ILPs), ovary ecdysteroidogenic hormone (OEH) and 20-hydroxyecdysone (20E) interact to regulate gonadotrophic cycles. Circulating hemocytes also approximately double in abundance in conjunction with a gonadotrophic cycle but the factors responsible for stimulating this increase remain unclear. Focusing on Ae. aegypti, we report that hemocyte proliferation is upregulated by insulin-like peptide 3 (ILP3). ILP3 upregulated the insulin signaling pathway in hemocytes but few immune genes with effector functions. ILP3 also stimulated circulating hemocytes to increase in two other anautogenous (Anopheles gambiae and Culex quinquefasciatus) and two facultatively autogenous mosquitoes (Aedes atropalpus and Culex pipiens molestus), but had no stimulatory activity in the obligately autogenous mosquito Toxorhynchites amboinensis. Altogether, results indicate ILPs are the primary regulators of hemocyte proliferation in anautogenous mosquitoes, but also suggest this response has been lost in the evolution of obligate autogeny.

Functional morphology and evolution of an elaborate mechanosensory organ: the subgenual organ complex in the tibia of stick insects

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Abstract: Insect mechanosensory organs consisting of scolopidial sensilla are studied in depth for their morphological diversity and sensory physiology. Such scolopidial or chordotonal organs respond to movements of joints and body parts, substrate vibration, airborne sound, or gravity. The neurophysiology of mechanosensory organs is studied in model species of orthopteroid insects like crickets, cockroaches, locusts or stick insects. Orthopteroid insects possess a mechanosensory organ complex in the proximal tibia, the so-called subgenual organ complex. This complex consist of the subgenual organ, the legs main receptor for substrate vibrations, with additional scolopidial organs close-by. Stick insects are important models in neurophysiology and the neuronal control of locomotion. While leg mechanoreceptors are analysed well studied for their functional contributions, the subgenual organ complex in the tibia was not investigated.

The subgenual organ complex of stick insects (Euphasmatodea) shows a unique neuroanatomical organisation, consisting of the subgenual organ and the distal organ, each with 20-40 sensilla. The subgenual organ is arranged perpendicularly to the tibia's main axis, and the sensilla of the distal organ are arranged linearly along the proximo-distal axis of the tibia. These anatomical differences indicate sensory specialisations between the two organs. In Sipyloidea sipylus, the subgenual organ complex is sensitive to sinusoidal vibration stimuli but not to airborne sound. In addition, the sensitivity is influenced by the stimulus direction, with highest sensitivities in response to vertical displacements along the tibias proximo-distal axis. Likely, this is due to the strongest propagation of vibrations if the stimulus direction and leg orientation are aligned. Notably, sensilla in the distal organ are organised linearly and also show a gradient in size, decreasing from proximal to distal. The functional properties of chordotonal organs depend on the attachment structures, which allow different mechanical inputs. Analysis by microcomputed tomography shows that the distal organ is placed in the hemolymph channel like the subgenual organ. It is attached by different tissue strands to the leg cuticle. There are no obvious attachments to a leg tendon, which could indicate a proprioceptive function. The origin of the elaborate, linear organisation of the distal organ raises both functional and evolutionary questions, since the distal organ in other orthopteroid insects, e.g. cockroaches or locusts, form a smaller, dense group of sensilla. From the functional morphology, the stick insect distal organ is likely also a receptor for vibration stimuli, which can be transmitted in the hemolymph or over the leg cuticle. For a better understanding of the adaptations of the distal organ into the linear set of sensory neurons, the specific biomechanical characteristics of the stick insect tibia need to be established.

Olfactory-visual integration and plasticity in mushroom body output neurons

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Abstract: Brains are fascinating miracles with a multitude of adaptations across the animal kingdom. They receive a tangle of multi-sensory input and hold the capacity to simultaneously select adequate modalities while ignoring others. Hence, the resulting percept reflects a multi-modal construct rather than the neural representation of only a single modality.

Multi-modal integration involves convergence of different sensory pathways at a higher brain level. The bee's mushroom body (MB) represents such an integration center. Its ~170.000 Kenyon Cells are organized in layers each receiving input from a different modality. MB output is conveyed to ~400 MB output neurons (MBON), which we record from on a reliable basis. We characterized olfactory, visual, as well as olfactory-visual (OV) induced activity in the same MBONs. We can show that the layered input of the MB is conserved in a subpopulation of MBONs responding to either odors or light stimulation, whereas a substantial proportion of MBONs was sensitive to both modalities and thus integrated OV information across MB input layers. Another subpopulation of MBONs did not respond to any of the presented stimuli. Previously we showed that such units become recruited after a classical conditioning experiment. We therefore propose that reward association to an OV compound stimulus may recruit initially non sensitive MBONs which will encode the OV-reward association during memory retention after classical conditioning.

Funding: This work is supported by DFG grand STR1334/3-1 to MSB.

LED enhanced yellow traps equipped with cameras for monitoring of whiteflies and fungus gnats

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Abstract: Yellow sticky card traps are used for monitoring and control of alate pests such as whiteflies and fungus gnats in greenhouses. The use of light emitting diodes (LEDs) has turned out as a promising approach to increase the efficiency and reliability of visual traps. The implementation of (semi-)automatic image acquisition and analysis methods is of great interest in order to improve and simplify the identification and counting of insects on traps.

LED enhanced yellow traps were constructed which combine a yellow card with specific edge lighting acrylic glass equipped with green high-power LEDs in a frame. In a next step, traps were equipped with cameras and white high-power LEDs were mounted in the frame and adjacent to the trapping surface to facilitate the acquisition of transmitted and incident light images at dark night-time conditions. The traps were compared with common yellow sticky traps in small-scale tomato crop stands in gauze cages with artificial whitefly infestation (Trialeurodes vaporariorum) and naturally occurring not further determined fungus gnats. A final experiment was conducted in a larger crop stand to evaluate the trap efficiency and the image acquisition method with subsequent pest counting on images.

The results show a significantly increased efficiency of the LED enhanced traps for whiteflies compared to yellow traps in experiments with high population densities and in choice situations with both trap types. A higher attractiveness for fungus gnats was observed throughout. The obtained images allowed reliable counting of both pests comparable with manual counting on traps.

Utility of metagenomic data for Platypezidae

Authors: Ståhls-Mäkelä Gunilla, Finnish Museum of Natural History, Finland

Abstract: Shotgun metagenomic DNA sequencing is a powerful sequencing approach that provides insight into community biodiversity and function. Here it was used to screen genomic DNA of platypezid flies as a first step to decipher the unknown biology of some lineages by characterizing the fungal and microbial biota associated with the flies. About 10GB of genomic information was sequenced per specimen. The mitochondrial genome and nuclear ribosomal gene sequences were extracted for phylogenetic studies.

Insect Community in Beijing Urban Area: Does Functional Type of Green Space Matter?

Authors: Su Zhimin[1] and Ouyang Zhiyun[1], [1]State Key Laboratory of Urban and Regional Ecology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing, China

Abstract: Urbanization is the leading cause of biodiversity decrease, while urban green spaces are considered as the important harbor of wildlife in urban area, raising questions about the abilities of different habitats to support the species surviving. The aim of this study was to: (i) understand the composition of insect community, (ii) evaluate how much the theoretical species richness is, (iii) analyze whether the insect diversity have significant differences, (iv) and how about the structure of community in different functional types of urban green space.

We collected insect specimen using suction trapping within 45 green patches across six types of urban green space of Beijing. A total of 11211 specimens, representing 213 species / morphospecies from 11 orders, 98 families, were collected from 1620 samples. Hemiptera, Coleoptera, Hymenoptera, Diptera, Orthoptera and Lepidoptera are the six major orders on the urban lawns, with several highly dominant taxa groups. For the entire study and each green space type, we plotted species-octave histograms to visualize abundance distributions following the method of Preston.

We found that octave-based relative abundance plots for all types of green space produced convincing lognormal distributions. The lognormal equation for species-abundance distribution in the institutional green space had the best goodness-of-fit ($r2 = 0.966$, $P < 0.0001$) than that for other five green types. On the basis of lognormal equation for species-abundance distribution, the theoretical total number of species in the universe being sampled was 320, 2/3 of which (213 species) were represented in the sample. There was not significantly different in insect diversity among different green space types. Vacant land had the highest Fisher's a diversity, followed by protective, institutional and residential green spaces. When using Shannon and Simpson indices as measure of insect diversity, protective green space was most diverse. Street green space had overall the lowest diversity. Insect community composition varied significantly among different green space types (adonis, $F = 2.098$, $P = 0.002$), with the vacant land significantly different from all the other green space types.

Our findings demonstrate that urban green spaces play important but different roles among different functional types in shaping urban insect diversity. Vacant land may be considered as a potential species pool. Its retention, removing, redesign and management needs to consider the environmental concerns, such as supporting biodiversity or improving infiltration of storm water. Therefore, reasonable allocation and management of different greenspace types may help to increase urban insect diversity.

Design and rationale for regional genetic monitoring scheme toward adaptive resistance management

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Abstract: Considering the aspect of temporal evolution in the resistance development of an insect pest to insecticides, an ideal management program should be adaptive: guidelines for the normal use of insecticides to delay resistance development (e.g. pesticide pyramiding, rotation, and untreated refuge), combined with the monitoring of field pest populations. Responding the “resistance risk level” based on the resistance allele frequency and/or mortality in bioassays, the insecticide use is halted at regional scale.

Monitoring and risk assessment of a field-evolved resistance comprise of several key techniques. One is the genetic diagnosis, including the development of genetic markers as well as analytical pipeline. Another important factor is the spatio-temporal sampling design to collect insects from field. A simulation suggests the risk of resistance prevalence in near future is correlated to the higher resistance allele frequency in the local mating pool, typically in adult males (Sudo et al. 2018 Evol Appl). Mass capturing methods e.g. sticky trap with attractants is a good way to grasp the tendency, showing high affinity with large-scale diagnosis exploiting next-generation sequence (NGS) analysis.

We preliminarily conducted a two-year, multi-site monitoring of the diamondback moth, Plutella xylostella, to multiple insecticides in Nagano Prefecture, central Japan. The NGS-based diagnosis revealed the spatio-temporal spread of resistance alleles, which can be used to determine the “optimal management unit” for future monitoring and regulation.

Gripping ease in southern green stink bugs Nezara viridula L. (Heteroptera: Pentatomidae) exploring highly variable terrains

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Abstract: The highly polyphagous southern green stink bug Nezara viridula L. (Heteroptera, Pentatomidae) prefers apically situated seeds and fruits on more than 150 plant species belonging to over 30 plant families all over the world. This forces them to move over highly variable terrains, including plant stems, leaves, pods and buds, which requires efficient attachment. Stink bugs have long slender legs and feet (tarsi)

equipped with paired curved claws, paired soft adhesive pads (pulvilli), and flattened lanceolate hairs (setae), which arise ventrally on the first and second foot segments (tarsomeres). To characterize their attachment abilities on well-defined test substrates, here we comparatively measured and analyzed the traction forces of bugs walking horizontally and vertically on hydrophilic (water attractive) and hydrophobic (water repellent) glass plates and rods (Voigt et al. 2019). The latter correspond to the geometry of preferred feeding sites of stink bugs in the field. The results show a clear contribution of tarsal flattened lanceolate hairs to the stink bug’s attachment. Higher traction forces are generated on a glass rod than on a glass plate, corresponding to up to individual maximum of 43 times the stink bug’s body weight. Substrate hydrophobicity promotes the attachment, while the measured forces are up to eight times lower when tarsal hairs are disabled. The combination of smooth and hairy tarsal pads results in a remarkable attachment ability, which enables N. viridula to climb unstable apical plant parts. The understanding of the foothold on plants and supports evaluations of stink bugs’ invasive behavior and global dispersion.

Reference:
Voigt D, Perez Goodwyn P, Sudo M, Fujisaki K, Varenberg M (2019): Gripping ease in southern green stink bugs Nezara viridula L. (Heteroptera: Pentatomidae): coping with geometry, orientation and surface wettability of substrate. Entomological Science 22: 105-118.

Effects of habitat conversion on plant-caterpillar-parasitoid networks in Ecuador

Authors: Sudta Chanchanok, University of Nevada, Reno

Abstract: Are global change parameters, such as increased mean temperatures, extreme weather events, and loss of biodiversity favoring generalist versus specialist organisms? To answer this question, we need to better understand ecological specialization and how it is affected by environmental change or how it varies across gradients. Using 18-years of empirical data from Ecuador on interactions between host plants and caterpillars collected from tropical forests along elevational gradients, we found that specialists are locally more abundant than generalists. The findings also revealed that generalist caterpillars achieve greater prevalence across the landscape. Loss of tropical forests and conversions to grassland can alter biodiversity, species interactions, and ecosystem functions. Concerns about habitat loss have prompted an additional question about associations between diet specialization and caterpillar abundance. Here, we examine variation in plant-arthropod networks across disturbance and elevational gradients in the Eastern Ades of Ecuador. The research will close knowledge gaps about how the complexity of biotic communities is affected by global change. The work will help tropical conservation efforts by identifying how specialist versus generalist organisms respond differently to global change and how that could affect ecosystem services that support local communities.

Biology of Mycetophila ruficollis (Diptera: Mycetophilidae), a fungus gnat pest of the Shiitake mushroom

Authors: Sueyoshi Masahiro, Japan

Abstract: Mycetophila ruficollis Meigen is a fungus gnat recorded from Europe and Japan. It is clearly delimited by some morphological features on the dark marking at the middle of the wing and the absence of any ventral setae on the mid tibia, and the gonotsylus of the male genitalia with narrow tip. This species composes the M. ruficollis species group, together with other 17 morphologically resemble species from Europe, Iran, China, Nepal, Mongolia, USA, and Canada. A molecular work supported the morphological species discrimination but is morphologically unable to identify female specimens to the species level in some species of the group. Mycetophila ruficollis is known as one of pests of the Shiitake mushrooms, Lentinula edodes, cultivated with bed logs of oaks in Japan. The larvae of this fungus gnat mine and injure the fruit bodies of the Shiitake. It also parasites fruit bodies of oyster mushrooms, Pleurotus ostreatus (Pleaurotaceae), and Omphalotus japonicas (Marasmiaceae). Adults of the group visit flowers of some jack-in-the-pulpits, and may pollinate them and contribute to pre-reproductive isolation of closely related Arisaema spp. of the Araceae.

The Shiitake is one of the edible fungi worldwide. They are cultivated with bed logs installed in forests since 17th century, or sawdust-based artificial media in an indoor facility since 1980s, in Japan. More than two 1.7 thousand farms product 65 thousand ton of the Shiitake in 2020. The amount of the Shiitake cultivated with bed logs represented 23% of the overall total in Japan but 60 % of Kyushu, south of Japan. The Shiitake cultivated with bed logs are rich in flavor and chewy taste and are traded at high prices, rather than the Shiitake cultivated with artificial media. Pest controls of M. ruficollis support sustainable use of the Shiitake cultivated with bed logs. I have studied on the biology of M. ruficollis in Kyushu, Japan, in recent years, resolving some aspects of biogeographical distribution, seasonal abundance, and parasitoids of this fungus gnat.

Mycetophila ruficollis has been recorded from Hokkaido to Kyushu in Japan. Based on the male specimens from more than 300 localities (elevation: 1-1292m, altitude: 32-45 degree north) of Japan, adults were found from March to December. Most number of adults emerged on March to June, with a peak on the late April, and some little numbers were also found on October to December in bed log laying yards. These observations support a hypothesis that it has at least two generations per year and overwinters as mature larvae and pupa. The larvae dwelt into soil and litter. Natural enemies of M. ruficollis have not been known well. Zero to 46% of larvae collected from fruit bodies of the Shiitake were infested by proctotrupid, and diapriid, and braconid wasps. The abundance of M. ruficollis in the bed log laying yards are much higher than that in other surrounding forests. It suggest that the population of this fungus gnat repeat generations every year, settling the yards.

Spatiotemporal distance between oilseed rape fields reduces cabbage seed weevil pressure without affecting biocontrol

Authors: Sulg Silva[1], Kaasik Riina[1], Willow Jonathan[1] and Veromann Eve[1], [1]Estonian University of Life Sciences

Abstract: Large monocrops provide sufficient vital resources for agricultural pests, but often do not support the presence of natural enemy populations (e.g. predators, parasitoids). This ecological imbalance can make intensive pesticide use a necessity for farmers. At the farm level, preventive methods in pest control (e.g. landscape complexity, crop-rotation, pathogen-free propagation material, cautious pesticide use) are well-established, whereas spatiotemporal field separation of same crop species remains understudied for most crop–pest systems, yet may be of great importance as a pest management technique. We carried out a three-year study in winter oilseed rape fields, where half of the fields were within 500 m from the previous year's closest oilseed rape field, and half outside this spatial distance. Cabbage seed weevil (Ceutorhynchus obstrictus) abundance was reduced in fields located further than 500 m from the previous year's nearest oilseed rape field, whereas parasitism by its key parasitoids was high in all fields. We demonstrate that spatiotemporal field separation is an effective preventive pest control technique at the landscape scale, and can work together with conservation biocontrol, which helps reduce the next year's pest population. The use of spatiotemporal distancing should be investigated as a key integrated pest management strategy in additional cash crops.

Conservation initiatives on privately owned and leased land can greatly benefit invertebrate fauna: a case study from Australia

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Abstract: The Australian Land Conservation Alliance (ALCA) is the peak group for eleven member organizations that manage privately owned in Australia with the aim of sustainable production and/or biodiversity conservation. The Australian Wildlife Conservancy, with more than 6.5 million hectares, is the largest private owner and manager of land dedicated to conservation in Australia. The land managed by members of the ALCA includes desert, grassland, savanna, heathland, eucalypt forest, rainforest and wetlands. Land management at the landscape level is focused on soil retention, soil health and revegetation or regeneration. Soil, vegetation and vertebrates are the primary foci of conservation actions. Specific initiatives of ALCA members include the restoration of endangered ecosystems, increasing the protected area estate, the control of invasive alien species and using nature-based solutions to tackle climate change. The major indirect beneficiaries of the intensive and extensive land conservation programs being managed by ALCA members across the vast Australian landscape are the invertebrates, mostly arthropods, a high proportion of which are endemic. Tens of thousands of invertebrate species, mostly insects and mites, are very likely inhabiting areas managed under the ALCA umbrella and management practices that increase ecological integrity and resilience can improve their chances of long term survival.

Genome comparisons and genetic diversity of 'Candidatus Liberibacter solanacearum' and its psyllid vectors

Authors: Sumner-Kalkun Jason, SASA; Scottish Government, United Kingdom

Abstract: The phloem-limited bacterium 'Candidatus Liberibacter solanacearum' (Lso) and its psyllid vectors are responsible for significant economic losses in Solanaceous and Apiaceous crops worldwide. Currently little is known about the genetic diversity of Lso and its psyllid vector with only a handful of draft genomes available. The recently described wild haplotypes U, Cras1, and Cras2 will be sequenced and compare to known pathogenic Lso haplotypes to examine genes that play a role in infection/ pathogenicity. We will examine psyllid populations of carrot psyllids (Trioza apicalis and Bactericera trigonica) from 7 European countries to understand their dynamics to infer psyllid movement. Ultimately, this will highlight areas that are at risk of psyllid invasion and help understand psyllid population movements.

Taxonomy at NCBI and GenBank -- An update for entomologists

Authors: Sun Lu[1], [1]National Center for Biotechnology Information (NCBI), United States

Abstract: NCBI Taxonomy database contains names and other taxonomic information for near 2 million organisms of which sequence data are recorded in GenBank and other databases. Additions of new taxa to science (and to NCBI Taxonomy) demonstrate an accelerating rate at present. More than one-fourth of all formal species names in NCBI Taxonomy belong to insects (about 140,000). Still, they account for barely over 10 percent of all published insect species, making Insecta the most "incomplete" group in the database. In addition, about half million insect names with various formats in NCBI Taxonomy are not identified into known species. Meanwhile, their naming and classifications have been undergoing constant, frequent, and often drastic changes.

This presentation provides an update to the curating of NCBI Taxonomy database and general guidelines for validating and registering related information generated among submissions and requests by users. Upgrades of the database software (Tax Editor) are developing and enabling large amount of complex taxonomic information (synonymies, authorities, references, types, etc.) to be registered and linked to other databases. On the other hand, timely data updates basing on newer study results maintain a challenge. Also, new types of research and enhanced, automated submission protocols demand revisions of policies. Resources, limitations and future improvements are discussed."

Identification of maleness factors escaped from doublesex dogma, a novel type of genital development pathway discovered in the silkworm, Bombyx mori.

Authors: Suzuki Masataka[1], Kasahara Ryota[1], Aoki Fugaku[1] and Yamamoto Fumiko[1], [1]Graduate School of Frontier Sciences, The University of Tokyo, Japan

Abstract: Reproduction of most animals is based on precise formation of sexually dimorphic genitalia. In insect species, sexually dimorphic genitalia development is regulated by a Zinc-finger type transcription factor gene, doublesex (dsx). dsx produces sex specific isoform called dsxM, dsxF by alternative splicing and regulate expression of maleness/femaleness factors in each sex. From past studies in many insects, insect sexual development is thought to be regulated by top-down, one-way cascade starts from sex determination gene, end in sex specific sexual development regulated by dsx. Thus, dsx has been believed to be an omnipotent regulator and only nexus in insect sexual development. However, recent studies are beginning to destroy that myth. The dispensable function of dsxF in female genitalia development has been observed in many basal insect species including Hymenoptera, Hemiptera, Dictyoptera. These facts indicate functional diversity of dsx and existence of sexual development factors that escaped from dsx control.

The domesticated silkworm, Bombyx mori is widely used lepidopteran model insect especially for genetics. This species has ZW/WW sex determination system, female sex determination gene Fem on W chromosome and male sex determination gene Masc on Z chromosome decide Bombyx mori dsx (Bmdsx) splicing pattern. Previous studies using forced expression and transient genome editing have demonstrated vital role of Bmdsx on genitalia development. Recently, we newly established stable mutant lines to examine more accurate functions of Bmdsx. During the study, we unexpectedly found unusual sexual development that is inconsistent with canonical model. The Bmdsx stable mutant, especially male, exhibited normal sexual development in some part of genitalia. This is also inconsistent with the case in species whose dsxF only has dispensable functions. From these facts, we are convinced this phenomenon is worth studying.

As first step, we performed transcriptomics (RNA-seq) for dsx mutants and sought responsible genes. Among about 100 candidate genes, we focused on 2 genes that were previously related to sexual development in the silkworm and the fruit fly, Drosophila melanogaster. RNA-seq analysis revealed they were not regulated by BmdsxM, but significantly suppressed by BmdsxF. Their expression was biased in testes during late larval to early pupal stage. Functional analysis of these genes using CRISPR/Cas9 proved their function in male genitalia development where Bmdsx mutation could not affect.

These findings allowed us novel viewpoint on genitalia development. It is said that Lepidopteran males have developed many unique genitalia features such as large testes and two types of sperm. We might be able to say that function of dsx in each species is correlated with sex-specific selection pressure.

Transgenic and knockout analyses of Masculinizer and doublesex illuminated the unique functions of doublesex in germ cell sexual development of the silkworm, Bombyx mori

Authors: Suzuki Masataka[3], Aoki Fugaku[2], Sezutsu Hideki[1], Sumitani Megumi[6], Matsuoka Misato[5] and Yuzawa Tomohisa[4], [1]1) Transgenic Silkworm Research Unit, Institute of Agrobiological Sciences, National Agriculture and Food Research Organization (NARO) 2) Department of Integrat, [2]Graduate School of Frontier Sciences, The University of Tokyo., Japan, [3]Graduate School of Frontier Sciences, The University of Tokyo., Japan, [4]Japan Water Systems Corporation, Japan, [5]SHINYUSHA, Japan, [6]Transgenic Silkworm Research Unit, Genetically Modified Organism Research Center, Institute of Agrobiological Sciences, National Agriculture and Food Research

Abstract: Background: Masculinizer (Masc) plays a pivotal role in male sex determination in the silkworm, Bombyx mori. Masc is required for male-specific splicing of B. mori doublesex (Bmdsx) transcripts. The male isoform of Bmdsx (BmdsxM) induces male differentiation in somatic cells, while females express the female isoform of Bmdsx (BmdsxF), which promotes female differentiation in somatic cells. Our previous findings suggest that Masc could direct the differentiation of genetically female (ZW) germ cells into sperms. However, it remains unclear whether Masc directly induces spermatogenesis or if it promotes male differentiation in germ cells indirectly by inducing the expression of BmdsxM.

Results: In this study, we performed genetic analyses using the transgenic line that expressed Masc, as well as various Bmdsx knockout lines. We found that Masc-expressing females with a homozygous mutation in BmdsxM showed normal development in ovaries. The formation of testis-like tissues was abolished in these females. On the other hand, Masc-expressing females carrying a homozygous mutation in BmdsxF exhibited almost complete male-specific development in gonads and germ cells. These results suggest that BmdsxM has an ability to induce male development in germ cells as well as internal genital organs, while BmdsxF inhibits BmdsxM activity and represses male differentiation. To investigate whether MASC directly controls male-specific splicing of Bmdsx and identify RNAs that form complexes with MASC in testes, we performed RNA immunoprecipitation (RIP) using an anti-MASC antibody. We found that MASC formed a complex with AS1 lncRNA, which is a testis-specific factor involved in the male-specific splicing of Bmdsx pre-mRNA.

Conclusions: Taken together, our findings suggest that Masc induces male differentiation in germ cells by enhancing the production of BmdsxM. Physical interaction between MASC and AS1 lncRNA may be important for the BmdsxM expression in the testis. Unlike in the Drosophila dsx, BmdsxM was able to induce spermatogenesis in genetically female (ZW) germ cells. To the best of our knowledge, this is the first report that the role of dsx in germ cell sexual development is different between insect species.

Environmental RNAi-mediated gene silencing in spider mites and its application to pest control

Authors: Suzuki Takeshi[1], Ghazy Noureldin[1], Arai Yuka[1], Takeda Naoki[1] and Hamdi Faten[1], [1]Tokyo University of Agriculture and Technology, Japan

Abstract: Environmental RNA interference (eRNAi) induced by exogenous double-stranded RNA (dsRNA) has been attracting attention as the mechanism of action of next-generation pesticides. eRNAi acts by suppressing gene expression in a sequence-specific manner, which ultimately enables pest management with species-specific resolution. eRNAi-based pest control is broadly classified into the use of crops expressing dsRNA of the target pest species and the spraying of synthesized dsRNA. The latter is called eRNAi-based biopesticides and is expected to be used in many countries and regions because it does not fall under the category of genetic modification. In this presentation, we discuss the potential application of eRNAi for controlling the two-spotted spider mite, Tetranychus urticae, which has the most serious resistance problem. Here we focus on midgut cells, the most promising target for eRNAi-based biopesticides in spider mites, and introduce the dsRNA uptake mechanism and subsequent dsRNA processing mechanism in the cells. In addition, we introduce a highly efficient method that uses a sheet-like structure mimicking plant leaves for the eRNAi screen in spider mites.

The role of the activin ligand Myoglianin in the developmental timing of metamorphosis in holometabolous insects.

Authors: Suzuki Yuichiro[3], He Lorrie[3], Shin Sara[3], Yuan Isabelle[3], Chiou Allie[3], Koyama Takashi[2] and Nijhout Frederik[1], [1]Duke University, [2]University of Copenhagen, [3]Wellesley College, United States

Abstract: In holometabolous insects, attainment of a threshold size specifies the final larval instar. We investigated the mechanism of threshold size assessment in the tobacco hornworm, Manduca sexta. The threshold size was found to vary with the level of exposure to poor nutrient conditions, whereas it was consistently lower under hypoxic conditions. Under these various conditions, threshold size was correlated with the mass of the muscles plus integuments and myoglianin (myo) expression. RNA interference-mediated knockdown of myo in Tribolium castaneum led to larvae that underwent supernumerary larval molts and stayed in the larval stage permanently even after passing the threshold size. We propose that increasing level of Myo in growing larvae serves a readout of their body size and trigger metamorphosis at the threshold size.

Green is good, grey is bad? - Landscape-level drivers of flying insect biomass

Authors: Svenningsen Cecilie[3], Tøttrup Anders[2] and Bowler Diana[1], [1] German Centre for Integrative Biodiversity Research (iDiv), [2]Natural History Museum of Denmark, [3]Natural History Museum of Denmark, Denmark

Abstract: The proportion of the Earth that is actively managed by humans continues to increase, with at least three-quarters of the global land area currently affected by human activities. Although biodiversity decline is linked to human activities, most evidence is derived from studies on plants and vertebrates with large data gaps on insects.

In this study, we investigated how land cover and land use affects flying insect biomass. To examine landscape level effects, we engaged citizen scientists in Denmark and Germany to sample flying insects using car nets along five km routes during the summer of 2018. We then extracted land use data from various sources, to examine how urban, farmland, grassland, wetland and forest affect flying insect biomass from a local (50 m) to a landscape (1000 m) scale.

By sampling across long transects of both grey and green urban areas, we show clear effects of reduced biomass associated with urban cover that were not evidenced before across a spatial large scale. In addition, we find that semi-natural areas, especially grassland and wetland, have higher insect biomass per relative percentage cover than both urban and farmland areas, signaling their importance for insect conservation.

A Predator as Prey: the evolutionary balancing act of praying mantises

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Abstract: The evolutionary interplay of predators as prey of vertebrates creates a dynamic organism that functions in its environment in unexpected and complex ways. Past research on the morphological, biogeographical, and ecological evolution of the lineage led to numerous findings that changed the way we think about their deep history and modern relationships. Recent research has focused on the evolution of a highly specialized predatory strategy within flower mantises, which includes shifts in sexual dimorphism, coloration, and crypsis. So extreme were these shifts that the mantis now functions with two signaling channels, one for prey and one for potential predators. New research is focused on the visual tracking, response, and pursuit of prey items and how these can change dramatically based on context. It points to a predator that is both flexible and dynamic, which challenges the traditional notion of these organisms functioning simply as ambush predators. Another project is focused on a highly specialized mantis lineage that has adapted into a very unmantis-like niche, which is even linked to novel ways of perceiving the environment. The final project evaluates the context of visual targets that are attractive as prey, but eventually pass a threshold and change into a threat. This shift in behavior indicates a clear strategy for when to hunt and when to hide. This presentation gives context to praying mantises as organisms that play the game between hunting and being hunted through their cryptic strategies, their level of hunger, and their perception of the environment.

Glial Kir channels as a target for novel mode- and mechanism- insecticides

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Abstract: Ion channels are ubiquitously expressed across animal tissue systems and they have been conserved throughout evolution to play essential roles in nearly all biological phenomena. Our group has aimed to characterize the physiological role of insect inward rectifier potassium (Kir) channels and have tested the broad hypothesis that inhibition of these channels will have deleterious consequences to insect tissue function and insect survival. Recent work has shown expression of various ion channels in insect glia cells, raising the intriguing possibility that glial cells contribute to neuronal function of insects and may represent a cellular target for insecticide design. Considering this, we tested the hypothesis that insect Kir channels expressed in glia cells contribute to central nerve firing and thus, Kir inhibition will have deleterious consequences to neuronal function and fly survivorship. To test this hypothesis, we used CRISPR/Cas9 in Drosophila to fluorescently tag the endogenous gene loci of Kir1, Kir2 and Kir3. Fluorescent microscopy imaging showed Kir2 channel subunits are localized at the membrane of glial cells, but not neurons. Functional studies support this localization pattern as patch-clamp electrophysiology showed an inward K+ conductance of 104 ± 60 pA/pF in Drosophila glia cells but no significant inward K+ current in central neurons. These data led us to speculate Kir channels constitute a mechanism for rapid clearance of K+ ions from the extracellular space during neuronal activity and thus, inhibition of glial Kir channels would result in membrane depolarization and increased firing. To test this, we performed extracellular recordings of Drosophila descending neurons and found pharmacological inhibition of Kir channels significantly ($P<0.05$) increased the firing rate and lead to nerve death. Importantly, tarsal contact of insect specific Kir channel inhibitors results in fly mortality (LC50: 700 ng/cm2). These data indicate it is possible to alter neural function of insects through inhibition of glia specific ion channels and highlights the potential for developing novel mechanism insecticides targeting glial Kir channels.

Soil-dwelling arthropods as indicators of erosion in a South African grassland habitat

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Abstract: Soil erosion is a natural process that drives the formation of lowland terrains in mountainous regions. Its role in ecosystem degradation has been strongly debated, due to the significant effect it has on a range of land types. Soil arthropods have been used as indicators of several disturbance types. However, little is known about arthropods in eroded sites in South Africa. The aim of this study was to identify possible indicators of erosion in the Golden Gate Highlands National Park, South Africa, and to determine differences in soil-dwelling arthropod assemblages found in non-rehabilitated and rehabilitated sites over a 24-month period. A total of 5661 soil arthropods were sampled during the study, with the highest species richness recorded in non-rehabilitated eroded sites. A higher number of unique arthropod species were recorded from the non-rehabilitated sites compared to other site types. Overlaps in assemblage structure between site types differed, dependent on site locality. IndVal results indicated a single strong indicator, the mite Speleorchestes meyerae Theron & Ryke, 1969, for the non-rehabilitated eroded sites. Linear model analyses of site richness with mineralogy identified the significance of Phosphorus (in the form of P2O5) in eroded sites. Given these results, soil mineralogy in conjunction with soil arthropod richness of eroded sites could be used to investigate the effect of erosion and form a basis for future study in soil biodiversity and function.

Opportunities for improving early detection of exotic jewel beetles

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Abstract: Our ability to survey for and detect the presence of potentially invasive, non-native longhorn beetles, bark and ambrosia beetles has improved significantly in recent decades, thanks in large part to the discovery of aggregation/sex pheromones in hundreds of species. On the other hand, the chemical ecology of jewel beetles (Buprestidae) is in its infancy and they are frequently under-represented in traps used in operational surveillance programs by regulatory agencies. The genus Agrilus has more than 3000 species worldwide, and even if only a small fraction of these have the potential to behave like the invasive emerald ash borer if established in a new habitat with naïve hosts and few natural enemies, we must develop improved tools and methods for their early detection. We briefly review some of the factors affecting detection of jewel beetles in surveillance traps such as trap colour, trap position, and semiochemical attractants, and present results from field experiments replicated in Europe, China, and North America.

The fragmented mitochondrial genomes of lice: how a rare and often fatal phenomenon persists in a group of parasitic insects

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Abstract: The mitochondrial genomes of most animals are contained on single chromosomes. However, in very rare cases mitochondrial (mt) genes are separated on multiple circular chromosomes. The greatest known abundance of these fragmented genomes is in lice (Insecta: Phthiraptera), parasitic insects of mammals and birds. 16 species from a single clade of mammal lice are known to have multiple mitochondrial chromosomes. Yet, some studies have indicated that other groups of lice also have fragmented mt genomes. Here we use whole genome sequence data to test how many times fragmented mt genomes have arisen across parasitic lice and address what factors might be associated with this fragmentation. We applied a bioinformatic approach to assemble and annotate mitochondrial genomes from 32 genera of parasitic lice and found that 19 of these genera have fragmented genomes ranging from 2 to 20 chromosomes. Based on an existing species phylogeny, our results suggest fragmented mt genomes arose at least 12 times within parasitic lice. The majority of these transitions appear to have occurred in avian feather lice. There was very little phylogenetic structure to patterns of genome architecture; however, there was relatively consistent genome structure within specific clades of lice, suggesting that a finer-scale approach is needed to understand how mt genome fragmentation occurs. Comparisons within these clades provided evidence for the order of mt genome fragmentation, and gave some insight into traits that are associated with mt genome architecture. Overall, this study highlights the complexity of mitochondrial genome architecture, particularly in parasitic lice, and provides an essential evolutionary framework for assessing the mechanisms and drivers of this complexity.

Viral-like particles for dsRNA delivery

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Abstract: Although RNAi has emerged as a promising strategy for insect pest control, considerable improvements are required to make it suitable for practical applications. One possible strategy would be based on the use of insect RNA viruses that produce dsRNA as part of their infection cycle. However, recombinant viruses would be considered as genetically modified organisms for which strong opposition exists by regulators and the general public. An alternative solution would be to use “viral-like particles” (VLPs) for encapsulation and delivery of non-replicative dsRNA molecules that are capable to induce silencing of essential genes in insect pests.

In this project, attempts are made to employ the baculovirus expression vector system (BEVS) for creating a biotechnological platform for production of VLPs and their encapsulation of dsRNA. VLPs will be derived from the dsRNA virus Cypovirus (Reoviridae) of which the structure has been extensively characterized by cryo-electron microscopy. In addition, the production of dsRNA molecules by the BEVS will be examined and strategies will be explored for their incorporation in VLPs during co-expression in insect cells. Finally, uptake of VLPs by cell lines and insect larvae will be evaluated as well as their capacity to deliver dsRNA and trigger gene silencing.

Influence of laboratory, semi-field and field conditions on Aedes albopictus vector competence

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Abstract: Experimental infections of mosquitoes with arboviruses are used to infer the potential role of vector populations in the transmission of diseases. The heterogeneity in the design of such studies can affect the results and reproducibility of experiments, making difficult the extrapolation of laboratory results to field conditions and comparisons between studies. Adaptation of mosquito’s colonies to laboratory and rearing conditions is a common step before conducting such studies and can affect the outcome of the research.

In this study we aimed to investigate the impact of Aedes albopictus rearing conditions on vector competence. Mosquito eggs were collected from the field and reared over five generations under different temperature and humidity conditions using cages of different size, to get a gradient of conditions from closer to those in nature to those typically used for colony maintenance in the insectary. Females were infected with Chikungunya virus and saliva and body parts were analyzed by plaque assay.

Results showed that rearing conditions typically used in the laboratory can lead to an overestimation of vector competence, with high values of infection rate and transmission efficiency compared to mosquitoes reared under semi-field conditions.

Molecular signatures for sexual communication in flies

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Abstract: Insects interpret the rich chemical landscape around them through a combination of physiological and behavioral adaptations. Exploiting vertebrates for a blood meal or, obtaining a sugar meal from plants demand extensive sensory and behavioral adaptations that are apparent across the evolutionary range of vector species. Since animal senses are biological features that have been shaped by natural selection to promote adaptive behavior, a variety of exciting patterns are apparent in what they sense and how. Vectors display robust olfactory driven behaviors. A distinct yet limited range of volatile organic compounds are parsimoniously used as major cues for tracking in various contexts. These chemicals elicit behaviors such as attraction or repulsion/avoidance while vectors seek habitats, hosts, mates, or oviposition sites. Chemoreceptors interact with the chemicals to elicit such essential behaviors: Odorant receptors (ORs), gustatory receptors (GRs) and ionotropic receptors (IRs) together detect and discriminate the chemical landscape. Additionally, they play important roles during adaptation and speciation. I will present data from our recent investigations into the molecular basis of sexual communication. Two critical events, viz., single nucleotide polymorphisms (SNPs) and gene copy number variation (CNVs) in the chemoreceptor repertoire appear to provide a compelling explanation to the chemical ecological findings and provide novel insights into the evolution of the chemosensation in a group of flies, as well as a framework for studies on the molecular basis of chemical communication.

When unhealthy lunch turns into a death trap: Mechanisms of direct and indirect host plant resistance against an invasive aphid

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Abstract: Indirect plant defenses are plant traits that increase the abundance and/or effectiveness of natural enemies (predators, parasitoids, pathogens) and thereby indirectly reduce herbivory

Most studies of indirect defenses have focused on chewing herbivores (e.g., caterpillars) or spider mites, even though phloem-feeding herbivores like aphids are associated with an abundant and rich natural enemy complex, and indirect defenses against aphids likely play important roles in both wild and crop plants. The goal of this work was to explore the effect of sugarcane aphid herbivory on induction of indirect defenses in sorghum and recruitment of natural enemies. We explored the expression of genes regulating biochemical pathways involved in volatile synthesis, quantified the emission of plant volatiles in response to aphids and measured their attractiveness to natural enemies in laboratory bioassays. We also assessed the preferential attraction of predators to HIPV-emitting plants in the field.

Anchored phylogenomics provides a robust evolutionary history for the Miltogramminae (Sarcophagidae: Miltogramminae)

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Abstract: The Miltogramminae (Diptera: Sarcophagidae) are known from ~600 species across 39 genera, and constitute ~20% of global Sarcophagidae (the flesh flies). While not the largest subfamily, this group contains the greatest diversity of life histories (particularly larval feeding strategies) among the sarcophagids, with species known as kleptoparasites, obligate parasites, parasitoids, predators and saprophages. Despite their significant contribution to flesh fly biodiversity, the miltogrammines remain one of the most poorly understood groups, particularly in terms of their evolutionary history.

To date, two phylogenetic studies, Piwczynski et al. (2017) and Buenaventura et al. (2019), have attempted to resolve miltogrammine relationships at the genus-level, with the latter study utilising next generation sequencing methods for the first time in this group. Unfortunately, these studies were heavily biased towards species from the Palearctic region; neither study saw the inclusion of any Australasian miltogrammine taxa and many important miltogrammine genera were excluded completely. As a result, there are several problems with the current phylogeny of this group: several paraphyletic genera, uncertainty surrounding the basal lineage of all miltogrammines, and poor resolution of many nodes.

The present study remedies these issues through the application of Anchored Hybrid Enrichment to the most miltogrammine taxa ever included in a single study. Flies are included from all zoogeographic regions and represent 1/6th of all described species of Miltogramminae. The resultant phylogeny, presented here, provides unprecedented insight into the genus-level relationships of this subfamily globally, allows insights into the evolution of larval feeding strategies and resolves the basal life history of all miltogrammines.

The first molecular phylogeny and species delimitation of the West Palaearctic Pollenia Robineau-Desvoidy (Diptera: Polleniidae)

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Abstract: Cluster flies, representing the genus Pollenia Robineau-Desvoidy, 1830, are known as mass invaders of human dwellings and plant pollinators in the temperate climatic zone. Despite being the most species-rich and widespread genus in the family Polleniidae, no study to date has tested infrageneric relationships using molecular data. Here we use three molecular markers, COI, Ef1α and CAD to reconstruct the phylogenetic relationships between 18 West Palaearctic species of Pollenia, representing 8 predefined morphological species groups, utilising both maximum likelihood and Bayesian approaches. We show several instances where morphological and molecular results are congruent as well as instances where they are discordant. We also develop a COI barcode reference library for 18 species, containing newly generated data (87 sequences) and sequences retrieved from the Barcode of Life Data System. We analyse this dataset using both BPP and ABGD methods to validate morphological species hypotheses and delimit species. The results of these species delimitation analyses were in the most cases identical and aligned with predefined morphological species concepts. Based on the results of our analyses we synonymise P. moravica (Jacentkovskỳ, 1941), stat. rev. with P. amentaria (Scopoli, 1763) and assign 191 unidentified sequences from BOLD to named morpho-species.

Post release evolution of natural enemies: blessing or curse?

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Abstract: The role of rapid evolution, both adaptive and non-adaptive, in biological control has been a core part of the field nearly since its inception and is an area of increasing focus today. Rapid evolution can drive establishment, population growth or decline. Growing experimental evidence shows that the effects on ecological dynamics can be quite large. We will show evidence from our work using Tribolium castaneum as a model species to study rapid eco-evolutionary dynamics, as well as review evidence from the literature on model systems. Further, we will present evidence from biological control systems, and outline a program for studying the role of evolution in biological control. With a focus on evolution following release, evidence suggests that adaptation generally facilitates establishment, population growth and successful control rather than leading to non-target effects. There is insufficient evidence from the field on evolutionary processes that can reduce fitness (for example, genetic drift and inbreeding), but work from model systems suggests such processes might play a role in the failure of natural enemies to control their target pests. Given that evolution of natural enemies following release will occur, we propose managing to favour adaptive over neutral processes.

Next Generation Biocontrol: Using experimental evolution to increase the effectiveness of native parasitoids at attacking invasive pests

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Abstract: We are in an era where the number of invasive species is steadily increasing while simultaneously classical biological control introductions are decreasing due to increasing regulations and costs. These trends are unlikely to change, and thus alternative methods need to be developed to control invasive pests that are safe, sustainable and publicly accepted. Native natural enemies represent a potential alternative as they often try to adopt invasive species but typically have low success rates on them. Laboratory selection, a long-recognized but rarely used method, can be used to speed up evolution and improve the performance of native parasitoids on exotic species within a few generations. We have started assessing the potential of experimental evolution to increase the virulence of native parasitoids on two highly detrimental agricultural pest species, spotted wing drosophila (Drosophila suzukii) and brown marmorated stink bug (Halyomorpha halys). We collected four native parasitoid species in Michigan: Leptopilina heterotoma (a larval parasitoid of drosophilids), Pachycrepoideus vindemmiae (a pupal parasitoid of drosophilids); and Telenomus podisi and Trissolcus euschisti that are egg parasitoids of stink bugs. Initial evaluations indicate that at least two of these four parasitoid species can develop on the target invasive species. We will present preliminary data on the potential of these species to increase their performance on invasive hosts within a few generations during laboratory selection. If this approach is successful, it could provide a safe and effective alternative or complimentary method to classical biological control.

Of Insects and Awareness: The ant colony as a test for scientific theories of consciousness

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Abstract: The appearance of consciousness in the universe remains one of the major mysteries unsolved by science or philosophy. Absent an agreed-upon definition of consciousness or even a convenient system to test theories of consciousness, a confusing heterogeneity of theories proliferate. In pursuit of clarifying this complicated discourse, we here interpret various frameworks for the scientific and philosophical study of consciousness through the lens of social insect evolutionary biology. To do so, we first discuss the notion of a forward test versus a reverse test, analogous to the normal and revolutionary phases of the scientific process. Contemporary theories of consciousness are forward tests for consciousness, in that they strive to become a means to classify the level of consciousness of arbitrary states and systems. Yet no such theory of consciousness has earned sufficient confidence such that it might be actually used as a forward test in ambiguous settings. What is needed now is thus a legitimate reverse test for theories of consciousness, to provide internal and external calibration of different frameworks. A reverse test for consciousness would ideally look like a method for referencing theories of consciousness to a tractable (and non-human) model system. We introduce the Ant Colony Test (ACT) as a rigorous reverse test for consciousness. We show that social insect colonies, though disaggregated collectives, fulfill many of the prerequisites for conscious awareness met by humans and honey bee workers. A long lineage of philosophically-neutral neurobehavioral, evolutionary, and ecological studies on social insect colonies can thus be redeployed for the study of consciousness in general. We suggest that the ACT can provide insight into the nature of consciousness, and highlight the ant colony as a model system for ethically performing clarifying experiments about consciousness.

Global Perspectives on Field-Evolved Resistance to Bt Crops

Authors: Tabashnik Bruce[2], Fabrick Jeffrey[3] and Carrière Yves[1], [1]University of Arizona, [2]University of Arizona, United States, [3]USDA ARS, U.S. Arid Land Agricultural Research Center

Abstract: Crops genetically engineered to produce insecticidal proteins from Bacillus thuringiensis (Bt) have revolutionized control of some key pests, but their benefits are reduced by evolution of resistance to Bt toxins in pests. The global monitoring data reviewed here reveal at least 22 cases of practical resistance to Bt crops, which is field-evolved resistance that reduces Bt crop efficacy and has practical consequences for pest control. Each case represents the responses of one pest species in one country to one Bt toxin. The 22 cases of practical resistance involve resistance of some populations of nine major pests (seven lepidopterans and two coleopterans), six countries, and nine crystalline (Cry) toxins. Field outcomes confirm predictions from theory that abundant refuges of non-Bt host plants can delay evolution of resistance to Bt crops. Also, multi-toxin Bt crops can most effectively delay resistance to Bt crops when each of the toxins is highly effective against the target pest.

Global Patterns of Field-Evolved Resistance to Transgenic Bt Crops

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Abstract: In each of the past two years, farmers worldwide planted over 100 million hectares of crops genetically engineered to produce insecticidal proteins from the bacterium Bacillus thuringiensis (Bt) These Bt crops have revolutionized control of some major pests, but evolution of resistance by pests has reduced their efficacy. Practical resistance to Bt crops, which is field-evolved resistance that has practical consequences for pest control, increased from 3 cases in 2005 to 21 cases in 2018 (Calles-Torrez et al. 2019, Smith et al. 2019, Tabashnik and Carrière 2019). Each case represents the response of one pest species in one country to one Bt toxin. The 21 cases of practical resistance represent resistance of some populations of nine major pests to nine crystalline (Cry) toxins, with each toxin produced by widely grown Bt crops affected by resistance in at least one case. The switch to multi-toxin Bt crops has not stemmed the tide of resistance. Indeed, the time from commercial introduction of Bt crops to practical resistance has decreased significantly over the past two decades.

The results with pink bollworm (Pectinophora gossypiella) and Bt cotton differ strikingly among the world's three leading cotton-producing nations. In the southwestern United States, farmers delayed resistance by planting non-Bt cotton refuges from 1996-2005, then cooperated in a program that used Bt cotton, mass releases of sterile moths, and other tactics to eradicate this pest from the region. In China, farmers reversed low levels of pink bollworm resistance to Bt cotton by planting second-generation hybrid seeds from crosses between Bt and non-Bt cotton. This approach yields a refuge of 25% non-Bt cotton plants randomly interspersed within fields of Bt cotton. Farmers adopted this tactic voluntarily and unknowingly; not to manage resistance, but apparently because of its perceived short-term agronomic and economic benefits. In India, where non-Bt cotton refuges have been scarce and pink bollworm resistance to pyramided Bt cotton producing Cry1Ac and Cry2Ab toxins is widespread, integrated pest management (IPM) emphasizing shortening of the cotton season, destruction of crop residues, and other tactics is now essential.

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Developing a camera trap for monitoring Sympetrum dragonflies and its application to resuming rice paddy fields in the Fukushima nuclear plant disaster area

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Abstract: The Fukushima Daiichi nuclear power plant accident in 2011 led to the establishment of evacuation zones across a large area. In the area, irrigation to rice paddy fields, which had provided various aquatic insects with habitats, was stopped. Although the evacuation order was cancelled at a large part of the area by the spring of 2017 owing to decrease in the radiation level and the rice paddy fields has been resuming, status of the aquatic insects has not been monitored adequately. To support monitoring of aquatic insects, we designed a novel camera trapping system, which can automatically detect and record perching dragonflies such as Sympetrum spp., known as an indicator species for environment of rice paddy fields. The camera trap system is based on a simple idea that perching dragonflies can be detected using inexpensive and energy-saving photosensors built in a perch-like structure. In the autumn of 2018, fifteen trial camera traps were set in the five plots of rice paddy fields of Fukushima for about two months, and successfully took photos of Sympetrum dragonflies. Furthermore, the frequency of detection was positively related to the result of dragonfly surveys based on observation by an investigator. Though there is room for improvement on the camera trap system, it can be a powerful tool for automatically monitoring dragonflies not only in the resuming rice paddy fields, but also in the areas where access by investigators is restricted.

The fauna of aquatic insects in the rice paddy fields on farming interruption and decontamination after an accident at the TEPCO Fukushima Daiichi Nuclear Power Plant

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Abstract: The Great North Eastern Japan Earthquake & Tsunami on March 11 2011 inundated the coastlines of Fukushima prefecture. This force damaged many human lives and biodiversity. In addition, many residents were evacuated due to the accident at the Fukushima Daiichi Nuclear Power Plant. In these regions farming was interrupted. After that, the farmland was decontaminated and farming was gradually resumed. But changes in biodiversity are not monitored in farmland where has resumed. Therefore, in rice paddy fields where resumed, we investigated Sympetrum and damselfly (Coenagrionidae, Lestidae), aquatic Coleoptera and Hemiptera according to the Functional Agro-biodiversity Indicators and Assessment Manual (2012).

As a result, three species of Sympetrum, S. frequens, S. infuscatum, S. kunckeli were confirmed in the paddy fields where farming resumed. Of these, S. frequens was the most common and the nymphal exuviae were confirmed even in the reopening year. In the damselfly, seven species were confirmed and the most common species was Ischnura asiatica. On the other hand, 23 species of aquatic Coleoptera and Hemiptera were confirmed in a 2019 survey. Among them, a large number of individuals were identified in Enochrus simulans, Gerris latiabdominis and the genus Sigara. In addition, we will report the results of analysis examining effects of cultivation method, decontamination, and farming interruption on these aquatic insects, and discuss on aquatic insect biodiversity in the resuming rice paddy fields.

The fauna of frogs and spiders in resuming rice paddy fields after an accident at the TEPCO Fukushima Daiichi Nuclear Power Plant

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Abstract: TEPCO Fukushima Daiichi nuclear power plant accident was occurred due to the Great North Eastern Japan Earthquake in 2011. Many residents of 12 municipalities Fukushima prefecture were force to evacuation due to diffusion of radioactive substances follow the accident. Decontamination, including soil stripping and soil dressing, has been conducted in these regions, and farming was gradually resumed. These changes of agricultural environment were anthropogenic disturbance of ecosystem, which was unprecedented in the history.

As a preliminary study, we surveyed the fauna in 5 paddy fields where resumed in Iitate village after decontamination in 2016. Although Tokyo Daruma pond frog (Rana porosa porosa) was common species before the accident, no individuals were found in 2016. It was assumed that interrupted rice cultivation at a large part of the area affected populations of this species, which mainly inhabits rice paddy fields. To assess effects of these changes of agricultural environment on agro-biodiversity, we investigated frogs (Ranidae, Hylidae), spiders (Tetragnatidae), Sympetrum dragonfly and damselfly (Coenagrionidae, Lestidae), aquatic Coleoptera and Hemiptera at 16 distincts in 7 municipalities including Iitate village, according to the Functional Agro-biodiversity Indicators and Assessment Manual compiled by the government of Japan. At this presentation, we report about frogs and spiders as potential predatory natural enemies of various insect pests in rice paddy fields.

From the field research at more than forty rice paddy fields in 2018 and 2019, R. porosa porosa were found in Iitate village. Moreover, Rana japonica, Rana rugose, Hyla japonica were observed. In the spiders, 5 species of Tetragnatidae were observed, with the most common being Tetragnatha caudicula. In addition, we will discuss effects of interrupted cultivation, decontamination and region on these frogs and spiders.

Apoptosis-mediated vasa down-regulation controls developmental transformation in Japanese Copidosoma floridanum female soldiers

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Abstract: Copidosoma floridanum is a polyembryonic, caste-forming, wasp species. The ratio of investment in different castes changes with environmental stressors (e.g. multi-parasitism with competitors). The vasa gene was first identified in Drosophila melanogaster as a germ-cell-determining factor, and C. floridanum vasa (Cf-vas) gene positive cells have been known to develop into reproductive larvae. Cf-vas seems to control the ratio of investment in C. floridanum larval castes. In this study, we identified environmental factors that control Cf-vas mRNA expression in Japanese C. floridanum by examining Cf-vas mRNA expression under competitor (Meteorus pulchricornis) venom stress; we treated the male and female morulae with M. pulchricornis venom. We also assessed the effects of multi-parasitism of Japanese C. floridanum with M. pulchricornis and found an increasing number of female soldier larvae. The results showed that several amino acid sequences differ between the Japanese and US Cf-vas. Quantitative reverse transcription polymerase chain reaction (qRT-PCR) showed that Japanese Cf-vas mRNA is expressed in both male and female larvae and pupae, but mRNA expression decreases in adults. Cf-vas mRNA expression significantly decreased, while C. floridanum dronc (Cf-dronc) mRNA expression increased, in female morulae after M. pulchricornis venom treatment at 20 h and 0 h of the culture period, respectively. Females and males showed different Cf-vas or Cf-dronc mRNA expression after M. pulchricornis venom treatment. Therefore, M. pulchricornis venom could affect the ratio of investment in different female castes of Japanese C. floridanum by decreasing Cf-vas mRNA expression via apoptosis.

Exploration of the ingredients which effect to human cancer cell line in the larval frass of Euploea mulciber

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Abstract: To date, many medicines have been discovered from natural products. However, exploration for the plant-derived natural products are almost completed, and other resources, which include ingredients for utilizing pharmaceutical agents, are required. Thus, there is an urgent need to find new pharmaceutical resources. Lepidoptera comprises 200,000 species of butterflies and moths, the majority of lepidopteran insects eat plants at the larval stage and take up secondary metabolites in the process of ingesting nutrients. Besides, insects have evolved a unique system that metabolizes secondary metabolites, including host plants, for escaping food competition. Furthermore, they keep the secondary metabolites that uptake from the plant in their body, and these secondary metabolites are utilized for escaping from predators. In this way, insects and plants have a strong relationship with the planets.
E.mulciber eats Ficus microcarpa and several kinds of Apocynaceae plants containing toxic ingredients such as alkaloids. E.mulciber might convert plant-derived ingredients into other substances through their metabolic system. We are interested in the ingredients produced through this species-specific metabolic system in E.mulciber. In this study, we investigated cell viability to several human cancer cell lines in the ingredients extracted from the frass of E.mulciber larva, which ate Ficus microcarpa. First, we extracted ingredients from the host plant or the larval frass using three types of organic solvents. Then, we examined morphological observation, cell viability to the several types of human cancer cell lines in these extracts.
Consequently, cell viability was significantly inhibited by the chloroform extract of larval frass. To seek the compounds which have inhibition of cell viability to the human cancer cell lines, we compared these ingredients from the host plants and larval frass using Thin-layer chromatography (TLC). Specific spots were presented only in the ingredients from the larval frass of E.mulciber. These findings suggested that E.mulciber larval frass might contain the compounds that changes the chemical structure and biological activity. In this presentation, we would like to discuss the metabolic factor that alters chemical structure and biological activity in E.mulciber.

Isolation of the ingredients which have biological activity for the human cancer cell lines in the frass of Papilio machaon and Papilio memnon

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Abstract: Lepidoptera comprises 200,000 species of butterflies and moths. The majority of lepidopteran insects eat plants at the larval stage and take up secondary metabolites in the process of ingesting nutrients. Byasa alcinous utilize secondary metabolites that are toxic to other organisms, including their host plants, to protect against predation. Pieris rapae eat poisonous plants, and they absorb poisonous secondary metabolites to their body. However, they can detoxify them by their unique metabolic system. Thus, some lepidopteran insects have a species-specific metabolic system. We are interested in ingredients produced through these unique metabolism systems in lepidopteran insects.

In this study, we investigated ingredients which have anti-cancer action to a human cancer cell lines from larval frass of Papilio machaon and Papilio memnon.

First, we extracted ingredients from the host plant and the larval frass using three types of organic solvents, and we examined morphological observation, cell viability, and SOD (anti-oxidative) activity to human cancer cell line in these extracts.

As a result, cell viability was inhibited by the chloroform extracts of larval frass from P. memnon fed Citrus paradisi. Cell viability was also inhibited by the chloroform extracts of larval frass from P. machaon fed Angelica keiskei.

Next, the frass extracts and plant extracts were compared by thin layer chromatography or nuclear magnetic resonance spectrometry, and we found specific spots or peaks only in the frass extracts from P. machaon fed A. keiskei.

To isolate ingredients which accelerates decreasing of cell viability, the chloroform extract from larval frass of P. machaon fed A. keiskei was separated using open column chromatography. One fraction significantly accelerated the decreasing of cell viability only in the human colon cancer cell line, HCT116. However, SOD activity did not change in HCT116.

Our findings strongly suggested that larval frass of P. machaon fed A. keiskei could contain the compounds that chemical structure and biological activity were changed by their unique metabolic system. In this presentation, we would like to discuss the metabolic factor that change the chemical structure and biological activity in P. machaon .

The new type of SOD knockdown leads to the abnormal leg movement and embryogenesis in T.castaneum

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Abstract: Superoxide dismutase (SOD) has been identified in the model insects. SOD is an essential key enzyme with the primary role of eliminating the superoxide anion which one of the reactive oxygen species (ROS). The red flour beetle (Tribolium castaneum) is a holometabolous insect belonging to the Order Coleoptera. The genome information of this species is well characterized, and systematic RNA interference (RNAi) is available. Previously, we found a new type of SOD gene which has three copper/zinc SOD domain in the T. castaneum genomic database, and we named this gene as T. castaneum SOD6 (TcSOD6) and then analyzed the function of TcSOD6 gene using RNAi. Quantitative RT-PCR experiments revealed that the transcript level of TcSOD6 mRNA was increased in the pupal developmental stages. To evaluate the TcSOD6 function in T. castaneum, we performed RNAi in the each developmental stage and observed these phenotypes. When TcSOD6 dsRNA was injected into larva, prepupa, or pupa, the phenotype appeared as short longevity and abnormal leg movements in the adult stage. Also, the amount of fat body was significantly decreased in the adult abdomen. Thus, it was suggested a short life span might be induced by fat body loss.

While we observed the tendons structure in their legs by pathological analysis to investigate their abnormal leg movements. However, tendons structure had a healthy structure.

Next, to carry out parental RNAi, TcSOD6 dsRNA was injected into a mature female adult and then performed the mating with a normal male adult. Almost eggs from the female adult which treated with TcSOD6 dsRNA did not progress embryogenesis. The phenotypes of the TcSOD6 knockdown were different depending on the developmental stage that injected dsRNA. Therefore, TcSOD6 might have a specific functions in each developmental stage. In this presentation, we would like to discuss how the TcSOD6 gene relates to adult leg movements, and egg embryogenesis.

Belowground microbiomes drive aboveground plant–pathogen–insect interactions

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Abstract: Plants interact with a large diversity of microbes and insects, both below and above ground. While studies have shown that belowground microbes affect the performance of plants and aboveground organisms, we lack insights into how belowground microbial communities may shape interactions between aboveground pathogens and insects. In this study, we investigated the effects of soil microbiomes and aboveground organisms on plant growth and development. We further examined whether differences in soil microbiomes influenced interactions between aboveground organisms. We conducted a growth-chamber experiment with oak seedlings (Quercus robur) growing in three soils with similar abiotic soil properties but with distinct natural soil microbiomes. Seedlings were subjected to single or dual attack by powdery mildew (Erysiphe alphitoides) and aphids (Tuberculatus annulatus), either in the presence or absence of prior attack by a free-feeding caterpillar (Phalera bucephala). Soil microbiomes were associated with differences in seedling height, and seedlings with multiple aboveground organisms had more but smaller leaves than healthy seedlings. The soil microbiome affected the severity of powdery mildew infection, and mediated the impact of co-occurring aboveground organisms on aphid population size. Our study highlights that plant performance is affected by natural soil microbiomes as well as aboveground organisms, and that natural soil microbiomes can shape interactions between pathogens and insects. These findings are important to understand species interactions in natural systems, as well as for practical applications, such as manipulation of soil microbiomes to manage agricultural pests and diseases.

The impact of latitude on patterns of voltinism and the host selection and performance of multivoltine herbivores within the oak-associated community

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Abstract: The phenology of insects consists of the timing of life events, as well as the number of generations (voltinism). While several studies have focused on the impact of climate change on the timing of seasonal events, or the voltinism of single species, we still have few insights in the factors that shape patterns of voltinism within ecological communities. Importantly, voltinism can have a major impact on population growth, trophic interactions, and the rate of evolution. We investigated the relative importance of latitudinal variation as a proxy of temperature in shaping patterns of voltinism within an herbivore community feeding on deciduous oak, and how these changes in voltinism, as well as plant phenology, can affect host selection and herbivore performance in the presence and absence of a third species (a plant pathogen). First, we used citizen science data on the seasonal flight periods of lepidopterans feeding on deciduous oaks (Quercus spp.) within Sweden and across Europe. Second, we conducted a multifactorial experiment to assess the influence of spring phenology and pathogen infection on the preference and performance of multivoltine herbivores during the different herbivore generations (spring, summer, autumn). The proportion of multivoltine species within Sweden decreased with latitude, caused by a lower number of partially multivoltine species in northern Sweden, while no clear latitudinal pattern in voltinism was found in Europe. We did not find consistent differences in the relative abundance of the first and subsequent generations along a latitudinal gradient in Sweden or Europe. Regarding the preference of herbivores, leaf-miners preferred to oviposit on late phenology and healthy plants during the entire growing season, while pathogen infection reduced aphid preference in spring and summer, but not in autumn. We found a weak influence of plant phenology on the performance of leaf-miners, and a high variability on aphid performance. Our findings highlight that latitude (as a proxy for temperature) explains part of the variation in the voltinism of herbivores, and that changes in voltinism will affect the distribution and performance of herbivores within plant populations, with important consequences for the ecology and evolution of species interactions and food web structure.

Biological activity of Ajuga iva extracts (phytoecdysteroids and clerodanes) against the African cotton leafworm Spodoptera littoralis

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Abstract: The African Cotton Leafworm Spodoptera littoralis, a major crop pest worldwide, is usually controlled by chemical insecticides that led to serious environmental problems. Ajuga plants produce phytoecdysteroids which are analogues of steroid hormones that regulate metamorphoses in arthropods) and clerodanes,diterpenoids exhibiting anti-feedant activities. Our objective was to evaluate their potential to control S. littoralis.

Using Liquid Chromatography-Time Of Flight-Mass Spectrometry (LC-Tof-MS) and Thin-Layered Chromatography (TLC), we analyzed the profilesof phytoecdysteroids and clerodanes in Israeli Ajuga iva leaf extracts and evaluated their efficiency in controlling S. littoralis using bioassays. To test the biological activity of A. iva crude extracts, leaves of Castor bean were treated with water suspended-dried methanolic crude extracts of phytoecdysteroid and clerodanes from A. iva leaves at the concentrations of 50, 100 and 500µg/µl. For each repeat, 10 1st and 3rd larvae of S. littoralis were feed with one treated leaf for 3 and 4 days, respectively. Mortality, Larval weight gain (LWG), relative growth rate (RGR) and survival rate were compared to control leaves. DAPI and phalloidin staining of actin filaments were used to test the effectof the A. iva crude extracts on the insect gut morphology and intactness.

The tested crude extracts at the aforementioned concentrations significantly increased mortality of S. littoralis 1st stage larvae and caused36%, 70% and 87%, respectively, compared to 6% in the the control. LWG and RGR of 3rd stage larvae were significantly decreased (52%, 44% and 30% respectively) as compared with the relevant controls. Larvae that survived the different treatments with A. iva extracts were used forstaining the cellular nuclei and actin filaments with DAPI and phalloidin, respectively. The major phenotypes that were observed following treatment with 250µg/µl of crude leaf extract were reduced gut size, dislocation of the nuclei, abnormal and malformed actin filaments organization. Those results strongly demonstrate the potential in developing extracts from A. iva as alternative environmentally-safe insect pest control materials.

Establishment of breeding condition and efficacy test methods for textile-attacking insect pests, the oriental silverfish, Ctenolepisma sp. and the booklice, Liposcelis bostrychophila.

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Abstract: Silverfishes and booklice give damages on fabrics or furnitures, and are usually found in warm, humid environments worldwide. Although they are not known to transmit any disease nor to physically damage mammals including human, the control methods involve chemical insecticides, mostly naphthalene or empenthrin. As of 2012, the European Union legislated Biocidal Product Regulation (BPR), and started to legally control the registration and the use of pesticidal products for textile-attacking insect pests. In South Korea, a similar regulation has started in effect on January 1st, 2019, under the Chemical Products Safety Act, all household insecticides including the ones intended for textile-attacking insect pests have to be registered to the Ministry of Environment for commercial use. While the new regulation is already in effect, the establishment of test guidelines for newly regulated insecticides, including for stored-product pests and textile-attacking ones is urgently necessary. The present study aims to provide collection and breeding methods for lab colonies setup and to suggest the evaluation procedure for active ingredients. In the collection study, three types of lure traps were designed and evaluated. For the growth condition study, two different food compositions (high protein : low carbohydrate or low protein : high carbohydrate) with three different temperature setup were tested. For the toxicity test, the bioactivity of chemicals and plant essential oils were examined via the contact and residual bioassay, fumigation bioassay, and repellent assay.

Synergistic effects of uninfested plants and honey on the attractiveness of the synthetic host-infested plant volatiles to parasitoid wasps

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Abstract: When infested by herbivores, plants start emitting specific blend of volatiles, so-called herbivory-induced plant volatiles (HIPVs) that attract carnivorous natural enemies of the herbivores. We already reported that a blend of four volatile compounds of HIPVs emitted from cabbage plants infested by diamond back moth (DBM; Plutella xylostella Lepidoptera: Plutellidae) larvae, attracted larval parasitoid wasps, Cotesia vestalis (Hymenoptera: Braconidae) under both laboratory and field conditions. The blend of synthetic four compounds is hereafter called the attractant.

DBM larva is one of the important pests of cruciferous crops worldwide. C. vestalis is considered to be an effective biological control agent for DBM larvae. To develop the biological control method of DBM larvae with C. vestalis, we have been studying the possible use of the attractant using komatsuna plants (Japanese mustard spinach; Brassica rapa var. perviridis) as a model. In this presentation, we will show that (1) C. vestalis females prefer DBM-infested komatsuna plants to uninfested komatsuna plants in an experimental greenhouse, and (2) the presence of the attractants next to infested komatsuna plants results in the increased attractiveness to C. vestalis when compared with infested komatsuna plants alone.

In general, infested plants were surrounded by conspecific and/or heterospecific uninfested plants under field conditions. Thus, we further tested the effects of the presence of uninfested komatsuna plants on the attractiveness of the attractant. In addition, the effect of the presence of honey (food for C. vestalis females) was also tested. In choice chamber experiments in the laboratory, the presence of the attractant together with either the uninfested plants or honey synergistically increased the attractiveness of the attractant. In the greenhouse, when infested plants were coupled with the attractant, uninfested plants and honey, the attractiveness was increased significantly when compared to infested plants coupled only with the attractant. These data indicated the importance of volatiles from uninfested plants and honey on the attractiveness of the attractants to C. vestalis. We will discuss the synergistic effects of uninfested plants and honey on the attractiveness of the synthetic host-infested plant volatiles to parasitoid wasps in the viewpoint of DBM control.

The induction of defense in eggplants exposed to conspecific volatiles induced by omnivorous predator, Nesidiocoris tenuis

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Abstract: In response to damage made by herbivorous arthropods, plants start emitting so-called HIPVs (Herbivory-Induced Plant Volatiles) that attract carnivorous naturel enemies of the currently infesting herbivores. Further, HIPVs mediate communication between plants. Plant-plant communication via HIPVs is now wildly recognised as one of the induced defence strategies of plants against herbivores.

HIPVs are also induced by omnivorous insects, and such HIPVs would also mediate plant-plant communication. In this study, we tried to clarify whether volatiles emitted from eggplants infested by omnivorous insects, Nesidiocoris tenuis Reuter (Heteroptera: Miridae) induce direct and/or indirect defence in neighbouring uninfested conspecific plants. Eggplants infested by N. tenuis adults emitted specific HIPVs that are qualitatively and quantitatively different from HIPVs emitted from eggplants infested by tobacco cutworm (Spodoptera litura Fabricius, Lepidoptera: Noctuidae), and two spotted spider mites (Tetranychus urticae Koch, Trombidiformes: Tetranychidae). In this study, intact eggplants were exposed to N. tenuis-HIPVs for 3 days, and then their defence traits were measured. Volatiles from the exposed eggplants were not significantly different from those from control eggplants (plants exposed to volatile from uninfested conspecifics). The exposure of N. tenuis-HIPVs to uninfested eggplants affected their production of HIPVs neither qualitatively nor quantitatively when they were infested by herbivore (S. litura) or N. tenuis. These data suggested that the exposure of N. tenuis-HIPVs did not affect the induced indirect defense in uninfested eggplants. By contrast, the direct defences were induced by exposure of N. tenuis-HIPVs. The exposed eggplants were more defensive against S. litura larvae when compared with the control eggplants: the reduction of the growth rate was recorded when the larvae were on the exposed eggplants. We will also report the performance of other herbivore species (T. urticae) and N. tenuis itself on the exposed eggplants. The possible effects of N. tenuis-HIPVs in plant-plant communication and in tritrophic interactions will be discussed.

A parental volatile pheromone triggers offspring begging in a burying beetle

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Abstract: Parental care is a notable aspect of reproductive effort in many animals. The interaction between offspring begging and the parental feeding response is regarded as an important communication mechanism that regulates offspring food supply. The costs of begging are hypothesized as necessary for evolutionally stable parent–offspring communication. Reducing the cost of superfluous begging is beneficial to both parents and offspring; thus, selection impels parents to emit signals informing that they are ready to provision, and offspring to respond to these parental signals. However, no study has demonstrated that parents send signals to elicit offspring begging. In this study, we concluded that parents of the burying beetle species Nicrophorus quadripunctatus inform their offspring of their preparation for provisioning by emitting a volatile signal, and we term this newly identified pheromone type the “provisioning pheromone”. Gas chromatography–mass spectrometry analysis and behavioral assay revealed that female parents emitted an antimicrobial aromatic compound, 2-phenoxyethanol, in their regurgitation before provisioning, and that this compound elicits begging behavior from their offspring. These results suggest that the provisioning pheromone originates from a germicidal agent that the female parent invests in the regurgitated food. Furthermore, begging incurs growth and survival costs, and parents spent more than 85% of their time in close proximity to their offspring without provisioning. Therefore, it is suggested that limiting offspring begging during provisioning is beneficial to both parents and offspring. We report here a novel aspect of parent–offspring communication in family life.

Key role of systematics in biological control of invasive stink bugs

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Abstract: Two species of pentatomid stink bugs have recently become worldwide pests of agriculture, the brown marmorated stink bug (Halyomorpha halys) and bagrada bug (Bagrada hilaris). Programs to manage these pests rely on accurate identification of natural enemies, especially egg-parasitoid wasps in the genera Gryon and Trissolcus (Scelionidae). The taxonomy of these wasps is thus essential for efficacious biological control programs in North America, Europe, Australia and New Zealand. Ecological studies, including surveys with sentinel eggs, have resulted in a greater understanding of parasitoid biology and the discovery of multiple adventive populations of Trissolcus in areas invaded by H. halys and B. hilaris. These include Trissolcus japonicus in Europe and North America, T. mitsukurii in Europe, and T. hyalinipennis in California. Classical biological efforts conducted in concert with research on parasitoids systematics have yielded a wealth of new information on parasitoid diversity, host-associations, and phylogenetic relationships. The role of systematics in multi-institutional, multi-continental projects will be discussed, highlighing recent advances in alpha taxonomy, emerging diagnostic technologies, and the challenges of identifying parasitoids on a world scale.

Disrupting the transmission of Liberibacter by psyllids

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Abstract: Psyllids are phloem feeding hemipterans that transmit plant bacterial pathogens Liberbacter. Control of diseases caused by Liberibacter relies on chemical control of the vector populations, with great economic and environmental consequences. ‘Candidatus Liberibacter solanacearum’ (Lso) has emerged as a serious bacterial pathogen of crops worldwide. In North America, two bacterial haplotypes, Lso A and Lso B, are transmitted by the potato psyllid Bactericera cockerelli, to solanaceous plants and cause zebra chip disease in potato. We are investigating this pathosystem to understand the key molecular mechanisms involved in the transmission of these pathogens in order to identify targets that could be used to disrupt their transmission. In this presentation we describe the differences in the transmission of these haplotypes and potential genes that could be targeted to disrupt Liberibacter transmission or its ability to infect its hosts.

Larval colour polyphenism in Lepidoptera: birds rule the game

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Abstract: We will advocate the view that bird predation forms by far the most important selective force on insect appearance: alternative factors appear to have limited contribution at best. In a series of experiments with colour-polyphenic, hairy larvae of Orgyia antiqua (Lepidoptera: Erebidae) we showed that empirical evidence is well consistent with this ‘bird hypothesis’. In particular, we did not find evidence of the effect of cuticular darkness on thermoregulation of these insects. Instead, the dependence between the colouration and body size of the larvae could well be explained by size-specific optima for cryptic appearance. Despite the yellow-red-black colour pattern of the larvae, there was little support for the alternative hypothesis based on size-dependent warning effect. Vertebrate ecologists have developed the idea that the colouration of an animal can reflect its ’quality’, with darker and brighter colouration being positively correlated with individual fitness. In contrast, in O. antiqua, we were not able to detect any phenotypic correlations between performance of the larvae and their colouration parameters. This question was further addressed in a quantitative genetic study on Ematurga atomaria (Lepidoptera: Geometridae), a species showing a complex pattern of larval colour polyphenism, encompassing both genetic and environmental effects (Journal of Evolutionary Biology, 31: 1959-1968). There was very weak to no evidence of either genetic or environmental correlations between a composite trait describing variation in larval colouration, and fitness-related parameters of growth performance of the insects. In other words, there was no support for trade-offs between colouration and performance, neither could we find any evidence for physiological cost of certain colour patterns. In contrast, we showed that the variation in appearance of E. atomaria is partly based on plastic responses to host plant species, which contributes to the situation-specific camouflage of the larvae. There is however considerable residual variance in colour-related traits which can be interpreted as a result of negatively frequency-dependent selection imposed by bird predators, which can both maintain genetic variance and select for coin-flipping plasticity in colour patterns.

A determining factor for insect feeding preference in Bombyx mori

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Abstract: Feeding preference is critical for insect adaptation and survival. However, little is known regarding the determination of insect feeding preference, and the genetic basis is poorly understood. As a model lepidopteran insect with economic importance, the domesticated silkworm, Bombyx mori, is a well-known monophagous insect that predominantly feeds on fresh mulberry leaves. This species-specific feeding preference provides an excellent model for investigation of host-plant selection of insects, although the molecular mechanism underlying this phenomenon remains unknown. Here, we describe the gene GR66, which encodes a putative bitter gustatory receptor (GR) that is responsible for the mulberry-specific feeding preference of B. mori. With the aid of a transposon-based, clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein-9 nuclease (Cas9) system, the GR66 locus was genetically mutated, and homozygous mutant silkworm strains with truncated gustatory receptor 66 (GR66) proteins were established. GR66 mutant larvae acquired new feeding activity, exhibiting the ability to feed on a number of plant species in addition to mulberry leaves, including fresh fruits and grain seeds that are not normally consumed by wild-type (WT) silkworms. Furthermore, a feeding choice assay revealed that the mutant larvae lost their specificity for mulberry. Overall, our genetic and phenotypic evidence demonstrates that GR66 is a major factor affecting the feeding preference of the silkworm.

A comparison of hyperuricemia model mice loaded with oxonic acid and the silkworm “o06” strain as an alternative for evaluating voluntary oral administration (II)

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Abstract: We proposed the silkworm “o06” strain as a hyperuricemia model. When silkworms were given either a single subcutaneous or single intestinal dose of medication for hyperuricemia (Feburic®, allopurinol, etc.), the medication effectively reduced the uric acid (UA) levels . Here, we examined the optimal conditions for evaluating long-term voluntary oral dosage, and dose response effects were considered.

Methods: The UA content was measured in the silkworm “o06” strain (from the 3rd to the 6th day of the fifth instar) from NBRP (National BioResource Project ; Kyushu University). The silkworm groups given the leaves soaked in CPPG solution, Feburic® suspension, Allopurinol solution, and Milli-Q water formed the evaluation, treatment, and control groups, respectively. All silkworms were treated and kept in a room maintained at 23°C ± 3°C with 40–70% humidity. We performed deproteinization using the chloroform-methanol method. Ten microliters of fresh silkworm hemolymph was placed in the sample reservoir of a Cosmospin Filter G spin filter with 100 µL of methanol, 100 µL of chloroform, and 90 µL of H2O; the solution was then sonicated. The filters were centrifuged at 10,000 rpm for 20 min to collect the aggregated protein. The filtrate was lyophilized for 90 min. Dried residue was dissolved in 15 µL H2O. The solution (3 µL) was injected into the HPLC instrument and was immediately analyzed in triplicate. Standard UA (0, 1.25, 2.5, and 5.0 mg/dL) solutions were prepared using reagent-grade chemicals at the time of use. Each (3 µL) solution was subjected to HPLC under the aforementioned conditions. The automatic peak area counts for each peak of interest were plotted against concentration (mg/dL) to generate a calibration curve. The areas of the peaks in the chromatogram were compared with the amount of UA injected. Each dose was determined using four or five independent samples, and each result is shown as a scatter plot. The determination coefficient for UA was 0.999. The HPLC assays were performed in triplicate, and the averages were calculated. All animal experiments used 12–17 silkworms, and the data are presented as means ± standard deviations. Differences between the means of the control silkworms and the sample-treated silkworms were analyzed using one-way analysis of variance and Student’s t-test with Bonferroni’s correction. A P-value of < 0.05 was deemed to indicate statistical significance. We hold significant difference authorization with OriginPro 9.1J and IBM SPSS Statistics 20.

Results:A significant difference in the UA level 20 hours after starting was observed between the treatment and control groups. Evaluation of the UA levels was possible. And each CPPG and allopurinol showed in terms of efficacy, but the effect of Feburic® was barely measurable. We plan to make comparisons with the sample dose (mg/g) in mice and evaluate whether the silkworm is a useful model of hyperuricemia.
lit. J. JSMUFF, 2(13), 77-90, 2019.

Excretion of uric acid (and allantoin) in the silkworm “o06” strain as an animal model of hyperuricemia

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Abstract: A large number of patients suffer from gout or hyperuricemia, a condition that significantly degrades the quality of life of patients with hypertension. The use of a sensitive method for uric acid (UA) analysis is necessary to diagnose and to facilitate the development of treatments for hyperuricemia. Hyperuricemia mice models involving the administration of potassium oxonate (a uricase inhibitor) have been developed to evaluate and screen medications used for the treatment of hyperuricemia. We have been developing methods for measuring compounds in small quantities of plasma that can be collected from a mouse-tail vein without anesthesia. This is now possible due to the development of a UA quantitative analysis that allows the use of microliter volumes of plasma. However, the use of hyperuricemia mice models involving the administration of potassium oxonate creates a number of problems, potentially. One is the difference between humans and mice in the end product of purine metabolism; mice excrete allantoin by urinary excreation because they have an uricase. The second problem is cost for the maintenance of experimental mice, are expensive. Third, ethical issues exist surrounding the use of mice and rats, which is regulated by law in European Union (enforce in March 2013). From this kind of circumstance, we need to renew the hyperuricemia model in medical studies.

Silkworms normally produce UA as a result of nucleic acid metabolism and reserve it in epidermal cells for use after the pupal stage. Mutant silkworms, called ”Aburako”, have decreased ability to store UA in the epidermis, which then builds up in the hemolymph and causes the skin of the mutants to become translucent.

Herein, we discuss the o06 strain as a possible substitute for the mouse hyperuricemia model in medical studies, and examine its UA (and allantoin; AL) excretion of feces, larval urine, and meconium.

Materials and Methods: AL and UA were measured in the o06 strain (3 to 6 days of the 5th instar) from the National BioResource Project silkworm collection. The UA content was analyzed using improved high-performance liquid chromatography with ultraviolet detection, and the quantity of AL was determined of hydrophilic interaction liquid chromatography. The silkworm mutants were then treated with allopurinol or Febuxostat (a xanthine oxidase inhibitor) for hyperuricemia.

Results: There was no difference in the total amount of UA excreted (mg/individual) between normal and diet groups. The UA level in the hemolymph of the diet group was lower than that of the normal group. Because 5th instar larva of strain o06 contain less AL, they do not express uricase, an enzyme that degrades UA to AL, as Hayashi showed in vitro. Purine metabolism is similar in silkworms and humans and the end product of both is UA. Our results indicate that strain o06 is a potential substitute for the mouse hyperuricemia model.

lit.1) Hayashi Y, Nature 186, 1053-1054, 1960.

Pollinators and Their Conservation Helps a Hungry Planet

Authors: Tanda Amarjit, Australia

Abstract: Major crops are mainly dependent upon managed honey bees and wild bee pollinators which are of great significance. Bee pollinated crops being a great part of the bio-diverse system, 4,000 native bees, and offer over US$1.5 billion each year in North America. In the US, the value of wild bees in food production was determined to be over $1.5 billion annually. However, the worth of wild bee pollination in insect cross-pollinated crops may be much more. These great wild players are now in a fast-declining phase or possibly extinct due to human-disturbed habitats. More studies are needed in population biodiversity, bee abundance and protection measures, suitable habitat, nesting sites especially their immediate conservation strategies. As progress is demanded in entomology, honeybees and the wild bee pollinators should be protected from the overuse of pesticides by conserving bee populations for better agricultural production to feed the hungry planet by sustaining global biodiversity. We highlight in this presentation, the various measures, and actions to conserve the wild bees so that they can serve the growers as co-players to managed honey bees in boosting agricultural food production worldwide.

Natural enemies of black soldier fly (Hermetia illucens L.) threaten the growth of emerging insect-based enterprise in Africa

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Abstract: Sustainable utilization of black soldier fly (BSF, Hermetia illucens) larvae as a novel protein source to substitute the major source of protein (fish and soya bean) in animal feeds has gained momentum globally. However, information on their natural enemies an implication for mass production has received limited research attention. We evaluate for the first time the threats posed by two important natural enemies (phoretic mite, Macrocheles muscaedomesticae Scopoli and newly described parasitoids, Eniacomorpha hermetiae Delvare) on potential colony collapse under on-farm conditions. Significantly higher infestation of the mites was observed on the fly's abdominal space with mortality occurring within 2 – 5 days. There was a significant negative effect of mite load on the survivorship and fecundity. For the parasitoid, pupation substrate type and depth of the pupae significantly influenced the parasitism rates with over 75% of fly pupae buried up to <10 cm deep in dry grasses and sawdust compared to sandy soil. We conclude that the mite and parasitoid described represent a serious threat to BSF colony viability and shed light of their possible contribution to a cascade of negative implications in the animal feed industry that might rely on BSF larvae meal as alternative source of protein.

Mosquito midgut epithelial profiles show shared trends amongst Aedes, Anopheles and Culex and uncover differences in cellular dynamics in response to infection and blood feeding

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Abstract: The cellular dynamics of the insect gut are key for the maintenance of epithelial integrity and, in hematophagous vector species, could have important implications for disease transmission. We studied mosquito midgut epithelial dynamics by measuring DNA synthesis and mitotic proliferation in the posterior midguts of Aedes, Culex, and Anopheles mosquitoes during post-emergence maturation, and in sugar-fed, pathogen-challenged, and blood-fed adults. We found that in the first 24 hours post-emergence ~15 cells/posterior midgut can be seen undergoing mitosis and by the end of the maturation period (72 h) ~20% of the midgut cells have synthesized DNA,. Mature mosquitoes (five to eight-days-old) maintained on sugar water had an average of ~3.5% of cells undergoing DNA synthesis over three days, and displayed ~5 mitotic cells/posterior midgut, indicating a modest but constant cell turnover. Pathological challenge by oral bacterial infection triggered a substantial increase in these parameters, suggesting an active modulation of cell dynamics to deal with stress. Interestingly, we found that the Aedes aegypti response to bacterial infection started a day earlier than Anopheles gambiae's, but both species responded strongly to infection, with final counts of 209 ± 102 and 207 ± 80.54 mitotic cells/posterior midgut respectively. Finally, responses to blood-feeding were significantly different across species and between blood sources (human, bovine, avian, and artificial). All mosquito species tested showed increased cumulative DNA synthesis in the period of blood digestion (72 hours post-blood-meal). Our results suggest that cell proliferation, differentiation, and endocycling can occur as a response to the blood meal in these mosquitoes, but how these events occur and their progression, are significantly different between Ae. aegypti and An. gambiae. Our results highlight the diversity and relevance of cell cycle regulation in hematophagy, and the implications of these observations for examining vector competence and designing transgenic strains.

The Biodioversity of Entomopathogenic nematodes and their use in IPM strategies

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Abstract: Important updates on different aspects of entomoparthogenic nematodes biodiversity and their role in microbial control strategies

Boosting phenomics: PhenoScript the new computer language for describing and comparing species

Authors: Tarasov Sergei, Finnish Museum of Natural History, Finland

Abstract: Analyzing phenotypes is central to much of the research in biology. In biosystematics, phenotypes are used for describing species and characterizing their evolutionary history. Although accumulating rapidly through species descriptions, phenotypic data, unlike molecular ones, are challenging to compare and analyze, which impedes phenomic-scale research in biology. This happens because organismal anatomies (= phenomes) have complex hierarchical structure (e.g., digits are parts of limbs which, in turn, are parts of body), while anatomical entities have diverse semantic qualities (e.g., shape and coloration of digits and limbs), which are largely neglected by available approaches. Both complex anatomical systems and their semantics can be modeled using ontologies – computer-understandable representation of knowledge, with well-defined terms, relationships, and logic. The application of ontologies to biosystematics is recent but extremely promising. In this talk, I will explore PhenoScript the computer language designed to stimulate the phenomic-scale research in biology and further reuse of phenotypic data. PhenoScript aims at providing a user-friendly environment for writing computer-parsable semantic species descriptions and running automatic species comparison. I will also discuss how future developments in ontology-driven approaches can change the way we analyze and represent phenotypes.

The potential role of queen reproductive potential in colony losses of honey bees

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Abstract: Both empirical and anecdotal evidence suggests that one of the primary problems for beekeepers is ‘poor queens,’ including premature supersedure (queen replacement), inconsistent brood patterns, early drone laying (indicative of sperm depletion), and failed requeening. There are many factors that affect queen reproductive potential (=quality), and it is therefore fundamentally important to promote high queen quality to maximize colony productivity and fitness. Our research has explored the connections among queen rearing, insemination success, management practices, and various measures of colony phenotype and health that has helped to elucidate the central role that queens play in modern bee management.

Cold hardiness of Tuta absoluta (Lepidoptera: Gelechiidae): implications and overwintering strategy

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Abstract: For many ectotherms, overwintering survival is achieved through entering diapause. However, this phenomenon has not been observed in the highly invasive tomato pinworm, Tuta absoluta (Meyrick) (Lepidoptera: Gelechiidae). Reports suggest the ability to survive during cold seasons in both protected and open-field crops in the Mediterranean region. However, it is unknown how the pest responds to sub-zero temperatures and whether it uses cold hardiness as an overwintering adaptation strategy. To assess T. absoluta winter survival strategy, we measured cold hardiness in T. absoluta larvae and adults. We measured the larval supercooling point (SCP) and investigated various factors that affect SCP vis cooling rates, feeding status, hydration status and inoculative freezing as well as the pest’s lower limits of activity (critical thermal minima [CTmin]). Furthermore, we investigated the freeze strategy, using lower lethal temperatures (LLTs) and supercooling point mortality assays. The effects of low temperature exposure and duration of exposure (i.e., LLT) on larval survival showed that the temperature at which 50% of the larval population survives was -10°C after 2 h exposure. Following supercooling, both the larvae and adults failed to survive a 24h post recovery period. Feeding status had no effect on adult SCP, however a significant SCP depression was noted in fasted larvae. Adults showed a superior CTmin (mean -1.9°C) as compared to the larvae (mean 3°C), however, no significant difference was noted between fed and fasted for both adults and larva. Low relative humidity treatments significantly decreased SCP from -19.1°C (control) to -20.3°C for larvae and no differences were noted in control vs desiccated adults. Inoculative freezing (by water contact) raised SCP to -7.5 °C (larvae) and –8.7 (adults) respectively. The slowest cooling rate (0.12°C) significantly improved larval SCP while significantly impairing adult SCPs. These results suggest both T. absoluta larvae and adults are chill-susceptible and that different ecological factors e.g. cooling rates, feeding status, hydration status and inoculative freezing may affect their cold hardiness and survival at extreme low temperatures. These results are important in determining this species range limits, its response to seasonal temperature variation, overwintering pest management and modelling pest risk status.

How do combinations of agricultural chemicals affect bee-microbe-plant interactions?

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Abstract: Population declines of wild bees are linked to the widespread use of pesticides and fungicides they encounter when foraging, yet whether combinations of chemicals alter pollinator visitation or floral microbial third parties remains unknown. Here I ask if the presence of a pesticide and fungicide alter bee visitation, fruit production, and the abundance of floral microbes. I treated Penstemon palmeri, (n = 126) with the neonicotinoid pesticide imidacloprid, the fungicide tebuconazole, their combination, or a water control (31 plants per treatment). Plants were placed in a randomized block array, and I observed the frequency and identify of floral visitors. I also collected flowers, rinsed them in 1x-0.15% PBS-Tween solution, and plated these rinses to culture floral microbes. Finally, I collected seed pods from each plant as a measure of reproductive success. Since plants face a tradeoff between growth and defense, chemical treatment may allow plants may allocate more resources to growth and reproduction, having more inflorescences and receiving higher pollinator visitation. Alternately, if treatment disrupts microbial communities, this could alter their attractiveness to pollinators by changing scent or nectar chemistry. Given the ubiquity of these chemicals, any findings will inform our knowledge of how wild pollinators cope with chemical stressors.

Reciprocal interactions between nutrition and immunity influence coinfection dynamics in flour beetles

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Abstract: Insect hosts are exposed to a suite of microbes over the course of their lives. Each microbe leaves an imprint on the within-host environment through their influence on immunity and stored energetic resources that modulates the fitness of other within-host community members. An open question, however, is whether direct competition for nutritional resources among parasite community members modifies the role of immunity in mediating apparent competition among parasites. On the one hand, by modifying the relative and absolute densities of each parasite population, resource competition could indirectly influence the magnitude and timing of immune defenses that respond dynamically to parasite density. Parasite-mediated depletion of host resources could also directly affect immunological investment, however, if immunity is competing for the same resources as the microbes. In this study, we manipulated the within-host parasite community of flour beetles (Tribolium castaneum) by infecting them with a relatively benign protozoan parasite (Gregarina spp) or mildly virulent bacterial strain (Bacillus thuringiensis Bt1). These parasites, as measured by metabolite assays and RT-qPCR on immune gene expression, modify different aspects of the immunological and nutritional within-host environments subsequently experienced by a more virulent Bt strain (Bt2). We used a nutritional geometry approach to manipulate macronutrient acquisition by beetles infected with the benign parasites, and then performed RNA-seq on beetles collected at multiple time points after Bt2 infection to determine the role of resource competition on immune system dynamics in singly- and co-infected beetles. Most notably, our results suggest that gregarines reduce within-host carbohydrates available to the bacteria but also suppress the expression of key antimicrobial peptides, with net outcomes for bacterial growth and survival that depend on both the developmental stage and protein to carbohydrate diet ratio of the host. Our study therefore sheds new light on the nutritional regulation of within-host parasite communities and the impact of multiple infections on the evolution of host life history and immune systems.

The stable fly conundrum

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Abstract: Stable flies, Stomoxys calcitrans, are pests of livestock, wildlife, and humans throughout much of the world. Adults, both males and females, require bloodmeals for reproductive success. Their painful bites reduce productivity of livestock, molest wildlife, and disrupt recreational activities of humans. Although traditionally considered pests of confined livestock developing in bedding contaminated with manure and urine, extreme outbreaks associated with post-harvest plant residues are becoming serious issues in several locations around the globe. The social, economic, and management issues associated with these outbreaks will be discussed.

Strategic nomination of insects and allied invertebrates for conservation management in Australia

Authors: Taylor Gary, The University of Adelaide, Australia

Abstract: Insects and allied invertebrates are the most numerous and diverse organisms in terrestrial and freshwater environments. They play critical roles in ecosystem function including pollination, herbivory, nutrient cycling, parasitism and predation, and providing food for most invertebrates and vertebrates. The Australian fauna is highly endemic, with numerous ancient lineages, relicts and evolutionary radiations. Yet, under increasing environmental stress, they may be disappearing rapidly, undocumented, in the face of key threatening processes such as habitat loss and fragmentation, exotic and invasive species, pollution and climate change. As impediments to conservation, terrestrial invertebrates are impacted by the Public dilemma (too small, too hidden and too little known), the Political dilemma (too little attention from decision-makers), the Scientific dilemma (too few scientists and scarce funding), the Linnean shortfall (many undescribed species), the Wallacean shortfall (too little known about distribution), and the Prestonian shortfall (too little known about abundance). Of the 285 species of insects and allied invertebrates listed under the Australian State/Territory Acts, the national EPBC Act and the international IUCN Red List shows a highly biased (mis)representation across the Australian landscape. Of the 89 Australian IBRA regions, six had more than 18 species, 23 had less than five species and thirty-six (40%) had no species at all. For a more uniform representation, the AESCC proposes a novel regional approach by selecting a relatively small number (3-5) ‘flagship taxa’ from each IBRA region to engage scientists, government agencies, local community groups and the general public in conservation management. The nomination of iconic flagship species that may include threatened species at risk of extinction, or species of important scientific, social or cultural value from under-represented IBRA regions is currently being advanced to better represent insects and allied invertebrates across the Australian landscape. Nominations will be progressively posted on the AES website at www.austentsoc.org.au.

Traditional medicinal uses of arthropods in francophone West Africa

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Abstract: From ancient times to the present day, insects, arachnids and other arthropods have been used worldwide for treatment. They play an important role in the traditional therapy of local populations because of their availability in the field, their cost and their effectiveness.

Arthropods were also present, until the end of the 19th century, in the pharmacopoeias of Western countries. But they have been gradually abandoned since, because they were considered harmful, vectors of diseases, or dirty.

In French-speaking West Africa, this knowledge has been little or not listed and disappears when traditional healers die, because it has been transmitted orally for generations.

During our investigations in the rural areas of Benin, Niger, Mali and Guinea-Conakry, we identified new data on arthropods used in traditional medicine.

Here we present these species and their therapeutic properties.

Cytochrome P450 metabolic resistance (CYP6P9a) to pyrethroids imposes a fitness cost in the major African malaria vector Anopheles funestus

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Abstract: Metabolic resistance threatens the sustainability of pyrethroid-based malaria control interventions. Elucidating the fitness cost and potential reversal of metabolic resistance is crucial to design suitable resistance management strategies. Here, we deciphered the fitness cost associated with the CYP6P9a (P450-mediated metabolic resistance) in the major African malaria vector Anopheles funestus. Reciprocal crosses were successfully performed between a pyrethroid susceptible (FANG) and resistant (FUMOZ) laboratory strains and the hybrid strains showed intermediate resistance level. Genotyping the CYP6P9a–R resistance allele in oviposited females revealed that CYP6P9a negatively impacts the fecundity as homozygote susceptible mosquitoes (CYP6P9a-SS) significantly lay more eggs than heterozygote (OR = 2.04: P =0.01) and homozygote resistant. CYP6P9a also imposes a significant fitness cost on the larval development as homozygote resistant larvae (CYP6P9a-RR) developed significantly slower than heterozygote and homozygote susceptible mosquitoes (?2=11.2; P = 0.0008). This fitness cost was further supported by the late pupation of homozygote resistant than susceptible mosquitoes (OR = 2.50; $P < 0.01$). However, CYP6P9a does not impact the longevity as no difference was observed in the life span of mosquitoes with different genotypes (?2 = 1.6; P = 0.9). A significant decrease of the resistant CYP6P9a-RR genotype was observed after 10 generations (?2 = 6.6; P = 0.01) suggesting a reversal of P450-based resistance in the absence of selection. This study shows that the P450-mediated metabolic resistance imposes a high fitness cost in malaria vectors supporting that a resistance management strategy based on rotation could help mitigate the impact of such resistance.

Simultaneous Identification of Mosquitoes, Their Microbiota and Blood Meal Sources Using Next-Generation Sequencing

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Abstract: Mosquitoes transmit many devastating and life threating diseases to humans, domestic animals and wildlife. Many mosquito species occur as complexes that are typically difficult to identify based on morphological characteristics. Yet, effective control of mosquito-borne diseases relies on proper identification of the major vectors and their ecological traits. One such ecological trait that is critical for mosquito-borne transmission is the blood feeding pattern. Only mosquito species that feed on vertebrate hosts that amplify a particular mosquito-borne pathogen are considered to be potential vectors of that pathogen. Moreover, previous studies have shown that the microbial communities that inhabit the mosquito body can influence vector susceptibility to pathogens. Here we describe the development and application of Illumina Miseq next-generation sequencing for simultaneous identification of mosquito species, their microbiota and host blood meal source. Our results show that PCR amplification and Miseq sequencing targeting the mitochondrial cytochrome c oxidase 1 (mosquito identification), 12S rRNA (blood meal source), and 16S rRNA (microbiota) genes can successfully be used for simultaneous identification of mosquito species, their microbiota and host blood meal sources. These findings demonstrate the capability of next-generation sequencing to improve the efficiency of mosquito-borne disease surveillance systems.

The role of plant nutrient quality on the survival and reproductive fitness of dengue vector Aedes aegypti

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Abstract: Overwhelming evidence indicate that female mosquitoes, including those of highly anthropophilic Aedes aegypti and Anopheles gambiae, intermittently forage on plant sources for nutrition. However, the role of these plant nutrients on their reproductive fitness is scarcely known. Recent advances have seen the advent of more robust analytical techniques such as DNA barcoding and mass spectrometry which allow identification of plant sources fed upon and their trophic interactions. Taking advantage these advances, we recently identified plant sources of four afro-tropical mosquito species that vector dengue, malaria and Rift Valley fever. Here, we further investigated the role of three of the identified plants on survival and reproductive fitness of dengue vector Ae. aegypti. Newly emerged adult male and female Ae. aegypti were fed on Leonotis nepetifolia, Pithecellobium dulce or Opuntia ficus-indica with females receiving an initial three rations of blood meal on day 3, 5 and 7 from anaesthised mice. The controls included those fed on 6 % glucose solution with the initial three blood meals and those fed on blood meal only provided on alternate days throughout the experimental period. We collected data over 30-day period on daily mortality, oviposition and eggs hatching rates. The mosquitoes, plant sources and mice blood were also analysed for sugar and amino acid content. Our results show that survival was strongest on glucose solution and P. dulce with L. nepetifolia and blood meal having comparable survival rates and O. ficus-indica having the least survival. On the other hand, fecundity was strongest on L. nepetifolia and least on O. ficus-indica. Hatching rate was least in eggs laid by females fed on O. ficus-indica but comparable among the rest of nutrient sources. Nutritional analysis revealed qualitative and quantitative similarities and differences between the different nutrient sources that may explain the observed differences in the fitness matrices of Ae. aegypti. Our findings highlight the central role of plant nutrients in the reproductive fitness of dengue vectors which may impact their disease transmission potential.

Semiochemical basis of Aedes mosquito attraction to Non-human primate and human hosts

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Abstract: Non-human primates (NHP) are important in the epidemiology of the Aedes-borne pathogens, dengue, Zika, Yellow fever and chikungunya viruses where they serve as reservoir hosts. However, they have been neglected in studies of Aedes odour-guided host-seeking behaviors, which have largely focused on human volatiles. We explored how host-derived skin odours from the NHP baboon, sykes, vervet, and humans influence Aedes mosquito responses in domestic and sylvatic environments where these viruses circulate. We found that the ketones cyclohexanone and sulcatone are i) important signature cues for Aedes mosquitoes to detect the NHP and humans, respectively, and ii) attractants to Aedes mosquitoes including Aedes aegypti in sylvatic and domestic settings. Both compounds have potential practical applications as lures for improved monitoring Aedes disease vectors as a critical component of risk assessment for transmission of these viruses.

Exploring sand fly plant feeding behaviour for development of nectar- based vector control strategies

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Abstract: Knowledge of plant feeding behavior is being exploited in vector control including sand flies. However, we have little understanding of this trait for Afrotropical sand fly species. Focusing in an endemic site for leishmaniasis in Kenya, we applied biochemical and molecular methods to i) compare the extent of plant feeding among different sand fly species/sexes belonging to Sergentomyia and Phlebotomus genera) from different habitat, ii) identify specific plants fed upon in nature, and iii) identity signature cues mediating sand fly attraction to the identified plants. We found variation in the proportion of sugar fed males and females with generally no significant difference within sand fly species. Identified plant species fed upon in nature mainly belong to the family Fabaceae. Chemical profiling of host plant odors identified specific volatile organic compounds (VOCs) that can be developed into lures for surveillance of sand fly vectors of Leishmania parasites and phleboviruses.

Exploiting chemical ecology of mosquito-plant interactions to develop surveillance tools for the dengue vector Aedes aegypti

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Abstract: Plants are important in the bioecology of mosquitoes as they provide breeding and resting sites, as well as nectar for energy metabolism. Plant feeding in mosquitoes is largely odor guided and therefore plant-derived odors represent candidate mosquito attractants. One example is (E)-linalool oxide (LO), an attractive plant volatile organic compound (VOC) for both malaria and dengue vectors. In addition to LO, plants produce a plethora of other VOCs, some of which have been found to elicit electrophysiological responses in the antennae of the dengue vector Ae. aegypti. In this presentation, we describe the performance of a blend of LO and two other antennally- active VOCs in field trapping of Ae. aegypti. We also share our findings on the nectar-feeding patterns of this vector in three ecologies of Kenya, additional candidate attractants identified, and the prospects thereof for targeting plant feeding behaviours for vector surveillance.

Advances in the management of the transmission of phytoplasmas: from the field to the lab

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Abstract: Phytoplasmas are a severe threat for several crops in the world and new control strategies are required to better prevent their occurrence and spreading.

Recent studies focusing on the vector transmission efficiency and on the potential of microbial symbionts to reduce vector competence will be presented opening new scenarios in the epidemiology of phytoplasma diseases and for their management.

For instance, new evidences on the infective risk of newly emerged adults of the psyllid Cacopsylla melanoneura when the migration to conifers is delayed for some reason, or on the ability of the leafhopper Scaphoideus titanus to acquire FD-C phytoplasma as an adult too, and to, successively, inoculate it in a short window of time impose a revision of the vector management strategiesMoreover, new tools for the analysis of the interactions between phytoplasmas and their vectors come from the analysis of the immunity system of these latters. An in vitro model based on immunocyte cultures has been developed enabling the study of their structure and activity in particular in relation to the synthesis of antimicrobial peptides. The knowledge of the presence/absence of the most common molecules involved in the immunity of the insect vectors may clarify if the phytoplasmas induce or modulate the insect immune responses, providing potential targets for the management of the insect vectors or of their vector competence.

Another interesting approach to reduce the vector competence comes from bacterial symbionts of insects. In particular, the acetic acid bacteria Asaia sp. induced a reduction of phytoplasma acquisition by the leafhopper vector model Euscelidius variegatus Kirschbaum, mediated by the production of and air-liquid interface biofilm. Moreover, the expression of immune genes in the leafhopper after exposure to Asaia symbiotic bacteria, revealed a specific activation of the Raf gene (a known component involved in the response to septic injury and in immunocyte proliferation and survival) in midguts after double infection by Asaia and flavescence dorée phytoplasma. This particular interplay can suggest the elicitation of a basal host immune activity by Asaia against other microrganisms, including phytoplasma. All these new findings provided evidence of the potential for Asaia to be used as a biocontrol agent capable of reducing phytoplasma infection in leafhopper vectors.

Biopesticides and botanical extracts as an IPM options against rice stem borers in Eastern Africa

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Abstract: The demand for rice has increased sharply in Sub-Saharan Africa (SSA) and is growing more rapidly than in any other continent. SSA has huge production potential for both upland and irrigated rice; however, availability improved varieties, fertilizer, farm mechanization, weeds, diseases and insect pests are the major limiting factors. The major insect pests of rice in Africa include stem borer complex, African rice gall midge, leaf hoppers, flea beetle and termites. The estimated rice yield loss due to insect pests in Africa range between 15% and 25%. Efficacy of two commercial biopesticides: Beauveria bassiana and Metarhizium anisopliae, two botanical extracts (Neorautanenia mitis and Derris elliptica), one synthetic insecticide Cypermethrin (144g/L) + Imidacloprid (200g/L, and untreated control, were evaluated against rice stem borers in Tanzania. The results show that both biopesticides and botanical extracts reduced damages and yield losses caused by rice stem borers as compared to control. Higher grain yield and higher stem borer mortality were also observed in the treated than un-treated control suggesting that biopesticides and botanical extracts can control rice stem borers as efficiently as chemical insecticides. The efficacy and compatibility of biopesticides and botanical extracts with other control options should be evaluated.

Attractiveness of yeast species, strains and combinations to Drosophila suzukii

Authors: Tempest Hayden[3], Jones Rory[1], Günther Catrin[2], Eady Paul[2], Fountain Michelle[3], Goddard Matthew[2], [1]University of Lincoln/NIAB EMR, United Kingdom, [2]University of Lincoln, United Kingdom, [3]NIAB EMR, United Kingdom

Abstract: Some herbivorous species can suppress plant defences. Plants in which defences are suppressed are beneficial for suppressors, as well as for their competitors, hence suppression can be considered a form of niche construction. Tetranychus spider mites are important pests of several crops. Within this genus, T. urticae induce whereas T. evansi suppress tomato plant (Solanum lycopersicum) defences of the jasmonic acid (JA) and salicylic acid (SA) pathways. Defence suppression is beneficial for both species. However, the degree of intraspecific variation for both suppression and induction within species is as yet unclear. Here, we characterize two highly variable outbred populations of T. urticae and T. evansi, regarding their ability to suppress defences. We also test defence suppression in the 7 populations used to found these outbred populations. To this aim, we infested tomato plants with 25 mites of each population during 4 days, then measured (i) the suppression of plant defences through differential expression of plant marker genes for JA and SA pathways and (ii) the consequences of defence suppression for the suppressing mites by recording their fecundity during the period of plant infestation. To assess whether defence suppression can also benefit the competing species, we measured the performance of individual of that species, for 2 days, on plants previously infested with populations of the other species. We found that outbred populations of both species and their founder populations suppressed defences with equivalent beneficial effects across populations. These results show that suppression is not uncommon in T. urticae. Only in some populations did suppression benefit the competitor. This suggests different degrees/pathways of defence suppression or that the suppressors interact differently with different and competitor populations. Thus, our results indicate that defence suppression is a form of niche construction. However, the ecological and evolutionary consequences of within-species variation for this form of niche construction remain to be elucidated.

Defence suppression by phytophagous spider mite as a form of niche constrution

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Abstract: Some herbivorous species can suppress plant defences. Plants in which defences are suppressed are beneficial for suppressors, as well as for their competitors, hence suppression can be considered a form of niche construction. Tetranychus spider mites are important pests of several crops. Within this genus, T. urticae induce whereas T. evansi suppress tomato plant (Solanum lycopersicum) defences of the jasmonic acid (JA) and salicylic acid (SA) pathways. Defence suppression is beneficial for both species. However, the degree of intraspecific variation for both suppression and induction within species is as yet unclear. Here, we characterize two highly variable outbred populations of T. urticae and T. evansi, regarding their ability to suppress defences. We also test defence suppression in the 7 populations used to found these outbred populations. To this aim, we infested tomato plants with 25 mites of each population during 4 days, then measured (i) the suppression of plant defences through differential expression of plant marker genes for JA and SA pathways and (ii) the consequences of defence suppression for the suppressing mites by recording their fecundity during the period of plant infestation. To assess whether defence suppression can also benefit the competing species, we measured the performance of individual of that species, for 2 days, on plants previously infested with populations of the other species. We found that outbred populations of both species and their founder populations suppressed defences with equivalent beneficial effects across populations. These results show that suppression is not uncommon in T. urticae. Only in some populations did suppression benefit the competitor. This suggests different degrees/pathways of defence suppression or that the suppressors interact differently with different and competitor populations. Thus, our results indicate that defence suppression is a form of niche construction. However, the ecological and evolutionary consequences of within-species variation for this form of niche construction remain to be elucidated.

Does climate change contribute to the rise of super pests?

Authors: Teodoro-Paulo Jéssica[4], Alba Juan M.[3], Valeriano-Santos João, Charlesworth Steven[1], Duncan Alison B.[2] and Kant Merijn R.[3], [1]Center for Ecology, Evolution and Environmental Changes, University of Lisbon, [2]Institut des Sciences de l'Évolution, University of Montpellier, CNRS, IRD, EPHE, [3]Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, [4]Universidade do Porto - Faculdade de Ciências, Portugal

Abstract: Rising temperatures due to climate change are predicted to accelerate the life cycle of arthropod herbivores thereby exacerbating pest formation of invasive species already adapted to warm conditions. Notorious pests such as Tetranychus spider mites thrive at higher temperatures, with some species suppressing defences by interfering with the plant's signalling pathways. This promotes mite performance but also that of co-occurring competitors. In this study, we investigated the effect of higher temperatures on plant-eating mites that either induce or suppress plant defences and the impact on their population growth. We found that survival of adults and their offspring was similar for inducer and suppressor mites under moderate temperature (25ºC). At 32ºC, mite damage and fecundity were increased, but survival of adults and their offspring decreased severely, especially for inducer mites. However, the overall pattern of defence induction and suppression was not affected by high temperatures. These results may be particularly relevant to sectors of plant breeding and biological control as they are expected to provide the alternatives that prevent an increase in pesticide use due to climate change. Finally, our results provide novel insights into how climate change could lead to the selection of super pests, such as suppressor mites.

Killers and competitors: the effect of invasive ants on the food web of Round Island, Mauritius, as revealed by dietary DNA metabarcoding

Authors: Tercel Maximillian, Cardiff University

Abstract: Invasive ants are highly damaging introduced species capable of significantly reducing native species richness and abundance. Our knowledge of how they mechanistically impact native ecological communities, however, is lacking. Here, we present the results of an island-wide dietary analysis of twelve species of introduced ants present on Round Island, Mauritius, a supposedly “pristine” island nature reserve supporting numerous endemic animals and plants found nowhere else. Using dietary DNA metabarcoding, we reveal the trophic interactions of the entire ant community of Round Island, representing one of the most complete dietary analyses to date in any system. We found that introduced ants are both predating upon and competing with native species of vertebrate and invertebrate. We also show how they rely on both introduced and native plants. For the first time, this describes the species-level interactions and mechanistic ecological underpinnings of how invasive ants can be so damaging to native species. Results are further discussed in the context of fragile island ecosystems and the increasing prevalence of introduced ants globally.

The Medicinal Use of Insects in Northern Vietnam

Authors: Teräväinen Marianna[1], Long Khuat Dang[2] and Muona Jyrki[1], [1]Finnish Museum of Natural History & University of Helsinki, [2]Institute Of Ecology and Biological Resources, Vietnam

Abstract: Animal-based traditional remedies have received less attention in pharmacological research than botanical ones. However, it is known that especially insects contain medicinally useful compounds. Such practices are found among northern Vietnamese ethnic minority groups, who continue to rely on self-made remedies, often preferring insects over plants because they are considered more potent. Traditional healers from ten ethnic minority groups (Cao Lan, Green/Blue H’Mong, Flower H’Mong, Muong, Nung, Dao, Red Dao, San Diu, Tay, and Thai) spread out across four provinces in northern Vietnam were interviewed about their use of insects for medicinal purposes. These practices and the pharmacological rationale for their use is discussed.

Applications of population genomics to fall armyworm integrative pest management

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Abstract: The fall armyworm (Spodoptera frugiperda) is a highly polyphagous agricultural pest that is currently of global concern. Although primarily a pest on grass and cereal crops such as corn and sorghum, this generalist insect can opportunistically feed on over 80 different host plants. Within the fall armyworm, there are two morphologically identical but genetically distinct host associated strains, commonly referred to as the corn-strain and the rice-strain. These host strains have a sympatric distribution in the New World, but show a slight difference in their host plant preferences and responses to chemical insecticides. The aim of this study was to use population genomics to characterize the spatiotemporal population structure and host strain hybridization patterns of fall armyworms in their central United States native range. To do this, we collected moths from five locations across the central US at three time points during the growing season, and used ddRADseq to identify genome-wide single nucleotide polymorphisms (SNPs). Using the SNPs, we gained new insights into fall armyworm population structure, and identified novel patterns of host strain hybridization Additionally, we identified new, high-resolution genetic markers that can be used to rapidly differentiate between host strains and their hybrids. Enhancing our understanding of fall armyworm population structure and host strain hybridization patterns will enable more targeted pest management strategies for this species both in the US and globally.

Imperatives for mass trapping thrips. What we know and what we don’t know

Authors: Teulon David[2], Arias Andres[1], Brochero Elena[1] and Nielsen Mette[2], [1]Facultad de Agronomía, Universidad Nacional de Colombia, Colombia, [2]The New Zealand Institute for Plant & Food Research Limited, New Zealand

Abstract: Mass trapping is a recognised tactic for the management of a range of insect pests including thrips. Despite the many references to the apparent successful use of mass trapping for thrips pest management in commercial and industry literature, the scientific literature supporting this approach is scarce. This paper summarises the available literature on this subject and identifies the building blocks necessary to develop a successful thrips mass trapping approach including aspects such as trap size and density, and the use of visual and odour cues. Finally, an experimental scenario is proposed where the scientific basis for mass trapping can be best demonstrated.

A cholesterol-sensing mechanism promotes growth and maturation through insulin and ecdysone signaling

Authors: Texada Michael[1], Rewitz Kim[1], Lassen Mette[1], Pedersen Lisa[1], Koyama Takashi[1] and Malita Alina[1], [1]University of Copenhagen

Abstract: Nutritional inputs strongly govern animal growth and developmental transitions, both as building blocks for metabolism as well as regulators of hormonal signaling. In particular, nutrient intake influences insulin-like signaling systems that drive systemic growth, while also promoting the timely activation of steroid-signaling axes that trigger maturation into a reproductive adult. We have found that the dietary lipid cholesterol promotes larval growth and maturation in Drosophila by inducing the expression and release of insulin-like peptides. Cholesterol absorbed from the diet activates the nutrient sensor Target of Rapamycin (TOR) in the cells of the fat body and the subperineurial glia of the blood-brain barrier, which remotely upregulate insulin production; the cholesterol transporter Npc1a, which removes cholesterol from the lysosome, regulates this cholesterol sensing. Furthermore, cholesterol signaling within the cells of the prothoracic gland strongly promotes TOR activity in this tissue as well, leading to increased endoreduplication and acceleration or bypass of the critical-weight checkpoint. Thus, Npc1/TOR-mediated signaling links cholesterol availability to cellular and systemic growth control as well as developmental timing, which may underlie aspects of associations between cancer and cholesterol as well as the connection between obesity and early puberty.

Second green revolution in India: Issues and challenges

Authors: Thakur D R, Department Of Biosciences, Himachal Pradesh University, Summer Hill, Shimla, India

Abstract: India has achieved the 1st Green Revolution in late 60s with the benevolent efforts of Prof. M S Swaminathan and Prof. Norman Borlaug, USA, “Father of the Green Revolution”, who received Nobel Peace Prize in 1970. This was package of industrial agriculture technologies, such as hybrid seeds, fertilizers, pesticides, and irrigation. Our Hon’ble Prime Minister, Shri Narinder Modi is dreaming to have second green revolution in India because to feed the ever increasing human population against the constant land mass. United Nations declared 2016 as “International Year of Pulses” with the aim to popularize the vegetarian food full of proteins and to eliminate the social evil of malnutrition. But even after the three years of the International Year of Pulses, UNICEF revealed the malnutrition behind 69% deaths among children below five year of age in India. Pulses have 20-27% proteins which is 2- 3 times higher than traditional cereals and constitute the main source of proteins for developing countries, like India where per capita consumption of the animal protein is low, thus pulses are rightly considered the poor man’s meat. Insects belonging to the family Bruchidae (Coleoptera: Chrysomalidae) commonly called “pulse weevils” or bruchids are cosmopolitan in distribution and cause serious loss to legumes both in fields and stores worth million dollars every year. Callosobruchus maculatus (F.), C. chinensis (L.), C. analis (F.), C. theobromae (L.), C. pisorum (L.) etc. infest Phaseolus mungo, P. aureus, Vigna sinensis, Cajanus cajan, Cicer arietinum, Pisum sativum, Glycine max, Dolichos biflorus, D. lablab and many more legumes both in stores and fields and spoil this valuable share of the legume proteins which otherwise be eaten by human being. No doubt chemical control results quick knock down of the pests but unfortunately leave behind many hazardous effects on biodiversity in general and human health in particular. Therefore, the present work has been carried out to explore the reproductive strategy and life history traits of idiobiont and koinobiont parasitoids on some bruchid species under laboratory conditions along with botanicals. Egg endoparasitoid, parasitized the 0-84 hours old eggs and rendered them unviable for future development. Both idiobiont and koinobiont parasitoids could be exploited as potential bio-controlling agents for legume and other stored grain pests after detailed investigations and field trials. In botanical management the use of natural plant products is an important alternative of chemical pesticides to keep the pest population below the economic injury level. Acetone and methanol extracts of leaves, stem, roots etc. were prepared and employed at concentrations of 5, 10 and 20% with three replicas each. Efficacy of extracts was observed on adult mortality, fecundity and F1 adult emergence and 100% adult mortality egg deterrence was observed on second and third day treatment at 20% concentration.

Systematics and Ecology of Southeast Asian Bumblebees

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Abstract: Tropical ecosystems contain high biological diversity including bees which are vital in ecosystem services on pollination. Bumblebees (Apidea: Bombus) show a different pattern as they are predominantly temperate in distribution and rarely occur in the tropics. In tropical Southeast Asia, mountains provide the most suitable habitats for bumblebees. There are approximately twenty-two species in this region. A question is whether these bumblebees are truly tropical species or whether they are restricted to temperate-like refuges at high elevation. Due to their rarity and the inaccessibility of their habitats, the bumblebees in this region are poorly known. This study aims to clarify their systematics, climatic distribution and ecological interactions from museum collections, ecological models and molecular analyses of field samples. This is a first step towards generating an improved understanding of these tropical bumblebees, which is ultimately directed towards pollinator conservation in this region.

Targeting insect synaptic and extrasynaptic nicotinic acetylcholine receptors

Authors: Thany Steeve, University of Orleans, France

Abstract: In insects, nicotinic acetylcholine receptors (nAChRs) are ligand-gated ion channels permeable to sodium (Na+), potassium (K+) and calcium (Ca2+). But, the pharmacological profile of native nAChR subtypes are limited and correlated to hybrid receptors. Insect nAChR remains of fundamental importance because they are the main target of neonicotinoids, sulfoximines and recently introduced pesticides. Several nAChR subunits have been cloned in insects such as the cockroach Periplaneta americana which is currently used to study the mode of action of pesticides. Pharmacological studies demonstrate that synaptic and extrasynaptic receptors may have different pharmacological properties against pesticides. Indeed, imidacloprid and clothianidin activate both synaptic and extrasynaptic nicotinic receptors whereas thiamethoxam activates synaptic receptors. In addition, clothianidin is a full agonist and imidacloprid a partial agonist of nAChRs expressed on the cell bodies. These results suggest that nAChR expressed on synaptic ganglia are distincts to receptors expressed on isolated cell bodies. Moreover, clothianidin effects on isolated cell bodies could involve internal regulation of Ca2+ pathways through the activation of cAMP activity. Comparative studies between nAChRs expressed on the synapses between afferents sensory neurons and giant interneurons, and isolated cell bodies could improve our understanding on the mode of action of pesticides on insect nAChRs.

LIFE “Patches & Corridors” - Development of a habitat network for the Violet Copper to promote a sustainable metapopulation in the northern Eifel (LIFE15 NAT/DE/000745)

Authors: Theissen Bernhard, Biological station Aachen, Germany

Abstract: The violet copper Lycaena helle (Lepidoptera: Lycaenidae) is protected by the European Habitats Directive as ‘a species in need of strict protection’. This project aims to improve the conversation status of this butterfly and its supporting habitat in the northern Eifel mountains in western Germany. A number of projects have targeted this species in this region in the past, however a key barrier to the long term maintenance of this species has been dispersal between sites supporting sub-populations. This project focuses on establishing a habitat network to facilitate migratory movement within and between different Natura 2000 sites through the restoration of mountain hay meadows, wet meadows and alluvial. To monitor the success different endpoints are used e.g. the diversity of vegetation, butterflies, moths, carabid beetles and ground dwelling spiders as well as the dispersal and egg deposition of L. helle.

Tongue length evolution in Prosoeca (Nemestrinidae), a group of specialised flower-feeding flies

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Abstract: Differentiation of traits involved in resource acquisition may be a key-innovation causing rapid radiation in some animal groups. In plant-pollinator mutualisms, morphology of interacting traits such as proboscis length and nectar tube length, may covary, especially in specialized systems. While nectar tubes have long been considered a key-innovation, almost nothing is known about the diversification of proboscis length in most groups of pollinators. In this study we use the Southern African Nemestrinidae, which have proboscides that vary between 5mm – 90 mm and are important pollinators of several dozen plants in the Southern African flora, to reconstruct tongue length evolution. Prosoeca is the most speciose and diverse genus of Nemestrinidae in Southern Africa with 37 described species. Species in this genus are almost always engaged in highly asymmetrical mutualistic interaction networks, in which multiple plant species rely on it as the primary pollinator species for reproduction. We evaluated two alternative scenarios for tongue length evolution. In particular we tested whether long proboscides evolved repeatedly, possibly as an adaptive response to host plant diversity or whether the evolution of a long proboscis occurred once as a key-innovation, followed by rapid radiation. To do this we generated a molecular phylogeny for Prosoeca using two mitochondrial (CO1 and 16S) and two nuclear (28S and CAD) genes. This phylogeny was then used to reconstruct the evolution of absolute proboscis length, which represents the trait with which pollinators interact with flowers, as well as proboscis length relative to body size to correct for allometric effects. An average of proboscis length relative to body length was determined by measuring multiple specimens of a species. Our study provides insight into the factors that influence the evolution of these flies and their unique proboscides.

Understanding the incidence and severity of fall armyworm (Spodoptera frugiperda J.E. Smith) infestations and exploring low-cost management practices in cropping systems of Southern Africa

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Abstract: Fall armyworm (FAW, Spodoptera frugiperda J.E. Smith), a voracious agricultural pest native to Latin America, was first detected on the African continent in 2016, has subsequently spread throughout Africa and then across Asia. National African Governments immediately responded with purchasing synthetic pesticides for widespread control without much success. Throughout the last three years, we researched how FAW has affected smallholder farmers in Zimbabwe and explored different low-cost pest management practices adapted to the context of smallholder farmers using climate-adapted “push-pull systems”. These practices are based on plant semiochemicals affecting pest behavior and pest-predator interactions to control this invasive pest. The objectives are: a) to provide smallholder farmers with more viable and economical feasible options that are safer for their health and the environment, b) to better understand control processes and foster biological control through agro-ecological management. We found that: i) maize-legume intercropping strategies were effective in reducing FAW damage; ii) the strongest effect was found in cropping systems that are based on the principles of Conservation Agriculture due to increase in biological control; iii) there is evidence that the use of Conservation Agriculture, different maize-legume intercropping strategies and their combination foster increases the abundance of alternative preys for FAW natural enemies; iv) some legume intercrops (e.g. velvet beans (Mucuna pruriens L.) in our trials had a direct effect on reducing FAW damage. The resulting cropping systems from this research can be well integrated into already existing initiatives of fostering sustainable agriculture intensification which include cereal-legume rotations and green manure cover crops. They will enhance greater resilience against this pest besides the other co-benefits of food- and nutrition security for smallholder farmers over time.

Parasitism and competition as structuring forces within host communities, and their sensitivity to experimental warming

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Abstract: To understand how host-parasitoid networks will respond to global warming, it is important to recognize how trophic and non-trophic interactions act together to structure ecological networks, and how parasitoids can control host populations. To do this, we used laboratory experiments on a co-evolved, tropical Drosophila-parasitoid community at two temperatures – 23°C and 27°C – to test if the mechanisms observed change with increased temperature.

We first investigated how the relative influence of competition and parasitism on host communities change in response to warming temperatures, looking at host community composition and parasitism rates in a co-infection experiment over one generation using different community configurations of three Drosophila species and two parasitic wasp species. Host communities were structured most strongly by trophic interactions with parasitoids. Increased temperatures reduced host community evenness and increased overall host abundances, without significant changes in parasitism rates. Climate change may therefore result in marked changes to the structure of host-parasitoid communities, and increasing the potential for host outbreaks.

We then investigated the stabilizing role of parasitoid on host communities, and if this role will change in response to warming temperatures in a multi-generational experiment using three different community composition of four Drosophila species and two parasitic wasp species. We identified trophic links from the pupae.

The interaction between parasitism and competition is essential for the stability of entire host-parasitoid networks by allowing host species to coexist, but global warming could weaken those interactions and destabilize entire networks. We show that parasitoid control of host population might be compromised with progressing climate change.

Competition for resources impacts phenological asynchrony in host-parasitoid interactions

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Abstract: One of the most apparent ecological consequences of climate change has been the ongoing phenological shift in important life-history events among species. Given that species within the same community typically show dissimilar phenological responses to climate change, such phenological shifts are altering the timing of species interactions. Thus, some of the most profound effects of climate change on communities will likely be though changes in the timing of species interactions. One way that climate change can alter the phenology of interacting species is by accelerating or decelerating the developmental rates of species. We examined how temperature and resource competition alter the outcomes of phenological mismatches in Drosophila-parasitoid food webs, by modifying the developmental rates of the Drosophila host community. Specifically we set out to address the following questions: 1) To what extent does increased temperature modify foraging success of parasitoids that are phenologically mismatched with their hosts? 2) Are the consequences of phenological mismatch between a host and parasitoid similar in pairwise and multispecies contexts? 3) Does competition among hosts mitigate the adverse impacts of phenological asynchrony by extending the development time of the host community? We found that the degree of wasp infestation was greater in higher temperatures, but successful rate of parasitism (e.g. those infestation events that resulted in adult wasp) was significantly less in the warmer environment. The effects of phenological mismatch on wasp fitness were lessened in the multispecies treatments, suggesting that pairwise investigations may overestimate the effects of phenological asynchrony on host-parasitoid species interactions. Finally, while competition among hosts did extend and increase the rate of infestation, hosts in competition resulted in fewer adult wasps. We suggest that host quality is significantly reduced in high resource competition environments, which limits the successful development of wasps. These results highlight the importance of inspecting the consequences of phenological mismatch in a multispecies context, and reveal that both abiotic and biotic environments can significantly alter the outcomes of phenologically mismatched communities.

Near-infrared optical sensors to monitor flying insects

Authors: Thomas Benjamin[1], Genoud Adrien[1] and Saha Topu[2], [1]New Jersey Institute of Technology, United States, [2]PhD Student, United States

Abstract: In this contribution, we present the results obtained using entomological optical sensors during both laboratory and field experiments. The optical and morphological properties of insects are probed from a distance using near-infrared optical sensors measuring either backscattered light or optical extinction. From optical signals, predicator variables are derived and used in supervised machine learning algorithms such as support vector machine algorithm with the objective to classify insects and specifically mosquitoes. These predictor variables include the wingbeat frequency, Mel Frequency Cepstral Coefficient of the wing signals, body and wing depolarization ratios, and body and wing spectral cross-sections. We present the identification accuracy obtained for various scenarios, such as the classification of the insect family, genus, species, sex group, or gravidity. In addition, we conducted two field campaigns, where we monitored insect's aerial density (# of flying insects/m3) continuously for 80 days in 2020 and 189 days in 2021 and over a range of approximately 50m. During both campaigns, a co-located weather station was used to record several key environmental parameters. The collected data allowed for the study of the circadian rhythm and daily activities as well as the aerial density dynamic over the whole campaign for each cluster individually.

A novel house-based intervention for malaria control: insights from a large-scale cluster randomized controlled trial

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Abstract: Current malaria vector control relies heavily on the core technologies of Long Lasting Insecticide Treated Nets (LLINs) and Indoor Residual Spraying (IRS). These tools have contributed to substantial declines in malaria burden. However, it is now widely recognized that new tools are required to complement these existing technologies if future control targets, such as those set out in the WHO Global Technical Strategy, are to be achieved.

Over the last few years a group of researchers have been working to develop and evaluate a novel control tool involving fitting sections of PVC pipe into the closed eaves of a house, with an insecticide-treated mosquito-screen insert placed inside the tubes. The tubes maintain airflow through the eaves and can be combined with housing improvements such as screening windows, closing eaves and sealing any other cracks, to make the house more "mosquito proof". The screening component alone should provide some protection for the household, as a physical barrier to mosquito entry. However, relying on cues that typically draw malaria mosquitoes into houses, the insecticide-treated tubes turn the house into a "lethal lure" and could provide community level protection at sufficiently high coverage.

Here we report the results of a large cluster randomized controlled trial conducted over 2 years in 40 villages in central Cote d'Ivoire to determine whether the combination of insecticide-treated tubes plus screening provides protection against malaria, on top of the current best practice of universal coverage of LLINs. We present data on efficacy, acceptability, and cost-effectiveness to provide an interdisciplinary evaluation of the "lethal house lure" approach.

The road to perfect immunity: absence of diseases in fungus-farming termites?

Authors: Thomas-Poulsen Michael, University of Copenhagen, Denmark

Abstract: Social insects have to protect both themselves and their obligate symbionts from specialised diseases. Research in this field has identified a number of specialised and general defence mechanisms that play pivotal roles in protecting social insect symbioses. Fungus-growing termites have coevolved with a basidiomycete fungal cultivar (genus Termitomyces) that is maintained in external fungus gardens (combs) on a substrate of plant material that passes through the termite gut before it is deposited in the fungus comb. This association originated 30 MYA in sub-Saharan Africa and has diversified to include more than 330 described termite species, 40 described Termitomyces spp., and complex and specific core gut microbial communities. Fungus-growing termites manure their fungus on harvested decaying wood, which is expected to contain a rich diversity of microbes that could compromise termite fungiculture, either by competing with or parasitizing Termitomyces or by infecting the termites themselves. However, efforts to identify whether specialised diseases have evolved to exploit farming termite nests have turned up empty handed. Here I review recent progress in our understanding of how these termites maintain high-efficiency monoculture farming to accomplish complete decomposition of any plant substrate without being compromised by pathogens.

Understanding how bumblebees interact with herbicide treated plants

Authors: Thompson Linzi Jay[3], Smith Stephen[2], Stout Jane[1] and Stanley Dara[2], [1]Trinity College Dublin, [2]University College Dublin, [3]University College Dublin, Ireland

Abstract: Herbicides are the most applied pesticides globally, and are used to kill weeds. Some herbicides, such as glyphosate, can be applied to flowering plants, meaning that bees could be exposed to these when foraging. Bumblebees may avoid plants treated with herbicide, since they die shortly after application, especially if there are untreated plants available.

Individual bees were presented with four plants in an exclusion cage; two treated with glyphosate and two controls. We recorded the number and duration of interactions with each plant. Observations were repeated when plants were freshly treated (within 24 hours) and again when they begun to die from glyphosate treatment (after 48 hours). We also collected corbicular pollen and tested for the presence of glyphosate.

We found that bees spent significantly less time collecting nectar from glyphosate treated flowers. However this effect was not strong enough to change their choice to forage overall, where we saw no significant effect on the number or duration of all other foraging and investigative interactions. We found glyphosate was present in pollen at both time periods tested. Therefore, we conclude that bees indiscriminately forage on glyphosate treated plants. This demonstrates a potential exposure route to herbicides in the wild.

Poorly understood effects of plant sessility on pollination success

Authors: Thomson James, University of Toronto Department of Ecology and Evolutionary Biology, Canada, United States

Abstract: The book Cognitive Ecology of Pollination arose from an invitation to organize a symposium on pollination for the International Botanical Congress; I decided that an audience of botanists could benefit from a more sophisticated, up-to-date view of the behavioural ecology of flower-visiting animals. At this anniversary, I will reverse that model by focusing on aspects of plant biology that tend to be overlooked by entomologists, particularly the consequences of plants' sessility. Most comparisons of the "pollination values" of different flower visitors tend to stress an animal's morphology, behaviour, and its morphological "fit" to the flower. It is less appreciated that pollination success also depends on a plant's spatial location—not only what neighbours are present at the time of visitation, but also the composition of the local community in the preceding days. Drawing upon field and lab studies, I will show how site fidelity and trapline holdover affect both the quantity (visitation rates) and the quality (heterospecific pollen deposition) of pollination service delivered by bumble bees.

Can non-crop habitat support biocontrol of the diamondback moth in organic Australian Brassica crops?

Authors: Thurman Jessa[2] and Furlong Michael[1], [1]School of Biological Sciences, The University of Queensland, Australia, [2]University of Queensland, Australia

Abstract: It has been suggested that non-crop habitat benefits biocontrol programs as natural vegetation can promote natural enemies of pests on farms. In-field surveys of arthropod communities were paired with natural enemy exclusion experiments to measure the potential indirect impact of adjacent, unmodified non-crop habitat on larval mortality of the diamondback moth (Plutella xylostella L.). Natural enemy diversity was higher in non-crop habitat, but the composition of the natural enemy communities in non-crop habitat was significantly different from that found within the crop, suggesting that non-crop habitat does not serve as a reservoir for natural enemies on farms. Predation of larvae was high throughout the crop, with significantly higher rates for neonate larvae on the crop edge compared to the middle of the crop. Diversity of natural enemies did not predict this increased predation rate, but there was a positive correlation between increased diversity and predation of second to third instar larvae. These results suggest that unmodified non-crop habitat does not support conservation biocontrol on farms, but that predation by natural enemies plays a significant role in the suppression the diamondback moth populations on farms. When considering these relationships, natural enemy diversity and mortality across life stages must be considered as these interactions vary between the life stages of the pest.

Development of cabbage stem flea beetle rearing to identify resistance in white mustard (Sinapis alba)

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Abstract: The cabbage stem flea beetle, Psylliodes chrysocephala, is major pest of oilseed rapein Europe. Since the ban of neonicotinoid insecticides in the European Union, flea beetle pressure has been severe, and the area of oilseed rape sown has decreased significantly in response. Alternative control measures are desperately needed, and host plant resistance is a promising option. Resistance genes can be sourced from within Brassica napus germplasm, or introgressed from relatives such as white mustard, Sinapis alba.

Currently, no cabbage stem flea beetle resistant varieties of Brassica napus are commercially available. Identification of resistance genes is hampered by challenges with typical phenotyping methodologies using field trials, due to unpredictable infestation rates and difficulty identifying nuanced resistance. In addition, no published rearing methods for this non-model insect currently exist for experimentation in a controlled laboratory setting.

This work optimised methodology for rearing the cabbage stem flea beetle to obtain a consistent source of insects. In addition, a novel phenotyping methodology was used to screen for resistance in the laboratory. Accessions of both Brassica napus and Sinapis alba were phenotyped, and two genotypes of Sinapis alba with contrasting antixenotic (deterrent) resistance were identified. Investigation of quantitative trait loci is underway.

Exploring Biomechanics of Water-Walking Arthropods according to Updated Archimedes' Principle

Authors: Tian Yu, State Key Laboratory of Tribology,Tsinghua University, China

Abstract: Water-walking insects, such as water striders and water spiders, have become the recent burgeoning interest subject. The swift locomotion of water striders and water spiders primarily relies on their hairy super-hydrophobic legs, which allow them to be supported by water surface and to achieve the motion momenton. Exploring the physical mechanisms behind this water-walking capability has become a considerably interesting topic for bioinspired areas. The elegant bright-edged leg shadows of water striders are used to make the tiny forces visible and measurable based on the updated Archimedes' principle. The leg shadows could be used to reconstruct the in situ three-dimensional topographies water surface dimples to achieve the corresponding supporting forces acted on legs. The mechanics of water striders in self-cleaning, swimming forward, jumping forward have been revealed. These results are helpful for understanding the locomotion principles of water walking insects and the design of biomimetic aquatic devices. Visually measure tiny forces applied on the top surface of a circular plate has been invented with a high stability and sensitivity.

An experimental test on the relative role of natural enemy diversity and intraguild predation on herbivore dynamics

Authors: Tighiouart Karim[3], Frago Enric[2], Sanders Dirk[4], Montoya José [5] and Montoya Daniel[1], [1]Basque Centre for Climate Change (BC3), Bilbao, Spain., [2]Centre for Biology and Management of Populations, Montpellier, France, [3]CIRAD-3P, UMR PVBMT, Saint Pierre, La Réunion, France, [4]Environment and Sustainability Institute, University of Exeter, United Kingdom., [5]Theoretical and Experimental Ecology Station (SETE-CNRS), Moulis, France.

Abstract: Natural enemy diversity usually relates positively with herbivore suppression, but this effect can be dampened when natural enemies engage in intraguild predation (i.e. when two predators feed on each other and on a shared resource). The mechanisms behind these effects are poorly understood, and experimental studies are lacking. We worked with a trophic web composed of four herbivores and four enemies, some engaging in intraguild predation. We manipulated this assemblage to create replicated webs following a gradient of natural enemy diversity, that we monitored over several months. Our results showed that community dynamics weakly depended on enemy diversity or intraguild predation because it was mostly driven by a highly-influential polyphagous predator. Our work reveals experimentally how the structure of natural enemy networks determines the dynamics of terrestrial communities, and the services these communities provide, particularly pest biocontrol.

Bacteriophages as tools to dissect mosquito-microbiome interactions

Authors: Tikhe Chinmay[1] and Dimopoulos George[1], [1]Johns Hopkins University, United States

Abstract: Mosquitoes are important vectors of arboviruses and plasmodium parasites globally. Mosquito microbiome plays an important role in larval development, metabolism and vector competence. Multiples studies have deciphered the taxonomic diversity of bacterial community associated with various mosquito species. However, little is known about the functional role of individual bacterial taxa and their interactions with each other within the mosquito microbiota. Targeted modulation of mosquito microbiota can provide insights into the functional role of individual bacterial taxa. Bacteriophages; viruses that infect bacteria, provide a target specific tool for the selective modulation of the mosquito microbiota. In this study we isolated three novel lytic bacteriophages that specifically target Enterobacter spp., Serratia spp. Elizabethkingia spp., three common members of the mosquito microbiota. We assessed the utility of theses bacteriophages to alter the larval development of monoxenic Aedes aegypti and Anopheles gambiae larvae. Our results showed that addition of lytic bacteriophages to the water altered the development of monoxenic Aedes aegypti and Anopheles gambiae larvae. These results provide a proof of principle that bacteriophages can be utilized as a tool to modulate the mosquito microbiota and can in-turn affect mosquito life history traits. We intend to utilize these bacteriophages further to study the effect of targeted microbiome modulation on mosquito life span, fecundity and vector competence. This is the first use of bacteriophages to modulate the mosquito microbiome and has the potential to be developed into a novel strategy to curb mosquito-borne diseases.

Insect Outreach in the UK with the Royal Entomological Society

Authors: Tilley Luke[1], Sconce Francisca[1], [1]Royal Entomological Society, United Kingdom

Abstract: The Royal Entomological Society aims to promote and improve entomology. Entomological outreach is important to increase wider public understanding of insect science and contributes to our charitable purposes.
For almost 15 years, the Society has coordinated a series of major outreach activities in the UK including National Insect Week, Insect Festivals and EntoSci. This has been achieved through collaboration with partners such as specialist insect societies, as well as those working with wildlife and natural history.
In this talk we will share some of the successes of these campaigns and events, and the lessons learned from these activities.

Arthropod community response to abnormal precipitation in Ohio agroecosystems

Authors: Tilmon Kelley[1], Pekarcik Adrian[1], Raudenbush Amy[1] and Richer Eric[1], [1]Ohio State University, United States

Abstract: Annual precipitation in Ohio was nearly 16 cm above normal in 2019. The excessive rainfall delayed or even prevented planting in an unprecedented number of cases. By June 9 only 38% of soybean and 50% of corn was planted which is well below the average of 89% and 96% for these crops, respectively. Additionally, oversaturated soils are known to cause yield losses, especially when planted late. While the negative impact of saturated soils on plants was obvious, it is unknown how the arthropod communities that co-inhabit these soils were affected. When soils are saturated, ground-dwelling insects can move onto the soil surface to escape oversaturation, which in turn may leave them vulnerable to predators they would not generally encounter. Otherwise, insects that remain in the saturated soils may drown. In 2018 and 2019 we monitored X fields in northern Ohio for Asiatic garden beetle, and there was a 3-fold reduction in beetle populations in 2019. We used pitfall traps for this sampling and also collected invertebrate bycatch. The goal of this study is to assess how oversaturated soils in 2019 impacted arthropod communities of corn-soybean rotated fields. Arthropods were sampled weekly throughout the summers of 2018 and 2019 from 20 plots established in a 5x4 grid over a 5-acre area of corn-soybean rotated fields in northern Ohio with a field history of Asiatic garden beetle infestation. All bycatch was identified to the Family level and various aspects of the communities were compared between the two years. We hypothesize that excessive rainfall in 2019 reduced the arthropod communities, particularly for species that are strictly ground-dwelling.

Harmonia axyridis Immigration and Oviposition in Response to Variable Aphid Density

Authors: Tilmon Kelley[1], Pekarcik Adrian[1] and Raudenbush Amy[1], [1]Ohio State University, United States

Abstract: The multicolored Asian lady beetle, Harmonia axyridis, shows a remarkable ability to respond positively to soybean aphid (Aphis glycines) prey density in soybean. We performed both field and greenhouse choice and no-choice studies examining the response of H. axyridis to variable prey density. H. axyridis showed a density dependent response attributable to both increased adult immigration and increased reproductive recruitment (oviposition) in response to higher prey density. This density-dependent response helps explain the success of H. axyridis as both a biological control agent and an invasive species.

Genomic approaches to characterize Wolbachia in arthropod communities of soil

Authors: Tischer Marta[2] and Bleidorn Christoph[1], [2]Georg-August-University Göttingen, Germany, [1]Georg-August-University Göttingen, Dept. Animal Evolution and Biodiversity

Abstract: Wolbachia is a widespread, intracellular, endosymbiotic Alphaproteobacteria known to infect arthropods and several groups of filamentous nematodes. The most important effects of Wolbachia on hosts include manipulation of reproduction, vitamin supplementation, and pathogen restriction.

Wolbachia distribution and diversity among soil arthropods are still poorly studied. There are many representants of soil arthropod hosts caring diverse and possibly new Wolbachia supergroups or strains that require precise examination. Most of the phylogenetic analyses and co-phylogenies made so far for Wolbachia were based on the multilocus sequence typing system (MLST), which comprises up to 5 conserved housekeeping genes. However, while supergroups can be well-distinguished by this system, it often result in a lack of resolution of strains. Currently, there are 16 identified and classified supergroups of Wolbachia, from different hosts and habitats, including nematodes, hexapods and other pancrustaceans, or arachnids. As an alternative for strain typing approaches sequencing and annotating draft genomes have been proposed.

In this project, we aim to investigate the molecular diversity of arthropod communities from the soil environment. After screening for the presence of Wolbachia, we used Illumina-based short-read sequencing to generate draft genomes of Wolbachia from soil organisms. Using phylogenomic approaches, we phylogenetically place the Wolbachia genome sequences, including putatively new supergroups. The diversity of Wolbachia in soil arthropods is discussed and we interpret the results in the light of the evolution of Wolbachia-arthropod symbiotic relationships.

A review of the social insect inquilinism in Histeridae (Coleoptera)

Authors: Tishechkin Alexey, Plant Pest Diagnostics Center, CDFA, Sacramento, CA, United States

Abstract: Histeridae along with Staphylinidae are two leading groups of inquilinous beetles in terms of taxonomic diversity and occurrence. There are two major obligate inquilinous lineages (subfamilies) in the family as well as numerous additional cases of inquilinism evolution in the rest of Histeridae. Distriobution, diversity, host taxa and specificity, integration mechanisms and other natural history features of inqulinous Histeridae are reviewed.

The ‘Cost’ of Wolbachia infections in Nasonia vitripennis

Authors: Tiwary Alok[2] and Raychoudhury Rhitoban[1], [1]Indian Institute of Science Education and Research Mohali Knowledge city, Sector 81, Manauli, PO, Sahibzada Ajit Singh Nagar, Punjab, India, [2]Indian Institute of Science Education and Research(IISER), Mohali, India

Abstract: Wolbachia is known to alter its host reproductive biology for its benefit. It also introduces both positive and negative fitness effects in the vast majority of its host population. The present study describes the effect of maintenance of Wolbachia infection in the parasitoid host Nasonia vitripennis. We have separated the two Wolbachia infections in N. vitripennis to get single lines of Wolbachia supergroup A and supergroup B infections. We compare the effect of Wolbachia infection on life-history traits between uninfected, single A, single B, and double infection strains. Contrary to the previous reports, our results suggest that there is a “cost” associated with the maintenance of Wolbachia infection where life-history traits like adult progeny family size, fecundity, longevity, and male mating potential are compromised in Wolbachia infected strains. The double infection of Wolbachia has more detrimental impacts on the host as compared to single infections. The findings of the study raise important questions on the mechanism of survival and maintenance of these reproductive parasites in arthropod hosts

Wolbachia infections in Nasonia vitripennis: A Host-Pathogen interaction study

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Abstract: Wolbachia is a maternally inherited endosymbiont that alters its host's reproductive biology to increase the number of Wolbachia-infected females in the population. One of these alterations includes sperm-egg incompatibility known as Cytoplasmic Incompatibility (CI). CI leads to a Wolbachia infected male produce viable offspring only with a female having the same Wolbachia type infection.

Wolbachia induces CI in the parasitoid host Nasonia vitripennis (Hymenoptera: Pteromalidae). The worldwide population of Nasonia vitripennis is infected with two Wolbachia infections, one each from the supergroups of A and B. In case of multiple infections in a single host, several unanswered questions remain. How these infections are being maintained over a long evolutionary time scale even though the two supergroups show CI between each other? To address these questions, we have separated the two infections in Nasonia vitripennis and have generated single lines for Wolbachia supergroup A and supergroup B infections. We have studied the dynamics of these infections at the different developmental stages of its host Nasonia vitripennis. The study demonstrates a trade-off in life-history traits like fecundity, longevity, male mating potential, etc, and the maintenance of Wolbachia infection.

Even though Wolbachia-induced CI has been an area of attraction in recent times, the genetic basis of CI remains poorly understood. Using Nasonia vitripennis as a model system, we are also trying to understand how Wolbachia alters its host reproductive behavior? We have identified the stage of Nasonia vitripennis male development where CI is introduced by Wolbachia. We intend to find out the genes playing a role in this alteration by doing stage-specific transcriptome studies. Our study will lead to deeper insights into the biology of Wolbachia-host interaction.

Understanding how oilseed rape crops are colonised by one of its main pests, the cabbage stem flea beetle Psylliodes chrysocephala

Authors: Tixeront Margot, Université Rennes 1, France

Abstract: Integrated pest management is an emerging solution to protect crops using less or no insecticides. However, predicting crop colonisation and the pest's spatial distribution is essential for effective control. The cabbage stem flea beetle Psylliodes chrysocephala (CSFB) can cause complete destruction of oilseed rape crops (Brassica napus, OSR). In the present study, the colonisation process of OSR fields by the CSFB was studied using sticky traps placed at the border and in the centre of the fields at different heights. Results show that more individuals were caught on the outer side of the traps, suggesting that more beetles were entering than leaving the crop, and beetles were moving into the centre quickly. Catches were more important at the bottom of the trap near the crop, and they were more important during the day than during the night. The sex-ratio of individuals caught was both equilibrated and stable over the study period. Dissections of female's genitalia showed that sexual maturity occurred during the experimentation. Finally, the integration of sampling data with local meteorological data showed that the caught depends on temperature, humidity, and wind speed. The information provided by this study could contribute to implement IPM strategies against this pest.

Establishment of clock gene knockout strains and analysis of diapause phenotype in the silkworm, Bombyx mori

Authors: Tobita Hisashi[1], Katsuma Susumu[1] and Kiuchi Takashi[1], [1]The University of Tokyo, Japan

Abstract: Insects endure unfavorable seasons by entering diapause, physiologically dormant state, and photoperiod is a major environmental cue for the diapause induction. It is well known that disruption of clock gene expression prevents diapause induction in several insect species. In the silkworm, Bombyx mori, several studies have revealed that clock genes are involved in the diapause induction. However, it is controversial how clock genes are involved in the photoperiodic and temperature-dependent diapause induction. We report here the results of knockout (KO) of positive regulators Clock and cycle, and negative regulators period and timeless, in B. mori to investigate their involvement in the diapause induction. We established each clock gene KO strain using CRISPR/Cas9 system in a bivoltine strain p50T (Daizo). In embryonic or larval stage, KO lines were kept under photoperiodic conditions that the wild type moths oviposit diapause eggs. As a result, all KO strains produced non-diapause eggs regardless of the embryonic and larval photoperiod. On the other hands, KO strains tend to oviposit diapause eggs when kept under high temperature conditions in the embryonic stage. These results suggest that clock genes are involved in the photoperiodic-dependent diapause induction in B. mori as a circadian clock.

Unraveling the trophic effects of cover crops on predatory communities in a cotton agroecosystem

Authors: Toews Michael[1], Schmidt Jason[1], Bowers Carson[1], [1]University of Georgia, United States

Abstract: Providing resource stability for natural enemy communities when crop habitat is low should lead to more stable arthropod communities and service provisioning by predatory arthropods in the form of biological control. Here we use molecular gut content analysis to investigate the response of predator communities and interaction networks to rye and crimson clover cover crop use as compared to conventional tillage practices in a cotton system. Predators were collected from the field during each major cotton development stage in 2017 and 2018, and PCR was used to screen predators for the presence of primary cotton pests, incidental pests, and alternative prey. Cotton strip-tilled into cover crop residue promoted unique predator communities in the early and mid-season as compared to cotton using conventional tillage (clean till), with correspondingly dissimilar prey consumption among cover crop treatments. Temporal dynamics observed in predator communities and their interactions with prey suggested higher stability in the late growing season. We identify limitations for biological control of some key pests in this system and discuss potential mechanisms for altered predator communities and their function in the early season.

Rye cover crops replace insecticide applications for sustainable cotton production

Authors: Toews Michael[3], Lahiri Sriyanka[1] and Roberts Phillip[2], [1]Gulf Coast Research and Education Center, Department of Entomology and Nematology, University of Florida, Wimauma, FL, United States, [2]University of Georgia Department of Entomology, United States, [3]University of Georgia, United States

Abstract: Thrips infestations on seedling cotton are a predictable impediment to cotton production in the southeastern US. Common thrips species in this region include Frankliniella fusca, Frankliniella occidentalis, and Frankliniella tritici. As early season thrips can cause stand and yield losses if not managed, growers utilize prophylactic insecticide applications including seed treatments, in-furrow liquid and granular insecticides, and foliar applied insecticides. Field trials were conducted to understand how to better manage these insect pests in the absence of insecticide availability. Responses included counts of immature and adult thrips, visual plant damage ratings, dry biomass estimates at 42 days after planting and lint yield. On conventionally tilled plots, an insecticide seed treatment followed by a foliar insecticide application were necessary for maximizing yield. However, studies also demonstrated that utilizing alternatives including strip tillage into a cereal cover crop minimized thrips infestations and plant damage, while maintaining plant biomass and lint yield. Additionally, utilization of starter fertilizer [93.5 liters of 10-34-0 (N P K) per hectare] complemented thrips mitigation efforts by enabling rapid plant growth that shortened the window of time when seedlings were most susceptible to thrips injury. Although there are no drop in replacements for the convenience of a seed treatment, these data suggest that growers could adapt practices that provide adequate levels of early season thrips protection to preserve lint yield.

Bioinformatics and ecological theory for understanding/designing complex webs of species interactions

Authors: Toju Hirokazu, Kyoto University, Japan

Abstract: In the Anthropocene, countless species are at the unprecedented risk of extinction, while we still have limited knowledge of biological dynamics in nature. Developing interdisciplinary platforms for drastically increasing the information of entangled webs of species interactions is an urgent task. By integrating high-throughput DNA metabarcoding, bioinformatics, and several mathematical tools, we have revealed how hundreds or thousands of species are associated in various types of natural and experimental ecosystems. In an analysis of terrestrial arthropod communities, for example, we have selected Hexapoda-specific PCR primers for detecting gut contents of spiders and then identified a number of prey species with Illumina sequencing. The data were subsequently used to examine how network structure of predator-prey interactions changes through time and how spiders link above- and below-ground food webs. The technical platform was also applied to plant-microbiome and microbe-microbe interactions, allowing us to explore “core species”, which were expected to have great impacts on whole ecosystem dynamics. Furthermore, with the aid of recently developed methods for time-series data analyses (e.g., empirical dynamic modeling), we inferred how the direction/strength of species interactions could change and how the stability of whole communities could fluctuate through time. Such time series datasets also provide a basis for predicting critical transitions between alternative stable states of biological community compositions. Based on these new lines of results on community structure and dynamics, we are now trying to build frameworks for designing complex webs of species interactions for the restoration of degraded ecosystems and the management of sustainable agroecosystems.

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Microsporidia as pathogens of Lepidoptera and their parasitoids

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Abstract: Microsporidia, obligate intracellular parasites, are widespread in arthropod hosts and play an important role in population dynamics of agricultural and forest lepidopteran pests, such as beet webworm, corn borer, cabbage white, green tortrix, spruce budworm, gypsy moth, winter moth etc. (Franz, Huger, 1971; Wilson, 1973; Hill, Gary, 1979; Canning, Wigley, 1983; Issi, 1986; McManus, Solter, 2003; Frolov et al., 2008). Presence of microsporidia in lepidopteran hosts of hymenopteran and dipteran parasitoids may adversely affect the latter due to premature death of the host, decreased host attractiveness for oviposition, physiological alteration of the host or direct infection of the parasitoids (Brooks, 1993; Hoch et al., 2002; Down et al., 2005; Malysh et al., 2013; Paes et al., 2019). On the other hand, parasitoids may facilitate the transmission of microsporidia among the Lepidoptera. In cabbage white Pieris brassicae, two endoparasitic wasps, Cotesia glomerata and Pteromalus puparum, become infected with a microsporidium Vairimorpha mesnili when the parasitoid larvae develop within the host larvae. The pathogen completes its life cycle both in P. brassicae and C. glomerata and the emerged parasitoids transmit V. mesnili to new hosts (Issi, Maslennikova, 1964). Dybrachys cavum, a hyperparasitoid of C. glomerata, may also become infected. Moreover, the wasps may transmit microsporidia mechanically from diseased to healthy larvae during repeated attacks (unsuccessful oviposition attempts) due to ovipositor contamination with the spores (Issi, 1986). Notably, epizootics of microsporidiosis in cabbage white followed the outbreaks of braconid parasitoids (Lipa, 1963), indirectly suggesting an important role of the latter in pathogen dissemination. Additionally, V. mesnili disrupted winter diapause in P. brassicae and C. glomerata causing death of both insects during hibernation (Issi, Maslennikova, 1966).

Ectoparasitic wasp Habrobracon hebetor is widely exploited in pest control (Brower et al., 1996). To understand its interactions with a microsporidium Nosema pyrausta from corn borer Ostrinia nubilalis, we have designed a laboratory model. A continuous laboratory culture of O. nubilalis infected with N. pyrausta has been established. The microsporidia-infected larvae were exposed to adult H. hebetor for oviposition. Development of ectoparasitic larvae was successful, ending up in pupation. However, no adults emerged from the cocoons. Microscopic examination showed that pupal tissues of the wasp were tightly packed with microsporidia spores, and molecular genetic analysis confirmed its identity to N. pyrausta. On the contrary, adult wasps successfully emerged when maintained on control (microsporidia-free) host larvae. Thus, the microsporidium from O. nubilalis is highly infective to H. hebetor larvae and cause fatal disease in its pupae. This may limit H. hebetor efficiency against corn borer populations extensively infected with N. pyrausta.

Increased mutation rate is linked to genome reduction in insect endosymbionts and other prokaryotes

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Abstract: The evolutionary processes that drive variation in genome size across the tree of life remain unresolved. Effective population size (Ne) is thought to play an important role in shaping genome size, a key example being the reduced genomes of insect endosymbionts, which undergo population bottlenecks during transmission. However, the existence of reduced genomes in marine and terrestrial prokaryote species with large Ne demand an alternative explanation. One such alternative is enhanced mutation rate, which might increase an organism's ability to adapt to novel environments, but might also promote gene loss. We analysed the reduced genomes of bacteria from three divergent phyla: Blattabacterium endosymbionts of cockroaches (Bacteroidetes), Buchnera endosymbionts of aphids (Proteobacteria), and free-living marine Prochlorococcus and Synechococcus (Cyanobacteria). We found that rates of gene loss strongly correlate with mutation rates in all of these groups, and show weak or no correlation with the ratio of nonsynonymous/synonymous substitution rates (dN / dS). This indicates that genome reduction is largely associated with increased mutation rate, while the association between gene loss and changes in Ne is less well defined. Lineages with relatively high dS and dN, as well as smaller genomes, lacked multiple DNA repair genes, providing a proximate cause for increased mutation rates. Our findings suggest that similar underlying mechanisms drive genome reduction in both intracellular and free-living prokaryotes, with implications for developing a comprehensive theory of prokaryote genome size evolution.

Metabolome profiles in the hindguts of the wood-feeding cockroaches collected from East Asia and North America

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Abstract: Wood-feeding subsocial cockroaches of the genus Cryptocercus (wood roaches) are close relatives of termites, which sparsely distribute in East Asia and North America. The wood roaches harbor numerous unicellular eukaryotic flagellates in the hindgut as is the case of termites. These flagellates contribute to digestion of recalcitrant lignocellulose, which contains only a trace amount of nitrogen. Previous studies suggested that some bacterial endosymbionts in the hindgut flagellates fix atmospheric nitrogen to produce amino acids. On the other hand, almost all cockroaches including the wood roaches harbor the bacterial endosymbionts Blattabacterium cuenoti in the fat bodies, which play a role in recycling nitrogen wastes of their hosts to produce amino acids and cofactors. Thus, it appears that there is functional redundancy between the bacterial endosymbionts in the gut flagellates and in the host tissue. Our previous studies indicated that the genome sizes in Blattabacterium inhabiting the wood roaches in North America were markedly reduced compared to those in East Asia and that Blattabacterium in the wood roaches in North America lost several genes involved in essential amino acid biosynthesis. Based on these results, we hypothesized that the hindgut microbiota in North America acquired ability to synthesize essential amino acids more efficiently. To address this issue, we performed capillary electrophoresis-mass spectrometry to analyze metabolome profiles in the hindguts of Cryprocercus punctulatus and C. kyebangensis, which were collected in the United States and South Korea, respectively. As a result, we identified 209 distinct metabolites in the hindguts of these Cryptocercus species. There were considerable differences of normalized quantities of the metabolites between these species, whereas the amounts of most essential amino acids in the hindgut were larger in C. punctulatus than in C. kyebangensis. These results suggest that the hindgut flagellates in the wood roaches of North America acquired bacterial symbionts that can efficiently produce essential amino acids, which might have led to relaxed selection of genes involved in essential amino acids biosynthesis in Blattabacterium.

Ecological divergence among morphologically and genetically related Asphondylia species (Diptera: Cecidomyiidae)

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Abstract: Ecological data is crucial for determining the degree of reproductive isolation among closely related species, and in identifying the factors that have produced this divergence. We compared the ecological divergence among ten morphologically and genetically closely related Japanese Asphondylia (Diptera: Cecidomyiidae) species in Japan. We found that the ten species were significantly differentiated in important life history traits, such as host range, galling-host organ, voltinism, lower developmental threshold temperature, thermal constant and diapausing season. The data support the hypothesis that ecological divergence evolves early in speciation as the result of divergent natural selection, and that it may drives the evolution of reproductive isolation. We present scenarios on how host range expansion, host plant shift and host-organ shift for galling initiate the early stages of speciation.

Morphological characters of the pupal dorsal thorax of gall midges (Diptera: Cecidomyiidae), with reconstructions of their ancestral states within the family

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Abstract: Gall midges (Diptera: Cecidomyiidae) are the largest group of gall-inducing arthropods and are expected to be the most specious taxon of flies on Earth. Their fascinating, diverse, and species-specific shapes of plant-galls have attracted the attention of taxonomists to collect them to obtain immature stages as well as to rear adults. Thus, gall midge systematics is based on the descriptions of larvae, pupae and adults, in addition to the biological information, such as host plants and gall structures. In pupae of gall midges, characters of anterior and ventral parts of head and dorsal tergites of abdomen have been described, but the dorsal thorax remains totally undescribed, except the prothoracic spiracles. This is because the dorsal thorax is usually unclear and folded in the traditional slide-mounting techniques in which the ventrally situated antennae, wings, and leg sheaths prevent from observing its characters comfortably. Scanning electron micrographs can partially help us to observe its general morphology, but usually insufficient to precisely examine the number and position of tiny papillae. In the present study, a new dissecting technique was adopted for pupal exuviae and it enabled us for the first time to examine the detailed morphology of the dorsal thorax in slide-mounted specimens of Cecidomyiidae. We described the morphological features of pupal dorsal thorax of 35 species of 14 genera belonging to several tribes of Cecidomyiinae, two species of two genera of Porricondylinae, and one species of Micromyinae. A new set of terms is provided for the newly found characters, and reconstructions of their ancestral states were inferred.

Unexpected broad existence of endogenous phytohormones in arthropods: implications for the evolution of phytophagy and gall-inducing habits in insects

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Abstract: Recent studies have shown that some insects including non-gall inducers have an ability to synthesize auxin (IAA) in their bodies. These facts suggest that a wide range of insects have the auxin-synthesizing ability for some reason, and it might be involved in the evolution of phytophagous and gall-inducing habits as a preadaptive trait. To confirm the origins of phytohormone synthetic abilities in insects, we analyzed endogenous levels of IAA as well as cytokinins (iP and tZ) and their ribosides (iPR and tZR) in various terrestrial arthropods. Surprisingly, certain concentrations of IAA were detected in all terrestrial arthropods analyzed. In addition, iP and/or iPR were detected in most insect orders and the common ancestor of insects was supposed to have possessed its synthesizing ability. In contrast, tZ and/or tZR were detected only in some orders belonging to Condylognatha and Holometabola in Insecta and the synthesizing ability was supposed to have acquired independently in these taxa. Endogenous levels of IAA were not significantly different among higher taxa and feeding habit, but gall inducers possessed significantly higher levels of iPR, tZ and tZR, suggesting that these phytohormones are critically related to the evolution of gall-inducing habit in insects. In conclusion, we revealed that unexpectedly a broad range of arthropod taxa, regardless of phytophagy, possess certain concentrations of endogenous IAA, implying that IAA is not merely used as hormones in plants but has some important function in terrestrial arthropods. Furthermore, the tZ and/or tZR synthesizing ability is likely to be acquired in limited insect taxa containing gall inducers, suggesting its critical role, as in microorganisms, in the acquisition of gall inducing habit.

Environmental factors affecting dragonfly diversity in the Saga Plain, Japan

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Abstract: Odonata species are important indicators of freshwater environments. In recent years, several Sympetrum species have declined in Japan and systemic insecticides used for rice nursery-box were suspected as their causes. However, to conclude the causal relationship, we need to discriminate direct and confounding factors affecting Odonata densities in the field. In this study, we investigated Odonata diversity and abundance in ten localities in the Saga Plain, Kyushu, Japan from 2017 to 2019. In addition, we surveyed environmental factors including aquatic vegetation cover (emergent plants, floating-leaved plants, submerged plants), water quality, concentrations of various insecticides, and land use patterns around the census cites. To exclude confounding factors, we analyzed factors affecting the subtractions between generations or years for each species. The abundance of most species belonging to the suborder Anisoptera was negatively related to coverage of aquatic vegetation. The abundance of Sympetrum eroticum eroticum was negatively related to concentrations of a systemic insecticide (fipronil), which consistent with previous studies. Moreover, the spring generation of Ischnura senegalensis seldom occurred at localities surrounded by paddy fields and the concentrations of fipronil negatively affected the abundance of spring generation, which strongly suggest that the insecticides causes population decline of this species.

A revision of the birch-associated genus Massalongia (Diptera: Cecidomyiidae), with discovery of an unidentified species from Japan

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Abstract: Betula L. (Betulaceae), or birch, is a Holarctic genus of trees and shrubs, and its species have ornamental, industrial and medical importance. Gall midges of the genus Massalongia Kieffer (Diptera: Cecidomyiidae: Cecidomyiidi) are known to be exclusively associated with birches in the Palearctic region. In 2018, we discovered an unidentified Massalongia species heavily forming leaf galls on midveins of B. grossa Siebold & Zucc. on Mount Tara, Saga Prefecture, Kyushu, Japan. In this study, we consider the taxonomic status of the unidentified species and review the genus Massalongia. In addition, we compared Massalongia with other known genera of Cecidomyiidi, and found that the Nearctic genus Apagodiplosis Gagné, containing a single species A. papyriferae (Gagné) associated with paper birch B. papyrifera, has no synapomorphic differences from Massalongia. Thus, we synonymize Apagodiplosis under Massalongia, and the genus Massalongia becomes a Holarctic genus as their host plant genus. All known Massalongia species are univoltine, and their third instars drop from galls in Autumn, crawl into the ground, and construct unique hyaline bottle-shaped cocoons on the leaf litter. These cocoons does not let the water get inside, thus we suggest they play an important role in the protection of the overwintering larvae against rain water and snow in winter.

Oregon’s experience with a Japanese Beetle Eradication

Authors: Toland Ashley[1], Bodart Jake and Rogg Helmuth[1], [1]Oregon Department of Agriculture, United States

Abstract: In 2016, the Oregon Department of Agriculture (ODA) detected 369 Japanese Beetles, Popillia japonica, in the Portland Metro area. This was the largest detection ever in the state. The following year ODA detected over 23,000 beetles, and initiated a multi-year project with the goal of containing and eradicating Japanese beetle. The project has grown in size and scope each year, but has also seen many successes. Since the project began, there has been an 85% decrease in Japanese beetle detections, over 20,000 acres have been treated, over 22,000 tons of potentially infested yard debris has been quarantined, and over 90% of residents within the treatment boundary have consented to treatment each year. ODA will outline their steps to the eradication program including planning, treatment methods, communications, maintaining public support, and lessons learned along the way.

First evidence of N1575Y mutation in pyrethroid resistant Anopheles gambiae in Nigeria

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Abstract: In view of recent findings that codon 1575 mutation increases the L1014F mediated resistance in Anopheles mosquitoes, we investigated the presence of this mutation in four sites with intense pyrethroid resistance in Nigeria. Pyrethroid: permethrin and deltamethrin susceptibility test was carried out using 2-3 days old adult Anopheles from larval collections. Based on the susceptibility test result, intensity test with 5x and 10x concentrations were carried out at sites with high resistance (% mortality>85). Resistant specimen from each insecticide concentration were identified to species level by PCR and screened for the presence of L1014F and N1575Y mutations using allele specific PCR and Taqman assay respectively. The frequency of kdr mutation for permethrin varied from 0.71-0.75 for 5x and 0.73-0.75 for 10x. The kdr frequency for deltamethrin was significantly low: 0.54-0.60 for 5x and 0.66-0.71 for 10x. Anopheles gambiae resistant to 5x and 10x concentrations of permethrin showed the presence of homozygous mutant allele (Y) and heterozygous mutant allele (NY) in two sites. This is the first detection of N1575Y mutation in Nigeria. From this study, there was no significant association with resistance intensity (?2=0.8, P=0.3711). It may take time for such mutation to reach significant frequency. However, there is need for frequent monitoring, to forestall the effect this may have on national malaria vector control programs

Conditions for collapse: chronic nutrient enrichment increases native insect density linked to salt marsh dieback

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Abstract: We examined how different conditions of nutrient enrichment affect densities of a native insect that feeds upon a salt marsh foundation plant species with subsequent effects on salt marsh dieback. Dieback is the abrupt death of salt marsh vegetation, leaving barren mudflats. In a natural salt marsh in the mid-Atlantic United States, we set up a full factorial experiment in which we crossed the amount (low, medium, high) with duration (one-year pulse or a two-year press) of nitrogen addition. We recorded stem-boring insect larvae densities, plant tissue percent nitrogen, and percent dieback within each plot. When we compared the effects of nitrogen amount and duration on dieback, we found an effect of nitrogen amount and a marginal effect of press/pulse. By comparing linked and independent Bayesian hierarchical models, we determined both plant percent nitrogen and stem-boring larvae densities contributed to salt marsh dieback. Our findings link nutrient enrichment with an increase in native insect herbivory as a cause of salt marsh dieback, whereas previous studies considered nutrients and herbivory as separate factors. Broadly, we provide evidence that high levels of nutrient enrichment that persist for multiple years amplifies native herbivory and is a condition leading to salt marsh dieback.

Deciphering Adult Behavior the Black Soldier Fly to Optimize Egg Production in Colony

Authors: Tomberlin Jeffery, Department of Entomology Texas A&M University, United States

Abstract: Black soldier fly adults have a unique lekking behavior that drives mating and resulting fertilized egg production. Various abiotic and biotic factors impact such behavior and egg production. During this presentation, those attending will updated on what is known about the impact of temperature, microbiology, and body size on adult mating behavior and resulting egg production.

Photic entrainment mechanism of the circadian clock in the cricket, Gryllus bimaculatus

Authors: Tomioka Kenji, Graduate School of Natural Science and Technology, Okayama University, Japan

Abstract: In insects, the circadian clock governs daily rhythms in various physiological functions, including behavioral activity, hormonal secretion, and sensitivity of visual system. One of the essential properties of the clock is the synchronization to the daily environmental cycle. Light is the primary cue for this synchronization or entrainment. However, the molecular mechanism of the photic entrainment is still largely unknown in insects and our goal is to understand the mechanism. We investigated the mechanism using the cricket Gryllus bimaculatus. Molecular and behavioral experiments revealed that it includes two separate pathways: one resets the clock by delayed light-off and the other resets the clock by light exposure in darkness. The former includes Pdp1 as the first responder to delayed light-off which is followed by upregulation of Clock, then of period and timeless (tim). In this pathway, tim plays an important role because its knocking-down by RNAi mediated gene silencing often prevented resynchronization of locomotor rhythm to 6 h delayed light-dark cycle. The latter mechanism includes c-fos and two cryptochrome genes (cry1 and cry2). Light exposure upregulated the c-fos mRNA levels within 60 min at both early subjective night (CT12) and late subjective night (CT20), while no significant changes were observed when light was given at the mid subjective day. RNAi of c-fos gene significantly decelerated resynchronization to both 6 h advanced and delayed light-dark cycles. Although single RNAi of cry1 or cry2 rather accelerated the resynchronization, double RNAi of cry1 and cry2 often prevented the resynchronization. No significant changes were induced by light exposure in cry1 and cry2 mRNA levels. Thus, post-transcriptional modification may be involved in the c-fos/cry pathway. Based on these results the entrainment mechanism of the cricket circadian clock will be discussed.

The first insights into the Colorado Potato Beetle (Leptinotarsa decemlineata Say) circadian rhythm

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Abstract: It has been unambiguously established over the past decades that almost all of the animals investigated thus far contain endogenous clocks that help them to adapt to the Earth's punctual daily cycle. They accomplish this task by tracking the time using intricate protein feedback loops and then giving output to the organism which ensures the correct timing of complex behaviors such as mating, foraging, molting, and sleeping. Colorado potato beetle (Leptinotarsa decemlineata Say) which is a serious pest of the plants in the Solanaceae family that can devour entire potato fields if left uncontrolled, exhibits an explicit photosensitive response when it comes to the diapause induction which might indicate the existence of a robust circadian clock in this beetle. We were interested in this insect's putative circadian clock and the hypothetical correlation between this clock and diapause behavior as the literature on this topic is still hazy. Clock genes have been studied extensively using the Drosophila melanogaster as a study model. In this study, the mRNA levels of major clock gene homologs isolated from the brains of adult beetles that were reared either under short(light/dark 8h:16h) or long day(light/dark 16h:8h) conditions were evaluated using Rt-qPCR technique at different Zeitgeber times throughout the day. In order to complement the Q-pcr data, we also studied the daily activity pattern of the beetle by monitoring them under different light/dark cycles. Lastly, we tried to locate the neurons that might be implicated in the circadian rhythm of this beetle by staining Diuretic hormone 31 and another neuropeptide, Allatostatin-C, which might be playing a role in the diapause induction.

Evolution of parasitism in Calliphoridae

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Parasites are attractive models for the study of the evolution of the parasitic habit, and the molecular mechanisms underlying adaptive changes. The Calliphoridae family, for example, is a good candidate for such a study. In this family of flies, different species have been recorded feeding on: living tissues of a vertebrate host; living tissues of an invertebrate host; decomposing matter; and blood. Considering the feeding habits of their larvae, califorids are classified in: saprophagous species, which feed on decomposing tissue; facultative parasites, which feed on decaying organic matter, or infest necrotic or living tissues of vertebrates; and obligate parasites, which feed only on the living tissues of their hosts. We combined three dimensions of information to try and understand the origins of the parasitic habit in this family of flies: (1) phylogenetic, mapping the transitions of habits that occurred in history of the family; (2) phenotypic, quantifying the index of preference for different food sources, and (3) genetic, comparing patterns of gene expression among different species. |The stochastic character mapping in the phylogeny of the family, revealed the most likely ancestral habit as saprophagy. Obligate parasitism and facultative parasitism evolved later, independently. Two-choice essays with females allowed the precise classification of the species regarding their feeding habits. Essays with larvae showed that both, saprophagous and facultative parasites, feed on decaying flesh and fresh meat. On the other hand, C. hominivorax, an obligate parasite, showed an aversive behaviour to decaying meat. These results led to the hypothesis that parasitism arose from a shift in the attraction of the female to new oviposition sites, followed by the specialisation of the parasitic larvae. The search for the genes involved in the specific feeding habits was done with a comparative gene expression analysis of RNA-seq data from six Calliphoridae species. We found 230 potential candidate genes for future research. In addition, we found that both, regulatory and coding regions, have predominantly undergone the action of purifying selection.

Subtle subterfuge: Parasite manipulation of underlying phenotypic plasticity in social insect hosts

Authors: Toth Amy, Iowa State University, United States

Abstract: Parasite and pathogen manipulation of host phenotypes is a dramatic phenomenon, often leading to aberrant, unusual, or even novel host behavior. However, in other cases host manipulation may take a subtler form, resulting in shifts in normal host phenotypes in a direction that benefits the parasite or pathogen. Here, I discuss two cases from social insects, a group widely known for possessing high levels of phenotypic plasticity. The first study suggests strepsipteran endoparasites can alter the social caste of their paper wasp hosts, leading would-be workers to show gene expression patterns that are more queen-like. The second study suggests viruses can alter social behavior in honey bee hosts, allowing infected bees to more easily be accepted into foreign colonies. Both of these examples illustrate cases in which alterations of host social plasticity may result in potential advantages in transmission for the parasite or pathogen. I suggest host manipulation via alterations of underlying phenotypic plasticity may be a common and under-appreciated phenomenon in the study of host-pathogen interactions.

How temperature affects the outcomes of protective aphid-bacterium mutualisms?

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Abstract: Many research efforts are being invested with the aim to identify the ecological and evolutionary drivers of insect-symbiont mutualisms in a rapidly changing world. Among these drivers are temperature fluctuations, which shape the cost-benefit fitness balance of hosting certain symbiont species or genotypes and their spread within insect populations. To provide a synthetical view on this topic, we first propose a meta-analysis to quantify the impacts of microbial symbionts on the phenotype of their insect hosts in different thermal contexts (benign or stressful heat conditions). We found that fitness traits (survival, development, morphology, reproduction, and defense against natural enemies) are unevenly protected from acute heat stress by the symbionts (or that hosting a symbiont may or may not be advantageous under heat stress, depending on the trait studied). We distinguish three groups of traits: those that are strongly enhanced by symbionts but poorly affected by temperature (defensive traits), those whose expression is strongly dependent on symbionts and temperature in an interactive manner (development and reproduction), and those that are negatively affected by symbionts independently of temperature (morphology, survival). From this literature survey, it appeared that the fitness impacts of heat-protective symbionts on their hosts have usually been examined under constant temperatures or acute heat pulse, whereas these interacting organisms experience more complex fluctuating temperatures in nature. Empirically, we then examined the joint effects of mean temperature and thermal variability (diurnal thermal range) on the tripartite interaction between an aphid host, its obligate bacterial symbiont, and a facultative heat-protective bacterium. We highlight complex trait-environment relationships that could help drawing a more integrative and nuanced picture about the eco-evolutionary trajectories of insect-symbiont partnerships in the era of climate change.

Loss of winter diapause expression in aphid parasitoids from mild winter climates

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Abstract: Temperature is both a selective pressure and a modulator of the diapause expression in insects from temperate regions. Thus, with climate warming, an alteration of the response to seasonal changes is expected, either through genetic adaptations to novel climatic conditions or phenotypic plasticity. We compared the capacity of four parasitoid species to enter winter diapause under nine different photoperiod and temperature conditions in the laboratory. Our results suggest rapid shifts over the last three decades in the overwintering strategies of aphid parasitoids in Western France, probably due to climate warming. Species that have very recently (last 10 years) invaded winter trophic networks in this region show a low proportion of winter diapause. Parasitoids not entering diapause but developing under short day-lengths had increased developmental time and higher weight than non-diapausing parasitoids compared to those developing under long day-length, at a similar temperature. Responses to novel day-length conditions may thus affect phenological adaptations in a changing climate. Our results overall imply that diapause can be replaced by active adult overwintering, with potential consequences for life-histories, species interactions (host-exploitation throughout winter, increased competition), insect community composition, and natural pest control. In cereal fields of Western France, we report that the host-parasitoid community structure and composition that were stable and prevailed before 2011 have recently shifted toward a more diversified community, with the presence of two new braconid parasitoid species, a few hyperparasitoid species and one aphid species. Modifications in minimal winter temperatures and frequency of frost events across the winter partially explain observed community changes.

Museomics of ground beetles using HyRAD-X exome capture

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Abstract: Museomics is a comparatively recent field allowing the inclusion of Museum-preserved specimens into molecular studies often using a combination of phylogenomics and high-throughput sequencing. Such studies are revolutionary because they permit, for instance, the placement of extinct species in a phylogenetic framework using an unprecedented amount of data. In this study, we investigate the performance of a new phylogenomic method in generating a robust evolutionary tree allowing to place a presumably extinct endemic species from Saint Helena island. Within Carabinae (ca. 1500 species), four tribes are recognized, the flightless Holarctic Cychrini (four genera, ca. 230 species), the flightless South American Ceroglossini (one genus, ca. 10 species), the flightless Pamborini (two genera, ca. 20 species), and the mostly flightless Carabini (two genera, ca. 1100 species). An additional genus comprising the unique species Haplothorax burchelli remains enigmatic because the placement of this Saint Helena endemic is highly uncertain. Using Hy-RAD-X, a recently developed exome capture method, we aim to generate genomic data for representatives of all tribes and most genera within Carabinae to place Museum specimens of Haplothorax in a phylogenomic framework. The phylogenetic implications as well as methodological aspects of this approach will be detailed in this presentation along with perspectives of development in the field of Museomics and in the study of ground beetle evolution.

Belowground battles in Brassicaceae. Molecular mechanisms of optimal glucosinolate allocation in roots under herbivore attack

Authors: Touw Axel[2], Sontowski Rebekka[3], Tsunoda Tomonori[1], Uthe Henriette[2] and van Dam Nicole[3], [1]Faculty of Biotechnology, Department of Bioscience, Fukui Prefectural University, [2]German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, [3]German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Germany

Abstract: Optimal defense theory (ODT) predicts that organs with highest value to plant fitness and highest vulnerability to herbivores should have highest levels of chemical defenses. Until recently, ODT was mostly tested for defense allocation over aboveground plant organs. We extended ODT to roots by studying constitutive and herbivore-induced defense allocation patterns over taproots, lateral roots and fine roots of glucosinolate (GSL)-containing plant species. We found that taproots contained highest overall levels of constitutive GSLs, followed by lateral roots and fine roots. In line with these findings, the generalist beetle Amphimallon solstitiale preferred feeding on fine roots, whereas larvae of the specialist Delia radicum (cabbage root fly) preferred feeding on taproots. Herbivory always induced strongest GSL increases in the taproot, independent of which root class was damaged. This induction coincided with upregulation of biosynthesis and transporter genes in taproot tissues, but not in fine roots. Since GSL levels in fine roots or aboveground organs did not decrease, we hypothesize that GSL transporters mainly help to retain GSLs in the taproot during root-herbivory. Future research will include structurally related defense compounds, in particular phytoalexins such as brassinins, which will be related to herbivore feeding patterns and risk of infection by soil-borne pathogens.

The role of cryoprotectants in insect freeze tolerance: lessons from crickets, butterflies, and other animals

Authors: Toxopeus Jantina, St. Francis Xavier University, Canada, United States

Abstract: Many terrestrial insects encounter temperatures low and sustained enough to freeze their body fluids. Remarkably, some temperate and polar insects are freeze-tolerant, surviving conversion of as much as 82 % of their body water into internal ice. However, although insect freeze tolerance was first described almost 300 years ago, we have a limited understanding of the mechanisms underlying this cold tolerance strategy. Many freeze-tolerant insects accumulate low molecular weight cryoprotectants (e.g. amino acids, polyols, sugars) prior to winter. However, many of these molecules are not unique to freeze tolerance (e.g. are accumulated by insects that survive low temperatures but not freezing), and no cryoprotectant (or group of cryoprotectants) is accumulated by all freeze-tolerant insects. Here, I discuss studies on a variety of cryoprotectants in three freeze-tolerant species: the spring field cricket Gryllus veletis, the small cabbage white butterfly Pieris rapae, and the great grig Cyphoderris monstrosa. Using a combination of metabolomics and targeted assays, I show that these insects accumulate moderate concentrations (< 100 mM in the hemolymph) of low molecular weight cryoprotectants in response to a range of treatments, including acclimation to typical autumn-like conditions, prolonged supercooling, and freezing. Through laboratory manipulations, I demonstrate that even small increases (c. 20 mM) increases in hemolymph cryoprotectant concentrations can improve freeze tolerance of G. veletis, likely through non-colligative mechanisms. I discuss whether plasticity in cryoprotectant composition is important for surviving freezing, and how these results inform our understanding of the mechanisms underlying insect freeze tolerance.

The incompatible insect technique: elimination of isolated Aedes aegypti populations is possible and why evaluations of field interventions should focus on the vector itself

Authors: Trewin Brendan[1], Pagendam Daniel[1], Griffin Lachlan[2] and Beebe Nigel[3], [1]CSIRO, Australia, [2]Queensland University of Technology CSIRO, Australia, [3]University of Queensland CSIRO, Australia

Abstract: The incompatible insect technique (IIT) is a new method of control that can effectively suppress populations of medically important vectors such as mosquitoes. This novel technique applies the symbiotic bacteria Wolbachia as the sterilising agent and has recently been applied to successfully suppress populations of Aedes aegypti and Aedes albopictus. Here we show results on how it may be possible for IIT to suppress an Aedes aegypti beyond detection from an isolated urban area in north Queensland, Australia. During the experiment over three million Wolbachia infected Aedes aegypti males were released into three treatment landscapes of 200+ houses, while three control areas with similar characteristics were also monitored. During the 20 week experiment the adult population was suppressed by over 80% across the three treatment areas. However, during subsequent monitoring over the next season, we observed one productive treatment area that did not yield adults until well into the summer, suggesting the standing egg bank had been depleted and the endemic population had been suppressed below detection.

Although randomized control trials (RCT) are the gold standard in evaluating field studies, their size, complexity and costs delay or prevent the implementation of potentially life-saving tools. Alternative and potentially simpler methods are required if we are to efficiently fund novel vector control interventions within human communities. Furthermore, epidemiological endpoints are important when mosquitoes are still present in treatment areas, as is the case when Wolbachia is used as a virus blocking mechanism, however, it may not be optimal to design RCTs when mosquito populations can be removed entirely. With assistance from next generation modelling and genomic surveillance approaches, it will be possible to design interventions that focus entirely on the vector itself. Direct measurements of the mosquito population are cost effective, while modern technologies such as biosensors or LAMP assays have the potential to directly measure viral prevalence within these populations. Given the evidence available for the power of IIT, an epidemiological endpoint of local disease elimination is certainly possible. This will be particularly important as we enter the fourth great era of vector control - the era of area-wide rear-and-release strategies.

SciComics! Biology and Entomology education through comics

Authors: Tribull Carly, Farmingdale State College (State University of New York), United States

Abstract: Comics often bring to mind images of overly muscled superheroes and stories of villains cavorting around with world-ending weapons. However, this is an incredibly limited view of what comics can accomplish and their ever-growing role as tools for science communication! This presentation will provide a justification for why comics should be used in science communication and entomology education - namely for their motivating qualities, ability to bridge difficult concepts through a combination of art and writing, and concept comprehension driven by the reader's personal pace. Along with a growing popularity in the production of biology and entomology comics, there have been a number of studies examining STEM comic successes in primary and secondary science education and as a tool for scientific communication. These studies, along with a survey of the comics themselves, will be discussed in order to encourage symposium participants' adoption of these materials in SciComm work. Additionally, Biology Comics (www.biologycomics.com), an Open Educational Resource that translates the standard introductory biology textbook into a freely accessible webcomic for college students, will be discussed. As many entomology professors also teach general biology at their institutes, Biology Comics can be used as a novel teaching tool, especially for reluctant students. For two semesters, Biology Comics and a traditional biology textbook have been used in a controlled study at Farmingdale State College (SUNY). Preliminary results covering introductory topics like the characteristics of life and atomic properties show that there is no significant difference in learning assessment performance, but a significant difference in attitude towards the material: As with other science comic studies, students receiving the comic reported a more positive attitude towards course materials. Finally, a new project specifically geared at General Entomology students will be presented: A comic guide to insect collecting and collection building as a way of reducing common student mistakes in introductory entomology courses.

A century of phytoplasma-host association records: possible implications for overlooked phytoplasmas in natural habitats

Authors: Trivellone Valeria[1] and Dietrich Christopher[1], [1]Illinois Natural History Survey, Prairie Research Institute, University of Illinois at Urbana-Champaign, United States

Abstract: Phytoplasmas are a diverse lineage of uncultured bacteria strictly associated with the phloem of vascular plants and internal organs of hemipteran insects. Because phytoplasmas often cause severe diseases of economically important plants, study of their diversity and host (vector and plant) ranges has focused almost entirely on agroecosystems. Earlier studies reported that non-crop plants and insect vectors not associated with cultivated plants may serve as inoculum sources that enable phytoplasmas to persist locally through alternative transmission routes. However, despite these efforts, new outbreaks involving previously known or new strains continue to occur regularly. Routes of transmission may involve bridge-vectors and a wider range of plant hosts in natural habitats interspersed with other habitat types. A few studies attempted to detect possible sources of inoculum in specific plants in forests and grasslands that surround crops to estimate the risk of emerging diseases. However, the broader ecological and evolutionary context remains poorly investigated, and available data may suffer from sampling bias; e.g., failure to systematically screen for phytoplasmas and potential vectors in the wild. Insect species that are restricted to natural habitats should be compared with known vectors in terms of their functional traits to detect alternative routes of transmission and bridge-vectors. Network analysis of a global Hemiptera-Phytoplasma-Plant associations database showed that plant- and vector-phytoplasma associations are significantly modular and nested, suggesting stability of communities and increase in numbers of coexisting species associated with lower competition. However, the nested pattern might become non-nested if further plant and/or insect hosts are discovered for one or more phytoplasmas in natural habitats. To examine whether observed patterns might be altered by including data from natural habitats of understudied areas we carried out a pilot study analysing 215 specimens representing 8 tribes of leafhoppers. The specimens were previously collected during several field expeditions to 3 biogeographic regions worldwide. Six specimens of Deltocephalinae tested positive. Among them, 4 species (Leofa dispar, Pravistylus exquadratus, Acharis n. sp., Mayawa n. sp.) belong to genera never reported as phytoplasma vectors and none are normally associated with crops. The sequenced phytoplasmas are related to the 16SrXI phytoplasma group. Another undescribed species of Macrostelini from Australia tested positive for a phytoplasma closely related to the 16SrII-E phytoplasma group. Macrosteles sordidipennis from Kyrgyzstan was infected by a phytoplasma belonging to the 16SrI group; the only phytoplasma group reported previously from Kyrgyzstan belongs to 16SrXII. A better understanding of phytoplasma-associated plant diseases can be achieved by documenting phytoplasma-host associations in natural habitats and screening of potential vectors.

Drivers of true fruit fly (Diptera: Tephritidae) invasions

Authors: Trombik Jiří[1] and Liebhold Andrew [2], [1]Czech University of Life Sciences Prague, Czech Republic, [2]USDA Forest Service

Abstract: Given the high costs associated with fruit fly (Tephritidae) invasions, there is a need to better understand and predict the risks of future invasions. We assembled a global database of historical Tephritidae invasions with the objective to identify the biological and socioeconomic drivers that explain these invasions.

We used various published sources and online databases to assemble a database documenting the occurrence (presence/absence) and status (native/non-native) of individual species for each country in the world. Values of several socio-economic and environmental variables were also assembled and considered as explanatory variables. A generalized linear mixed-effects model framework was used to evaluate the utility of these variables for predicting the country-level occurrence of each species outside of its native range.

A total 44 species were identified as having been accidentally introduced in the world. The number of invasions has rapidly increased since the 1950s. Climatic similarity between native and invaded countries, gross domestic product of the invaded country and distance from the native range are significant predictors of tephritid invasions.

Chinmo is the Larval Member of the Molecular Trinity that Directs Drosophila Metamorphosis

Authors: Truman James[1] and Riddiford Lynn, University of Washington, United States

Abstract: The molecular control of insect metamorphosis from larva to pupa to adult has long been a mystery. The Broad and E93 transcription factors, which can modify chromatin domains, are known to direct the production of the pupa and the adult respectively. We now show that chinmo, a gene related to broad, is essential for the repression of these metamorphic genes. Chinmo is strongly expressed during the formation and growth of the larva and its removal results in the precocious expression of broad and E93 in the first stage larva, causing a shift from larval to premetamorphic functions. This trinity of Chinmo, Broad and E93 regulatory factors are mutually inhibitory. The interaction of this network with regulatory hormones likely ensures the orderly progression through the insect life history.

Genetic structure of stable fly, Stomoxys calcitrans (Diptera: Muscidae): a reference for the quarantine management in Taiwan

Authors: Tsai Cheng-Lung[1], Lu Chia-Ning[1], Yeh Wen-Bin[1] and Tu Wu-Chun[1], [1]Department of Entomology, National Chung Hsing University, Taiwan

Abstract: The stable fly, Stomoxys calcitrans (Diptera: Musidae, Stomoxyini), a blood sucking species with global distribution, is considered as an economically important medical and veterinary pest. It could cause enormous economic loss of cattle by reducing the milk production, losing body weight, and arresting development. Thus, the clarification of genetic structure of S. calcitrans is crucial for its management. To understand the genetic composition of S. calcitrans in Taiwan, two mitochondrial genes, cytochrome oxidase subunit I (COI) and 16S rDNA, and one nuclear internal transcribed spacer 2 (ITS2) of 110 specimens representing 13 localities are analyzed. Moreover, a total of 593 COI sequences from 22 countries including six zoogeographical regions are further applied to resolve the possible origin of Taiwanese population. Phylogenetic inference based on COI gene revealed that a specific genetic lineage was found in Ethiopian Region. For the two Taiwanese lineages, i.e. one from Palearctic/Oriental Regions and the other is associated with the worldwide populations including Nearctic, Neotropical, and Palearctic Regions, might have represented two possible origins for S. calcitrans in Taiwan. A calibration estimation showed that these two lineages were diverged in the middle Pleistocene approximately 0.35 million years ago. However, intermingled ITS2 sequences of the two lineages and low differentiation index (FST) informed that gene flow might have occurred frequently either in Taiwan or among countries. The prevalence of livestock industries and human activities might be the possible explanation for current differentiated pattern. Genetic exchange among populations which belong to the two lineages may change the genetic composition and cause severe impact on livestock industries. Thus, the prevention of foreign populations exhibiting peculiar genetic composition such as Ethiopian Region is important for quarantine task in the world.

Where do apple pollinators live? Understanding nest-site selection of solitary ground-nesting bees in UK orchards

Authors: Tsiolis Konstantinos[4], Fountain Michelle[2], Potts Simon[4], Garratt Michae [4], Tilston Emma[3], Burman Joseph[1] and Rintoul Naomi[1], [1]Canterbury Christ Church University, [2]NIAB EMR, [3]NIAB EMR / Enviresearch Ltd, [4]University of Reading, United Kingdom

Abstract: In the UK, ground nesting bees are the most economically important pollinators of apple crops. However, very little is known about where they nest in orchard landscapes and what their specific habitat preferences are. This presentation will provide novel insights into the habitat preferences of ground-nesting andrenid bees and show how simple management interventions can be used enhance populations several ground-nesting bee species. The findings shared here will underpin more general implications for the sustainable management of a largely overlooked pollinating taxa which have a central role in food security.

The molecular basis of chemosensory receptors in the olive fruit fly, Bactrocera oleae (Diptera: Tephritidae) and manipulation of the reproductive behavior by Orco knock down

Authors: Tsoumani Konstantina[1], Spanomitrou Antonia[4], Gaitanidis Alexandros[3], Skoulakis Efthimios[3], Mathiopoulos Kostas D[1], Belavilas-Trovas Alexandros[1] and Gregoriou Maria-Eleni[2], [1]Department of Biochemistry and Biotechnology University of Thessaly, Greece, [2]Department of Biochemistry and Biotechnology, University of Thessaly, Larissa, Greece, [3]Division of Neuroscience, Biomedical Sciences Research Centre “Alexander Fleming”, [4]University of Thessaly, Greece

Abstract: The olfactory and gustatory systems of an animal possess central roles in several physiological functions, including food localization and choice, mate search or oviposition selection. For insect pests, the ability to manipulate such systems could lead to efficient and species-specific reduction of the insect’s reproductive capacity and damaging ability. To achieve this, however, a profound knowledge and understanding of these systems is a prerequisite. The olive fruit fly, Bactrocera oleae, (Diptera: Tephritidae) is the most destructive pest of the olive tree worldwide. Its specialist larvae feed exclusively on the olive pulp, causing significant production losses and olive fruit impoverishment.

In this study we have identified and explored the families of receptor proteins involved in olfactory perception and taste, including odorant receptors (ORs), ionotropic receptors (IRs) and carbon dioxide-sensing gustatory receptors (GRs) on the B. oleae genome. Gene structure analysis was performed, functional and structural characteristics were determined, and basic phylogenetic clustering were examined. Further phylogenetic comparisons with relative species were also performed based on sequence similarities to uncover the diversity among these receptors and determine divergence or species-specific expansions that might have facilitated the adaptation of the olive fruit fly to its unique plant-host.

We further knocked down the expression of the olfactory co-receptor Orco by RNAi through dsRNA injections. Disruption of Orco expression impaired the copulation and reduced oviposition rates. These results demonstrated that both pre- and/or post- mating processes were affected. The observed changes in the reproductive behavior of B. oleae render Orco a critical key gene that could be considered a potential pest control target for the development of environmentally friendly insect management strategies of the olive fruit fly populations.

We are currently deorphanizing odorant receptors which would allow the design of novel and species-specific pest control agents and set new perspectives towards the improvement of the olive fruit fly control approaches.

Effects of photoperiod on the induction of dormancy in Glaucias subpunctatus (Walker) (Heteroptera: Pentatomidae)

Authors: Tsunashima Ayaka[2] and Itoyama Kyo, Meiji University, Japan, [2]Meiji University, Japan

Abstract: The fruit-piercing stink bug, Glaucias subpunctatus (Walker) (Heteroptera: Pentatomidae) is a pest attacking various fruits in the southwestern area of Japan. In recent years, it has been reported that their distribution has gradually expanded northward and the incidence has tended to increase in some areas. The basis of forecasting is the ecological characteristics of target pests, especially understanding of phenology and life cycle is necessary. Although the expansion of the damage of this bug in the future is concerned as mentioned above, its ecological characteristics remain largely unknown. For overwintering, G. subpunctatus adults are known to enter reproductive dormancy in temperate climates. However, G. subpunctatus winter dormancy has not been explicitly evaluated to determine whether it is a diapause or a quiescence state. Therefore, the objective of this study was to clarify effects of photoperiod on the induction of dormancy in G. subpunctatus. We investigated the critical day length and the sensitive developmental stage to photoperiod of G. subpunctatus under laboratory conditions. In the first experiment, bugs were reared from eggs to adults under five photoperiodic conditions ranging from 12L12D to 16L8D at 25 ± 1°C. In the second experiment, egg masses were first placed in long-day condition (16L8D) and then moved to short-day condition (12L12D) at each developmental stages. The results of these experiments suggested that the critical day length was between 13 h and 14 h and that it may not had a clear sensitive developmental stage to photoperiod. We discuss the expansion of the distribution of southern insects based on the dormancy characteristics of G. subpunctatus.

Evolution of the repeat-rich Y chromosomes in mosquitoes: new insights from long read sequencing

Authors: Tu Zhijian, Department of Biochemistry, Virginia Tech Blacksburg, VA, United States

Abstract: Sex is critical to the survival and evolution of sexually reproducing organisms including mosquitoes. Only female mosquitoes feed on blood and transmit disease-causing parasites or viruses while the non-biting males are harmless in this context. A dominant male-determining factor (M factor) from the Y chromosome or the male-determining locus (M locus) provides the master switch that initiates male development in mosquitoes. Such male-determining factors have been recently discovered in a few mosquito species (Hall et al., 2015; Criscione et al., 2016; Krzywinska et al., 2016). However, Y chromosomes are still very difficult to study due to their repeat-rich characteristics (Hall et al., 2016). Y chromosomes were entirely missed when the 16 Anopheles mosquito genomes were published in 2015 (Neafsey et al., 2015). Towards the goals of improving our understanding of the function and evolution of the Y chromosomes in mosquitoes, we have recently sequenced the males from divergent Anopheles species using Oxford Nanopore and other platforms. In this presentation, I will describe the various methods that we are developing to facilitate Y gene discovery and Y chromosome assembly. These methods include coverage-based informatic analysis, targeted assembly, and sequencing of hybrid F1 progeny followed by trio binning. Experimental verification of these genomic analyses will also be presented. I will also present comparative genomics analysis of the distribution and turnover of M-locus and Y-chromosome genes among divergent mosquito species. The potential for using “Y”-linked “maleness” genes to control mosquito-borne infectious diseases will be also discussed.

Demographic comparison of rearing media (or meridic diets) for the predator Orius strigicollis (Hemiptera: Anthocoridae)

Authors: Tuan Shu-Jen[1], Chen Yeuh-Wen[1] and Hung Yi-Ting[1], [1]Department of Entomology, National Chung Hsing University, Taiwan

Abstract: The generalist predator Orius strigicollis (Poppius) (Hemiptera: Anthocoridae) is commonly used in the biological control of minute pests because of its high searching ability and high predation rate. In order to develop a cost-effective mass-rearing medium for O. strigicollis, thirteen meridic diet recipes with different proportions of egg yolk, honey, sucrose, beef extract, yeast extract, milk powder and eggs of Ephestia kuehniella Zeller were evaluated for rearing nymphs and adults of O. strigicollis at 25°C by comparing life table data derived from using the age-stage, two-sex life table. Two artificial diets (10YE+5MK and LarvaC, composed mainly of yeast extract, milk, and egg yolk) proved to be outstanding replacements for the two most commonly used natural prey species (i.e., deutonymphs of the mite Tetranychus urticae Koch and 3-day-old nymphs of Rhopalosiphum padi (L.) aphids). The fecundities of O. strigicollis reared on the two meridic diets were at least 20% above those reared on mites and >7+ times higher than when reared on aphids. Our results demonstrated that the artificial medium 10YE+5MK appears to be an effective substitute for mass rearing of O. strigicollis. The sustainable mass-rearing system was constructed based on life table analysis and rearing costs.

Halyomorpha halys (Hemiptera: Pentatomidae), a new alternative host for egg parasitoid Ooencyrtus kuvanae (Hymenoptera: Encyrtidae)

Authors: Tunca Hilal[1], Venard Marine[2], Tabone Elisabeth[3], Cosic Benjamin[3], Colombel Etty-Ambre[3] and Capelli Mathilde[2], [1]Ankara University, Agriculture Faculty, Dept. of Plant protection, Turkey, [2]Biocontrol laboratory, Experimental Unit of Entomology and Mediterranean Forest from the National Institute of Agronomic Research (INRA), France, [3]INRA, UEFM site Villa Thuret, Laboratoire BioContrôle, France

Abstract: One of the most important egg parasitoids of gypsy moth is Ooencyrtus kuvanae (Howard) (Hymenoptera: Encyrtidae). We have already developed a method to rear O. kuvanae on the laboratory host Philosamia ricini (Danovan) (Lepidoptera: Saturniidae). In order to try to optimize the rearing of this oophagous parasitoid, we used an alternative host Halyomorpha halys (Heteroptera: Pentatomidae). However, H. halys has rapidly become an important pest of several crops in many countries. The study was conducted at the INRAE-PACA Mediterranean Forest and Entomology Unit, Laboratory of Biological Control located in Antibes, France. The laboratory conditions were 25 ± 1°C, 60 ± 5% RH and a photoperiod of 18:6 hr L:D. Halyomorpha halys was successfully reared in our biocontrol laboratory . The reproduction of the parasitoid is arrhenotoky and O. kuvane was reared for more than ten generations on the eggs of H. halys. O. kuvanae could be a candidate for future research as a biological control agent against an important pest, H. halys, and that insect may be a suitable alternative host for rearing of egg parasitoid O kuvanae.

Development of a biocontrol program against the Box Tree Moth Cydalima perspectalis (Walker, 1859)

Authors: Tunca Hilal[1], Venard Marine[2], Tabone Elisabeth[3], Colombel Etty-Ambre[3], Thévenet Jean[2] and Capelli Mathilde[2], [1]Ankara University, Agriculture Faculty, Dept. of Plant protection, Turkey, [2]Biocontrol laboratory, Experimental Unit of Entomology and Mediterranean Forest from the National Institute of Agronomic Research (INRA), France, [3]INRA, UEFM site Villa Thuret, Laboratoire BioContrôle, France, [6]INRA, UEFM site Villa Thuret, Laboratoire BioContrôle, France

Abstract: The Box Tree Moth (BTM), Cydalima perspectalis (Walker, 1859), an invasive East-Asian pest, spread out in Europe and in France since 2008. These Lepidopteran Moths caused serious damages by defoliating box trees. Strategies have to be setting up in order to limit pest impact. In preparation for this control, the aim of the researchers is to evaluate and to develop biocontrol solutions. In Antibes, INRA laboratory goal is to improve moth biology knowledge and to develop a biocontrol strategy with parasites and predators.

With this aim in mind, the team has reared BTM in laboratory (25°C, 75%RH, 16L: 8D). Since 2017, collections were made in situ on damaged box trees of different stages of BTM in order to find indigenous parasites, between May and September, on several sites of five French departments. Then, parasites have to be tested on BTM eggs or larvae to evaluate their efficiency to control the pest. The most present parasite in BTM pupae is a Diptera from the Tachinid family. Some Hymenoptera have also been found.

Other collections of arthropods were made at the same moment in situ by the beating method on box trees with presence of BTM. This study aimed to spot which species consume the moth. For this, the predators' digestive tract content is analyzed to see if there is BTM DNA in it. The most represented orders are the Hemiptera, Hymenoptera (Formicidae), Aranea, Acari, Psocoptera and Colembolla. Each individual is dissected and analyzed by PCR method. The results of this study will be presented.

Box Tree protection against BTM could be effective only by combining several environmental friendly strategies.

Where is the northern limit of the potential range of citrus longhorn beetle (Anoplophora chinensis) in EU based on climate suitability?

Authors: Tuomola Juha[1] and Hannunen Salla[1], [1]Finnish Food Authority

Abstract: To support appropriate use of biosecurity resources, we studied which climatic factors limit the potential range of citrus longhorn beetle (CLB, Anoplophora chinensis) in the EU, and where the northern limit of its potential range is based on these factors. First, we built a Climex model for CLB in Europe. Sensitivity and uncertainty analyses revealed that two Climex parameters, 1) the lower development threshold temperature and 2) the annual growing degree days (GDD) required for establishment, determine the northern limit of the potential range of CLB in the EU. Next, we delineated the northern limit using the annual GDD required for establishment and assuming that CLB needs to complete its life cycle in 3 years. The analysis was done using JRC-MARS climate data for 2000-2020. Our results suggest that the northern limit goes through southern Denmark and Sweden, and south-eastern Estonia. This suggests that CLB surveys, required in the EU legislation, are unlikely to be necessary in areas north from this limit. However, our assessment does not consider the uncertainty in the GDD that CLB needs to complete its life cycle, and that the pest might be able to establish also if its life cycle takes longer than 3 years.

Whiteflies can fool their host plants, but not their parasitoids

Authors: Turlings Ted[1], Zhang Peng-Jun[2] and Yu Xiao-Ping[2], [1]FARCE Laboratory, Institute of Biology, University of Neuchâtel, Switzerland, [2]Zhejiang Provincial Key Laboratory of Biometrology and Inspection & Quarantine, College of Life Sciences, China Jiliang University, Hangzhou, China

Abstract: Herbivorous insects and plant pathogens commonly trigger chemical defenses in plants, which include the release of specific blends of volatiles. Herbivore-induced plant volatiles play a key role in the host searching behavior of many parasitoids. An additional role of inducible volatiles is to alert undamaged plant tissues of incoming attack. When neighboring plants perceive these alert signals, they also prepare themselves in a way that they respond faster and stronger when they themselves are assaulted by the same attacker. This is referred to as defense priming and in the case of chewing insects, priming involves the plant hormone jasmonic acid (JA), but in the case of an attack by a biotrophic pathogen, the enhanced defense responses are usually dependent on salicylic acid (SA).

Phloem-feeding whiteflies appear to manipulate their host plants by making them mobilize SA defense, at the cost of JA-dependent defenses, which makes the plants more suitable for whitefly development. We found that this apparent manipulation extends to the volatiles that are induced by whitefly feeding, which also are similar to volatiles to volatiles released after pathogen attack, for instance the monoterpene ß-myrcene. As a result, neighboring plants that perceive whitefly-induced volatiles wrongly prepare themselves for pathogen attack and become more vulnerable to insects and thus more suitable for the next generation of whiteflies. The specialist parasitoid Encarsia Formosa, which parasutize whitefly nymphs is not misled by this signal manipulation. In greenhouse trials, with various Arabidopsis mutants we showed that the parasitoid uses SA-triggered emission of ß-myrcene for host location. Hence, unlike host plants, the parasitoid is not fooled by the whitefly's signal trickery.

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Sequestration of cucurbitacins by Diabrotica balteata larvae and their protective role against natural enemies

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Abstract: Cucurbitaceae plants produce cucurbitacins, bitter triterpenoids, to protect themselves against various insects and pathogens. Adult banded cucumber beetles (Diabrotica balteata), a common pest of maize and cucurbits, sequester cucurbitacins, presumably as a defensive mechanism against their natural enemies, which might reduce the efficacy of biological control agents. Whether the larvae also sequester and are protected by cucurbitacins is unclear. We profiled cucurbitacin levels in four varieties of cucumber, Cucumis sativus, and in larvae fed on these varieties. Then, we evaluated larval growth and resistance against common biocontrol organisms including insect predators, entomopathogenic nematodes, fungi and bacteria. We found considerable qualitative and quantitative differences in the cucurbitacin levels of the four cucumber varieties. While two varieties were fully impaired in their production, the other two accumulated high levels of cucurbitacins. We also observed that D. balteata larvae sequester and metabolize cucurbitacins, and although the larvae fed extensively on both belowground and aboveground tissues, the sequestered cucurbitacins were mainly derived from belowground tissues. Cucurbitacins had no detrimental effects on larval performance and, surprisingly, did not provide protection against any of the natural enemies evaluated. Our results show that D. balteata larvae can indeed sequester and transform cucurbitacins, but sequestered cucurbitacins do not impact the biocontrol potential of common natural enemies used in biocontrol. Hence, this plant trait should be conserved in plant breeding programs, as it will provide protection against plant pathogens and generalist insects.

Development of microsatellite markers for the endangered butterfly, Luehdorfia japonica (Lepidoptera: Papilionidae)

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Abstract: An endangered butterfly species, Luehdorfia japonica Leech, 1889 (Lepidoptera, Papilionidae), is endemically distributed in the central and western parts of Honshu, Japan. This species inhabits the Satoyama landscape neighboring deciduous forests populated with an evergreen wild ginger species of the genus Asarum sect. Heterotropa on which the larvae feed. However, habitat loss due to the development and the abandonment of regular forest management has caused L. japonica to be classified as “Vulnerable” in the latest version of the Japanese Red List. Here, we developed 17 microsatellite loci for L. japonica based on de novo genome sequence data and observed that 16 loci exhibited polymorphisms in four populations of L. japonica among Osaka, Hyogo, Fukui and Yamanashi in central Honshu, Japan. A principal coordinate analysis based on this genetic information revealed genetic differentiation among geographic populations of L. japonica. The genetic diversity of the Osaka population was found to be lower than that of other populations, suggesting that this population should quickly be targeted for conservation. The developed markers can potentially be used to evaluate temporal changes in genetic diversity in a local population of the species over a period of more than 30 years.

Phylogenetic revision of Bedbugs and their relatives, with an emphasis on their evolution of Traumatic insemination

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Abstract: Bedbugs and their relatives are members of the heteropteran superfamily Cimicoidea that comprise economically important species, ranging from predaceous biocontrol agents to ectoparasitic blood feeders. Beyond this lifestyle diversity, cimicoids are best known for practising traumatic insemination (TI), where the male pierces the abdomen of the female and ejaculate directly into the haemoceol. To better understand the evolution of these sexual characters, a robust phylogeny of the superfamily is needed. Currently, knowledge of the relationships within the Cimicoidea is in its infancy, with several alternative phylogenetic hypotheses. Here we present the first combined morphological and molecular analyses that includes data from next-generation sequencing (NGS), targeting ultra-conserved elements (UCEs) and flanking regions. We aim to optimise TI character evolution in a phylogenetic context to determine their origins and diversification.

Molecular Identification of Insect Vectors for Zoonotic Diseases from District Faisalabad, Pakistan

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Abstract: Correct identification of insect vector species is a very critical step toward the implementation of successful Integrated vector management programs. Based on molecular data the most important insect species involved as vectors for Zoonotic diseases in Pakistan were identified. The precise and accurate identification of such a type of organism is only possible through molecular-based techniques. Morphological species identification in insects at any life stage is very challenging, therefore, DNA barcoding was used as a tool for rapid and accurate species identification in a wide variety of taxa across the globe and parallel studies revealed that DNA barcoding data can be effectively used in resolving taxonomic ambiguities, detection of cryptic diversity, invasion biology, description of new species, etc. A comprehensive survey was carried out for the collection of insects (both adult and immature stages) in district Faisalabad, Pakistan and their DNA was extracted and mitochondrial cytochrome oxidase subunit 1 barcode sequences were used for molecular identification of immature and adult life stages. This preliminary research work opens new frontiers for developing sustainable insect vector management programs for saving the lives of mankind from fatal diseases.

Effect of Different Temperature regimes on the Development, Survival and parasitization rate of Parasitoids of Phyllocnistis citrella (Gracillariidae; Lepidoptera)

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Abstract: We studied the effect of three different temperatures on the development and survival of parasitoids, Citrostichus phyllocnistoides and Cirrospilus ingenuus (Eulophidae; Hymenoptera). The temperature regimes were set to 20, 25 and 30? with 65±2% relative humidity (R.H.) and 16h: 8h (L:D) photoperiod. The longevity of C. phyllocnistoides and C. ingenuus was highest (14.20 and 16.80 days respectively) at 20 ? that gradually decreased with an increase in temperature. The minimum longevity was recorded at the highest temperature (30?) for both parasitoids. The pre-oviposition period was found higher in C. phyllocnistoides and C. ingenuus (2.20 and 2.4 days respectively) at lower temperatures (20?) while this period became shorter by increasing the temperature levels. The oviposition period of both parasitoids was delayed at 20?. The post-oviposition period of C. phyllocnistoides was very short (< 1.5 days) at all the temperatures, as most of the parasitoids died shortly after the final egg-laying. On the other hand, the post-oviposition period of C. ingenuus was prolonged (2.8 days) at 20? while it became shorter at higher temperatures. Maximum fecundity of C. phyllocnistoides (17 eggs) and C. ingenuus (17.6 eggs) was recorded at 25? while minimum fecundity was recoded at 30? (10.60 and 9.4 eggs respectively). The parasitization rate of C. phyllocnistoides and C. ingenuus was highest (42.50 and 29.33% respectively) at 25? while lowest parasitization was recorded at 20? in both parasitoids.

Using dead-end trap plants in the biological control of the spotted-wing drosophila (Drosophila suzukii)

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Abstract: Drosophila suzukii, the spotted-wing Drosophila, is an exotic fruit fly from Asia that has recently invaded Europe as well as North and South America in the past decade. Being highly polyphagous, this fly has quickly become one of the major pests of small fleshy fruit crops such as strawberry, raspberry, blueberry, cherry, blackberry, etc. Females lay their eggs in the flesh of ripening fruits, causing them to rot prematurely. The economic damages to fruit production systems are considerable and increasing since few satisfactory means of controlling its populations are available. Indeed, chemicals are not entirely satisfying and their use tends to be reduced in agricultural practices because of their impact on the environment. Biological control technics have been intensively studied but are currently not effective enough to be used in the field. The use so called “dead-end trap plants” has recently shown promising results in the control of various pests. These plants attract the pest and but do not allow the development of its offspring. Previous studies (Poyet et al 2015) allowed us to identify several potential dead-end trap plant species, among which the firethorn Pyracantha coccinea. In our controlled laboratory conditions, the number of eggs laid by D. suzukii in strawberries was reduced by more than 50% in the presence of fruits of P. coccinea compared to a control where the strawberries were the only fruits available. The number of eggs laid by the pest was up to 2 times higher in the fruits of P. coccinea than in the strawberries, even when the distance between the two plant species increased up to 30 cm. Despite this preference shown by the female D. suzukii, the egg-to-adult survival rate of their offspring in P. coccinea was null, while it was approximately 80% in strawberries. A study of the survival of the larvae in the fruits of P. coccinea showed a significant developmental delay and a death happening before the pupation in the 10 days following the egg-laying. Our work shows the promising potential of P. coccinea as a dead-end trap plant that could be used as an alternative and complementary way to reduce the population of D. suzukii. Borders of P. coccinea could be planted around strawberries field or potted individuals could be positioned within greenhouses to provide an efficient IPM tool against D. suzukii that could be used in combination with chemicals or biological control agents such as predatory arthropods.

Population dynamics of Drosophila suzukii throughout the year in urban environment

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Abstract: The spotted-wing drosophila (SWD) Drosophila suzukii is a polyphagous pest of ripening small fleshy fruit (eg. Strawberries, cherries). It is native to Asia and appeared in Europe in 2008. It is the only Drosophila that causes agricultural damage in Europe and it is considered one of the main biological invasions of the 21st century. For instance, in the French region of Dordogne in 2013, D. suzukii caused the loss of 600 tons of strawberries, estimated to a total of 1.8 M€ and a shortfall of 9000 €/ha in cherry crops (Sicoloy 2016).
Despite much research on this insect, its ecology and the temporality of its life cycle (in natural and urban ecosystems) are still little known. In particular, its use of different urban habitats (eg. parks, river banks, buildings) which are warmer than rural habitats, could help it survive during winter time. The aim of this study was to investigate the ecological niche of SWD in urban areas and gather information on the local, landscape and climatic factors that could explain the variation of this invasive insect populations over time. Fly traps were randomly set in the town of Amiens (Haut-de-France, France) from September 2018 to August 2019 in five different habitat types (town centre, shops and houses, river bank, park, wood). For each trapping session, 75 traps were left for one week, fly species were then determined and biometrics measures were taken on SWD flies (winter/summer morph, size and number of eggs in ovaries). Overall, the two most important species were D. suzukii and D. subobscura, but their relative importance (co-occurrence) varies with the seasons. SWD could favor the presence of decaying fruit available for D. subobscura (facilitation). SWD was more common in the less urbanized sites of the city (wood, park and river). Our study gives new insights into the life cycle of SWD in an urban environment. The summer morph, still present in October, would give way to the winter morph in November / December, which would go dormant up to February and leave its place in May to a new summer generation. Wooded areas close to/in towns could be a winter refuge habitat for winter morphs of SWD which could in the spring move to other urban habitats from where it could then colonize agricultural places where small fruits are produced.

Behavioural plasticity in response to the social environment in a clonal ant

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Abstract: The composition of social groups can have wide-ranging and profound effects on their behaviour and function by influencing, for example, collective decision-making, foraging efficiency, or mating systems. In social insects, the demographic, genetic, and morphological composition of colonies is expected to affect their behaviour and, in turn, fitness. However, measuring the effect of each of these factors is challenging because they inherently co-vary in many systems. To avoid this issue, we analysed the relationship between group composition, division of labour (DOL), and fitness in the clonal raider ant Ooceraea biroi, a queenless, parthenogenetic species that affords maximum control over several important aspects of colony composition. We manipulated each of these factors independently by setting up experimental colonies with controlled variation in genetic composition (single vs. mixed genotypes), demographic composition (single vs. mixed age cohorts), and morphological composition (mixing workers with low and high ovariole numbers). Automated behavioural tracking of individual ants in 120 colonies allowed us to quantify DOL, and we also measured several fitness components. We find clear effects of age, genotype and morphology on individual behaviour, as well as unexpected effects of mixing individuals of different ages, genotypes, or morphology on colony-level behaviour.

By manipulating the main aspects of colony composition that are proposed to affect DOL and measuring their effects on colony performance, we provide a thorough picture of the causes and consequences of DOL in an emergent model system for social behaviour.

Eco-evolutionary dynamics in a real tangled bank: from genomics to field monitoring

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Abstract: Researchers have acknowledged that ecological and evolutionary time-scales can converge. Genetic variation and rapid evolution within populations can shape interspecific interactions, which in turn influence population demography, community dynamics, and ecosystem function. The ecological changes also feed back on evolutionary changes in space and time. With a growing number of experiments showing the interactions between ecology and evolution, the field of eco-evolutionary dynamics is developing rapidly.

Most experimental studies have elucidated impacts of phenotypic variation for ecological processes and patterns in highly standardized, simplified environments, using a common gardening design. However, toward an understanding of eco-evolutionary dynamics in nature, we should take into account that species co-occur in diverse communities in real ecosystems. In other words, the challenge remains to transfer the insights from standardized and simplified experiments to natural conditions, where multiple species directly and indirectly interact with each other and the dynamics are far more complex than those studied previously.

Recent advances in genomics and analytical tools can help to overcome difficulties to identify eco-evolutionary dynamics in complex nature. In this study, we took various approaches to elucidate eco-evolutionary dynamics in a community context in a “real tangled bank”, linking genomics approach, large-scale experiment in semi-natural settings, and spatio-temporal monitoring in the field.

The willow leaf beetle (Plagiodera versicolora), which occurs around a riparian “bank”, has a genetic variation in a foraging trait: specialist- and generalist-type. The specialist-type exclusively feeds on new leaves of willows, while the generalist-type displays non-preferential feeding for leaf-age types. We performed restriction-site associated DNA sequencing and genome-wide association study to develop SNP markers for tracking rapid, ongoing evolution in the foraging trait of the non-model organism. Next, we conducted a large-scale experiment in semi-natural settings to investigate real-time eco-evolutionary feedback between evolution and ecological community in the field. We covered a whole mature tree, inoculating leaf beetle populations. We initially manipulated leaf beetle populations in inoculation as follows: 1) specialist-type, 2) generalist-type, and 3) mixed treatment, based on the frequency of the specific marker allele. Effects of initial beetle treatment significantly reverberated in subsequent community dynamics of insects.

And then we detected rapid evolution of the foraging trait of the leaf beetle in response to the changes in arthropod community structure. Finally, we identified rapid, ongoing evolution of the leaf beetle foraging trait on “a real tangled bank”. Multi-spatial convergent cross mapping provides evidence of the rapid, ongoing evolution in a community context.

Sequence of (mtCO1) gene of Chilo partellus Swinhoe (Lepidoptera: pyralidae) by using molecular tools in Lahore Pakistan

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Abstract: Taxon barcodes using DNA sequencing is the only aspect for an endurable recognition of any biological systems. Molecular studies of an organism are very endorsing in specie diagnosis. Taxonomic knowledge is breaking up due to over reliance on conventional knowledge of identification. Mitochondrial gene Cytochrome C oxidase I (COI) is considered as a major constituent in global identifications of all biological systems. CO1 profiles are constructed temporarily to examine taxa and raw samples of that specific order and phylum. Authentic profiles for CO1 are developed on specie level that will guide and gave knowledge about that specie comprehensively. This knowledge lead towards a good, dependable, gainful analysis of close featured species and one sample is good enough to overcome the recognition crises. Chilo partellus Swinhoe (Lepidoptera: Pyralidae) is one of the major biotic constraints of maize and sorghum production areas of Pakistan. Present study reveals the molecular identification of the mitochondrial cytochrome oxidase (CO1) gene of C. partellus. DNA sequencing and specie identification by using the molecular tools were also parameters of this study. Samples were collected from maize fields in Lahore Pakistan. Molecular characterization of C. partellus was done by using mitochondrial cytochrome oxidase 1 (mtco1) genomic region. The DNA was extracted after performing PCR and sequencing was analyzed from Advance Bioscience International, Pakistan. The 717bp product was obtained, DNA sequencing results identified the specie on molecular level and it showed 100% homology with C. partellus specie present in Kolhapur India upon BLAST search. This homology is also shown with the help of phylogenetic relationship by using different softwares. This is the first report of molecular identification of any lapidopteran in Pakistan. This study reveals the gainful knowledge about molecular advancement. This study also concluded the vitality of CO1 gene is detectable in identification of insect species at molecular level.

Adoption of native parasitoid Habrobracon hebetor Say (Hymenoptera: Braconidae) in biological control of invasive coconut insect pest, Opisina arenosella Walker (Lepidoptera: Oecophoridae)

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Abstract: The coconut black-headed caterpillar (BHC), Opisina arenosella Walker is an invasive insect pest of coconut damaging Thai coconut industry in recent years. Biological control program was then chosen by using 2 BHC's braconid parasitoids including a native parasitoid, Habrobracon hebetor Say and an imported parasitoid, Goniozus nephantidis (Muesebeck). Comparative study on fecundity and parasitization ability of H. hebetor and G. nephantidis on two lepidopterous insect hosts was conducted revealing that the native parasitoid specie could obviously better adopt to its hosts than the imported one either on BHC or rice moth, Corcyra cephalonica Stainton larvae. H. hebetor could be then mass produced on BHC or C. cephalonica depending on availability of its insect hosts. Reproductive study on strains of H. hebetor; Japanese (JPN) and Thai strains proved that the reciprocal crosses of JPN x TOA1 and JPN x TCC4 produced only male's offspring. Economic impact of biological control program of BHC by utilizing H. hebetor in coconut field was finally performed by decreasing of the insect pests from the second months after parasitoid releasing with profit given of 550 USD/acres/year. This indicated that biological control using H. hebetor as biological agent can be well adopted to management program on BHC for sustainable coconut production.

Eliciting plant defenses by exposition to HIPV's: a new sustainable approach to manage agricultural pests

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Abstract: Plants communicate with each other using specific volatiles to warn of attacks and thus are able to activate defense mechanisms that make them more robust against external aggressions. In this research we have activated defense responses of tomato plants by exposing them to two synthetic Herbivore Induced Plant Volatiles (HIPVs). Tomato plants induced by both volatiles turned out to be less attractive to key tomato pests such as Bemisia tabaci and Tuta absoluta and more attractive to natural enemies. Using transcriptomics we were able to identify how exposure to both HIPVs modified the transcripts genes related with defenses. Under semi-field conditions one of the HIVP-mediated activation reduced the subsequent attack of Tetranychus urticae and T. absoluta to less than half. With this knowledge, dispensers to release this HIPV under field conditions were designed and calibrated. The use of these selected dispensers in commercial tomato greenhouses maintained defensively activated plants throughout the crop and reduced the impact of T. absoluta by almost 60%. Our work demonstrates for the first time under real field conditions how the use of HIPVs as elicitors of plant defenses can be successfully integrated as a new biorational and sustainable tool within pest management programs.

Zoophytophagous predator-induced defences restrict infection of plant viruses

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Abstract: Biological control in protected crops has been widely adopted to manage pests. In recent years, the incidence of plant viruses has decreased in crops using zoophytophagous predators. Because these predators induce plant defences with their plant feeding behaviour, we hypothesized these responses could be, in part, responsible for the decrease in virus occurrence. Here, we investigated whether the plant defence activated by two mirid predators can limit infection and multiplication of the Tomato spotted wilt virus (TSWV) in sweet pepper. Our results revealed TSWV accumulation in mirid-punctured plants to be significantly lower when compared to intact plants; this is probably associated with the upregulation of the JA pathway triggered by mirid phytophagy. We demonstrate for the first time how cultivated plants can be more robust against viral diseases when their induced defence system is activated. This novel approach can offer new control strategies for the management of plant diseases.

Contrasting invasion history in two ambrosia beetles of the Xylosandrus genus

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Abstract: Xylosandrus compactus and X. crassiusculus are two ambrosia beetles originating from Southeastern Asia and invasive on several continents.

We used COI and RAD sequencing to disentangle the origin(s) of their non-native populations on the invaded continents and analyse their genetic diversity and pathways within each invaded region.

Our results showed that, despite their ecological and phylogenetic proximity, the two species have different genetic patterns and invasion histories.

For X. compactus, both markers suggested three colonisation events. First, Africa was invaded more than a century ago from Southeastern Asia. Then, the American-Pacific region and Europe were invaded independently from close sources in or near Shanghai, in the mid-XXth century and at the beginning of the XXIst century, respectively.

X. crassiusculus' invasion was more complex. Both markers support the existence of two divergent clusters, mostly allopatric. Cluster 1 independently invaded the Pacific islands and Africa. Cluster 2 invaded the Americas, Europe, Africa and Oceania, with several independent introductions from multiple sources, including through bridgehead scenarios followed by intra-continental dispersion. Hawaii, Papua New-Guinea and South Africa were invaded by both clusters. Our study raises the question of the taxonomical status of the two clusters identified within X. crassiusculus.

OakeyLIFE: Ecological restoration of forest steppe habitats in Hungary benefitting Cucujus cinnaberinus, Bolbelasmus unicornis, Aphydryas maturna (LIFE16 NAT/HU/000599)

Authors: Vadász Csaba[3], Hajagos Gabriella[3], Andrési Dániel[2], Erdélyi Arnold[1], Hadi Barnabás, Peregovits László[4] and Győri Gabriella[1], [1]Hungarian University of Agriculture and Life Sciences, [2]KEFAG Kiskunsági Erdészeti és Faipari Zrt., [3]Kiskunság National Park, [4]PARS Kft.

Abstract: The Peszér-forest Natura2000 site is assigned to the conservation of several species of Community Interest. In the OAKEYLIFE project we aimed to present fine-scale distribution maps; carry out reliable estimations on populations size; determine the local conservation status and restore habitats of particular insect species (Cucujus cinnaberinus, Bolbelasmus unicornis, Aphydryas maturna).

C. cinnaberinus was present in all available/suitable microhabitats, even at isolated forest patches containing little amount of suitable deadwood (both native and alien tree species). By the preparation of dead wood, extent of habitats colonized was increased.

With high effort sampling, B. unicornis was proved to be present at most of those foreststeppic habitats and grasslands, which were never ploughed and were characterized by the mosaics of dry and mesic grassy patches. By increasing the extent of that kind of patches, we targeted to expand the habitats of this species. Within 1-2 years, colonization of restored habitats was not confirmed.

Aiming to increase the extent of habitats of A. maturna, ecological corridors were established, where spawning plants (especially Ligustrum vulgare) secondary host plants and nectar-providing plants were planted/seeded. The occupancy rate of restored habitats was 100%. Also, A. maturna was reintroduced to isolated forests unreachable by spontaneous colonization.

Smart Pheromone Traps for Automatic Remote Monitoring of Genus Osmoderma (Coleoptera, Scarabaeidae, Trichiinae) Species

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Abstract: The present study shows a novel solution to remote Osmoderma species monitoring using smart traps based on the Linux controller and equipped with an IR night vision video camera and moisture/temperature sensor. The traps take photos at regular intervals and record environmental parameters. All data is stored SD cards and via GPRS modem send to the remote repository (database) accessible through the web. Traps work from the autonomous power source and can work approximately 2 months without charging. Smart traps can be used in any area covered by the GPRS or 3G network. The hermit beetles imago activity is highly dependent on environmental conditions; therefore, monitoring of these species with standard pheromone traps often has situations when the placed pheromone traps are empty for a long period, and in such case, time, as well as financial resources, are unnecessarily spent for surveying. Environmental sensors that are integrated into the traps allows obtaining data on the ecological characteristics of Osmoderma species that are essential for the implementation of conservation measures.

The research was supported by European Union LIFE+ programme project "Ecological network for Osmoderma eremita and other species dependent on veteran trees" LIFE16 NAT/LT/000701.

Herbivory in novel native oak stands: Disentangling the effects of landscape context, leaf defences and tree genotype

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Abstract: Forests form a network of patches of woody habitats that can alter the relationships among organisms such as plant-herbivore interactions. However, little is known about how insect herbivores are affected by individual tree scale factors such as functional traits and tree genotype, and by environmental factors such as forest size and isolation. We investigated the effect of landscape and individual scale factors on herbivory in 15 newly established oak forest stands in rural landscapes of SW France. These stands differed in size and isolation. To that aim, we investigated if the patterns of herbivory could be explained by individual scale factors as the leaf defences, tree growth, tree genotype and/or by factors acting at larger scale as stand size and isolation. We found that both scales influenced insect herbivory. The herbivory increases with stand size, but decreases in fast growing trees and trees with high leaf phenolic compounds. The landscape-scale driver stand size has the largest overall effect. Tree genetipe sligly influenced herbivory and leaf defences. Stand isolation did not affect the herbivory. Our study shows that insect herbivory is driven by both landscape and individual tree scales. Overall, our results have important implication for the management of small isolated and expanding forest patches in complex landscapes.

The need for a New IPM, for the management and control of emerging Superpests, as those arthropods (insects and mites), rapidly adapting to Climate Change and Global Warming.

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Abstract: Climate Change represents a major driving force, drastically affecting planet earth, but also many of the human activities and agriculture, is and will be one of the most affected. Several insect pests are exhibiting characteristics of adaptation to Climate Change, that will require a brand-new approach to Pest Management, for us to overcome this new mega-challenge. One of the aspects of Pest Control to be more directly impacted by Climate Change, will certainly be the duration of the Life Cycle of many arthropod pests, which in general trends to be shorter, even under the slightest increases of temperature. A gross estimation of this Adaptive Response of arthropod pests to the increase of temperature, can be that in general, per each degree Celsius augmented, the Life Cycle of many insect pests will be one day shorter. As a result and due to an accumulative response of a pest to Climate Change, the overall Life Cycle can be several days shorter during the crop season. In spite of the apparent severity of this situation, this happens to be only “the tip of the iceberg” of the problem related to Climate Change, due to the following consequences of a shorter life cycle: 1. A significant increase of the potential damage to the host crop, as a result of the higher number of generations of the pest. 2. A more rapid population dynamics of the adaptive pest, which poses more difficulties to achieve its control by biological and chemical insecticides. 3. A minor shortening of the Life Cycle of a host pest, will represent a major challenge for many of the Biological Control Agents and for the Natural Enemies of the pest, which depend on its life cycle and not always are able to adapt to Climate Change at the same pace that the pest does. 4. More generations of the pest per crop season, represent a higher risk of Resistance to insecticides. Due to this situation and maintaining IPM as the Central Paradigm of Pest Control, it is apparent that a New IPM approach, with some important adjustments, might be required for the management of the Global Superpests, as follows: 1. Early Detection of the pests. 2. Emphasis on Preventive Control measures. 3. Priority on Natural Pest Control already existing in the crops. 4. Emphasis on Native Natural Enemies and indigenous entomopathogen species. 5. Use of Bioinsecticides within special-favorable application windows and under specific Action Sub-Thresholds, taking advantage of their Sub-lethal Effects. 6. When necessary, only specific-selective chemical insecticides should be applied under an Action Threshold criteria. 7. Development of Co-formulated mixtures of Biological and Chemical insecticides exhibiting synergism at lower rates and with a longer efficacy and 8. Integration of Technologies for the New IPM, where the additive, synergistic and complementary effects between the technologies applied, will facilitate to achieve an efficient, cost-effective and competitive IPM, on the face of Climate Change globally.

Expressing the Cry10Aa Toxin of Bacillus thuringiensis in transgenic Coffea arabica L. plants: sustainable development for integrated management of the coffee berry borer.

Authors: Valencia-Lozano Eliana[1], Eugenio Ibarra-Rendon Jorge[1], Luis Cabrera Ponce Jose[1] and Angel Gomez-Lim Miguel[1], [1]Center for Research and Advanced Studies of the National Polytechnic Institute, Mexico

Abstract: This report presents an efficient protocol of the stable genetic transformation of coffee plants expressing the Cry10Aa protein of Bacillus thuringiensis. We used Embryogenic cell lines with a high potential of propagation, somatic embryo maturation, and germination. We evaluated Gene expression analysis of cytokinin signaling, homedomains, auxin responsive factor, and the master regulators of somatic embryogenesis genes involved in somatic embryo maturation. We introduced Plasmid pMDC85 containing the cry10Aa gene into a Typica cultivar of C. arabica L. by biobalistic transformation. With this, we achieved a transformation efficiency of 16.7% according to the number of embryogenic aggregates and developed transgenic lines. We proved stable transformation by hygromycin-resistant embryogenic lines, green fluorescent protein (GFP) expression, quantitative analyses of Cry10Aa by mass spectrometry, Western blot, ELISA, and Southern blot analyses. Cry10Aa showed variable expression levels in somatic embryos and the leaf tissue of transgenic plants, ranging from 76% to 90% of coverage of the protein by mass spectrometry and from 3.25 to 13.88 µg/g fresh tissue, with ELISA. qPCR-based 2-??Ct trials revealed high transcription levels of cry10Aa in somatic embryos and leaf tissue. This is the first report about the stable transformation and expression of the Cry10Aa protein in coffee plants with the potential for controlling the coffee berry borer.

Wolbachia in sympatric parasitoid cryptic species

Authors: Valerio Federica[1], Martel Cornelia, Stefanescu Constanti, van Nouhuys Saskya, Kankare Maaria and Duplouy Anne, [1]University of Helsinki

Abstract: Identifying the mechanisms supporting the reproductive isolation between sympatric species often remains challenging, as it may be induced by multiple factors other than geographical distance.

Endosymbiotic bacteria can lead to reproductive isolation between conspecific lineages due to the infection inducing either post-mating incompatibility or pre-mating avoidance. Wolbachia, one of the most common endosymbiotic bacteria of insects worldwide, manipulates its host reproductive system or other life-histories towards its benefit to spread in the host population. Based on this, Wolbachia-induced phenotypes can support partial to complete reproductive isolation between host lineages up to speciation.

The genus Cotesia (Hymenoptera, Braconidae) includes over 1000 species and even more cryptic species, making it one of the most diverse groups of social parasitoids. In North-eastern Spain, several species of Cotesia occur in sympatry and parasitize Melitaeini butterfly species. Previous phylogeographic studies have suggested that local resource partitioning, competitive exclusion, as well as host-specialization may each have contributed to species radiation within this unique Spanish parasitoid community. However, the mechanisms by which gene flow has been restricted remain unclear.

Here, we investigated the biogeography of Wolbachia across European populations of several Cotesia species, including the North-eastern Spanish region. We characterized the mitochondrial diversity associated with infected and uninfected specimens. Moreover, we screened for Wolbachia infection all publicly available Cotesia whole genome sequencing data to gain insights into Wolbachia strain diversity in this genus. Our results proposed that different strains of the symbiotic bacterium might be key-players in the reproductive isolation and radiation of these Cotesia cryptic species.

Towards mass-rearing of Nsenene (Ruspolia differens) in Uganda

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Abstract: Ruspolia differens (Orthoptera: Tettigoniidae), Nsenene, is one of the most consumed insects in East Africa, with high nutritional and cultural value and high economic potential especially in the Lake Victoria region. Currently, they are harvested with powerful lights from the natural populations during the two annual swarming seasons. In order to prevent overexploitation of the natural populations, and to improve food and nutrition security in the region, methods allowing mass-rearing of this species are urgently needed. Mass-rearing could provide a sustainable and a more reliable way to produce valuable proteins and fatty acids for local communities in the future and could bring income to local farmers.

To achieve methods for mass-rearing, understanding on species' basic biology and ecology, optimal feeds, chemical composition, and optimal rearing conditions are essential. We aimed to shed light on these in our Academy of Finland -funded project (2015–2019) entitled "Developing mass rearing technology for the highly valued edible grasshopper, Ruspolia differens". This presentation summarizes the findings of our project.

We showed that it is possible to rear Nsenene successfully in laboratory for several consecutive generations, which means that mass-rearing in captivity is possible in controlled conditions. Nsenene can be reared from newly hatched nymphs to adult in relatively short time (49 d), on artificial diets, and in relatively high densities. The optimal rearing temperature is 28-30°C. Slightly lower temperatures, which slow down the development rate, can be used to synchronise the development of different batches of nymphs in mass-rearing conditions. With rearing densities =36 nymphs per liter, a survival rate of 60% can be expected up to 28 days. The weight of individuals can be modified with rearing duration, so that by rearing the insect up to a week after final moult, up to 50% increase in weight can be achieved. A promising egg-laying medium using folded plastic cloth was developed, enabling large-scale production of eggs in the future.

We found that Nsenene can develop and mature on highly variable feeds including both its natural host plants and artificial feeds. It benefits from diet mixing; more diversified diets result in shorter development time and greater adult fresh weight and female fecundity compared to the single diet or less diversified diets. Also feeds including by-product protein sources from food-industry can sustain its development – this information can be used in future to increase the sustainability of rearing efforts. Finally, the dietary fatty acids alter the content and composition of Nsenene fatty acids. This means that its nutritional value for human can be improved by adding a source of omega-3 fatty acids and proteins in its feeds. We emphasize that there is now enough information on the species' basic biology to start experimenting with mass-rearing of R. differens.

Evolution of life history traits in response to artificial selection for virulence and non virulence in a Drosophilaparasitoid, Asobara tabida

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Abstract: Co-evolution of host–parasitoid interactions is determined by the costs of hostresistance, which received empirical evidence, and the costs of parasitoid virulence, whichhave been mostly hypothesized. Asobara tabida is a parasitoid, which mainly parasitizesDrosophila melanogaster and D. subobscura, the first species being able to resist tothe parasitoid development while the second species is not. To parasitize resistant hosts,including D. melanogaster, A. tabida develops sticky eggs, which prevent encapsulation,but this virulence mechanismmay be costly. Interindividual and interpopulation variation inthe proportion of sticky eggs respectively allowed us to (i) artificially select and comparelife-history traits of a virulent and a nonvirulent laboratorystrain, and (ii) compare avirulent and a nonvirulent field strain, to investigate the hypothetical costs of virulence.We observed strong differences between the 2 laboratory strains. The nonvirulent straininvested fewer resources in reproduction and walked less than the virulent one but livedlonger. Concerning the field strains, we observed that the nonvirulent strain had largerwings while the virulent one walked more and faster. All together, our results suggest thatvirulence may not always be costly, but rather that different life histories associated withdifferent levels of virulence may coexist at both intra-and interpopulation levels.

Global environmental change may benefit Conservation biological control in temperate-climate areas

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Abstract: The increase of mean temperatures during winter caused by global warming in temperate climatic regions has induced change in organism phenology and may lead to interactions within and between trophic levels. In agro-ecosystems of the West part of France, aphids and their natural enemies are reproducing during the whole winter. These agro-ecosystems may benefit from a change in plant phenology, such as flowering plants often used in Conservation biological control programs. We investigated the consequences of flowering plants in winter to assess if they may constitute favourable habitats to biological control agents and increase their pressure on aphid pest populations in adjacent cereal crops. We hypothesised that (i) aphid parasitism would increase close to sown flowering cover rather than close to spontaneous grassy margins (SGM) by providing food resources or alternative hosts and (ii) that sown flowering strips would better promote ground predator activity than SGMs, by providing shelters with better micro-climatic conditions. Higher aphid parasitism has been observed close to flowering cultivated plants and the density of activity of ground predators was higher within sown flowering strips. The results suggested that the winter period should constitute the target period for conservation biological control programs under changing environmental conditions.

When additional floral resources fail to enhance aphid control by parasitoids: food web structure reveals increased intraguild competition and predation

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Abstract: Understanding which factors affect ecological community structure is essential to predict resultant ecosystem functioning, but remains a key challenge. For instance, biological control of herbivores by predators and parasitoids is a major ecosystem function, but how it is impacted by community structure modifications remains poorly understood. While trophic theory predicts that increased plant diversity will enhance diversity and abundance of higher trophic levels and increase top down control on herbivores, field results are not often consistent with those predictions. Studying community-level foodwebs could enlight the mechanisms involved in resultant top down effect in multi-natural enemy systems. For instance, it can be expected that increased plant resource provision will increase negative interactions among natural enemies, such as intraguild competition and predation. In that case, top down effect on herbivores may be limited.

In Brittany, intercropping legume plants within cereal fields is a common agroecological practice which provides an interesting model to study the effect of addition of floral resources on cereal aphid-parasitoid-hyperparasitoid foodweb structure. Legume plants provide carbohydrate resources (here, Vicia faba extra-floral nectar) and alternative hosts (such as the pea aphid Acyrthosiphon pisum) which can be used by generalist parasitoids. We conducted a two-year field studycomparing aphid parasitism rate and foodweb structure in cereal monocultures and cereals intercropped with legumes (mixed crops). Generalist parasitoids are more enhanced by additional floral resources than specialists, which probably resulted in increased intraguild competition. Moreover, hyperparasitoids also benefited from the increase in floral resources and the parasitoid community change in mixed crops. The resulting parasitism rate was higher in monocultural crops at the end of the season compared to mixed crops, showing no benefit of additional floral resources on aphid control.

While increasing resource provision is generally assumed to enhance herbivore control, our study showed that it could in fact disrupt top down effect due to a modification of the foodweb structure and the increase of intraguild interactions. Such effects may depend on the studied system, thus enlighting the need to deepen our understanding of additional resources on four-level trophic foodwebs to improve biological control methods.

Are you searching for insects? Here is where to look! - The effect of land use intensity on insect biomass

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Abstract: Insect abundance and diversity is declining across the globe. One major contributor to the decline is anthropogenic land use causing degradation of natural areas and essential insect habitats. There is currently a shortage of studies using a standardized sampling strategy across several land use categories, and hence the understanding of drivers that affect insect biomass distributions across multiple land use intensities remain unclear.

In this study, 177 citizen scientists sampled flying insects with rooftop mounted car nets on 278 routes in Denmark and Germany in June 2018. The 462 bulk insect samples were sorted in two size fractions and dry weight was used as a measure of total insect biomass. We incorporated land use categories as explanatory variables for variation in insect biomass, abundance and size structure using linear mixed-effect models lmer and lme (R packages lme4 and nlme). We included fine-scale land use metrics along a buffer zone of each route and accounted for sampling time, weather and spatial structure. Thus, we tested the hypothesis that insect biomass is lower along routes with increased land use intensity e.g. intensive agriculture or urban areas, and higher along heterogeneous and extensive land use types, e.g. forest. The same samples are currently processed with a DNA metabarcoding approach to obtain taxonomy data.

How to survive in the dark - Interactions of root flies with host plant defence compounds and their gut microbiome

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Abstract: Using a plant as a diet source is a major challenge for insects. Next to hard digestible particles, such as lignin, insects are often confronted with toxic plant defence compounds. The agricultural important crop family Brassicaceae evolved a defence system containing glucosinolates (GSLs) and their breakdown products the isothiocyanates (ITCs). Several insects have adapted to this defence system, such as the cabbage (Delia radicum) and turnip root fly (D. floralis). Both species are specialists and frequent pests on Brassicaceae roots. It is currently unknown how these larvae handle the Brassicaceae defence system. Our aim is to disentangle detoxification mechanisms of the GSL-ITC system in both belowground herbivores. We experimentally assess the effect of GLSs and ITCs on Delia performance. Second, we tested the breakdown of GSLs and ITCs in larvae using HPLC-UV and GC-MS. In addition, we compared gut microbial communities in both species using 16S barcoding and their role in detoxification processes. We found that ITC differently affected fly performance in both species. However, both larvae breakdown GSLs as well as ITCs. Although feeding the same, the gut microbial community differed in both species. Despite specialized on their host plant defence system, larvae suffer from defence compounds, even when they developed multiple breakdown pathways. Understanding the detoxification process of these pests is a first step toward the development of sustainable resistance.

The effects of low-dose exposure to Cry proteins on Fall armyworm and its practical implications for IRM in Africa

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Abstract: The planting of Bt maize is limited to only a few countries in Africa. In a response to mitigate fall armyworm impact, this expected to increase in the near future. FAW rapidly evolves resistance to Cry toxins, which is exacerbated by exposure to low-dose events, such as those that will be deployed in Africa. We report on effects of low-dose exposure to Bt maize on life history parameters and flight ability of moths reared for eight generations on Bt/non-Bt maize. Larval survival on Cry1Ab and Cry1A.105 + Cry2Ab maize ranged between 16 and 95% over eight generations. F1-larval survival on two-toxin maize was 19% and 82% for the F7-generation. Larval and pupal periods were delayed on Bt maize, resulting in poor synchronization of moth emergence patterns between Bt and refuge plantings. Moth flight ability was reduced and only between 29 – 45% of moths reared on two-toxin maize was able to fly out of a 40 cm high cylinder, compared to 88% for the non-Bt treatment. Limited capacity to fly may limit random mating and contribute to selection pressure, reducing the effect of the high-dose / refuge strategy on smallholder fields where several other IRM challenges also exist.

Vector competence of Belgian Anopheles plumbeus and Culex pipiens mosquitoes for Japanese encephalitis virus

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Abstract: Japanese encephalitis virus (JEV) is a mosquito-borne virus that is considered an emerging disease. It is therefore important to know if indigenous mosquitoes would be able to spread JEV upon introduction in a new area. Here we determined the vector competence of Belgian field-collected Anopheles plumbeus and Culex pipiens mosquitoes for JEV. Mosquitoes were orally exposed to an infectious blood meal containing $10^{6'39}$ TCID50/ml JEV (Nakayama strain), followed by a 14-day incubation period at 25°C. Infection and dissemination of JEV was investigated by detection of viral RNA by qRT-PCR in the abdomen and legs/wings/heads, respectively. In Culex pipiens, infection and dissemination rates of 34.7 and 21.3 % were found by qPCR while this was 13.8 and 13.8 % for Anopheles plumbeus. The majority of qPCR positive samples were confirmed positive in virus isolation. These findings suggest the existence of a stronger midgut infection barrier for JEV in Anopheles plumbeus than in Culex pipiens. The latter species also seems to have a midgut escape barrier for JEV. Saliva is currently being tested to determine the transmission ratio and the effect of temperature on the vector competence will be studied in the coming months.

What is the likelihood of entry of Navel orangeworm (Amyelois transitella) into European Union?

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Abstract: The Navel orangeworm (Amyelois transitella) (Lepidoptera: Pyralidae) is a polyphagous and multivoline pest in Americas, known to occur on nuts, so called ‘mummies’ (walnuts, almonds and pistachios), citrus, plums and other fruits. As a potential threat to EU nut and fruit production the European Commission requested the European Food Safety Authority (EFSA) to provide a quantitative risk assessment. The likelihood of the pest’s entry into EU27 was investigated following EFSA guidance on quantitative risk assessment. Understanding pest biology, crop phenology and industry practices is crucial when building a pathway model to assess the likelihood of pest entry. Taking into consideration pre-and post-harvest industry practices to minimise infestations for the export, we describe how the EFSA process integrates information and data on pest biology with agricultural practices to apply expert knowledge elicitation to quantitatively evaluate the likelihood of Amyelois transitella entering EU27 via the import of host nuts and fruits. Further work on establishment, spread and potential impact in the EU is planned together with the identification and evaluation of risk reduction options.

The European Commission will use the results of this assessment to make future decisions regarding the regulatory status of Amyelois trasnitella in EU27.

Fitness consequences of timing asynchrony at the individual and population level in the winter moth

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Abstract: Climate change can severely impact species that depend on ephemeral resources because of induced phenological asynchrony: a mismatch between consumer and resource seasonal timing. In the winter moth, climate change induced asynchrony increased selection on the temperature sensitivity of egg development rate. However, we know little about the fine-scale fitness consequences of asynchrony at the individual level and how this affects population dynamics in the winter moth. We determined the fitness curve of timing of egg hatching relative to timing of oak budburst in a feeding experiment and combined this with our long-term data series on relative abundances of four Dutch populations to model the effect of asynchrony on population dynamics. Already one day of mismatch greatly increased mortality rates of freshly hatched caterpillars. This was reflected in our population models in which we found a significant effect of timing mismatch on population growth rates. These severe fitness consequences of asynchrony have driven the rapid genetic adaptation to climate change in the winter moth in the past 20 years. We are now using whole genome sequencing of historic winter moth samples to gain insight into how the selection pressure strength and population dynamics we investigated here have impacted the speed of adaptation in the wild.

Dispersal, population development and symptom development of A. lycopersici and relationship between mite density, visual symptoms and yield loss in a Western European protected tomato crop

Authors: Van Heghe Benedikte[2], Bosmans Lien[2], Vervaet Lore[1], De Groote Stefanie[4], Aussems Evelien[3], De Vis Raf[3], De Clercq Patrick[1] and Van Leeuwen Thomas[1], [1]Laboratory of Agrozoology, Ghent University, Ghent, Belgium., [2]Research Centre Hoogstraten, Meerle, Belgium., [3]Research Station for Vegetable Production, Sint-Katelijne-Waver, Belgium., [4]Vegetable Research Centre, Kruishoutem, Belgium.

Abstract: Abstract as an attached file.

Managing the Russian invasion in Australia…

Authors: van Helden Maarten[3], Pirtle Elia[1], Al-Jawahiri Farah[2], Maino James[1], Lye Jess[1] and Heddle Thomas[2], [1]Cesar, Australia, [2]South Australian Research and Development Institute, Australia, [3]South Australian Research and Development Institute, University of Adelaide, Australia

Abstract: Russian wheat aphid, Diuraphis noxia Kurdjumov (Hemiptera: Aphididae) was considered a serious biosecurity risk to Australian grains since the 1980s (Hughes & Maywald 1990). When RWA was first detected in South Australia in May 2016, it had already spread over a large area. It is now (Jan. 2020) established across South Australia, Victoria, Tasmania and most of New South Wales. The front moves hundreds of km northwards each year, and is expected to reach Queensland soon. Western Australia seems protected by the arid Nullarbor Plain. Climex modelling shows that RWA should be able to persist in all cereal-growing regions of Australia (Avila et al 2018).

Since damage was expected, emergency permits were issued and curative insecticide sprays (2016 season) were applied. From then on, neonicotinoid seed treatments were adopted widely (estimated 40% increase in imidacloprid use nationwide).

Subsequent research, incorporating advice from overseas experts (F. Peairs, J. Vitou), focussed on biotype confirmation, varietal susceptibility, population growth, natural enemies, crop damage and yield loss.

Screening RWA populations against cereals with Dn-genes showed that Australian RWA are nearly identical to the American RWA1 biotype. There are currently no commercial cereal varieties with resistance to RWAau1 available in Australia.

The most recent GRDC investment, undertaken by SARDI and cesar, aims to assess the regional pressure of RWA and impact on yield, to provide risk estimates, thresholds and IPM options.

Field observations (2016) and experiments (2016-2020) looked into RWA dynamics and yield loss in relation to cereal commodity, sowing date and regional risks. Over the last (dry) years, regional RWA pressure was low. Infestation levels were higher when crops were sown very early (April) or late (July), when RWA migrate. RWA summer survival is linked to the green bridge: native and introduced grasses and volunteer cereals, requiring summer rainfall.

Inoculated trials show higher RWA development in crops experiencing severe drought stress, and yield loss was observed. In higher rainfall environments, even quite severe infestations of >15% of tillers with RWA did not result in yield loss. Elimination of high infestations at GS35-40 reduced the risk of yield loss. Intervention thresholds are being finalised.

Overall, the risk posed by RWA to cereal production in Australia seems low. Increased risk might occur in low rainfall areas, in years with high summer rainfall. For lower risk situations, the use of prophylactic seed treatments is not warranted, an IPM approach seems more sustainable: Symptom expression is very clear, quantifying RWA through scouting easy and (if needed) an insecticide application before GS40 will avoid yield loss.

Native and invasive wireworm pests of Canada: Increasing threats, and increasing options for their management

Authors: van Herk Wim[1], Vernon Bob[2] and Mitchell Terisha[1], [1]Agriculture and Agri-Food Canada, Canada, [2]Sentinel IPM Consulting, Canada

Abstract: Three invasive Agriotes click beetle species have become significant pests of vegetables and field crops on the west coast of British Columbia and in eastern Canada since the early 1900s. Pest populations of these species are currently increasing and they are continuing to spread to new areas. Populations of native Selatosomus, Limonius, and Hypnoidus pest species have also increased significantly over the last 20 years, and currently cause considerable crop damage in central Canada. However, with the increasing threats these developments pose for crop production, a suite of promising new chemical and semiochemical control approaches are offering hope.

The nutritive value of black soldier fly larvae reared on common organic waste streams in Kenya

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Abstract: In Africa, livestock production currently accounts for about 30% of the gross value of agricultural production. However, production is struggling to keep up with the demands of expanding human populations, the rise in urbanization and the associated shifts in diet habits. High costs of feed prevent the livestock sector from thriving and to meet the rising demand. Insects have been identified as potential alternatives to the conventionally used protein sources in livestock feed due to their rich nutrients content and the fact that they can be reared on organic side streams. Substrates derived from organic by-products are suitable for industrial large-scale production of insect meal. Thus, a holistic comparison of the nutritive value of Black Soldier Fly larvae (BSFL) reared on three different organic substrates, i.e. chicken manure (CM), brewers' spent grain (SG) and kitchen waste (KW), was conducted. BSFL samples reared on every substrate were collected for chemical analysis after the feeding process. Five-hundred (500) neonatal BSFL were placed in 23 × 15 cm metallic trays on the respective substrates for a period of 3–4 weeks at 28 ± 2 °C and 65 ± 5% relative humidity. The larvae were harvested when the prepupal stage was reached using a 5 mm mesh size sieve. A sample of 200 grams prepupae was taken from each replicate and pooled for every substrate and then frozen at -20 °C for chemical analysis. Samples of BSFL and substrates were analyzed for dry matter (DM), crude protein (CP), ether extracts (EE), ash, acid detergent fibre (ADF), neutral detergent fibre (NDF), amino acids (AA), fatty acids (FA), vitamins, flavonoids, minerals and aflatoxins. The data were then subjected to analysis of variance (ANOVA) using general linear model procedure. BSFL differed in terms of nutrient composition depending on the organic substrates they were reared on. CP, EE, minerals, amino acids, ADF and NDF but not vitamins were affected by the different rearing substrates. BSFL fed on different substrates exhibited different accumulation patterns of minerals, with CM resulting in the largest turnover of minerals. Low concentrations of heavy metals (cadmium and lead) were detected in the BSFL, but no traces of aflatoxins were found. In conclusion, it is possible to take advantage of the readily available organic waste streams in Kenya to produce nutrient-rich BSFL-derived feed.

Widespread loss of formerly dominant insect species and global biodiversity change

Authors: van Klink Roel, iDiv, Germany

Abstract: Widespread declines of terrestrial insect abundances are now well established. What remains unclear, however, is whether other aspects of biodiversity, such as species numbers, evenness and relative abundances, are also changing. We compiled long-term insect monitoring data to study global patterns of biodiversity change. We found that despite declines of terrestrial insect abundances, there is no average decline in species numbers, and no change in evenness. This can be explained by declines of dominant species and high rates of species replacement. In the freshwater realm, we found, apart from increases in abundance, strong increases in species numbers, and an increase in evenness. This could be explained by increases in the number of rare and intermediately common species, whereas the formerly most dominant species declined. The loss of formerly common species has probably already led to the widespread rewiring of food webs, and a change in ecosystem functioning and services, given the ecological importance of abundant species.

Essential and useless ecological knowledge for applied biological control

Authors: van Lenteren Joop, Wageningen University, Netherlands

Abstract: Ecology and biological control are intensely interconnected. Population regulation theory provides an understanding of the working mechanism of natural, inoculative and conservation biocontrol. Information about multitrophic relationships show intricate networks between soil biota, plants, herbivores, their natural enemies and organisms at the fourth trophic level. Ecological insight has helped in finding and evaluating natural enemies for specific types of biocontrol. However, ecologists have also proposed the necessity of certain research approaches for biocontrol that have not contributed to progress and even delayed implementation of biocontrol projects. I will illustrate this with examples related to studies on functional response, attack rate, handling time, host discrimination, associative learning, chemical ecology, etc. Biocontrol researchers would appreciate help from ecologists, for example in the development of reliable and quantifiable criteria to quickly exclude biocontrol agents that might not be effective or cause unacceptable negative effects. Other areas where help would be welcome are the design of quality control, mass production, storage and release methods for natural enemies, a better understanding of host plant resistance to pests and its effect on biocontrol agents etc. etc.

Mapping of resistance traits in diverse arthropods by bulked segregant analysis

Authors: Van Leeuwen Thomas[3], Dermauw Wannes[4], vandenhole Marilou[3], Kurlovs Andre[2], Wybouw Nicky[2], M. Clark Richard[5] and Snoeck Simon[1], [1]Department of Biology, University of Washington, United States, [2]Department of Plants and Crops, Ghent University, Belgium, [3]Department of Plants and Crops, Ghent University, Belgium, [4]Flanders research institute for Agriculture, Fisheries and Food (ILVO), Belgium, [5]School of Biological Sciences, University of Utah, United States

Abstract: The development of resistance to insecticides and acaricides is a major problem in agriculture. It is therefore of crucial importance to understand the mechanisms of resistance. However, these mechanisms of adaptation can be complex. In the past, some major discoveries were made via the genetic tools in model organisms such as Drosophila. As recently more and more good-quality genomes are becoming available and high-throughput short-read sequencing is becoming very cost effective, we present here a population-level Bulked Segregant Analysis (BSA) that can be used to map resistance genes in high resolution and uncover the genetic architecture of both monogenic and polygenic trait variation. Another advantage of population-level BSA is that it can be applied to a wide variety of arthropod species with life histories or physical attributes (as for micro-insects) that render genetic mapping with other methods impractical. Although this technique can be used for any sexual reproducing insect that can easily be crossed and maintained in high population size in the laboratory, we present here the work conducted with the spider mite Tetranychus urticae, an important crop pest. We give an overview of how this technique has resolved a number of complex cases of resistance against some of the major classes of acaricides. These advanced BSA experimental designs can thus resolve causal loci to narrow genomic intervals, facilitating follow-up investigations for a wide variety of arthropod species.

Potential of iolinid predatory mites for the control of tomato russet mite, Aculops lycopersici, in protected tomato cultivation

Authors: Van Leeuwen Thomas[1], De Clercq Patrick[3], Vervaet Lore[2], Vanlommel Wendy[4], Reybroeck Eva[5], Parapurath Gokul[6], Bosmans Lien[4], De Vis Raf[5] and van Havermaet Robin[5], [1]Department of Plants and Crops, Ghent University, Belgium, [2]Laboratory of Agrozoology, Department of Crop Protection, Ghent University, Belgium, [3]Laboratory of Agrozoology, Department of Plants and Crops, Belgium, [4]Research Centre Hoogstraten, Belgium, [5]Research Station for Vegetable Production, Belgium, [6]University of Padova, Italy

Abstract: The tomato russet mite (TRM), Aculops lycopersici (Tryon, 1917), is a key pest in tomato crops and occurs in all countries where tomatoes and related solanaceous crops are grown. The tomato russet mite can be highly destructive to the tomato crop and can cause significant yield losses. Early detection of this pest is difficult due to its minute size and the time-gap between infestation and the first symptoms. TRM is very small and moves easily on the leaf and stem surface, thereby not hindered by the (glandular) trichomes. These glandular trichomes, however, hamper all of the commercially available natural enemies of TRM. Moreover, low efficacy of acaricides against TRM has been reported. Actually, growers control TRM by repetitive sulphur sprayings but this has a negative effect on other biocontrol systems. Lack of successful control sparked a search for new natural enemies that can efficiently feed and reproduce on TRM and that are not hindered by the trichomes of the tomato plant. A survey for potential predators in Europe yielded two iolinid predatory mites. Laboratory experiments were done to compare their predation potential on different life stages of the pest. The value of pollen as a supplementary food for these predators was also tested, as well as its effect on their predation activity.

The contribution to adaptation of cis versus trans gene regulation in a polyphagous arthropod, the spider mite Tetranychus urticae.

Authors: Van Leeuwen Thomas[1], vandenhole Marilou[1], Kurlovs Andre[1], de Beer Berdien[1] and M. Clark Richard[2], [1]Department of Plants and Crops, Ghent University, Belgium, [2]School of Biological Sciences, University of Utah, United States

Abstract: The spider mite Tetranychus urticae is a global pest known to feed on 1,100 different hosts from 140 plant families, including most major crops. Due to a very strong adaptation potential, it is one of the most notorious organisms for insecticide/acaricide resistance development.

We have previously shown how spider mites can mount a strong transcriptional response when challenged with a novel hosts, or after adaptation to acaricides. However, gene regulatory mechanisms underlying this plasticity and adaptation potential are not well studied. We have generated a large collection of fully inbred and resistant mite strains and describe the sampled genomic variation in the context of selection and adaptation. Using dedicated crosses between these inbred lines, we have started to study gene regulation mechanisms on a genome wide scale and unravel the global architecture of gene expression variation in a generalist herbivore.

Development and impact of Environmental Risk Assessments on the use of Biological Control

Authors: van Lenteren Joop C., Wageningen University

Abstract: During the first 100 years of biological control of arthropod pests, natural enemies usually did not undergo environmental risk analyses. This changed in the 1980s after concern was expressed about non-target effects caused by import and release of exotic biocontrol agents. Non-target effect concern was amplified when many amateurs started to mass produce and market new natural enemies as a result of the strongly increasing popularity of augmentative biocontrol,. The development of environmental risk assessment procedures in Europe started with the design of a code of conduct for the import and release of exotic biological control agents in the 1990s. This was followed by devising specific environmental risk assessment protocols that initially were rather complicated, but were refined and simplified, resulting in a comprehensive, stepwise method. Worldwide, protocols for regulation of import and release of exotic biocontrol agents are very different and seriously limit implementation of biocontrol.

Introduction, history of natural enemy evaluation, current challenges and proposal for ecological evaluation criteria for candidate selection.

Authors: van Lenteren Joop C., Wageningen University

Abstract: Ecology and biological control are intensely interconnected. Population regulation theory provides an understanding of the working mechanism of natural, importation (=classical) and conservation biocontrol. Information about multitrophic relationships show intricate networks between soil biota, plants, herbivores, their natural enemies and organisms at the fourth trophic level. Ecological insight has helped in finding and evaluating natural enemies for specific types of biocontrol. However, ecologists have also proposed the necessity of certain research approaches for biocontrol that have not contributed to progress and even delayed implementation of biocontrol projects. I will illustrate this with examples related to studies on functional response, attack rate, handling time, host discrimination, associative learning, chemical ecology, etc. Biocontrol researchers would appreciate help from ecologists, for example in the development of reliable and quantifiable criteria to quickly exclude biocontrol agents that might not be effective or cause unacceptable negative effects. Other areas where help would be welcome are the design of quality control, mass production, storage and release methods for natural enemies, a better understanding of host plant resistance to pests and its effect on biocontrol agents etc.

Exploring the potential of microbial volatiles to enhance biological control of pest insects

Authors: van Neerbos Francine[1], Jacquemyn Hans[2] and Lievens Bart[1], [1]Laboratory for PME&BIM KU Leuven, [2]Laboratory of Plant Conservation and Population Biology KU Leuven

Abstract: Biological control using parasitoids has become an important method of pest management. However, its efficacy may be hampered by parasitoid dispersal from the crop and the occurrence of hyperparasitoids. This low efficacy may be addressed by employing an infochemical-based approach. A growing body of research has identified volatile organic compounds (VOCs) emitted by microorganisms to be an interesting source of these infochemicals. However, to date little is known about the olfactory response to microbial VOCs within and across different trophic levels, and whether they can be exploited as a source to enhance biological control. Here, we used Y-tube bioassays to assess how bacterial VOCs (bVOCs) affect the olfactory response of the aphid-parasitoid-hyperparasitoid food web. Next, using chemical analyses of the bVOC blends and correlation analysis with insect behavior, we identified interesting compounds and created synthetic mixtures which were both evaluated in Y-tubes. Results revealed that linalool was repellent for the hyperparasitoid Dendrocerus aphidum but repellent for the parasitoid Aphidius colemani. Furthermore, we found that a blend of styrene and benzaldehyde had the opposite effect. In subsequent greenhouse experiments, the styrene and benzaldehyde blend was evaluated in different doses and over different distances to attract parasitoids and repel hyperparasitoids.

Luring hyperparasitoids away from their parasitoid host in greenhouses

Authors: van Neerbos Francine, CMPG laboratory of PME&BIM KULeuven, Netherlands

Abstract: Parasitoids are among the best biocontrol agents of aphids but their efficacy may be reduced when hyperparasitoids are present. Hyperparasitoids are natural enemies of parasitoids and are thus in the fourth trophic level. They are often reported to kill virtually all parasitoids of aphids in greenhouse horticulture, impairing sustainable pest management of indoor-grown vegetables. In sweet pepper greenhouses in The Netherlands, a diversity of hyperparasitoids occurs, and they may kill up to 100% of aphid mummies, preventing population establishment of primary parasitoids. In this presentation, I introduce the possibility of managing aphid hyperparasitoids by developing lures (baits) that divert hyperparasitoids away from their beneficial parasitoid host. This strategy requires an understanding of the cues that hyperparasitoids use to find their host. Experimental data suggest that the hyperparasitoid Dendrocerus aphidum may use cues from plants but host-derived cues (the aphid mummy) are most attractive. I will discuss the opportunities and challenges of applying this knowledge to develop a sustainable management strategy for hyperparasitoids.

Host plant availability drives the spatio-temporal dynamics of interacting metapopulations across a fragmented landscape

Authors: van Nouhuys Saskya[2], H. Opedal Øystein[3], Laine Anna-Liisa[5], Saastamoinen Marjo[1], Ovaskainen Otso[4], [1]Helsinki Life Science Institute, University of Helsinki, Finland, [2]Indian Institute of Science, United States, [3]Lund University University of Helsinki, Sweden, [4]University of Helsinki Norwegian University of Science and Technology, Finland, [5]University of Zürich, Switzerland; University of Helsinki, Finland

Abstract: The dynamics of ecological communities are likely to depend on species interactions within and among trophic levels. The Glanville Fritillary butterfly, its specialist parasitoid wasp Cotesia melitaearum, and the specialist fungal pathogen Podosphaera plantaginis infecting Plantago lanceolata, a host plant of the Glanville Fritillary, live as metapopulations in Åland, Finland. These species are known to interact locally directly and indirectly. We assessed the influence of these interactions on their spatio-temporal dynamics. To do this we analysed a 19-year time-series of each species across a network of more than 4000 habitat patches. We first included the presence of potentially interacting species in the previous year as a predictor in models describing the local colonisation and extinction rates of each species. Then, we performed simulations of metacommunity dynamics based on models trained for each species independently, and compared these predictions to the observed dynamics. All focal species responded strongly to variation in plant abundance. Single-species analyses suggested that colonisation and to a lesser extent extinction rates differ depending on the presence of interacting species within patches. However, the directions of most effects differed from expectations, and simulations assuming species independence replicated reasonably well the observed metacommunity dynamics. These results suggest that although local interactions among the butterfly, parasitoid, and mildew occur, their roles in metacommunity spatio-temporal dynamics are weak compared to other environmental drivers. Instead, all species respond to variation in plant abundance, which fluctuates in response to climatic variation. Consequently, changes in climate affect the structure of entire metacommunities.

Historical and transgenerational effects of fungal infected diet for a butterfly

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Abstract: Sharing host plant with a plant pathogen may have important consequences for developing larvae but the degree of plant disease resistance may be difficult for an ovipositing female to evaluate. The Glanville Fritillary butterfly, Melitaea cinxia, inhabits a landscape with variation of risk of powdery mildew infected host plants and feeding on infected plants is detrimental to M. cinxia larvae. Here, we studied if females choose to oviposit on plants that are resistant to powdery mildew, thus minimising the risk their offspring will feed on infected plants, and if this choice depend on whether they came from populations with or without a history of mildew infected diet. We also study whether larvae differentiated between food that is infected or not, and how their efficiency of conversion depends on diet. In addition, we tested the effects of the mothers diet on offspring preference and performance. We found that the adults from both mildew infected and uninfected areas do not select plant genotypes that are resistant to mildew infection. However, larval diet selection and efficiency of conversion depends both on their own feeding experience and their mother's diet. Thus, larval preference is subject both to intra- and transgenerational plasticity depending on earlier experience of mildew infected diet. These results contribute to our understanding of how multitrophic interactions and transgenerational effects mediate insect behaviour.

Increased fluctuation in a butterfly metapopulation leads to diploid males and decline of hyperparasitoid

Authors: van Nouhuys Saskya[1], Nair Abhilash[3] and Nonaka Etsuko[2], [1]Indian Institute of Science, United States, [2]Sweden, [3]University of Helsinki, Finland

Abstract: Climate change can increase spatial synchrony of population dynamics, leading to large-scale fluctuation that destabilizes communities. High trophic level species such as parasitoids are disproportionally affected because they depend on unstable resources. Most parasitoid wasps have complementary sex determination, producing sterile males when inbred, which can theoretically lead to population extinction via the diploid male vortex. We examined this process empirically using a hyperparasitoid population inhabiting a spatially structured host population in a large fragmented landscape. Over four years of high host butterfly metapopulation fluctuation, diploid male production by the wasp increased, and effective population size declined precipitously. Our multitrophic spatially structured model shows that host population fluctuation can cause local extinctions of the hyperparasitoid due to the diploid male vortex. However, regionally it persists because spatial structure allows for efficient local genetic rescue via balancing selection for rare alleles carried by immigrants. This is the first empirically based study of the possibility of the diploid male vortex in a natural host-parasitoid system.

Two decades of temporal genetic changes in an introduced parasitoid population infected by a deleterious Wolbachia strain

Authors: van Nouhuys Saskya[1], Duplouy Anne[2] and Nair Abhilash[2], [1]Indian Institute of Science, United States, [2]University of Helsinki, Finland

Abstract: By influencing their host reproduction, or their host susceptibility to parasitism to favor proliferation of the infected hosts, endosymbiotic micro-organisms, such as the bacterium Wolbachia, can affect the spread of particular host genotypes in natural populations. This might have important consequences for the study of spatio-temporal changes in the genetic structure of introduced populations. and bias our understanding of how such populations establish, persist and disperse across habitats. We used 14 microsatellites and one mitochondrial marker to genotype 323 specimens of the parasitoid wasp Hyposoter horticola collected between 1992 and 2013 from five localities in the highly fragmented Åland archipelago, between the Finish and Swedish coasts in the Baltic Sea. A Wolbachia strain was previously shown to persist at an intermediate prevalence (~50%) in this population, and to affect the susceptibility of the wasps to a hyperparasitoid. We identified that migration occurred between some isolated populations, potentially facilitating the persistence of local introductions, and all island populations, despite occasional local population crashes. We show that the fixation of Wolbachia on some islands due to locally reduced predation pressures by the hyperparasitoid species, has selected for particular host genotypes in those isolated populations. We discuss the importance of including symbiotic partners in the study of trophic networks.

Viruses of mass reared insects – a lot of dark matter

Authors: van Oers Monique, Wageningen University and Research, Laboratory of Virology, the Netherlands

Abstract: Successful application of mass-reared insects heavily relies on healthy insect colonies. However, insect pathogens, including a number of before unknown viruses, easily emerge in large scale cultures, often leading to colony collapse. To be sustainable and cost-effective, insect production urgently needs to become more resilient to a variety of insect pathogens. The major drawback though, is that the knowledge needed to prevent such infectious diseases is very scarce and specific diagnostic tools are hardly available, leaving the insect rearing companies at serious risk for re-occurring outbreaks. To overcome this knowledge gap, develop the necessary techniques for diagnosis and management, and to increase the number of specialized researchers, the European INSECT DOCTORS programme was initiated. In this presentation, I will focus on what we know about viruses occurring in a variety of mass reared insects (e.g. crickets, tsetse, medflies, and caterpillars), thereby highlighting research data from the INSECT DOCTORS programme. I will also include our recent data on the discovery of insect specific viruses in mosquitoes and how the genome properties of these viruses differ from related human and animal viruses vectored by mosquitoes.

Valence-driven feature binding in the fly brain

Authors: van Swinderen Bruno[2] and Grabowska Martyna[1], [1]Queensland Brain Institute The University of Queensland, Australia, [2]Queensland Brain Institute Tee University of Queensland, Australia

Abstract: Selective attention describes the brain's capacity to prioritize one set of related stimuli while ignoring others. What defines a related set is driven in part by valence, or the value assigned to key stimulus features. Animals as dissimilar as insects and primates display valence-driven attention, but it is unclear if similar mechanisms are employed. Here, we used distinct frequency tags to disambiguate attractive and aversive visual objects in fly brain activity and found that valence cues governed the binding of associated visual features. Feature binding was evident even during covert attention and could be redirected by activating a reward circuit in the fly brain. Attended stimuli were phase-locked to endogenous beta (20-30Hz) oscillations, suggesting a conserved function for this frequency range in regulating feature binding.

Haze of glue determines preference of western flower thrips (Frankliniella occidentalis) for yellow or blue traps

Authors: van Tol Rob[3], Tom Jolanda[3], Roher Monika[2], Schreurs Anne[1] and van Dooremalen Coby[3], [1]Bosch, Netherlands, [2]Greb, Croatia, [3]WUR

Abstract: In a wind tunnel we compared the colour preference for western flower thrips to four types of colour plates (clear, white, blue and yellow) applied with two types of glue (diffuse Stikem versus clear D41). Further the results for blue and yellow preference were validated in two greenhouses. In the wind tunnel, we found a clear preference of yellow over blue when a clear glue (D41) was used. However, with a more diffuse (whitish) glue (Stikem) the preference for yellow over blue disappeared, whereby the attraction to yellow decreased (58%) while the attraction to blue increased (65%). In the greenhouses, we found similar effects as in the wind tunnel with a decrease in attraction to yellow (35%) and increase in attraction to blue (32%) for Stikem compared to D41. Light measurements showed an increase of 18% of blue, 21% of violet light, 8% of yellow and 9% of green light reflected

on the yellow Stikem trap versus the yellow D41 trap. On blue plates there was only 4% increase of blue light, 8% decrease of yellow light reflected when Stikem glue was used compared to D41 glue.

Response of the Western flower thrips to blue and yellow varies according to diffused versus specular reflection of glue on the trap

Authors: van Tol Rob[3], Schreurs Anne[1], van Dooremalen Coby[4], Tom Jolanda[4] and Roher Monika[2], [1]bosch, Netherlands, [2]greb, Croatia, [3]Wageningen University and Research, Netherlands, [4]WUR

Abstract: In a wind tunnel and greenhouses we compared the effect of different reflection of glue on the preferred colour for Western flower thrips. We compared colour choices of thrips in a wind tunnel for two types of glue (diffuse Stikem versus specular D41) on four types of colour plates (clear, white, blue and yellow) and repeated this experiment in two greenhouses (Chrysanthemum and Rose).
We found in the wind tunnel a clear preference of yellow over blue when a specular (clear glue) reflective glue (D41) was used. With a more diffuse (whitish) glue (Stikem) the preference for yellow over blue disappeared whereby the attraction to yellow decreased (58%) while the attraction to blue increased (65%). There was no significant effect of glue found for clear or white plates.
In the greenhouses we found similar effects as in the wind tunnel whereby the overall effect was a decrease in attraction to yellow (35%) and increase in attraction to blue (32%) when changing the glue type from specular to diffused. Light measurements showed an increase of 20% of blue light and 8% of yellow light reflected on the yellow Stikem trap versus the yellow D41 trap. On blue plates there was only 3% increase of blue light and 8% decrease of yellow light reflected. It remains to be seen if the change of ratio blue to yellow caused by the glue type plays a role in the change of attraction or whether the diffused particles in the glue itself cause these changes in attraction.
The reflective properties of glue are so far an unknown factor in colour choice and may explain partially the different results on colour preference as found by others.

Advances in studying the role of neuropeptides and their receptors in locust physiology and behavior

Authors: Vanden Broeck Jozef, Catholic University of Leuven, Belgium

Abstract: Despite their diversity, some fundamental characteristics are shared by all animals. Like other metazoans insects are heterotrophs, implicating a need for the intake of food. Many post-embryonic processes depend on this nutritional and energetic input. It is crucial that insects can rely on regulatory mechanisms controlling and integrating their development, physiology and behavior. Hormonal and neuronal signalling systems are playing an important role in this complex regulation.
In this presentation, we will consider neuropeptide-mediated signalling pathways that are implicated in the regulation of developmental-physiological and behavioral processes in insects. In particular, we will discuss recent data obtained in locusts, which are swarming pests that irregularly devastate the agricultural production in large areas of the world. In a physiological and neurobiological context, locusts have proven to be interesting experimental research organisms. We have molecularly characterized several neuropeptide precursors and receptors in locusts, and will report on our recent physiological and molecular biological studies that further illustrate the important role of neuropeptide-mediated signalling systems. We have also evaluated the potential of peptide-mimetic analogues as molecular pharmacological tools to interfere with these signalling systems, as well as with the downstream physiological processes they are controlling. Moreover, RNA interference was employed as a highly efficient and robust method to post-transcriptionally silence the expression of peptide precursors and/or receptors.

The general aim of our work is to contribute to a better understanding of the regulation of insect post-embryonic processes, as well as of the functional networking interactions between different regulatory pathways in an integrative, organismal context.

Acknowledgements:
We gratefully acknowledge the EU (Horizon-2020 project nEUROSTRESSPEP), the Research Foundation of Flanders (FWO-Flanders) and the Special Research Fund of KU Leuven (C14/15/050) for financial support.

Knockdown of ecdysone receptor in male desert locusts affects relative weight of accessory glands and mating behavior

Authors: Vanden Broeck Jozef[1], Van Lommel Joachim[3], Lenaerts Cynthia[1] and Delgouffe Charlotte[1], [1]Catholic University of Leuven, Belgium, [3]KULeuven, Belgium

Abstract: Recently (2018–2021) the world has faced the largest swarms of desert locusts, Schistocerca gregaria, in decades and food security in large parts of Africa and Asia was under extreme pressure. We investigated the possible role(s) of the ecdysteroid receptor in the reproductive physiology of male S. gregaria. Ecdysteroids are best known for their role in moulting and exert their function via a heterodimer consisting of the nuclear receptors ecdysone receptor (EcR) and retinoid-X receptor (RXR). To gain insight into the role of SgEcR and/or SgRXR in the male reproductive physiology of S. gregaria we performed RNAi-induced knockdown experiments. A knockdown of SgEcR, but not SgRXR, resulted in an increased relative weight of the male accessory glands (MAG). Furthermore, the knockdown of these genes, either in combination or separately, caused a significant delay in the onset of mating behavior. The high transcript levels of SgEcR in the fat body, especially towards the end of sexual maturation in both males and females, represent a remarkable finding since as of yet the exact role of SgEcR in this tissue in S. gregaria is unknown. Finally, our data suggest that in some cases SgEcR and SgRXR might act independently of each other.

Cryptic Fire Ant Species in South America

Authors: Vander Meer Robert[4], Alberto Calcaterra Luis[1], Ascunce Marina[3] and Porter Sanford[2], [1]Foundation for the Study of Invasive Species, Argentina, [2]United States Department of Agriculture (retired), United States, [3]United States Department of Agriculture, United States, [4]USDA-ARS, United States

Abstract: In South America, the home land of the fire ant, Solenopsis invicta, where their population densities are 5-10 less than they are in the United States. The rationale for this is that they left their natural enemies behind when they arrive in the USA. The search for natural enemies in South America has been going on for decades. The most successful result has been the introduction of several species of parasitic phorid flies. Results with pathogens has been less successful. We propose that the problem is a result of several cryptic species in South America that is confounding the search for pathogens. We use chemical, behavioral, and genetic methods to establish the presence of cryptic fire ant (Solenopsis invicta) species in northern Argentina.

Crosspollinating Urban Community Gardens and Forests: A Network Approach to Conserving native bees in Cities

Authors: Vanderstock Amelie[1] and Latty Tanya[1], [1]The University of Sydney, Australia

Abstract: Conserving native bees in cities involves understanding how they use floral resources across urban habitat types. Community gardens, a form of urban agriculture tended to by the public, are thought to support pollinators by providing diverse flowers all year-round. Native and regenerated urban forest is assumed to not only provide food-flowers, but also habitat including bare ground for nesting as well as cavities and hollows in trees. However, insect conservationists are yet to understand how the location of community gardens and forest sites can influence native bee diversity in an urban context.

We studied how connectivity between these two urban green spaces influences pollinating insect communities and the structure of plant- pollinator networks in Sydney, Australia. Specifically, whether community gardens adjoining urban forest have greater abundance and diversity of native bees compared with isolated gardens. We also compared native bee biodiversity of isolated forest sites with those adjoining community gardens. We surveyed fifty-six sites for characteristics including size and floral density. Insect visitors to all flowering species were caught at each site in time-standardized surveys. Using visitation data, we constructed plant-pollinator networks to explore how the interaction between community gardens and urban forest sites influenced key network metrics.

Our results demonstrate that a greater species richness and abundance of native bees, flies and wasps were found in community gardens compared with bushland sites, regardless of their habitat connectivity. Density and diversity of flowering plants is a more important explanatory factor for native bee biodiversity than their proximity to bushland. Aside from honeybees Apis mellifera, the most abundant bees across sites were Blue Banded bees Amegilla cingulata and Sweat bees, Liptotriches phenerura; both ground nesting species, as well as Leaf cutter bees Megachile Serricauda; who nests in wooden cavities. These native bees are likely finding ample food and nesting resources in the urban environment regardless of immediate proximity to native habitat.

Understanding the interactions between cultivated crops and remnant vegetation in the urban matrix is an important contribution to the research on pollination network and food resilience in global cities.

Who profits from the invasion – a preliminary study towards biological control of mosquitoes

Authors: Vanslembrouck Adwine[3], Scheers Kevin[5], Vermeersch Xavier[1], Hendrickx Rens[4], Deblauwe Isra[2], Schneider Anna[2], De Witte Jacobus[2], Van Bortel Wim[2], Reuß Friederike[6] and Müller Ruth[2], [1]Brussels Environment, [2]Institute of Tropical Medicine, Antwerp, [3]Institute of Tropical Medicine, Belgium, [4]Province of Antwerp, [5]Research Institute Nature and Forest, [6]Senckenberg Biodiversity and Climate Research Center, Frankfurt

Abstract: The spread of mosquito-borne diseases (MBDs) is restricted by the occurrence of competent vectors. In addition to the native Culex pipiens, a vector for West Nile and Usutu virus, invasive species such as Aedes albopictus are flourishing in Europe. Their spread towards more temperate regions poses an increasing threat because of their high vector competences for different viruses. They can establish rapidly in suited regions, reaching high abundances and posing a potential risk for MBDs.

The control of these populations will be necessary to prevent MBDs outbreaks. One possible biological control agent is the use of several species of diving beetles as natural predators of mosquitoes. Twenty-four common dytiscid species were wild-caught in Belgium and kept at insectary for a feeding experiment and prey choice on Cx. pipiens and Ae. albopictus larvae.

First results on the feeding experiment suggest at least five good dytiscid predators that are known to inhabit small, temporal habitats. Further experiments on prey choice reveal a clear preference for the ground dwelling Ae. albopictus rather than Cx. pipiens. A distribution overlap between these good predators is given on the point of entries where Ae. albopictus has been found in Belgium in the past years.

Exploring the parasitoid diversity for viral domestication

Authors: Varaldi Julien, University Lyon 1, France

Abstract: In some endo-parasitoid wasps, viruses have been endogenized within and domesticated by wasp genomes. Those endogenized viral genes are used by the wasps as a delivery tool to inject virulence factors, essential to the development of their offspring. So far, most cases of such viral domestication have been described in the Ichneumonoidea superfamily. First, I will show that convergent evolution led to virus domestication outside this superfamily. Second, we hypothesized that endo-parasitoidism may have favored the domestication of viruses or conversely that virus domestication may have favored the evolution of endo-parasitoidism. By analyzing the genomic composition of 124 Hymenoptera genomes spread over the diversity of Hymenoptera including free-living, ecto and endo-parasitoid species, we tested whether wasp lifestyle correlates with endogenized virus content. First, dsDNA viruses were more often endogenized and domesticated than expected based on their estimated abundance in insect viral communities compared to other virus genomic structures. Second, our analysis revealed that endogenization and domestication of dsDNA viruses was more frequent in lineages with endo-parasitoid lifestyle compared to ecto-parasitoid or free-living species. This result suggests that the evolution of endo-parasitoidism has favored the domestication of dsDNA viruses or conversely that dsDNA virus domestication has favored the evolution of endo-parasitoidism.

Evading invasive ants: investigating an ant repelling fly and its potential as a control method for exotic pest ants.

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Abstract: Many studies have shown that invasive ants can have a devastating effect on the invertebrate environment in areas where they become established. With steadily increasing human trade around the globe, we are creating ever more opportunities for hitchhiking invaders. Increasing, stricter pesticide laws and different regulations around the world call for constant innovation for new control strategies for invasive ants. An unlikely new candidate could come from a fly. While most species of the Diptera are excellent fliers in their adult life stage, during their development however, they are soft-bodied, slow, vermiform packets of nutrients for any predator that might come by. Commonly called maggots, the juvenile life stages of dipterans have to find a method to avoid predation. While many are adapted to a cryptozoic lifestyle, the species used in this study regularly thrives in close proximity to foraging ants. Apparently, these maggots have developed a defensive strategy to prevent this kind of predation. This study used the tawny crazy ant (Nylanderia fulva), the red imported fire ant (Solenopsis invicta) and the Argentine ant (Linepithema humile) as examples to identify the activity and origin of a repellent compound found on these maggots. Survival assays under ant predation were conducted including assays with maggots raised on antibiotics to investigate the origin of the repelling compound. The common fruit fly (Drosophila melanogaster) was used as positive control for predation. Results show a drastic increase in survivorship for the untreated and antibiotics raised maggots, indicating an inherent origin of the repellant. This is strong evidence for a novel strategy of these flies to avoid predation by ants and future results could potentially yield a new natural repellent for ants.

Sexually antagonistic selection promotes genetic divergence between males and females in an ant

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Abstract: In Hymenoptera, males and females display striking phenotypic differences despite lacking sex chromosomes. The constraint of a shared gene pool has been thought to prevent them from separately reaching sex-specific fitness optima by fixing different alleles in each sex. However, their entire haplodiploid genomes display an X-linked pattern that predisposes them to sexually antagonistic selection (SAS), whereby an allele is beneficial to one sex but harmful to the other. Here we report the first instance of SAS in a haplodiploid organism, the invasive ant Nylanderia fulva, with distinct alleles across a large portion of the genome differentially selected in each sex. Our findings shed light on a newly described genetic pattern and provide further insight into sexual conflicts in haplodiploids.Genetic diversity acts as a reservoir for potential adaptations, yet selection tends to reduce this diversity over generations. However, sexually antagonistic selection (SAS) may promote diversity by selecting different alleles in each sex. SAS arises when an allele is beneficial to one sex but harmful to the other. Usually, the evolution of sex chromosomes allows each sex to independently reach different optima, thereby circumventing the constraint of a shared autosomal genome. Because the X chromosome is found twice as often in females than males, it represents a hot spot for SAS, offering a refuge for recessive male-beneficial but female-costly alleles. Hymenopteran species do not have sex chromosomes; females are diploid and males are haploid, with sex usually determined by heterozygosity at the complementary sex-determining locus. For this reason, their entire genomes display an X-linked pattern, as every chromosome is found twice as often in females than in males, which theoretically predisposes them to SAS in large parts of their genome. Here we report an instance of sexual divergence in the Hymenoptera, a sexually reproducing group that lacks sex chromosomes. In the invasive ant Nylanderia fulva, a postzygotic SAS leads daughters to preferentially carry alleles from their mothers and sons to preferentially carry alleles from their grandfathers for a substantial region (~3%) of the genome. This mechanism results in nearly all females being heterozygous at these regions and maintains diversity throughout the population, which may mitigate the effects of a genetic bottleneck following introduction to an exotic area and enhance the invasion success of this ant.

Influence of hedgerows on plant and invertebrate diversity in Niagara vineyards

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Abstract: Historically perennial agroecosystems, like vineyards, are known for their limited plant diversity, ultimately hindering the potential for the provision of ecosystem services. Due to the fact that plants display bottom-up control, increased plant diversity in the margins of agroecosystems, known as hedgerows, may support local abundance of natural pest-enemies, through increased habitat complexity. This research aims to better understand the interaction between increased plant diversity in various types of perimeter plantings throughout the Niagara region, Ontario, Canada, and the potential impact on a common vineyard pest, leafhoppers (Cicadellidae), and a natural pest enemy, spiders (Arachnids) communities. Plant surveys in the perimeters and interior of vineyards and invertebrate community data was collected in 7 vineyard sites, encompassing a wide range of management practices. It was found that plant communities and functional diversity differed from the hedgerow to the interior and among on-farm managements. Leafhoppers communities were affected by on-farm management but not by the presence of the hedgerow. Spider communities benefitted from the presence of a hedgerow due to the increased structural complexity both within the hedgerow and between the hedgerow and vineyard interior. In conclusion it was found that hedgerows did not increase weed or pest pressure, and did support the maintenance of spider assemblages both within the hedgerows as well as vineyard interiors.

Responses of invertebrate communities in Lettuce (Lactuca Sativa) and Radish (Raphanus Sativus) monocultures and intercrop

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Abstract: Agroecosystems are ecosystems that are often vulnerable to diversity loss, which reduces crucial ecosystem services such as pest and weed controls, and resilience in the face of climate or environmental changes. In agroecology and sustainable agriculture, intercropping is a cultivation method that shows promise in its ability to increase diversity at the first trophic level thereby increasing diversity in successive levels (i.e. insects and other invertebrates). There is a need however to better understand how invertebrate assemblages as well as plant yields within the system may respond according to the type of plants being cropped. To try to gain a better understanding of how increasing crop diversity influences subsequent trophic levels, three separate but related experiments were implemented in Southern Ontario, Canada, a region where intercropping is still not very often used, even in organic farming. The experiments included a greenhouse control with no invertebrates present, a controlled field environment at the community garden at Brock University (regular irrigation and mechanical weeding provided), and an operational field setting (an organic farm). The main objectives of this project were to 1) examine responses of insect and other invertebrate assemblages in operational and field-controlled settings of lettuce-radish intercropping and monocultures; and 2) evaluate under controlled greenhouse conditions lettuce-radish intercropping and monoculture yields in the absence of invertebrates. Differences in invertebrate assemblages, and plant growth and herbivory rates were quantified for cultivated monocultures and intercrops of lettuce (Lactuca sativa) and radish (Raphanus sativus). Species diversity (invertebrates) and interactions (plants) were also calculated and compared across treatments. In some cases, herbivore abundance and richness in intercrops was shown to decrease and predator abundance increase in the intercrops compared to monocultures. Intercrop treatments showed significant increase in invertebrate species diversity in a controlled field setting yet little difference was found at the operational farm. For plants, herbivory rates were significantly lower in intercrop treatments relative to monoculture, but radish was a significantly stronger competitor than lettuce in all intercrops and had highest yield in the controlled field location. Lettuce did not appear to benefit in terms of yield when in the presence of radish. Overall, results showed that existing interactions might be site specific. Future research should include a greater number of functional groups such as detritivores and pollinators in novel plant combinations to improve our understanding of how increased biodiversity at the first trophic level influences agroecosystem invertebrate composition and overall productivity.

Integrating nutritional and cognitive ecology to study complex floral rewards

Authors: Vaudo Anthony[1] and Francis Jacob[1], [1]University of Nevada, Reno, United States

Abstract: Our current understanding of the role floral rewards play in pollinator cognition and plant fitness largely revolves around a single currency, nectar. Yet, many plants reward visitors with both nectar and pollen, which are both chemically complex and variable across co-flowering plant species. Embracing the nutritional complexity of floral rewards represents both a challenge and an opportunity for pollination biologists. On one hand, our recent work shows that multiple aspects of reward composition (e.g. pollen alkaloid content vs. nectar sugar concentration) can interact to guide floral choice in bumblebees (Bombus), complicating our ability to predict pollinator preferences based on a single reward trait in isolation. On the other hand, recognition of this nutritional complexity holds promise for understanding what guides floral choice among generalist bees, and thus predicting how co-flowering plants interact via shared pollinators. We share our ongoing research on the nutritional ecology of floral rewards in a community context. To understand how reward composition predicts pollen movement in montane (NV and CA, USA) communities, we quantified the macronutrient content of pollen and nectar offered by Bombus-visited plant species co-flowering in Sierra Nevada meadows. We combined this information with high resolution aerial imagery (10m radius plots around 155 focal plants across 7 species) to identify co-flowering individual plants at pollinator-relevant spatial scales. Further, we apply a network approach to understand how pollen macronutrient ratios link bees and co-flowering plant species. Together, these efforts suggest that a nutritional perspective on the cognitive ecology of pollination may help explain how the drivers of individual bee foraging decisions scale up to a community level.

Dengue superspreading and its impact in surveillance and control strategies

Authors: Vazquez Prokopec Gonzalo, Department of Environmental Sciences. Emory University. Atlanta, GA, United States

Abstract: Abstract. Transmission heterogeneity (TH), whereby a disproportionate proportion of pathogen transmission events aggregates in a small fraction of individuals or geographic locations, is an emerging property of most infectious disease systems. For vector-borne diseases, TH is commonly inferred from the distribution of the number of vectors per host, which could lead to significant biases in situations where vector abundance and transmission risk do not correlate. The combination of human daytime mobility and the low and spatio-temporally heterogeneous density of Aedes aegypti significantly limit the value of entomological measures such as number of females per host as a measure of DENV transmission risk. Longitudinal cohort studies performed in the Amazon city of Iquitos, Peru, since 2007 have identified the activity space (AS), the array of locations that form part of a person’s daily routine, as the unit of DENV transmission. We extended such contact-cluster studies to quantify the distribution of acute DENV cases by AS during two consecutive outbreaks (DENV-4 and DENV-2) that occurred in Iquitos, during 2008-2014. A total of 257 ASs led to the virological detection of 220/1,474 (14.9%) DENV-infected contacts. Significant overdispersion in the distribution of contacts was observed in the presence of subclinical infections, with 34% ASs leading to 64% of all infections. Up to 16% ASs were quantified as super-spreading events. DENV super-spreading was predicted by the non-linear interaction of Ae. aegypti abundance and by host susceptibility to the circulating DENV serotype across the AS. Entomology is, thus, a valuable predictor after considering the intensity of transmission and the susceptibility of the human population. Furthermore, the marked heterogeneity in case distribution, and the role of asymptomatic infections in defining it, highlight important difficulties faced by reactive interventions if those spatial units contributing most to transmission are missed.

Biosurveillance for invasive xylophagous beetles using a DNA metabarcoding approach

Authors: Veillat Loïs[2], Roux Géraldine[1], Roques Alain, Boyer Stéphane and Lopez-Vaamonde Carlos, [1]INRAe, [2]INRAE, France

Abstract: Invasive xylophagous beetles represent a threat to forests worldwide. There is an urgent need to develop a biosurveillance system for early detection of invasive species. New approaches such as DNA metabarcoding allow rapid and accurate identification of species. However, many insects are not detectable with these approaches because they are not referenced in barcode databases. Moreover, these approaches are often expensive, time consuming and based on short DNA sequences, thus limiting taxonomic information.

The aim of this study is to develop an approach based on the MinION long-read sequencer which provides a cheap, direct and fast analysis within the framework of a biomonitoring study of invasive xylophagous insects.

We have used multi-component blends for mass trapping both native and exotic longhorn beetles at several European ports of entry. With this biological material at our disposal, we are developing reference databases of Cerambycides to improve the number of species detectable in metabarcoding analyses. We are also working on the design of beetle-specific primers to amplify short overlapping amplicons and re-construct the entire bracode fragment (658 bp), which would impove the detectability rate of these species using Oxford Nanopore Technology’s MinION portable sequencing platform.

RNA-seq transcriptomics reveals differences in gene expression patterns of Anastrepha obliqua colonizing different fruits: a potential diversification strategy

Authors: Velasco-Cuervo Sandra[1], Galindo-González Leonardo[2], Toro-Perea Nelson[1], [1]Universidad del Valle, Colombia, [2]University of Alberta, Canada

Abstract: Due to the close relationship of phytophagous insects with their host plants, many of them have been specialized in infesting one or several plant species related phylogenetically. In this context, the host-use is considered as a factor that impacts evolutionary trajectories of insects. Despite its importance, research in host-use effect in neotropical insects is scarce, being necessary to identify if the use of different hosts can drive ecological specialization or, if this behavior contributes to formation of generalist species in the Neotropics. One of the main tools to understand plant resources use by phytophagous insects is differential gene expression analysis. In the current study, we propose the fruit fly A. obliqua as a model to understand phenotypic plasticity at the transcriptomic level. since A. obliqua infests host plants from different families that co-exist in sympatry. We sampled fruits from three host-plants: (i) red mombin (Spondias purpurea, Anacardiaceae), their native host; (ii) mango (Mangifera indica, Anacardiaceae), the main host of this pest in the Neotropics; and, (iii) star-fruit (Averrhoa carambola, Oxalidaceae), which belongs to another family also infested by A. obliqua. We assembled the first de novo transcriptome of third stage larvae of this fly using RNA-seq technology. Results identified changes in expression in response to the host plant, which could be indicative of a plastic response of A. obliqua. Preliminary analyses identified an enrichment of serine hydrolase activity in larvae infesting red mombin. These enzymes are commonly associated with digestion in insects, although they have also been reported to be associated with physiological functions of development and the immune system. Other transcripts upregulated in the larvae associated with red mombin included genes of innate immune response, proteolysis and digestion. We also found downregulation on some transcripts associated to inflammatory responses and in the Mariner Mos1 transposase, when larvae of red mombin were compared with mango and start-fruit larvae. Transposons have been suggested to have an adaptive role into the genomes to environmental stresses and can cause rapid evolutionary change in their hosts. This transcriptional plasticity could be related to polyphagy allowing flies to infest new hosts and respond to specific secondary metabolites. We are analyzing if there are SNPs in differentially expressed transcripts, which may indicate genomic differentiation that could contribute to ecological specialization within a continuum of diversification. From the results and data obtained so far, we hope to contribute to the knowledge of metabolic pathways involved in the feeding and survival of A. obliqua and to infer potential strategies of host use diversification.

Role of plant defenses in host-parasitoid interactions

Authors: Venkatesan Radhika[1], Ghosh Enakshi[2] and Aswathi Sasidharan[2], [1]National Centre for Biological Sciences, Bangalore, India, [2]National Centre for Biological Sciences, India

Abstract: Plant defenses play a major role in shaping tri-trophic interactions between plants, insect herbivores, and parasitoid wasps. The characteristic blend of volatiles released by plants upon herbivory, function as attractive cues to parasitoids and as an indirect plant defense. Further, the secondary metabolites in plants alter insect host physiology that might indirectly affect parasitoid choice. This talk will explore the role of glucosinolates, a major class of secondary metabolites found in Brassicaceae in altering parasitoid performance. Using Plutella xylostella as host and two parasitoid wasps, we examine herbivore physiology and parasitoid choice and development. Our study shows that host plant quality mediated changes in insect physiology impacts trophic interactions and parasitoid behavior differentially.

Olfactory perception in elevated ozone: the role of ozone reaction products

Authors: Venkateswaran Vignesh[1], Knaden Markus[1] and Hansson Bill[1], [1]MaxPlanck Institute for Chemical Ecology, Germany

Abstract: Ozone can degrade VOCs mediating insect olfactory perception. How may reaction byproducts affect olfactory perception? Such products may be attractive or aversive or may change blend perception by altering the background. Using Drosophila melanogaster, we target nearly 600 odorants in the DoOR2.0 database (a database of odor-receptor responses), and predict their oxidative breakdown with ozone. We generate a ranked list of the most consistently occurring ozone byproducts and targeted the top ten most occurring products to investigate behavioral and neurophysiological responses. We test the intrinsic valence of flies to compounds, and in the context of the background. We investigate single sensillum responses. Almost all byproducts are perceived as olfactants and range from being attractive to neutral but not aversive when tested individually. When present in the background behavioral change to an attractive, ecologically relevant odour blend of balsamic vinegar was not altered. We observe that most products are perceived by one of the three tested sensilla investigated. Overall, the byproducts of ozone degradation may play only a minor role in disrupting odor perception of ecologically relevant signals. Our study provides a crucial foundation for accounting for ozone degradation of odors by air pollution for insect olfactory perception.

Arthropod assemblages of urban meadows - a multitaxa study

Authors: Venn Stephen, University of Helsinki, Finland

Abstract: Bees, carabid beetles and butterflies were sampled from a set of meadows in the Helsinki capital region. Bees were sampled using coloured pan-traps and netting along transects; carabid beetles were sampled by pitfall trapping and butterflies were sampled using netting along transects. Few meadow butterfly species were recorded, and carabid and bee assemblages were diverse, though did not include threatened species. I recommend that meadow networks are managed by mowing and grazing if possible, and more attention should be given to the management of patches of supplementary open habitat to support meadow assemblages. I suggest that species and taxa traits, particularly relating to dispersal, determine their capacity to persist in an urban environment.

Carabid species structure in grassland habitats is determined by soil and moisture conditions

Authors: Venn Stephen, University of Helsinki, Finland

Abstract: Carabid beetles are a speciose taxon that has been widely used in empirical ecological research studies. I sampled the carabid fauna of diverse grassland habitats in the capital region of Helsinki during the period 2007-2009, to characterize the assemblages of threatened habitat types, such as rocky dry meadows and sheep fescue (Festuca ovina) dry meadows and to determine how urbanization affects the carabid assemblage. Carabid beetles were sampled using pitfall traps, operated from May-September and emptied at 2-3 week intervals. I used NMDS ordination to compare the similarity of the carabid assemblages of different types of grassland, which showed a gradient of changing species composition from fresh grasslands on clay soils to dry grasslands on sandy soils. GLMM modelling of predicted species responses to level of urbanization and grassland type showed complex responses to three classes of urbanization and three habitat types. For instance, Amara nitida and Harpalus luteicornis were sensitive to urbanization, whereas Calathus erratus and Poecilus cupreus were more abundant in urban grasslands. Calathus melanocephalus was more abundant in dry grasslands, Ophonus rufibarbis favoured managed grasslands and Synunchus vivalis favoured fresh grasslands. The rarest species recorded were Amara equestris and Amara consularis, which are currently classified as LC, though until 2010 they were classified as VU.

Urban Effects on Diving Beetles (Coleoptera: Dytiscidae) and Implications for Wetland Management

Authors: Venn Stephen[1], Liao Wenfe[1] and Niemelä Jari[1], [1]University of Helsinki, Finland

Abstract: Urban blue infrastructure plays important roles in the ecology of cities, such as supporting aquatic biodiversity. Urban blue has received less attention than urban green. As consequences, it is unclear how urbanization has affected biodiversity in urban blue and what habitat features are essential for biodiversity to give management advice. We surveyed diving beetles in 26 urban ponds at 11 sites in Helsinki, Finland, with 1-litre activity traps. With generalized linear mixed models (GLMM) and non-metric multidimensional scaling (NMDS), we analyzed how dytiscid species richness and abundance were associated with the percentages of impermeable surfaces, pond margin slopes, and emergent plant coverage in ponds with and without fish. We found that the surrounding impermeable surfaces had negative effects on dytiscid species richness but not their abundance. Both species richness and abundance of dytiscids were lower in ponds with fish than in ponds without fish; both features decreased with increasing margin slopes and decreasing emergent plant coverage in ponds with fish, but not in ponds without fish. Urban wetlands can support a diversity of dytiscids at the regional level. Ponds free from predatory fish are ideal habitats for dytiscid diversity. In ponds with fish, emergent vegetation can be planted to create microhabitats for dytiscids to avoid predators. A diversity of wetland habitats are needed to maintain aquatic biodiversity in urban areas.

Comparison of leaf litter ant communities between core and buffer forests in the UNESCO Crocker Range Man and Biosphere Reserve, Sabah, Malaysia

Authors: Verble Robin[1] and Sumnicht Theodore[1], [1]Missouri University of Science and Technology, United States

Abstract: Borneo is home to the oldest and most diverse tropical forests in the world, but these forests are threatened by conversion, logging, agricultural clearing, and resource overexploitation. In an effort to preserve and conserve this biodiversity, the United Nations Educational, Scientific, and Cultural Organization (UNESCO) established a Man and Biosphere Reserve in the Crocker Range in 2014. The region is managed by the Sabah Biodiversity Centre and Sabah Parks. This reserve consists of three zones-- a highly protected interior core (144,492 ha), a buffer zone where development, tourism and agricultural activities are limited (60,313 ha), and a transition area where economic activities are less restricted (144,579 ha). We examined leaf litter ant biodiversity and community structure in the montane tropical forest of the core and buffer zones in Summer 2019 with the goal of evaluating the ant community structure between the two zones. Tropical leaf litter ant communities are spatially biodiverse and can vary on the 1-m scale. Leaf litter ants were collected via Berlese extraction of 0.25 m2 quadrats of leaf litter among core and buffer forest sites at Inobong Substation, Crocker Range. Ants were sorted to morphospecies using published keys. Total species richness, evenness, similarity, and relative abundance were compared among sampling quadrats, sites and forest zones. Results show predictably patchy ant communities, with differences among quadrats and sites, but limited differences between forest zones. Our results indicate that small place-based organisms are adequately protected by the core and buffer forests.

Pushed to the edge: dispersal syndromes and the eco-evolutionary dynamics of pushed vs. pulled range expansions in micro-wasps

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Abstract: While species ranges have always moved, the eco-evolutionary dynamics of range expansions have become especially relevant today, as human influence reshapes communities worldwide. Contrary to classical “pulled” dynamics, in which the low-density front populations provide most of the “fuel” for the advance, some expansions exhibit dynamics in which high-density rear populations actually “push” the expansion forward. Combining the pushed/pulled expansion concept with evolution at range edges highlights the importance of understanding how density-dependent dispersal or growth evolve during expansions. It has been suggested that not accounting for this may explain failures to predict colonization dynamics of e.g. invasive species or biocontrol agents. The comparative eco-evolutionary consequences of pushed vs. pulled dynamics remain to be studied however, especially in the context of preexisting life-history differences. To better understand these dynamics, we will create replicated range expansions using colonizations of experimental landscapes by Trichogramma micro-wasps, a biocontrol agent. We will compare the ecological and evolutionary dynamics of strains and species varying in dispersal ability, dispersal density-dependence, and in the association of these traits with life history traits. This will allow us to determine to what extent the evolution of density-dependent dispersal is predictable from initial trait architecture, and the consequences for the fate of pushed vs. pulled expansions. We will conclude by linking these experimental results to insights from individual-based models including more realistic trait architecture.

The open bar is closed: restructuration of native parasitoid communities following successful control of an invasive pest

Authors: Vercken Elodie[3], Muru David[3], Borowiec Nicolas[2], Thaon Marcel[1] and Ris Nicolas[3], [1]INRAE Sophia-Anitpolis, [2]INRAE Sophia-Antipolis, France, [3]National Institute for Agronomical Research (INRA), France

Abstract: When an invasive species establishes in a new area and reaches high densities, some antagonists may benefit from this bonanza situation. How such a native community may then evolve after the regulation of the invaders by external outputs – e.g. the deliberate introduction of specialized natural enemies – remains however poorly documented. To investigate this issue, we used the case study of the invasion of the Asian chestnut gall wasp Dryocosmus kuriphilus Yasumatsu in France and its subsequent control by the exotic parasitoid Torymus sinensis. From the survey of 26 locations during 5 years after the T. sinensis introduction, we more precisely analyze how the patterns of co-occurrence between the different native parasitoid species changed through time.

Our results demonstrate that native parasitoid communities show more competition as the D. kuriphilus levels of infestation decreased. During the last year of the survey, two alternative patterns were observed: either native parasitoid communities were almost inexistent, either the native parasitoid communities were dominated by one main parasitoid: Mesopolobus sericeus. We hypothesize that the scarceness of the newly-acquired resource forced the most generalist parasitoids to return to their original hosts, while only the most specialist native parasitoid remained. These results highlight how the “boom-and-bust” dynamics of an invasive pest followed by successful biological control can challenge the structure of native communities of natural enemies.

Optimizing the dose of biocontrol agents depending on local conditions: a mechanistic population growth model for soil-dwelling predatory mites

Authors: Vercken Elodie[4], Pasquier Antoine[2], Ferrero Maxime[3] and Andrieux Thibault[1], [1]Bioline agrosciences, France, [2]French National Institute for Agricultural Research / Bioline agrosciences, France, [3]Independant consultant, France, [4]National Institute for Agronomical Research (INRA), France

Abstract: Western Corn Rootworm (WCR), Diabrotica virgifera virgifera (LeConte) is an important pest of Maize, for which biological control options remain very limited. As WCR eggs and larvae inhabit the first centimeters of soil, soil-dwelling predatory mites are promising candidates as biocontrol agents against this pest. Recent work by our team led in controlled conditions revealed that the mite Gaeolaelaps aculeifer is able to feed on first and second instar larvae of WCR, and substantially reduce damage on maize plants when introduced at the timing of larvae emergence. These results open a promising perspective of biological control against this wildly spread pest.

However, the large-scale use of these mites to control WCR populations is currently facing two major constraints, as (i) the quantity of mites that would need to be spread to efficiently protect the maize is incompatible with economic viability, and (ii) the precise timing of WCR's larvae emergence in a given area is highly sensitive to environmental variations, which makes it difficult to predict. To address both these issues and improve the cost-efficiency balance of these candidate biocontrol agents, we propose an innovative strategy based on the deployment of a small quantity of mites early in the season, that will grow to reach a large-size population in time for WCR larvae emergence. The efficiency of such a strategy will strongly rely on the optimal correspondence between WCR population density, development time, and mites' population growth, all of which will depend directly on local parameters like soil temperature, precipitations, previous year's infestation, or the density of alternative preys.

In order to predict the optimal deployment strategy for soil-dwelling predatory mites, we built a 3-D spatial individual-based model accounting for mites' population growth and distribution in the soil. The model showed that variation in temperature and prey availability among regions directly impacts the initial dose of mites to introduce to reach optimal population size for WCR control at the time of larvae emergence. These results highlight the need for developing individually based advise methods that improve the cost-efficiency of biocontrol products in arable crops.

More bang for your knock(down): Methods and advancements for the cost-effective production of bacteria-derived double stranded RNA

Authors: Verdonckt Thomas-Wolf, KU Leuven, Belgium

Abstract: RNA interference is a highly conserved pathway for the post-transcriptional regulation of gene expression. It has become a crucial tool in life science research, with promising potential for pest-management applications. A major obstacle to applying this technique is the need to produce sufficiently large amounts of qualitative dsRNA in a cost-effective manner. To overcome this issue, much attention has been given to the development and optimization of biological production systems. One such system is the E. coli HT115 strain transformed with the L4440 vector. We recently demonstrated methods for the cost-effective extraction and purification of HT115 derived dsRNA, and its efficacy at inducing knockdowns in a lepidopteran cell line. In the presented study, we further elucidate the qualitative aspects of produced dsRNAs, their effect on the biological target system, and their impact on knockdown success. The insights and results from this poster will empower researchers to conduct otherwise prohibitively expensive knockdown studies, and greatly reduce the production times of routinely or large-scale utilized dsRNA substrates.

Co-occurrence models for global distribution of Robin’s pincushion (Diplolepis rosae) based on citizen science and open-source environmental data

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Abstract: Species Distribution Models (SDMs) constitute an important tool to assist decision-making in environmental conservation and planning in the context of anthropogenic effects and climate change. Nevertheless, SDM projections are affected by a wide range of uncertainty factors (related to training data, climate projections and SDM techniques), which limit their potential value and credibility. Here we present a case study, where we used citizen science distribution data for Robin’s pincushion, a plant gall induced by Diplolepis rosae (Hymenoptera: Cynipidae) on Rosa spp. (Rosaceae), and explore multiple scenarios regarding the two species joint global distribution. For the generation of joint global distributions, we used pseudo-absence data generated with three different algorithms along with open-source global Bioclim climate, soil and land use data. For pseudo-absence generation, we used the “mopa” R package which provides multiple data generation algorithms and tools for designing JSDMs while combining multiple sources of uncertainty (e.g., baseline climate, pseudo-absence realizations, future projections). The aim of our study was to surpass challenges involving pseudo-absence data generation for presence only data and to develop a general pipeline for global JSDMs based on citizen science and open-source environmental data with the R package “sdm”.

Molecular basis and evolution of sexual dimorphism in Nasonia vitripennis

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Abstract: Insects are well-known for their eye-catching colour differences or extreme size differences between the sexes. These sexually dimorphic traits are subjected to strong evolutionary forces and diversify rapidly within closely related genera or even within a genus, ultimately driving speciation. One essential transcription factor for sexual differentiation in insects is Doublesex (Dsx), which is involved in sex- and species-specific differences of e.g. pigmentation patterns, wing size, wing colour patterns and leg bristle number. The target genes on which Dsx acts, and the developmental and regulatory mechanisms underlying the rapid evolutionary changes are still poorly understood. However, a variety of studies show that most evolutionary novelties are caused by changes in the regulatory elements of pre-existing genes, so called cis-regulatory elements that contain binding sites for transcription factors to regulate gene expression.

The parasitoid wasp genus Nasonia (Hymenoptera) has a suite of sexually dimorphic traits that vary not only between sexes but also between species. One notable feature is wing size which is only sexually dimorphic in N. vitripennis. Males have short wings and cannot fly, while females have long wings and do fly. All three other male and female species in the genus have long wings and flight capabilities. In addition, leg pigmentation is a sexually dimorphic trait in all four Nasonia species; females have dark brown pigmented antennae and legs, while males lack pigmentation and have bright yellow antennae and legs. Lastly, all four Nasonia species have their own blend of sex pheromones that play a role in mate recognition and sexual communication which both evolve and diversify rapidly. This suite of traits makes Nasonia the perfect system to study the molecular basis of sexually dimorphic trait variation.

Here we present our results of Dsx developmental RNA interference experiments on the expression of the sexually dimorphic traits in N. vitripennis. Moreover, we present our identification of the Dsx binding site using the novel techniques, DNA Affinity Purification sequencing (DAP-seq), and our in-house developed DAP-qPCR. We found that N. vitripennis and Drosophila melanogaster Dsx homologs recognize the same extremely conserved sequence, suggesting that the rapid evolution of sexually dimorphic traits happens through gains or losses of regulatory regions of Dsx target genes, rather than in Dsx itself. Knowing the Dsx binding site sequence, we are able to study the Nasonia Dsx interactome and subsequently couple this with our study into the regulatory role of Dsx in the differentiation of the three sexually dimorphic traits: leg pigmentation, sex pheromone composition and wing size within the subfamily, on genus and species level. With this we aim to integrate our molecular understanding of sex determination and sexual differentiation with the rapid evolution of sexually dimorphic traits in insects.

Sex determination in the moth Ephestia kuehniella: Masc duplication and a candidate Fem piRNA

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Abstract: Insect sex determination is a rapidly evolving developmental process with varying levels of gene conservation. Genes at the bottom of the sex determination cascade are highly conserved, while genes at the top of the cascade are mostly very diverse, with the exception of the recently discovered Maleness-on-the-Y (Moy) gene in tephritid fruit flies. Consistent with this evolutionary trend, the sex determination cascade identified in the silkworm, Bombyx mori (Lepidoptera), reveals low conservation with Diptera and Hymenoptera, i.e. only the bottom gene, doublesex, is conserved between these three orders. However, little is known about the molecular mechanism of sex determination in Lepidoptera other than B. mori.

Here we present data on the sex determination system in the Mediterranean flour moth, Ephestia kuehniella. We identified an ortholog of the Masculinizer (Masc) gene through comparison with closely related species, and we discovered a duplication of this gene on the Z chromosome. Knock-down experiments confirmed a conserved role of EkMasc in masculinization as reported in several other lepidopteran species. Subsequently, we did an extensive search of the W chromosome of E. kuehniella and identified multiple copies of Masc. In addition, we identified a short sequence with a high homology to Masc and designated this sequence as a candidate Feminizer piRNA (EkFem piRNA). Using molecular cytogenetic methods, we confirmed that the locus generating EkFem piRNA is located on the W chromosome as expected. Analysis of small RNA sequencing data showed that expression of the candidate EkFem piRNA is initiated during early embryogenesis. These findings indicate a sex determination system involving gene silencing through short RNAs. A comparison of the sex determination systems of B. mori and E. kuehniella thus suggests a similar primary feminizing signal in these species.

Assessment of the role of vectors for lumpy skin disease virus (LSDV) transmission

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Abstract: Lumpy skin disease (LSD) is an OIE listed viral disorder of cattle as a consequence of severe infections leading to high economic losses. Until 1989, the occurrence of LSD was restricted to the African continent. In 2015, the first European outbreak occurred in Greece, and in 2016 many countries of the Balkan region (Serbia, Kosovo, Bulgaria, Romania, Albania, Montenegro and FYR Macedonia) were affected resulting in a large economical loss. As a result of intensive vaccination campaigns, only Greece and FYR Macedonia were still reporting LSD cases in 2017 in Europe. In 2018 Turkey, Russia and Georgia still reported cases and in 2019 only Russia and Israel. The explosive spread of LSD in the Balkan countries, however, was reminiscent to the recent spread of the Culicoides-transmitted bluetongue virus in Europe. Although the role of arthropods in the transmission of LSDV is still unclear, it has been postulated Stomoxys calcitrans being the main incriminated vector based on circumstantial evidence and mathematical models.

This work is presenting data of a two-year project (2018-2020) funded by the Swiss Federal Food Safety and Veterinary Office (FSVO grant nr. 1.18. d) investigating the transmission efficiency (mechanically and biologically) for LSDV among field-collected and laboratory-reared mosquitoes (Aedes japonicus, Culex pipiens, and Aedes aegypti), Culicoides (Culicoides obsoletus, Culicoides pulicaris spp., and Culicoides nubeculosus) and flies (Stomoxys calcitrans). Arthropods were exposed to LSDV spiked blood, followed by their incubation under realistic fluctuating climatic conditions. Quantification of viral DNA was carried out from body parts (mouth part, head and abdomen) and faecal shedding at different time post oral infection.

Bluetongue virus reassortment and vector competence in Culicoides biting midges

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Abstract: Bluetongue virus (BTV) is transmitted to its ruminant host almost exclusively during blood-feeding of Culicoides biting midges and causes haemorrhagic disease, bluetongue, especially in sheep. The complex interactions between mammalian hosts, insect vectors and viruses are very challenging to examine experimentally, and studies maybe compromised by needle-inoculation of the virus into the host. By allowing previously infected Culicoides vectors to blood-feed directly on the host, we use a more natural transmission model by feeding naïve insects on infected hosts to explore Culicoides-borne virus transmission dynamics and the impact of genetic drift and reassortment (the exchange of genome segments during coinfection) on the phenotype of virus strains.

The characteristics of three parental BTV strains of different serotypes (BTV-1, BTV-8 and BTV-4) and two field-isolated natural reassortment progeny strains (BTV4), that shared segment identity with either two or three of the parental strains, were examined in sheep. Infection of all sheep by feeding infected Culicoides was achieved, irrespective of BTV strain, even where only 1-3 individual infected Culicoides took a blood-meal. The reassortant strains displayed differential vector competence rate and pathogenicity phenotypes from the parental strains from which they derived. We demonstrate phenotypic differences in viremia and pathology in sheep and vector competence in Culicoides between the 2006 and 2015 re-emergent European strains of BTV-8 despite their genetic similarity.

Additionally, we use an immunofluorescence technique to visualise the infection and replication of BTV in whole organs of infected Culicoides and investigate potential barriers to infection, dissemination and virus transmission from individual insects. We aim to align molecular diagnostics by PCR and virus isolation with the probability of an individual carrying a transmissible BTV infection.

Irradiation as an effective phytosanitary treatment for Drosophila suzukii

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Abstract: The spotted wing drosophila (SWD), Drosophila suzukii, is a pest native to Southeast Asia that has caused significant economic losses to soft fruit crops. Given that fumigation is the only postharvest treatment currently available for SWD, phytosanitary irradiation has been considered as a promising treatment option for the species. Yet, the validation of a phytosanitary irradiation dose is pending for SWD. We tested whether 80 Gy can provide quarantine security against SWD considering prevention of F1 generation as treatment endpoint. Naturally infested blueberries containing late pupae were either irradiated using gamma rays or left unirradiated as controls. Irradiated and non-irradiated pupae were then removed from the blueberries, counted, and transferred to emergence cages. Emerged females mated with siblings from the same treatments were provided with blueberries as oviposition substrates. Eggs laid in those blueberries were counted and held until the completion of the insects' development. The total number of late pupae irradiated at 80 Gy was 30,058. The females emerged from pupae that had been irradiated at 80 Gy laid a total of 49 eggs, none of which hatched. Our findings suggest that the radiation dose of 80 Gy can be effectively used as a phytosanitary treatment for D. suzukii.

Improving an attract & kill strategy targeting wireworms: influence of biotic and abiotic parameters

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Abstract: Wireworms, the larvae of click beetles, are one of the most important insect pests of agricultural and horticultural crops worldwide. In recent decades, wireworm damage has continuously increased repeatedly reaching severe economic levels in particular in potatoes. Efficient and sustainable control measures are desperately needed, specifically in organic but as well as in conventional potato production.

The innovative capsule system ATTRACAP®, based on a biological attract-and-kill strategy against these soil dwelling insect pests takes advantage of the fact that larvae are attracted to CO2. The capsules produce and emit CO2, and an isolate of Metarhizium brunneum grows out of the capsules, with which the wireworms come into contact. Thus, a maximum probability of infection is achieved with a minimized application rate. Field applications on farmer fields and specific experiments have predominantly yielded efficacies up to 70%; however outliers downwards have been observed as well. In order to better understand the reasons for the variable efficiency ranges, we investigated the influence of either improved capsule formulations and production methods and abiotic parameters (soil moisture, humidity, and microorganism activity, respectively), wireworm species composition or application systems in experimental fields. Results identified soil condition during the first days and weeks after capsule application as a crucial factor influencing the efficiency of this Attract & Kill strategy. Technical solutions are available to take these different influencing factors into account. However, the very limited flexibility of the EU registrations conditions makes the implementation of site-adapted capsule types unlikely.

Defensive shimmering responses in the giant honeybee Apis dorsata are triggered by dark stimuli moving against a bright background

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Abstract: Due to the absence of physical barriers, the open-nesting giant honeybee Apis dorsata has evolved a spectacular collective defence behaviour – known as “shimmering” – against predators, which is characterised by travelling waves generated by individual bees flipping their abdomens in a coordinated and sequential manner across the bee curtain. We examined if shimmering is visually-mediated by presenting moving stimuli of varying sizes and contrasts to the background (dark or light) in bright and dim ambient light conditions. Shimmering was strongest under bright ambient light, and its strength declined in dim-light. A. dorsata shimmered only when presented with the darkest stimulus against a light background, but not when this condition was reversed (light stimulus against dark background). We suggest that this is an effective anti-predatory strategy in open-nesting A. dorsata colonies, exposed to high ambient light, as flying predators are more easily detected when they appear as dark moving objects against a bright sky. Moreover, the stimulus detection threshold (smallest visual angular size) is much smaller in this anti-predatory context (1.6° - 3.4°) than in the context of foraging (5.7°), indicating that ecological context affects visual detection threshold.

Combining new strains of predators, feeding strategies and hairless mutant cultivars to improve preventive control of pests on tomato

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Abstract: Aculops lycopersici is a key pest on tomato on a worldwide scale, causing severe damages in protected crops. The difficulty in controlling this pest with pesticides has enhanced the interest in biocontrol. Transeius montdorensis was reported as a promising predator. In this study preventive strategies have been evaluated by IRTA and Agrobío, based on introductions of this predator combined with releases of astigmatid mites as complementary food.

Rijk Zwaan Breeding BV has selected a tomato mutant that does not produce the type VI glandular trichomes. Utilizing these tomato cultivars gives new opportunities to apply biocontrol with natural enemies that otherwise would not survive on tomato plants. It has been stated that these varieties are less affected by A. lycopersici. However, preliminary trials have showed that these plants may be more vulnerable to other pests, such as thrips.

Two field trials by Rijk Zwaan and Agrobío have showed that a new strain of Orius laevigatus, performing better with suboptimal diets, can be established on tomato when combined with in-crop feeding strategies, improving the control of thrips. New designed mixed diets to favor a ‘standing army’ which improves the preventive control in the mutant varieties are discussed.

Beyond Arge, a phylogenetic hypothesis for argid sawflies (Hymenoptera: Tenthredinoidea) based on adult/larval morphology and genetic data

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Abstract: Argidae belongs to the ancient phytophagous lineages (“Symphyta”) of the megadiverse order Hymenoptera; this is the second most diverse family of sawflies including more than 900 species and 60 genera distributed worldwide, with more than 300 species in the cosmopolitan genus Arge. However, the highest diversity of Argidae genera is found in South America. The Gondwanan family Pergidae has frequently been retrieved as the sister group of Argidae. To develop a phylogenetic hypothesis for Argidae and explore its relationship with Pergidae, we analyzed a data set of more than 220 adult morphological characters for adults, 65 larval characters, and six molecular markers (mitochondrial, ribosomal and nuclear). The most complete dataset was achieved for the adult morphological component, with a total of 110 terminals, representing all argid genera and 22 outgroup taxa from other tenthredinoid families, including 10 Pergidae. For morphological characters we use maximum parsimony criterion, while for the molecular markers different models of DNA evolution were used under Maximum likelihood and Bayesian inference estimations. In the analyses, Argidae was usually retrieved as monophyletic and sister to a monophyletic Pergidae, except for the Australian genus Zenarge, which is placed as sister to (Argidae s. str. + Pergidae). We propose a new subfamily classification for Argidae, analyze character evolution, historic biogeography and discuss taxonomic changes, including raising Zenarge (Zenarginae) to family status.

Abstracts of presentations at ICE2022Helsinki

Bugdex – changing the way we learn about insects

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Abstract: The world is filled with an overwhelming diversity of insects that is innately fascinating, but hard to get to grips with initially. Learning how to identify insects is very difficult and represents a threshold that might deter newcomers. Bugdex is an educational app that combines mobile technology, awe-inspiring animations and interactive design; it aims to both simplify insect identification and inspire future generations of entomology students. The app at its core is an identification key to common northern European and North American insect orders and families and is richly illustrated with interactive multimedia elements designed to inspire students to discover the wonders of entomology around them. Bugdex is being produced by DKB Digital Designs and the Natural History Museum of Denmark in collaboration; the app will be made freely available both for iOS and Android devices. The first planned output is a key to Insect orders of the world that will be published in multiple languages. Next, family level guides to common of northern European and North American Lepidoptera, Coleoptera, Diptera, Hemiptera and Hymenoptera will be released as updates. The complete set of guides is expected to be available before the end of 2023.

Molecular identification of Blowflies used in Maggot Debridement Therapy

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Abstract: The use of maggots to clean necrotic wounds, known as maggot debridement therapy (MDT), has long been known to the scientific world. Various species of flies have been used for MDT, the most commonly used being Lucilia sericata, a greenbottle blowfly. This fly is closely related to another greenbottle, L. cuprina, but L. cuprina feeds on live as well as necrotic tissue, which is undesirable in MDT. L. cuprina is commonly named the ‘sheep blowfly’ because it is responsible for fly-strike in sheep, a form of myiasis that can kill sheep. L. sericata and L. cuprina are similar in morphology and it is extremely difficult to correctly identify them (especially females) using the literature as many characters in these works are subtle and subjective.

Flies were sampled from a laboratory colony of putative Lucilia cuprina at the Eugene Marais Hospital in Pretoria, South Africa and another of putative Lucilia sericata at Alexandria University in Egypt. DNA was extracted and polymerase chain reaction (PCR) amplification was performed. A total of 654 base pairs were sequenced for the 28S gene and a total of 601 base pairs were sequenced for the COI gene. Maximum Parsimony and Bayesian Inference analyses were used to analyse the data. The results indicated that L. sericata was being cultured at the Eugene Marais Hospital and L. cuprina was being cultured in Alexandria. This was unexpected and suggests that (1) these two flies are easily confused even in laboratory settings, and (2) L. cuprina can be safely used for maggot debridement therapy under controlled conditions.

The effects of larval density of Black Soldier Fly (L., 1758) (Diptera: Stratiumyidae) under scalable conditions

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Abstract: Contemporary research has focussed on the mass rearing and up-scaling of Black soldier fly for feed production for livestock (i.e. poultry, swine and aquaculture) around the world due to H. illucens’ unique and sustainable characteristics. However, larval density is poorly known in terms of scale and the reliability of data that has been produced. Therefore, this study looks at optimizing larval feeding densities and attempts to show the effects of larval population scaling effects on survival and feeding efficiency of BSF. The first study examines what effects feeding/provisioning rations (mg/larva/day) have on varying larval densities and their feeding efficiencies using treatments between 75-150 and 200 mg/larva/day at set depths and feed particle sizes. The second study uses five treatments of population size in orders of magnitude between 5 and 50 000 individuals to test how this variable affects feeding efficiencies. Various dependent variables were investigated at set environmental conditions over a 15-day period on 6-day-old larvae for the 1st study while larvae were portioned and left to feed undisturbed for a full 21 days. In study 1, larvae fed on catering waste showed significant differences in most feeding efficiency variables at densities above 100 mg/larva/day, and positive trends in larval mass, prepupation rates and survival rates with increasing provisioning rations. Larvae could access feed within the first week and aggregations were at their hottest within the first three days of experimentation. Additionally, significant differences were noted between treatments in waste reduction, bioconversion, and crawl-off biomass. Study 2 showed, larval body mass reduces as population size increases but variation decreases above 500 larvae treatments. Bioconversion showed a promising linear increase with treatment but it is recommended that harvesting methods should be evaluated for future research. Recommendations and optimal conditions are suggested and discussed from the shown results and future considerations are mentioned.

Computational assisted development of novel insect control traits

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Abstract: Genetically modified crops expressing Bt toxins have been a mainstay of insect control in the row crops industry since the late 1990s. However, with only a handful of resistance traits available to date in the market, these traits control merely a subset of the target pests and are being steadily broken due to their extensive use. Development of new resistance traits is, therefore, an urgent market need.

Over the past six years Evogene has been waging a computational discovery and optimization effort to deliver novel bacterial toxins applicable against major and emerging pests of Corn, Soybean and Cotton from the Lepidoptera, Coleoptera and Hemiptera insect orders. Dedicated big data composed of proprietary as well as publicly available genomes and metagenomes were mined using custom-made computational predictive tools, capable of associating insecticidal activity and complimentary attributes, required for trait functioning, with proteins having no prior insecticidal indication. Experimental validation in vitro and in planta led to establishment of novel toxins and toxin families that address different pests utilizing non-Bt mechanism of action. Rationale-based sequence optimization further drove toxin efficacy towards industrial grade.

In this talk the enabling technology and trait development advancements made with selected toxins and toxin families will be presented.

Wing shape variability and flight performance of invasive box tree moth

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Abstract: Box tree moth (Cydalima perspectalis, Walker) is an invasive species that has been present in Croatia since 2012, causing great damage to plants of the genus Buxus. The pest spreads rapidly, has high reproductive potential and good adaptability. The known natural dispersal velocity is up to 10 km per year. The objective of this study was to assess wing shape variability, flight propensity and of C. perspectalis and to evaluate its invasive character using geometric morphometric methods and the flight mill technique. An inter-site analysis was conducted, and the dataset was partitioned by geographic area, with intraspecific variation determined independently. Results indicate that wing shape is influenced by agroecological factors, with forewings being more plastic than hindwings. Regarding sexual differentiation, multivariate regression of wing shape revealed minimal differences between male and female forewings, with female wing shapes being more variable and covering a large percentage of the shape space. C. perspectalis flew a maximum distance of 15.6 km (virgin females) and spent a maximum flight time of 241 minutes (4 hours). The average speed of C. perspectalis ranged from 1.1 m/s to 1.6 m/s. Knowledge of the wing characteristics and flight performance of C. perspectalis is imortant in assessing dispersal and provides insights into migratory activities. Understanding the flight characteristics of insect pests is critical to developing effective strategies and programs for their management.

Is culture-based method effective for identification of insect gut mycobiome?

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Abstract: Next-generation metabarcoding is becoming an indispensable tool in microbial community ecology and with the implementation of this is rapidly changing our understanding of the insect symbiosis by uncovering high fungal and bacterial diversity, which is often host specific. Due to the progress in molecular methods for the characterisation of the composition of the microbial community, NGS methods (DNA metabarcoding) have been used recently, while traditional cultivation followed by Sanger technology was used only for the isolation and more accurate identification of specific species. In fact, both approaches with their pros and cons are considered complementary. In particular, the availability of cultures allows species-level identification using the entire ITS barcode and alternative genes, whereas metabarcoding provides rather a genus or family-level identification.

Our study is a comparison of culture-dependent approaches (strain isolation plus molecular identification) and culture-independent approaches (metabarcoding) to characterize the diversity of the gut mycobiota of lepidopteran larvae. We sampled larvae from four tree species (Acer platanoides, Corylus avellana, Carpinus betulus, and Quercus robur). The guts of more than 60 individual larvae were subjected to ITS2 rDNA metabarcoding on the Miseq Illumina platform and simultaneously to Sanger based DNA barcoding of ITS rDNA of fungal strains.

Our results show that cultivation using a single medium did not allow us to characterize the mycobiome as accurately as metabarcoding. The diversity of genera in cultivations was 16 times lesser than those obtained by metabarcoding. In total metabarcoding covered 98.7% of genera found by cultivations, i.e., only 8 genera were unique for culture-based method. Other species identified by cultivation were evaluated as the most abundant fungal taxa obtained in metabarcoding. Our results clearly show that NGS methods are the most effective method for the identification of the insect gut microbiome with minor information losses. Information obtained from metabarcoding should be careful with respect to the possibility of contamination and identification of genetic material from dead organismal cells. On the other hand, culturing has allowed for more precise identification, which is invaluable when studying the ecology of individual components of the mycobiome.

The research was supported by the Czech Science Foundation (GA18-08803S, GA22-29971S) the Student Grant Competition projects of the University of Ostrava (SGS14/PrF/2022).

Close the circle: recycling by-products to develop standardized diets for edible insects

Authors: Vitale Maria Luisa[1], Verrastro Vincenzo[1], Avosani Sabina[1] and Lamaj Flutura[1], [1]CIHEAM Bari, Italy

Abstract: Tenebrio molitor was the first insect approved as a novel food by EFSA in 2021 and is currently one of the leading edible insects due to its nutritional value and food conversion rate. Within the European project CoRoSect, we aim at formulating a standardized diet for T. molitor based on agriculture and food industries by-products, to promote a more sustainable food production chain. Potato peels, tomato peels, brewer's spent grain and olive oil pomace were selected considering local availability, seasonality, and already-existing recovery paths. The by-products were dried, ground and chemically analyzed to define their physical and chemical composition. Wheat bran was used as control. Each by-product was provided ad libitum alone, although small pieces of pumpkin were used as water source. The diets' performance was evaluated considering larval mortality, larval weight gain and the amount of diet consumed. Ten replicas (n=20 larvae per replica) were performed and allowed the identification of the most promising by-products. The latter are going to be combined to formulate mixed diets that will be tested with a higher number of individuals, simulating intensive farming conditions, to provide a standardized and more sustainable food source for T. molitor. Results are presented and discussed at ICE22.

Investigating the black soldier fly's mycobiome composition "natural habitats" and it's metabolic effect on the larvae

Authors: Vitenberg Tzach[1] and Opatovsky Itai[1], [1]MIGAL, Israel

Abstract: In recent years, extensive information regarding the interactions between insects and bacteria was found, however, the interactions between the insects and fungi remain vague. Yeast and yeast-like fungi have significant metabolic complexity that can provide nutrients such as proteins, fatty acids and vitamins for insects. This study focuses on the interactions between fungi and the black solider fly (Hermetia illucens; BSF), which is efficient in the process of converting diverse organic wastes into nutritional valued biomass for animal feed. As BSF lives in environments of rotten organic material, which thrive with bacteria and fungi, we hypothesis that the coexistence of this insect and the fungi will lead to metabolic interactions that will benefit the BSF. In this study, BSF were collected from natural environment and the mycobiome composition, in the insect's gut and environment was analyzed using next generation sequencing. The main yeast species that was found in both the insect's gut and the insect environment was Candida spp.. In order to test whether this yeast like fungi affects the BSF life cycle and metabolic pathways, a metabolome analysis was conducted to BSF larvae that were fed with the fungi in laboratory experiments.

Microbial management and social immunity in burying beetles

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Abstract: The tremendous evolutionary success of insects is at least in part owed to microbial symbionts which help them to explore novel ecological niches such as the ability to utilize unusual diets. Selective pressures from xenobiotics, nutrient limitations and natural pathogens may contribute to driving insects to adapt towards and enable exploitation of these diets.

An intriguing example of food preservation and controlling food-associated microbiomes are the burying beetles (Nicrophorus spp) that have evolved to occupy a unique ecological niche by reproducing on small vertebrate cadavers buried in the soil. Carrion-feeding insects that breed on decaying carcasses must overcome the challenges arising from competing microbes, which decrease its nutritional value and render it unpalatable or even toxic to animals. Adult burying beetles use effective counterstrategies to reduce detrimental microbial activity by treating the carcass with anal and oral secretions. We show that the burying beetle modifies the microbial communities of carrion, since beetle-tended carcasses showed no signs of degradation and supported the growth of the beetles' gut microbiota, including the yeast Yarrowia, in a biofilm-like matrix. In contrast, untended carcasses showed visual and olfactory signs of putrefaction and supported the growth of endogenous and soil-originating microbial decomposers. The beetles and their microbiome thus coordinate a specialized adaptive strategy of carrion management, enabling them to preserve carrion quality and support larval growth on a challenging resource.

Large-scale mitogenomics as a phylogenetic framework for insect biomonitoring across Earth's biomes

Authors: Vogler Alfried[1], Creedy Thomas[2], Liu Huaxi[2], Dawson Beth[1], Garner Beulah[3] and Zhou Zichen[1], [1]Imperial College London, [2]Natural History Museum

Abstract: Hyperdiverse insect groups such as Coleoptera are too poorly known for a global monitoring program. Mitochondrial genomes can be sequenced with relative ease and are a powerful marker to provide an increasingly complete phylogenetic tree of global lineage diversity and biogeographic distributions. We bulk sequence high-biodiversity samples from sites around the world (see www.site-100.org) and generate mitogenome sequences via a genome skimming technique to produce the phylogenetic framework of insect diversity composed of numerous regional samples. The resulting densely sampled tree is used to place any species encountered in (meta)barcoding using COI or other mitochondrial markers with high accuracy. Vice versa, the (meta)barcodes are added to the tree, for an ever more complete inventory at the species level, and themselves can help the placement of additional species not present in the tree. The approach thus goes beyond the standard biomonitoring schemes recording species presence/absence, and instead provides a phylogenetic fingerprint of local sites relative to a global sample of biodiversity, for measures of endemicity, phylogenetic diversity (PD), and functional diversity etc. of local communities, and their responses to global change.

The phylogenetic diversity of beetles in tropical forests

Authors: Vogler Alfried[3], Yeo Darren[4], Liu Huaxi[5], Nie RuiE[1], Ounjai Sarawut[2] and Creedy Thomas[5], [1]Chinese Academy of Sciences, China, [2]Imperial College London and Natural History Museum, United Kingdom, [3]Imperial College London, United Kingdom, [4]National University of Singapore and Imperial College London, Singapore, [5]Natural History Museum

Abstract: Tropical forests hold huge species diversity, but global patterns remain poorly known because of the greatly incomplete taxonomic inventories. We use 'genome skimming' from bulk samples of Coleoptera to generate mitochondrial genome sequences for a comprehensive set of species in several tropical forests around the world. Combining these data across sites provides a phylogenetic fingerprint of each local species assemblage. Sequencing from numerous such sites also provides a picture of the biogeographic distribution of the lineages present, and when combined with short DNA barcode and metabarcode sequences, these phylogenetic trees can produce an increasingly complete inventory of the biogeographically confined lineages of beetles on Earth. We demonstrate the power of this approach for characterising insect diversity in local forest sites in the context of the global phylogeny and, vice versa, how the inclusion of individual sampling sites improves the understanding global biodiversity patterns. The SITE-100 (www.site100.org) project implements this approach as a collaboration among researchers studying forest sites around the world.

Social environment and pathogen exposure influencing ant survival and gene expression

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Abstract: Social structures that involve group living can induce a high rate of disease transmission and leave many individuals vulnerable to the infection. Eusocial insects are particularly under high disease pressure due to a close genetic relatedness and dense living conditions. To resist an epidemic, individuals perform behaviors that can reduce the disease outbreak among the infected members; broadly termed as social immunity. To observe the effects of social living and social immunity on the pathogen resistance, acorn ants Temnothorax curvispinosus were inoculated with the entomopathogenic fungus. After inoculation, ants were either kept in isolation or placed into groups and their survival was recorded. Subset of ants were dissected and tested for differently expressed genes one-day post pathogen or sham exposure. This study shows that the ant social environment plays a crucial role in the pathogen resistance, with differentially expressed genes in the head, mesosoma and gaster.

Diverge or converge: Differential trends in the macroevolution of defences among lowland and highland willow species

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Abstract: Plants produce astonishing diversity of defensive metabolites in response to selection by the environment. To find the underlying mechanisms behind the variation in plant chemical defences, we need to understand how the prevailing environmental conditions contribute to their quantity, richness and variation between plant species. Species-rich plant genera with large elevational rages, such as willows (genus Salix L.), are ideal model systems for studying the macroevolution of defences in plants experiencing different selection pressures. Here we used willow species growing at different elevations to explore if macroevolution of defences follows different trajectories in plants exposed to different levels of abiotic and biotic stress. Our results show that lowland and highland plant species invest into different defensive traits as suggested by previous studies. However, we also show that the different macroevolution of traits among lowland and highland plants does not concern just the identity of the traits but also the trajectories by which they evolve. Lowland environment seems to promote variation in the type of defences employed and to generally promote divergence in defences among willow species. Contrastingly, highland environment selects willows for conservatism in their chemistry and supports directional trends towards escalation or de-escalation in individual traits, depending on their importance for the highland plants. These directional trends have pronounced effects on the macroevolution of chemical diversity in plant in terms of both richness and structural variation in metabolites employed by plants experiencing various environmental pressures.

Functional analysis of ichnovirus particles production

Authors: Volkoff Anne-Nathalie[1], Lorenzi Ange[2], Ravallec Marc[1], Jouan Véronique[1], Eychenne Magali[1] and Girard Pierre-Alain[1], [1]INRAE, [2]University of Georgia

Abstract: A crucial question considering endogenous viral elements (EVEs) found in parasitic wasps remains which viral functions have been retained during the virus domestication process. In ichneumonids, EVEs consist in tens of viral loci dispersed in th wasp genome. They include clusters of endogenized viral genes that compose the functional machinery allowing the wasp to produce virus-like particles. The other viral loci correspond to sequences that serve as templates to generate circular molecules encoding virulence genes and which are packaged into the particles to be delivered to the parasitoid’s host.

Ichneumonid EVEs derive from the integration of a non-determined virus and the genes composing the viral machinery have no similarity with known sequences. As a consequence, the function of such viral genes cannot be predicted. Our objective is to unravel their specific role in the different steps leading to the production of particles in the wasp ovaries. For that, we used RNA interference (RNAi) to silence a number of candidate viral genes. Using this approach combined with transmission electron microscopy observations, we were able to identify endogenized viral genes involved in particle assembly and particle trafficking.

A remarkable legion of guests: diversity and host specificity of army ant symbionts

Authors: von Beeren Christoph, TU Darmstadt, Ecological Networks, Germany

Abstract: Tropical rainforests are among the most diverse biomes on Earth. While species inventories are far from complete for any tropical rainforest, even less is known about the intricate species interactions that form the basis of these ecological communities. One fascinating but poorly studied example are the symbiotic associations between army ants and their rich assemblages of parasitic arthropod guests. Hundreds of these guests, or myrmecophiles, have been taxonomically described. However, because previous work has mainly been based on haphazard collections from disjunct populations, it remains challenging to define species boundaries. We therefore know little about the species richness, abundance and host specificity of most guests in any given population, which is crucial to understand co-evolutionary and ecological dynamics. Here, we report a quantitative community survey of myrmecophiles parasitizing the six sympatric Eciton army ant species in a Costa Rican rainforest. Combining DNA barcoding with morphological identification of over 2,000 specimens, we discovered 62 species, including 49 beetles, 11 flies, one millipede and one silverfish. At least 14 of these species were new to science. Ecological network analysis revealed a clear signal of host partitioning, and each Eciton species was host to both specialists and generalists. These varying degrees in host specificities translated into a moderate level of network specificity, highlighting the system's level of biotic pluralism in terms of biodiversity and interaction diversity. By providing vouchered DNA barcodes for army ant guest species, this study provides a baseline for future work on co-evolutionary and ecological dynamics in these species-rich host-symbiont networks across the Neotropical realm.

High-tech droplet digital PCR (ddPCR) diagnostics for pesticide resistance monitoring and management in major agricultural pests

Authors: Vontas John[2], Mavridis Konstantinos[1], Papapostolou Kyriaki Maria[6], Riga Maria[6], Michaelidou Kleita[7], Tsagkarakou Anastasia[5], Van Leeuwen Thomas[3], Bass Chris[8], Ilias Aris[4], [1]Agricultural University Athens, Greece, [2]Institute of Molecular Biology and Biotechnology, Foundation for Research and Technology Hellas, Heraklion, Crete, Greece, [3]Department of Plants and Crops, Ghent University, Belgium, [4]Foundation for Research & Technology Hellas, Institute of Molecular Biology & Biotechnology, Heraklion Crete, Greece, [5]Hellenic Agricultural Organization "DIMITRA", Heraklion, Greece, [6]IMBB-FORTH, Heraklion, Greece, [7]School of Medicine, University of Crete, Heraklion, Greece, [8]University of Exeter, United Kingdom

Abstract: Decisions on which pesticide to use in agriculture are expected to become more difficult, as the number of available chemicals is decreasing. For major pests for which a number of candidate markers for pesticide resistance are available, molecular diagnostics could support decision-making for the rational use of pesticides. A suite of twenty TaqMan assays was developed to assay target site mutations in T. urticae mites, B. tabaci whiteflies and F. occidentalis thrips, validated against Sanger-sequencing, and adapted for use with ddPCR in bulk pooled samples. The achieved LoD was as low as 0.1% (detection of a 1 mutant in a background of 999 wild type pests). The assay panel was assessed in terms of agreement with phenotypic resistance, through a pilot application in field populations, with strong correlation and thus diagnostic value of the molecular assays in some cases. It was also able to capture incipient resistance that was missed by phenotypic bioassays in other cases. DdPCR diagnostics could prove a valuable tool for pesticide resistance management. This work was supported by the European Union's Horizon 2020 research and innovation program (Grant: 773902-SuperPests) and the project 'SmartPP', funded by the Crete Operational Program 2014-2020 and ERDF (Action 1.b.1, RIS3Crete).

Molecular characterization of insecticide resistance in malaria and arbovirus vectors and access to advanced diagnostic tools (INFRAVEC2)

Authors: Vontas John[2], Chaskopoulou Alex[7], Mavridis Konstantinos[1], Grigoraki Linda[8], Kefi Mary[4], Fotakis Max[5], Bellini Romeo[3] and Balabanidou Vasileia[6], [1]Agricultural University Athens, Greece, [2]Institute of Molecular Biology and Biotechnology, Foundation for Research and Technology Hellas, Heraklion, Crete, Greece, [3]Centro Agricoltura Ambiente, Department of Sanitary Entomology and Zoology (EZS), Italy, [4]Department of Biology, University of Crete, Heraklion, Greece, [5]Department of Crop Science, Laboratory of Pesticide Science, Agricultural University of Athens, Athens, Greece, [6]Institute of Molecular Biology and Biotechnology, Foundation of Research and Technology, Heraklion, Greece, [7]USDA-ARS European Biological Control Laboratory, Thessaloniki, Greece, [8]Vector Biology, Liverpool School of Tropical Medicine, Liverpool, United Kingdom

Abstract: Abstract The intense use of insecticides in vector and agricultural pest control programs has resulted in a dramatic selection of resistance in mosquito populations to such an extent that their control becomes exceedingly challenging. We investigate the mechanisms of insecticide resistance, by using a variety of classical and modern approaches, including bioassays, transcriptomic studies, functional expression and characterization of recombinant proteins, immunohistochemical stainings and genome-editing CRISPR/Cas9 approaches, aiming to understand the role of specific genes and mutations in the resistance phenotype. Examples from our most recent studies include: (1) the elucidation of leg-based pyrethroid resistance mechanisms in the major malaria vector Anopheles gambiae, (2) the characterization of temephos and pyrethroid resistance in Aedes albopictus, (3) the characterization of target site diflubenzuron resistance in Culex pipiens and (4) the development of sample-to-answer multiplex molecular diagnostics for malaria and arbovirus vectors. FORTH-IMBB is a partner in the INFRAVEC2 Horizon2020 EU project and provides access to infrastructures for insecticide resistance research at no cost to the end-user, such as: (a) the genotyping of mosquito vectors of malaria and arbovirus for species ID, insecticide resistance traits (metabolic resistance and target site mutations) and detection of pathogens (plasmodium, arboviruses etc) and (b) the analysis of the mosquito cuticle thickness and composition, as a marker of cuticular resistance.

Abstracts of presentations at ICE2022Helsinki

The emergence of multiple insecticide resistance in Tuta absoluta and the implications in the management of the most important tomato pest

Authors: Vontas John[1], Roditakis Emmanouil[3], Tsagkarakou Anastasia[3], Ilias Aris[2], Vasakis Emmanouil[3] and Stavrakaki Marianna[3], [1]Institute of Molecular Biology and Biotechnology, Foundation for Research and Technology Hellas, Crete, Greece, [2]Foundation for Research & Technology Hellas, Institute of Molecular Biology & Biotechnology, Heraklion, Crete, Greece, [3]Hellenic Agricultural Organization "DEMETER", Institute of Olive Tree, Subtropical Crops and Viticulture, Department of Viticulture, Vegetable Crops and Plants, Greece

Abstract: The tomato borer Tuta absoluta Meyrick (Lepidoptera: Gelechiidae) is the most important pest of tomato. It is mainly controlled by chemical insecticides, which resulted in the development of resistance. The first and most striking resistance case at a global scale was that of diamide insecticides. Significant pest control problems were associated with the rise of diamide resistance thus it was thoroughly investigated. Indoxacarb resistance is now widespread and high levels of resistance were detected in both Greece and Cyprus associated with known target site mutations. To date, moderate to no resistance levels have been documented to insecticides spinosad and emamectin benzoate, allowing the use of these chemicals as the last resorts of effective control agents for T. absoluta infestations. Studies were performed on laboratory selected strains and novel resistance mechanisms were detected for both insecticides. However, in 2019 populations from Tympaki area exhibiting multiple resistance levels against all tested insecticides were identified for the first time. More specifically, strain GR-TYMP-19-2 exhibited 1777-, >1000-, 250- and 157-Resistance Ratio to the insecticides chlorantraniliprole, indoxacarb, spinosad and emamectin benzoate respectively. The control failure likelihood was significant (p<0.05) in all cases, suggesting that the particular multi-resistant strain could not be controlled by any of the register insecticides, thus the current pest management schemes have to be drastically revised with minimal reliance to chemicals. Currently, novel insecticides, microbials and plant extracts are tested in search of novel pest management tools. Still most of these novel candidates are several years away from the market and their incorporation in agricultural practices. Also, it is admitted that greenhouse tomato production is still largely based on chemical insecticide applications and a shift to IPM schemes that don't predict use of insecticides is technically impossible for the majority of the farms at this stage. Therefore, we intend to aid the rational and sustainable revision of pest management tactics for T. absoluta in tomato crops with the contribution of academia and the support of the policy makers.

Parasitoid pre-adaptation improves biological control of symbiont-protected aphids

Authors: Vorburger Christoph[1] and Rossbacher Silvan[1], [1]Eawag & ETH Zürich, Switzerland

Abstract: Aphids are commonly infected by the heritable bacterial endosymbiont Hamiltonella defensa, which increases aphid resistance to parasitoid wasps. Laboratory cage experiments have shown that the release of parasitoids rapidly selects for symbiont-protected aphids, resulting in failed biological control, while other experiments have shown rapid counter-adaptation of parasitoids to the presence of H. defensa in their hosts. Taken together, these findings suggest that parasitoid pre-adaptation could be a viable strategy to improve biological control of symbiont-protected aphids. We tested this prediction in laboratory cage populations of black bean aphids (Aphis fabae) and their main parasitoid Lysiphlebus fabarum. Aphid populations comprised a mixture of H. defensa-free aphids, aphids infected with a moderately protective strain of H. defensa, and aphids with a strongly protective strain. These populations were exposed to five different treatments: (i) no parasitoids, (ii) parasitoids experimentally evolved on H. defensa-free aphids, (iii) parasitoids evolved on aphids protected by the less protective strain of H. defensa, (iv) parasitoids evolved on aphids protected by the more protective strain, and (v) a mixture of iii and iv. As expected, all treatments with parasitoids resulted in strong selection for H. defensa-protected aphids, but parasitoids adapted to H. defensa-free aphids and parasitoids adapted to the less protective strain of H. defensa failed to reduce aphid infestations relative to the parasitoid-free control. Parasitoids adapted to the more protective strain and the mixed parasitoid treatment, on the other hand, strongly reduced aphid densities, resulting in significantly improved host plant condition. This study thus showed, for the first time, that parasitoid pre-adaptation can improve the control of partly resistant aphid populations harbouring a protective endosymbiont.

The evolutionary ecology of defensive symbioses in aphids

Authors: Vorburger Christoph, Eawag & ETH Zürich, Switzerland

Abstract: Aphids engage in symbioses with a diverse menagerie of maternally transmitted bacterial endosymbionts. Maternal transmission couples host and symbiont fitness. This has facilitated the evolution of host protection: Several endosymbionts are known to increase aphid resistance to parasitoids or pathogens. A well-studied case is the gamma-proteobacterium Hamiltonella defensa, which occurs in many aphid species and provides protection against parasitoid wasps. Using the example of the black bean aphid (Aphis fabae) and its main parasitoid Lysiphlebus fabarum, I demonstrate that Hamiltonella plays an important role in mediating host-parasitoid coevolution. Hamiltonella increases the heritable variation available to selection, it alters the specificity of the host-parasitoid interaction as a consequence of genotype-by-genotype interactions between symbionts and parasitoids, and it modifies the trade-off between aphid resistance to parasitoids and other components of fitness. A better understanding of these complex interactions will be important to address the challenge endosymbionts pose for aphid pest control with parasitoids.

Endophytically colonized plants influence on thrips foraging behaviour

Authors: Vu Anh[1], Meyhoefer Rainer[2], [1]Leibniz Universität Hannover, Zoological Biodiversity, Applied Entomology, [2]Leibniz Universität Hannover, Zoological Biodiversity, Applied Entomology, Germany

Abstract: As a major pest in onions foraging behaviour of onion thrips, Thrips tabaci, has been investigated in detail. Many studies show that host plant selection by onion thrips is affected by visual as well as chemical host plant cues. Moreover, recently symbiotic interactions between host plant and fungal endophytes, with capacity to increase host plant resistance, has come into focus. Nevertheless, how endophytes influence onion thrips foraging behaviour still remains unexplored. In order to address this question, foraging behaviour of female T. tabaci was investigated in the laboratory with onion plants colonised by endophytic fungi, i.e. Trichoderma harzianum or Beauveria bassiana. Especially orientation towards the host plant was investigated by choice tests and feeding activity on the host plant by electrical penetration graph (EPG). Results show, that onions colonised by endophytic fungi were strongly avoided by onion thrips, and in consequence feeding damage and egg laying activity was largely reduced. Endophytic colonization also clearly showed an influence on thrips feeding behaviour, since the number of probes and probing duration of T. tabaci were significantly reduced on inoculated plants. Results will be discussed in the context of thrips foraging behaviour and possible advances in biological control.

Beetles LIFE: Positive effects of restoration burning on saproxylic insects in Finland (LIFE17 NAT/FI/000181)

Authors: Vuorio Ville, Finland

Abstract: Protected beetles that play an important role in Finland's boreal forests and bog woodlands are under threat due to loss of habitat and fragmentation, and due to a reduction in wildfires as a result of human intervention. To improve the conservation status of eight insect species across 26 project sites in Finland, degraded forest habitats are being restored and new habitats created through controlled burning and simulations of storm damage to increase the amount of decaying wood. Bog woodlands are also being restored through blocking of ditches and removing trees to improve water retention. Project monitoring has revealed that restoration measures have been successful: project target species were recorded in Kakonsalo (Stephanopachys linearis) and UK National Park (Stephanopachys substriatus and Aradus angularis) project sites as well as several fire-dependant Coleoptera and Hemiptera species including Aradus laeviusculus, a species classified as vulnerable in the 2019 Red list of Finnish species.

GOS Traps, NS1 kit and climatic factors for early surveillance of dengue in multi storey dwellings in Malaysia

Authors: Vythilingam Indra[1], Wee Kent Liew Jonathan[1] and Selvarajoo Sivaneswari[1], [1]Department of Parasitology, Faculty of Medicine, University of Malaya, Kuala Lumpur, Malaysia

Abstract: Dengue is a serious public health problem in Southeast Asia and has increased 37- fold in Malaysia compared to decades ago. New strategies are urgently needed especially with the current change in climatic conditions. A two-year study was conducted in a high human density dengue-endemic urban area in Selangor, where Gravid Ovipositing Sticky (GOS) traps were set up to capture adult Aedes spp. mosquitoes. All Aedes mosquitoes were tested using the NS1 dengue antigen test kit. All dengue cases from the study site notified to the State Health Department were recorded. Weekly microclimatic temperature, relative humidity (RH) and rainfall were monitored. 95.6% of the mosquitoes trapped were Ae. aegypti of which 23% was found to be positive for dengue using the NS1 antigen kit. Confirmed cases of dengue were observed lag of one week after positive mosquitoes were obtained. It was also observed that Ae. aegypti increased by lag of 2-3 weeks when temperature increased from 28oC to 30oC, and lag of 3 weeks with increase in rainfall. Currently a randomised-control trial is ongoing. Surveillance using the GOS traps should be able to efficiently provide adequate coverage for multi-storey dwellings where population per unit area is likely to be higher. Furthermore, trapping dengue-infected mosquitoes using the GOS trap, helps to halt the dengue transmission carried by the mosquito. It is envisaged that the results of this randomized controlled trial will provide a new proactive, cheap and targeted surveillance tool for the prevention and control of dengue outbreaks.

How a minute mite promises to make big waves in biocontrol

Authors: Wackers Felix[2], Pijnakker Juliette[1], Moerkens Rob[1], Duarte Marcus[1], Benaventa Alfredo[1] and Vangansbeke Dominiek[1], [1]Biobest Group, [2]Biobest Group NV, Belgium

Abstract: Eriophyid pests and powdery mildew are two main problems in crop cultivation for which no effective biocontrol solutions exist to date. In greenhouse trials we investigated the potential of a new group of miniscule mites (Iolinidae) to control these problem pests and key pathogens. Using Typha pollen, the Iolinid Pronematus ubiquitus established well on all tested crop plants. On tomatoes the established population was capable of controlling subsequent infestations with both russet mites and powdery mildew. This represents the first case, where an omnivorous arthropod has been shown to control a pest- and pathogen problem concurrently. The additional experiments in other crops also showed strong mildew suppression potential.

Preventatively establishing P. ubiquitus could be a real game-changer in biological crop protection as it eliminates the need for repeated pesticide use or sulphur applications. The finding that arthropods can effectively control diseases opens up entire new opportunities for biological crop protection.

Manipulating the behavior of the African weaver ant, Oecophylla longinoda, to promote biological control of mango fruit flies

Authors: Wackers Felix[1], Chailleux Anaïs[3], Correa Philippe[2], Detrain Claire[4] and Brévault Thierry, [1]Biobest Group NV, Belgium, [2]-CIRAD, UPR HortSys, Centre Commun ISRA-IRD, Senegal -Biopass, Cirad-IRD-ISRA-UCAD, Dakar, Senegal -UCAD-FST, ED SEV, Dakar, Senegal, [3]Senegal, [4]Unity of Social Ecology, University of Brussels, Belgium

Abstract: Damage to mangoes caused by tephritid fruit flies, particularly the Oriental fruit fly, Bactrocera dorsalis (Hendel) (Diptera: Tephritidae), leads to significant crop losses in Senegal. Though African weaver ants, Oecophylla longinoda (Latreille) (Hymenoptera: Formicidae), are effective predators of fruit flies, they are often considered as pests by farmers due to indirect damage caused by mealybug tending to collect honeydew. Moreover, growers blame ants for other nuisances such as biting and nesting on trees. It is thus essential to reduce the negative effects of ants to improve their adoption as a biocontrol agent in fruit tree orchards. Providing sugar to weaver ants could be a way to manipulate ant behavior and interspecific interactions with mealybugs and fruit flies. Here, we hypothesize that provision of sugar sources to ants will (i) reduce both mealybug tending, abundance of nests and ant aggressiveness, and (ii) increase their predation of fruit flies. To that end, a long-term study was launched in an organic orchard in Senegal. Three treatments have been compared: (1) mango trees with both ants and sugar feeders, (2) mango trees with ants but no feeders, and (3) mango trees without ants nor feeders. The population dynamics of mealybugs and weaver ants has been monitored over one year. Ant abundance decreased during the dry season following mango harvest and increased in the early rainy season in connection with fruit production and increase of food resources. The effect of sugar feeders on ant foraging, predation, nesting, aggressiveness, and mealybug tending was lower than expected and varied across time. Results will be key for the development of strategies for the biological control of fruit flies in African mango orchards.

Precipitation Changes as Drivers of Insect Decline

Authors: Wagner David, University of Connecticut, United States

Abstract: Changes in historical patterns of rain and snowfall have many consequences for the flora and fauna of terrestrial ecosystems. Insects, with their enormous surface body-to-volume ratios and dependence on spiracular ventilation, are particularly vulnerable to drying. In addition to the immediate threat of desiccation, decreases in precipitation have weighty knock-on effects for affected regions: they result in lowered surface waters, water tables, and soil-moisture levels; diminish snow cover, which can insulate in-ground faunas, and provide water over summer months via snow melt; elevate fire risks; lower hostplant fitness and affect plant defense systems; diminish nectar availability; and ultimately lead to hostplant death (and range contractions). Given that nearly one-half of all described insects are specialist herbivores, the reshaping of global plant communities, due to changed patterns of precipitation, will have enormous consequences for global food webs, that will cascade across the tree of life. The talk will anchor to data from the Southwestern USA but explore other regions where changes in rain and snowfall may be driving declines.

Estimating the contribution of beekeeping to household wellbeing and conservation motivations in the Tanzanian Miombo

Authors: Wagner Kata[1], Meilby Henrik[2] and Cross Pau[1], [1]Bangor University University of Copenhagen, United Kingdom [2]University of Copenhagen, Denmark

Abstract: Beekeeping is used by numerous development agencies in their efforts to promote livelihood activities that constitute alternatives to slash-and-burn agriculture in order to reduce poverty and provide incentives for forest conservation. Besides short-term monetary focused project evaluation reports, there is little evidence on the effectiveness of beekeeping to achieve these goals. We examine the contribution of beekeeping to household wellbeing and conservation motivations in four rural communities in Central Tanzania using a mixed methods approach. First, we identified predictors of beekeeping adoption, dependence and success. We found that beekeepers were often also livestock keepers and wild honey hunters. The results also indicate that beekeeping uptake was mainly motivated by the prospect of cash income, but the lack of suitable land, means to acquire hives and technical knowledge were significant inhibitors. We also found that beekeeping training provided by governmental organisations did not lead to improved beekeeping success when compared to local training provided by neighbours and family members. Lastly, elite capture of project benefits was a frequent occurrence when project participation was linked to the requirement to form associations. We then assessed whether beekeepers were better-off in ten crucial life domains than their non-beekeeping peers and whether beekeeping was effective in filling an income gap during the agricultural year. We observed that while beekeepers were slightly more food secure, positive effects on other life domains were limited to beekeepers marketing more than just honey. Beekeepers were slightly more resilient and had marginally more farm-and non-farm assets, but the differences to non-beekeepers were relatively negligible. We found that beekeeping income was not sufficient to effectively bridge income gaps throughout the year. Finally, we analysed the associations between beekeeping and conservation by assessing a range of factors contributing to forest-friendly behaviour. While we found beekeeping to be linked to slightly more intensive forest use, more positive attitudes towards the forest and a stronger appreciation of conservation benefits, the observed differences between beekeepers and non-beekeepers were again relatively small. Beekeepers also engaged in forest destructive behaviours or did not have sufficient influence within their communities to protect forest resources. These findings are of importance, as considerable efforts are being paid to the promotion of beekeeping in developing countries, including in the context of REDD+. The results of this study can inform better-targeted investment in beekeeping as an alternative livelihood option by improving the selection of beneficiaries and the design of project delivery mechanisms, by creating realistic expectations of potential beekeeping benefits and identifying further measures potentially needed to achieve livelihood and conservation goals.

A modeling approach to improve the efficiency of augmentative biological control with arthropod natural enemies

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Abstract: Identifying key life-history traits of biocontrol agents and their effect on population dynamics is important to obtaining more efficient pest control and generating higher economic returns for biocontrol practitioners. An optimality simulation model was built to identify the most important life-history traits of natural enemies to improve their efficacy as biocontrol agent, taking into account the costs and benefits for biocontrol practitioners. Two different optimized life-history strategies for the agents were found with higher potential economic returns. These strategies differ in the plant-leaving decision and host handling time of the biocontrol agents, but also in their respective fecundity, longevity and dispersal ability. The preferred strategy depends on the number of agents released and the growth rate of the plant.

What shapes leaf miner abundance on oak trees in a forest: leaf quality or movements?

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Abstract: The abundance of leaf miners on a tree may be affected by leaf quality and the rate of movements among trees. Factors affecting leaf quality include genetic traits, responses to herbivory, and interactions with neighbouring trees. Insect movements may be limited by distantly related neighbours. We recorded leaf mines in the crowns of mature oaks (Quercus petraea) in a forest in western Poland in July and October of three years. We evaluated the effects of budburst phenology, microsatellite traits, genome size, physical and chemical traits of leaves, leaf damage by other insect herbivores, and the phylogenetic distance to neighbours as predictors of leaf miner density and community structure. We found that leaf miner abundance was higher on trees that appeared less nutritious (low nitrogen content) and more defended (high polyphenol content). The phylogenetic neighbourhood of the tree did not appear to affect leaf miner abundance. Our results suggest that leaf miner abundance is mainly affected by oviposition behaviours and establishment success. In addition, leaf miners may avoid competition with other herbivores by selecting trees with low leaf quality, while they suffer little costs because they may be able to locally alter leaf chemistry.

Grant No. 2018/29/B/NZ8/00112 National Science Centre (Poland).

Native and non-native egg parasitoids of Halyomorpha halys: variation among regions and habitat types in the U.S.A.

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Abstract: Halyomorpha halys is an invasive insect found throughout many regions of the U.S. and in a diversity of managed (orchard, vegetable and field crops) and natural (wooded edges) habitats. Its abundance and pest status varies by region and habitat type. To determine the identity of natural enemies associated with H. halys and their impact on H. halys eggs, a large collaborative survey was conducted over two years in five U.S. regions, involving 13 states and 26 scientists. Surveys using sentinel and naturally laid H. halys eggs elucidated differences in native and non-native egg parasitoid identity and their impact on H. halys eggs among regions and habitat type. As expected Trissolcus japonicus was the only non-native egg parasitoid emerging from H. halys eggs and native parasitoids included Trissolcus spp., Anastatus spp., Telenomus spp., and an Ooencyrtus sp. The native and non-native parasitoids associated with H. halys varied by region and habitat type, and between the first and second year of the study. For example, non-native T. japonicus was found in only one region in 2017 and in 3 regions in 2018 (of 5 regions), while native Anastatus spp. was found mainly in the mid-Atlantic and Southeast regions, with very low numbers on the Pacific Northwest region both years. Parasitoid diversity was greatest in the mid-Atlantic region, which was predicted since this is where H. halys was detected and became an outbreak pest first. While overall parasitism (emerged parasitoids) was low (4%), it was greatest in semi-natural, forests and ornamental habitats. Parasitoid species varied in their relative abundance among habitat types. For example, Anastatus and Trissolcus are arboreal and Telenomus and Ooencyrtus were found only in vegetable / field crop habitats. Knowledge of differences in parasitoid species identity and their impacts on H. halys among diverse habitats and regions will assist in identifying measures to maximize biological control programs in the U.S. and other invaded countries.

Problems Created by the brown marmorated stink bug invasion, and the scientific and industry response.

Authors: Walgenbach James, North Carolina State University, United States

Abstract: In North America, the brown marmorated stink bug (BMSB), Halyomorpha halys Stål, first appeared as a major pest in 2010 in the mid-Atlantic states of the USA, approximately 15 years after it was first detected in that region. With the agricultural community largely unprepared for this abrupt population explosion, BMSB caused near catastrophic damage to a wide range of tree fruit and vegetable crops, especially apples, peaches and fruiting vegetables. This was followed by large invasions of homes in residential areas when adults dispersed to overwintering areas in the fall of 2010. The pest subsequently spread to other regions of the country, and now has been detected in 46 states with established populations in 38 states. The response of the scientific community, grower organizations, and crop protection industry was swift. A BMSB working group was formed to identify research and outreach priorities, and a large Federal grant that included over 50 PI's from nine states was successfully obtained to guide research. Initially, tree fruit IPM programs that took decades to develop, and which relied on soft chemistry, mating disruption, and biological control, were replaced by frequent applications of broad spectrum pyrethroid insecticides. This predictably led to secondary pest outbreaks and additional pesticide use. However, multidisciplinary research teams have made considerable progress in understanding the biology and ecology of BMSB, developing monitoring programs, semiochemical based management tactics, and expanding biological control of BMSB with Asian parasitoids. This symposium will highlight progress that has been made in rebuilding IPM programs following the invasion of BMSB.

Insect venoms: Biochemical weapons used to facilitate and defend against predation

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Abstract: Venom use to facilitate or defend against predation has evolved independently at least 13 times among the insects. However, almost nothing is known about the venom systems or toxins of most venomous insect groups excepting the Hymenoptera (wasps, ants, and bees). To address this gap in knowledge, we have investigated the venom systems of three diverse but neglected insect groups, specifically the assassin bugs and allies (Heteroptera: Reduviidae), robber flies (Diptera: Asilidae) and nettle caterpillars (Lepidoptera: Limacodidae) using proteomics, transcriptomics, imaging technologies, and toxicity assays.

Assassin bugs and giant water bugs have morphologically complex venom glands that produce two different venoms that they can inject independently. Venom from the posterior main gland rapidly paralyses and kills prey insects when injected, and activates mammalian peripheral neurons that sense pain. Although assassin bug venom contains peptide toxins with similar structural folds to spider venom 'knottin' toxins, much of its bioactivity depends on currently uncharacterised protein toxins with higher molecular mass.

Robber fly venom displays similar insecticidal and pain-causing bioactivities as assassin bug venom, but contains a more diverse range of peptide toxins. We have solved the structure of two heterologously expressed robber fly venom peptides that cause rapid paralysis when injected into insects. One of these, Dg3b, is a member of the cystine-stabilised a/ß defensin family and is closely related to insect innate immunity peptides, but shows greater similarity to scorpion venom peptides both structurally and in its ability to modulate neuronal potassium channels.

In contrast to the orally produced venoms of assassin bugs and robber flies that are used primarily for predation, venoms of nettle caterpillars (Limacodidae) are produced in cuticular spines and used only for predator deterrence. Their venoms contain more peptides and fewer enzymes, and do not kill but cause pain and aversion, and include both 'knottin' peptides and modified insect neurohormones.

Currently, we are seeking to identify the individual venom toxins from each of these three families that underlie the biological effects of venom, and to characterise them structurally and functionally. We believe this will provide new insights into the molecular weaponry used by insects, both to facilitate predation and defend against it.

Codling moth sterile insect releases: A supplementary phytosanitary measure for New Zealand apple exports

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Abstract: The New Zealand apple industry ships almost 50% of its export production to Asian markets that require strict phytosanitary measures to eliminate the risk of codling moth (CM) larval infestation in fruit. Apple growers follow Integrated Fruit Production (IFP) principles and the industry adheres to the New Zealand Ministry of Primary Industries' 'systems-based' programme, for additional CM risk mitigation in crops destined for Asia. Despite the high phytosanitary performance of this regulatory programme, some Asian countries have a zero tolerance for CM and require mandatory postharvest disinfestation with the fumigant methyl bromide. New Zealand aims to eliminate the last remaining uses of this greenhouse gas so the apple industry is investigating localised eradication of CM as a potential supplementary phytosanitary measure for apple exports to markets with a zero tolerance.

The sterile insect technique (SIT) is being attempted on six IFP orchards (total 350 ha), and one 38 ha organic orchard, in Central Hawke's Bay (CHB). The orchards are isolated by farmland from each other and other orchards which greatly reduces the risk of CM immigration. IFP programme measures include threshold-based insecticide applications and use of pheromone mating disruption. We are supplementing these measures with weekly releases of sterile CM (~250 per ha) delivered by a fixed-wing, unmanned aerial vehicle (UAV) flying at a height of 40–50 m. Three orchards are currently in the fifth year of releases and catches of wild CM on these orchards in 2018–19 were 93–96% lower than in 2013–14, the year before releases began. Three orchards have had 3 years of moth releases and average annual catches have decreased 84–92% since 2015–16. The BioGro™ New Zealand certified organic orchard has had 2 years of SIT releases and catches are down by 79%, but initial populations were much higher than other orchards.

Catches of wild CM on the IFP orchards are now extremely rare (range 0.03–0.22 moths/ha/season in 2018–19) and packhouse records show no codling moth damaged or infested fruit have been detected since SIT moth releases commenced in 2014. There are relatively few wild apple host trees within a >5 km radius of the SIT-treated orchards. Pheromone trapping found mixed densities in these host trees; season-long moth catches in 30 traps were: 0 moths (7 traps), 1–5 moths (11 traps), 9–13 moths (6 traps) and 22–53 months (6 traps). Recent expansion of the SIT programme (+80 ha) onto the Heretaunga Plains (New Zealand's major apple growing region) using a DJI M600 Pro hexacopter has enabled more manoeuvrable flight at lower altitudes (25 m) and recapture of sterile moths averaged 10 times and three times higher, respectively, than that of moths released via the fixed-wing UAV. Special measures to reduce pest prevalence, such as additional sterile insect releases or alternate host tree removal, would be needed to reduce the risk of immigration and achieve local eradication.

An atypical moth pheromone receptor in the genus Spodoptera

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Abstract: In the highly diversified insect order Lepidoptera, male pheromone receptors (PRs) tuned to female-emitted type I pheromones (which make up the vast majority of pheromones identified) form a dedicated subfamily of odorant receptors. Using a combination of heterologous expression and in vivo genome editing via CRISPR-Cas9, we identified in males of the cotton leafworm Spodoptera littoralis one PR that does not belong to this subfamily but to a distantly related lineage. It suggests two independent apparitions of PR for type I pheromones in moths. This PR is specifically tuned to the major sex pheromone component emitted by females and mutant males for this receptor are not able to mate. Using available genomic and transcriptomic data, we also identified orthologues and paralogues of this receptor in other Spodoptera species and compared their response spectra, in order to rebuild the evolutionary history of this receptor and to understand how it became specifically tuned to the major pheromone component in S. littoralis and its sister species S. litura.

Virus discovery and dynamics in a wild Drosophila community

Authors: Wallace Megan, University of Exeter, United Kingdom

Abstract: The fruit fly Drosophila melanogaster remains a key model system for the study of insect-virus interactions, and recent metagenomic sequencing studies have identified over 140 naturally-occurring viruses of the Drosophilidae. This could enable the study of study of 'typical' wild co-evolutionary dynamics between insects and their viruses, which might help us to understand the evolution of insect-vectored viruses with economic and public health impacts.

In this study, we make the first attempt to quantify the dynamics of wild drosophilid virus communities. We used metagenomic sequencing to describe the 41 new and previously described viruses present in populations of Drosophila in South-east Scotland, along with their host range, finding that over 90% of these viruses infect multiple host species. We also examined how ten of these viruses vary in prevalence in the wild using repeated, spatially and temporally structured sampling of a total of 2227 flies of 15 species, over three years. We describe prevalence variation across host species, and season, along with the frequency of co-infection. We then investigate what predicts patterns of host range and prevalence in insect viruses using phylogenetic mixed models. Together, these data capture a rare snapshot of multi-host, multi-virus community dynamics in wild insects.

Attraction of pollinator Eupeodes corollae is mediated by odorant receptor 25 narrowly tuned to aromatic floral compounds

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Abstract: Flowering plants have evolved strategies to attract pollinators with volatile compounds that are accurately perceived by the sensitive olfactory system of insects. Syrphid flies are the largest flower visiting Diptera, but little is known on how they detect floral scents at the molecular level. In this study, fourteen aromatic compounds were used in Electroantennogram (EAG) recordings, and all of them elicited responses from the antennae of Eupeodes corollae. In order to identify ORs of E. corollae tuned to aromatic volatiles, we analyzed functional profiles of Drosophila melanogaster odorant receptors (ORs), DmelOR46a and DmelOR71a, which are narrowly tuned to phenolic compounds and represent the orthologues of E. corollae OR25 and OR28, respectively. The full-length genes encoding EcorOR25 and EcorOR28 are expressed in the antennae of both sexes and were functionally characterized. EcorOR25 is narrowly tuned to several structurally-related floral scent volatiles, including eugenol, p-cresol and methyl eugenol. Finally, choice behavior assays showed that eugenol and methyl eugenol were strong attractants for both sexes of E. corollae adults. In summary, our study indicates that EcorOR25 of E. corollae may be involved in flower foraging and pollination.

Prevalence of Three Common Urban Pests in Low Income Housing

Authors: Wang Changlu, Department Entomology, Rutgers University, United States

Abstract: Urban pests infestations commonly occur in residential buildings. The prevalence of different urban pests infestation is affected by both building occupant behavior and efficacy of pest management service. To address the infestations, residents often take matters into their own hands, which can result in the misuse of insecticide applications, and pose potential health risks to residents. In this study, community-wide pest surveys were carried out. More than 4000 apartments from twenty low-income apartment buildings, occupied by senior citizens in New Jersey, United States, were included. The objective of this study was to analyze the presence, prevalence, and spatial distribution of German cockroaches, house mice, and common bed bugs in relation to the environmental conditions, resident demographics, and pest control history of each apartment. We conducted resident interviews and visual inspections and assessed apartment conditions. To detect the presence of most common urban pests, sticky traps for German cockroaches, baited-mouse stations for house mouse, and interceptors for common bed bugs were employed. The inspection found the top three urban pests to be as follows: German cockroaches (Blattella germanica L. [Dictyoptera: Blattellidae]), rodents, and bed bugs (Cimex lectularius L. [Hemiptera: Cimicidae]). The results will help pest management professionals, public housing authorities, and residents in selecting for optimum strategies in managing indoor pest infestations.

Spatial distribution of German cockroaches in a high-rise apartment building before and after implemetation of an IPM program

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Abstract: The German cockroach, Blattella germanica (L.) (Blattodea, Ectobiidae), is one of the most common indoor pests in multifamily housing communities. Our objectives were to investigate the spatial distribution patterns of German cockroach infestations in a multiunit dwelling before and after building-wide integrated pest management (IPM) implementation. The study was conducted in a high-rise apartment building with 188 residential units in Paterson, New Jersey, USA. At 0 month, 49% of the apartments were infested with German cockroaches. All the identified infestations were treated by researchers using IPM implementation, and monitoring was repeated at 6 and 12 months after the initial survey. The building-wide infestation rate decreased from 49% to 24% and 12%, at the 6- and 12-month inspections, respectively . We examined cockroach spatial distribution patterns within and between apartments. Traps placed by the stove and refrigerator caught significantly more cockroaches than traps placed in the kitchen cabinet under the sink or in the bathroom. At month 0, cockroach infestations within the building were spatially correlated. At 12 months after implementation of IPM, only infestations cross the floors remained to be correlated. Therefore, IPM not only eliminates cockroach infestations in individual units, but also reduces cockroach dispersal between units.

Olfactory coding of sex pheromone blends with reverse ratios in two Helicoverpa moth species: so similar, yet so different

Authors: Wang Chen-Zhu, State Key Laboratory of Integrated Management of Pest Insects and Rodents, Institute of Zoology, Chinese Academy of Sciences, China

Abstract: Sex pheromones released by female moths are detected by the olfactory sensilla with high specificity and sensitivity in antennae of conspecific males. The two sympatric closely related species, Helicoverpa armigera and Helicoverpa assulta share two major sex pheromone components, cis-11-hexadecenal and cis-9-hexadecenal, but in reversed relative concentrations, 97:3 and 7:93, respectively. We combined molecular biology, electrophysiology, optical imaging and behavior to investigate the olfactory coding mechanisms in males to their sex pheromone blends. Five pheromone receptors from the two species were identified functionally in the Xenopus laevis oocyte expression system. Specific olfactory sensory neurons (OSNs) in three types (including some subtypes) of antennal sensilla were proved to be involved in the pheromone coding. The projection of the axons of OSNs to the male specific macroglomerular complex in the antennal lobe was also compared between the two species. I will report how we assign different PRs to OSNs and types of sensilla responding to the pheromone components and the related compounds. We find that the PR orthologs in the two species do not necessarily have the same selectivity, and their species-specific changes in the tuning selectivity in male moths could be achieved with just a few amino acid mutations. We conclude that evolution of the olfactory coding mechanisms for pheromones of the two species satisfies the need of specific-species pheromone detection, which shed new light onto the reproductive isolation between these species.

The functional correlation between pheromone binding proteins and pheromone receptors in Helicoverpa armigera

Authors: Wang Chen-Zhu[1], Guo Hao[2], Huang Ling-Qiao[2] and Guo Ping-Ping[2], [1]Institute of Zoology, Chinese Academy of Sciences, Beijing, China, [2]Institute of Zoology, Chinese Academy of Sciences, China

Abstract: Three pheromone-binding proteins (PBPs) are abundantly expressed in antennae of moth species. Despite they have widely been studied by the competitive fluorescence binding assay, the roles of the PBPs in olfactory peripheral events remain contradictory. Helicoverpa armigera, wreaking havoc on agriculture and horticulture worldwide, utilizes (Z)-11-hexadecenal (Z11-16:Ald) and (Z)-9-hexadecenal (Z9-16:Ald) as its principal sex pheromone components. A pheromone receptor (PR), HarmOR13 when co-expressed with HarmORco in Xenopus oocytes is strongly activated by Z11-16:Ald, albeit with mediocre but appreciated sensitivities to other structural analogs. Here, by devising the olfactory system in Drosophila T1 sensilla, we studied the functional correlations of HarmPBPs with HarmOR13. First, RNA in-situ hybridization together with in-depth immuno-fluorescence staining revealed the three PBPs were colocalized in the supporting cells underneath trichoid sensilla, implying a specific role for pheromone detection. HarmOR13 olfactory receptor neurons (ORNs). Next, we expressed each PBP into the supporting cells of Drosophila T1 trochoid sensilla by LUSH-GAL4 drivers and investigated whether the presence of PBP could modulate the sensitivity and selectivity of HarmOR13 that is concomitantly expressed in OR67d ORNs using ORCO-LexA driver line. We found that the three PBPs were ineffective to change the selectivity of HarmOR13. Moreover, the presence of each PBP increased the sensitivity of HarmOR13 to Z11-16:Ald and other analogs in similar manners. Taken together, our results suggest that PBPs are essential to maintain the full peripheral sensitivity but play a negligible role to modulate the specificity.

A taxonomic study on the genus Odonterpyris Kieffer (Hymenoptera, Bethylidae) from China

Authors: Wang Chunhong, Institute of Insect Sciences, Zhejiang University, China

Abstract: The genus Odontepyris Kieffer 1904 belongs to the subfamily Bethylinae and it’s one of the most recognizable genera of Bethylinae for the large size and the present of median longitudinal as well as transverse carinae in the propodeal disc.
Currently, 42 species of this genus have been recorded in the world. Among this genus, 8 species are known from China . After carefully examined the specimens of this genus collected from China, we provided descriptions of 14 new species as well as a key to Chinese species.

Mechanisms underlying whitefly manipulation of plant defence response by a salivary protein

Authors: Wang Fang, Institute of Insect Sciences, Zhejiang University, Hangzhou, China

Abstract: Many phloem-feeding insects are able to manipulate host plant defence using salivary effectors. We demonstrated previously that expression of the whitefly Bemisia tabaci salivary protein BtQ0F1 enhanced whitefly performance on its host tobacco, and we hypothesized that this enhancement effect may be associated with leveraging crosstalk between jasmonic acid (JA) and salicylic acid- (SA-) signaling pathway in the plant. In this study, we show that the whitefly salivary protein BtQ0F1 increases the susceptibility of host plant by suppressing SA signaling pathway as well as JA signaling pathway. Overexpression of BtQ0F1 gene in planta promotes the susceptibility of tobacco to whitefly and suppresses SA signaling pathway as well as JA signaling pathway. In contrast, silencing whitefly BtQ0F1 gene significantly decreases whitefly performance on host plants. Our results indicate that the whitefly salivary protein BtQ0F1 suppresses plant defence by interfering the crosstalk between JA-SA signaling pathways in host plants.

Study on the Resurgence and Steam Treatment of Bed bugs in Mainland China

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Abstract: BACKGROUND: Bed bugs (Cimex lectularius L. and Cimex hemipterus (F.)) are obligate blood-sucking insects that feed upon humans and other animals. Recent two decades, the reports of bed bugs infestation have increased gradually in Mainland of China, especially for the Pearl River Delta Region. However, the species of bed bugs in this area is less reported. Based on our previous lab studies, steam treatment can be applied as an effective method to kill bed bugs on bed or sofa surface and under a cloth fabric, as well as in crack; and can temporarily reduced bed bug mobility and blood-feeding ability. However, less report was concerned on the field control of bed bugs through steam treatment. In this study, firstly, morphological identification and molecular technique that based on the differential of genetic distances of mitochondrial Cytochrome C oxidase subunit I gene (COI), were conducted for identifying the species of bed bugs collected from Guangzhou and Foshan City. Secondly, the efficacy of one affordable consumer-grade commercial steamer for killing bed bugs was evaluated in field study. The results of our studies may have important implications on the use of steam treatment for bed bug management in China.

RESULTS: There was no significant difference in the width to height ratio of Guangzhou (2.6) and Foshan (2.4) samples' pronotum, but both of them were significantly lower than those of Cimex lecturlarius (Ft. Dix strain, 3.1) which was used as a reference substance. The genetic distances of test samples with Cimex hemipterus were 0-0.2%, and 22.2-22.6% with Cimex lecturlarius. In the Maximum likelihood phylogeny tree, the tested samples were clustered into a same branch with C. hemipterus, and the support rate was 100%. In field study, the consumer-grade steamer at an affordable price can achieve a high control efficacy of bed bugs that exposed on mattresses, as well as hided in cracks.

CONCLUSION: Bed bugs collected from Guangzhou and Foshan belong to C. hemipterus. Proper use of steamers can kill all life stages of bed bugs. Even the affordable consumer-grade steamer can also be effective for eliminating bed bugs resting on mattresses, or hiding in cracks.

Multi-Omics Integration and CRISPR-based Genome Editing to Improve Poplar for Bioenergy and Stress Response

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Abstract: Multi-Omics integrative analysis of lignin biosynthesis can advance the strategic engineering of forest trees for adaptation and utilization. Lignin is a heterogeneous phenolic polymer deposited in secondary cell walls of vascular plants. It provides mechanical support to plant cell walls, hydrophobicity for water transport, and augments defenses against biotic and abiotic stresses. Lignin is polymerized from three monomers (monolignols) produced by a grid-like pathway. The pathway in wood formation of Populus trichocarpa has at least 21 genes, encoding enzymes that mediate 37 reactions on 24 metabolites, leading to lignin and affecting wood properties. We perturb these 21 pathway genes and integrate transcriptomic, proteomic, fluxomic and phenomic data from 221 lines selected from ~2,000 transgenics. Stem-differentiating xylem of the transgenics and wildtype were analyzed by 239 full transcriptomes and 239 proteomes to regress the abundances of transcripts and proteins. Using recombinant proteins from the 21 monolignol pathway genes, we determined 207 reaction and inhibition enzyme kinetic parameters to predict the effects of protein abundances on pathway metabolic-fluxes and metabolite concentrations. To determine the effects of metabolic-fluxes and metabolite concentrations on lignin and wood properties, we quantified the chemical composition of 220 wood samples, and 76 lignin samples using 2D HSQC NMR for lignin composition and structures. We measured the growth of 221 lines, the modulus of elasticity of 416 wood samples, and the density of 213 wood samples. All these data were then systematically integrated to describe the transduction of biological information from the 21 monolignol genes through transcripts, proteins, metabolic-fluxes, and metabolite concentrations, leading to 25 wood traits, including lignin content, composition, and interunit linkages. The analysis then predicts improvements in any of these 25 traits individually or in combinations, through engineering expression of specific monolignol genes. The analysis informs CRISPR-based editing strategies to improve wood utilization and may lead to a greater understanding of plant adaptation to biotic and abiotic stresses.

Neuropeptide signaling in the male reproductive system of Drosophila

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Abstract: Myosuppressin peptides (Ms) are well-conserved insect brain-gut peptides with a -FLRFamide C-terminus and have roles in regulating muscle activity of the gut, heart and female reproductive tissues. The Drosophila genome has two GPCR type receptor genes (MsR1 and MsR2) that bind Drosophila Ms peptide. The pharmacology of these two receptors appear to very similar, when heterologously expressed in cell lines. We have been investigating a role for Ms signaling in the male reproductive tract of D. melanogaster and possible involvement in regulating ejaculation. Both sperm and non-sperm components (seminal fluid) of the male ejaculate are important for reproductive success in insects. In Drosophila, mature sperm is released from the seminal vesicles (SV) and mixed with seminal fluid prior to ejaculation. Copulation takes around 20 min and seminal fluid and sperm transfer (SFST) is complete by 12 min. The paired male accessory glands (MAG), the ejaculatory duct (ED) and the ejaculatory bulb (EB) all contribute to the seminal fluid with the MAG providing the bulk of the material. Initiation and termination of ejaculation will rely on the coordinated activity of the muscle layers surrounding these male structures. Four corazonin/cholinergic interneurons of the male abdominal ganglion promote SFST by activating 5-HT neurons that project directly to the MAG, ED and SV. We find distinctive Ms neurons from the abdominal ganglion, two rectal cells and a single cell positioned close to the ED innervating the male reproductive tract, suggesting a role for Ms in muscle inhibition. We show that the MAGs display bursts (~25 s) of strong muscular contractions that are asynchronous with the sustained peristaltic contractions of the ED. The MAG contractions are strongly inhibited by exogenous Ms, with full inhibiton at 10 µM. Null mutant alleles of both Ms receptors (MsR11 and MsR21) were generated by targeted gene-editing using CRISPR/Cas9 technology. Ms inhibited MsR11 MAG contractions, but no Ms induced suppression was observed with MsR21 glands, demonstrating a specific role for the latter receptor in transduction of the Ms signal. Strong expression of MsR2-GAL4, but not of MsR1-GAL4, in the MAG muscle is consistent with this conclusion. Direct evidence of the importance of male Ms signaling in reproduction was obtained by silencing male Ms-neurons and by phenotypic analysis of the performance of MsR21 males. We conclude that Ms plays an important role in male reproductive physiology and that this is dependent on MsR2.

Discovery of culturable bacteria and fungi in mosquito saliva: potential players in mosquito-borne virus infection?

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Abstract: Pathogens transmitted by mosquitoes result in the death of almost 1 million people every year. As mosquito saliva plays a key role in virus transmission and pathogenesis in human skin, here we explore if salivary microbes are potential contributors to this effect.

The saliva of Aedes aegypti and Culex pipiens was harvested and plated on agar plates to detect actively growing fungal and bacterial colonies. We identified the fungal species Penicillium crustosum for the first time in mosquitoes. Culturable bacteria we detected include Serratia marcescens, Serratia nematodiphila, Enterobacter spp. and Klebsiella spp. which were identified previously as mosquito or insect endosymbionts. Blood-feeding positively affected the bacterial but not fungal load in Aedes aegypti saliva. Our in vitro study showed that pre-incubation with mosquito saliva significantly reduced Semliki Forest virus replication in skin fibroblasts compared to cells without saliva. Interestingly, the removal of all salivary microbiota resulted in a significant reduction of virus replication compared to saliva with microbiota.

This study concluded for the first time that the saliva of Aedes aegypti and Culex pipiens contains bacteria and fungi. Furthermore, saliva and salivary microbes may play a negative role on viral replication in human skin cells.

First report of kdr L1014F and ace-1 G119S insecticide resistance in Belgian Culex (Diptera: Culicidae) mosquitoes

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Abstract: The emergence of West Nile virus and Usutu virus in Europe is a significant risk to public health. In the absence of efficient antiviral therapy or vaccine candidates, the only strategy to control these arboviruses is to target the Culex mosquito vector. However, the selection pressure caused by exposure to insecticides in vector control or agricultural pest control can lead to the development of insecticide resistance reducing the efficacy of insecticide-based vector control interventions. In Culex mosquitoes, two of the most common amino acid substitutions associated with insecticide resistance are the kdr L1014F in the voltage gated sodium channel and G119S in the acetylcholinesterase.

In this study, Culex pipiens biotype pipiens, Culex torrentium, and Culex modestus were sampled from 2019 to 2021 in three distinct environmental habitats (urban, peri-urban, and agricultural) in and around the city of Leuven in Belgium. Two mutations resulting in L1014F and G119S amino acid substitutions were screened for in individual mosquitoes. Both mutations were observed in Culex pipiens and Culex modestus mosquitoes across the four collection sites, but not in Culex torrentium. Furthermore, multi-resistance or cross-resistance could be a developing threat, since both mutations were observed at low frequencies (resistant allele frequency <30%) and always in heterozygosity.

These results provide the first report of kdr L1014F and ace-1 G119S resistance in Culex pipiens and Culex modestus mosquitoes from Belgium, highlighting the importance of mosquito surveillance for the development of effective arbovirus control strategies in the event of an outbreak in Belgium.

The toxicity of triflumezopyrim and its sublethal effect on red imported fire ant Solenopsis invicta Buren

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Abstract: The red imported fire ant, Solenopsis invicta Buren, is a serious invasive pest in its invaded range. The use of insecticide remains the frontline method in controlling red imported fire ant (Solenopsis invicta Buren), which is one of the top 100 worst invasive organisms worldwide. Neonicotinoids are effective ingredients found in toxic baits that are used to suppress S. invicta population. To search for new and effective insecticides, we evaluated the toxicity of the novel neonicotinoid analog triflumezopyrim against S. invicta, and examine its sublethal effect in S. invicta food consumption (sugar water and locusts) and aggressiveness. Triflumezopyrim exposure to S. invicta did not cause high mortality, even at 120 μg/mL dosage for 72h treatment. Long-term exposure showed that 10 μg/mL triflumezopyrim caused 100% mortality after 2 weeks, but 1 μg/mL did not cause any significant effect on colony growth within the 56-day treatment period. Triflumezopyrim at 10 μg/mL did not inhibit S. invicta food consumption including sugar water and locust within the 7-day treatment period. Similarly, the addition of 1 μg/mL of triflumezopyrim did not inhibit the food consumption of S. invicta during the whole trial period. S. invicta treated with 10 μg/mL triflumezopyrim displayed a significant reduction of aggressiveness during interspeci?c confrontations and showed higher mortality than the control group after aggressive encounters. However, S. invicta treated with 1 μg/mL did not show any significant impact both on aggressiveness and mortality after aggressive encounters. Overall, our results showed that triflumezopyrim has a significant negative effect on fire ant population fitness. These findings imply that triflumezopyrim could be used as a bait toxicant against S. invicta.

Multiple responses of Diadegma semiclausum and its host Plutella xylsotella to elevated temperatures are asymmetrical and more detrimental to the parasitoid.

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Abstract: Understanding how temperature affects host-parasitoid interactions is crucial for predicting the likely effects of climate change. The solitary, endo-larval, koinobiont parasitoid Diadegma semiclausum is a specialist attacking Plutella xylostella and it is an important biological control agent of the pest. The development, pupal weight and fecundity of non-parasitized P. xylostella and D. semiclausum developing in P. xylostella hosts were investigated at constant temperatures of 10, 15, 20, 25, 30°C. Parasitoids reared at 30°C had the shortest adult life span, lowest egg load, lowest pupation rate, smallest pupal weight and incurred the largest costs arresting host development. Investigations of the outcome of parasitism, the effects of parasitism on host development, intergenerational population growth between the parasitoid and the non-parasitized hosts showed that higher temperatures were more detrimental to the parasitoid than its host. A higher proportion of parasitoid larvae could not complete development when reared at 30°C, the temperature at which host biomass was smallest and the metabolic demands of the parasitoid even greater than at lower temperatures. These responses might have contributed to previous failures of the parasitoid to establish in lowland tropical regions. Elevated temperatures affect host and parasitoid growth and development in multiple ways. These effects are consistently more detrimental to parasitoids than their hosts, explaining why parasitoids are more susceptible to elevated temperatures, a consistent response that might affect their impact on pest populations under conditions of predicted climate change.

Worldwide historical biogeography of termites (Blattodea: Isoptera)

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Abstract: Termites are well-known for their importance in organic matter decomposition and soil fertilization in tropical and subtropical ecosystems. Termites diverged from other cockroaches ~170 Ma, and all modern termite species share a common ancestor dated at 149 Ma. Given the antiquity of termites, both vicariance, through plate tectonics, or dispersal, through oceanic rafting or across land bridges, can explain the current distribution of termites. The phylogenetic relationships among termite families and subfamilies are well-studied. However, the relationships among lineages that diverged more recently have been unknown until recently. In our project, we used complete mitochondrial genomes to build time-calibrated phylogeny of termites, with the final aim of resolving the global historical biogeography of termites. We selected a representative set of samples, including species from all lineages, and from across the geographic locations where termites are known to occur. This dataset allowed us to reconstruct the precise origins and dispersal patterns of termites. Finally, we will sequence mitochondrial genomes of around 2000 samples including almost all termite species of the Neotropical regions.

RNA interference strategy triggered the abnormal reproductive development through silencing the crucial genes of the Sphingolipid pathway in the Brown Planthopper (Nilaparvata lugens)

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Abstract: Insect fecundity is defined as the number of offspring produced by an individual female during a set time period. Their robust fecundity not only ranks insects as the most diverse class of animals on earth but also makes insect pests a tremendous threat to human health and agricultural production. Sphingolipids are major structural components of endomembranes, which plays a crucial role in differentiation senescence, proliferation, apoptosis, programmed cell death and stress responses. In past studies in our laboratory on Sphingolipid pathway, the fecundity-related mechanisms have been studied at the levels of pathways and genes. Serine palmitoyltransferase (SPT) and Sphingomyelin phosphodiesterase (SMPD) are the key enzymes of sphingolipids, silencing the SPT and SMPD via RNA interference showed abnormal development and low fecundity.MicroRNAs(miRNAs)are a group of small non-coding RNAs involved in various development and biological processes through negative regulation of mRNAs at both transcriptional and post-transcriptional levels. It's also act in insect development and reproduction by regulating genes involved in these physiological processes. Although hundreds of insect miRNAs have been identified, the biological roles of most remain poorly understood.The brown planthopper (BPH), ilaparvata lugens (sta(o)l), which belongs to Homopteran, Delphacidae, is one of the most serious and destructive insect pests of rice. BPH have two wing phenotypes, long-winged (LW) and short-winged (SW) morphologies. LW morphs are capable of long-distance migration,while SW morphs have high reproduction capabilities. In the present study, small RNA libraries from (dsGFP, dsSPT, dsSMPD) short-winged morphologies female adults were constructed and sequenced. Subsequently, we examined the expression patterns of these miRNAs at three libraries. We used a multi-algorithm approach for miRNA target prediction in 3'UTRs of fecundity-related genes in the brown planthopper (BPH) Nilaparvata lugens and identified 43 putative miRNAs targeting SPT, 70 miRNAs targeting SMPD. High-ranked miRNAs were selected for target validation. Though QRT-PCR from different development phases and tissues, we experimentally verified N. lugens SPT may as an target of microRNA-1a. SMPD may targeting miR-71 and miR-184. In the females, SPT relative expression was down-regulated after injection of a miR-1a-3p agomir but up-regulated after injection of a miR-1a antagomir. In addition, overexpression of miR-1a disrupted ovary development in N. lugens. These findings showed that miR-1a is involved in regulating N. lugens fecundity by targeting SPT. Moreover, this study may lead to better understanding of the fecundity of this important agricultural insect pest.

Density-dependent aging plasticity in the migratory locust, Locusta migratoria

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Abstract: Locusts are one of the world's most destructive agricultural pests. At 2020, the locust swarms in East Africa and Middle Asia made more than 19 million people at risk of severe food insecurity. The lifespan and aging of locusts is one of the most important factors that determine the extent of locust plague. Thus study of the aging characteristics of gregarious locusts will help predict the hazard area and duration of locust plague. Here we systemically study the aging signatures of gregarious locusts at the physiological, cellular, and molecular levels. We first characterized the lifespan of adult locust males and found the locust has a short lifespan with median 22 days after exclusion. Then we assessed the changes of two key physiological traits, flight ability and sperm states which is important to locust plague. Our results revealed a remarkable and fast declines in flight ability and relative slight declines in sperm states upon aging. The cross-species comparisons of aging-related transcriptomes revealed the common signatures of aging-related genes between locusts and other model species, suggesting the overall conserved aging mechanisms between locusts and other species. Furthermore, we assessed the tissue-specific transcriptional changes in locusts, characterized by fast and intense alterations in flight muscle and fat body but stable testis and brain. Aging of flight muscle is accompanied by dramatic decline in the expression of genes involved in energy metabolism and aged fat body displayed intense upregulation of genes related to detoxification and immunity, revealing the intense homeostatic disruptions of metabolism and stress responses in aged locusts. The histological experiments also revealed remarkable aging deterioration in flight muscle and fat body but not brain. Lastly, we identified 4 representative locust aging genes (LIPT1, JUN, IAP1, and PGRP-SA) through screening locust transcriptomes, the knockdown of these 4 genes and 3 well-known aging genes (SOD1, LAMIN, and PINK1) in locusts all lead to short lifespan and aging phenotypes. Our results revealed although locusts have a large extent of conservation of aging characteristics with other species, they also displayed specific aging signatures such as fast deterioration of fat body and insensitivity to aging of brain, activation of detoxification, and several locust-specific aging genes. These findings will help us understand the aging process of gregarious locusts and contributed to accurately predict the extent of locust plague by considering the aging-related deteriorations.

Yeast-dependent population differentiation in Drosophila melanogaster

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Abstract: Adaptation to different ecological environments through divergent natural selection could result in reproductive isolation between populations and drive the formation of new species. Reproductive isolation will be accelerated when heterogeneous food resources not only promote divergent adaptation but also provide the substrate for reproduction. In many taxa, semiochemicals play a crucial role in food localization. Therefore, semiochemicals derived from food sources may attract different individuals to different food sources and hence reduce mating opportunities with one another. Over the course of many generations of selective pressure from heterogenous food resources, populations may evolve different behaviours including feeding and mating preferences. We test this hypothesis using Drosophila melanogaster and its main food source, yeast, which is essential for almost all stages of fly life cycle. Given the enormous diversity of yeast species and the global distribution of Drosophila melanogaster, different Drosophila populations may have adapted to different local yeast species. To explore the relevance of Drosophila-yeast interactions, we examined the influence of yeast and its semiochemicals on major Drosophila life history traits including: attraction, feeding, mating, oviposition and offspring development. We quantified these traits in a Drosophila-yeast matrix of 7 globally distributed fly populations and 4 yeast species. Our results reveal that different Drosophila populations respond differently to different yeast species in mating rate, fecundity and offspring development. There is thus an interaction between Drosophila populations and yeast species, suggesting that yeast and its semiochemicals may drive fly population differentiation and hence may have impacted Drosophila evolution.

Suppression of period and timeless arrest the photoperiodic induction of summer diapause in a cabbage beetle

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Abstract: In insects, facultative diapause is a state of developmental arrest mainly induced by photoperiod or temperature that allows insects to survive adverse environmental conditions. Understanding how insect initiates facultative diapause and prepares diapause can provide us new insights to study developmental and evolutionary biology. It has been shown that the circadian clock genes can participate in photoperiodic measurement and regulate reproductive diapause initiation through JH signaling in short-day-induced winter diapause. However, how circadian clock genes translate photoperiodic information into downstream JH signaling for diapause destiny and then affect diapause preparation remains largely unknown. In the present study, we investigate this in the cabbage beetle Colaphellus bowringi which undergoes reproductive diapause under long-day condition. We respectively knocked down two circadian clock negative regulators, period (per) and timeless (tim), in the 3-day-old larvae (most sensitive to photoperiod), and dsgfp treatment was served as a control. Under the diapause-inducing photoperiod (16L:8D), knocking down per and tim significantly decreased the rate of burrowing behavior. And many female beetles of the per and tim RNAi showed developed ovary, decreased lipid accumulation and downregulated expression of stress resistance genes. The JH-induced genes, Kr-h1, JHE1, Vg1, and Vg2, significantly increased in the females with suppression of per and tim. It implied that suppression of per and tim during diapause initiation phase (DIP) could activate the JH signaling in the female adults. Before the beetles enter into diapause preparation phase (DPP), we used RNA sequencing to analyze gene expression profiles after per and tim RNAi. It showed that many differentially expressed genes were enriched in environmental information processing, such as mTOR and TGF-beta signaling pathway. To ask whether per and tim also regulate diapause preparation, we knocked down these two genes in the female adults during DPP. It showed that the diapause destiny was not affected, but the lipid storage in diapause-destined females was significantly reduced after per and tim RNAi. Interestingly, per- and tim-regulated lipid storage during DPP was independent on JH signaling. We further found that per and tim promoted lipid storage by regulating the expression of genes that control lipogenesis and lipolysis. In summary, these results suggest that per and tim participate in photoperiodic measurement and initiate reproductive diapause through JH signaling during DIP in long-day-induced summer diapause. The mTOR and TGF-beta signaling pathways may be involved in the regulation of JH signaling by circadian clock genes. Meanwhile, per and tim transduce photoperiodic signal and promote lipid storage during DPP in a JH-independent manner. These results provide us new clues to study the molecular mechanism of photoperiod-regulated diapause induction in insects.

Begomovirus ßC1 attenuates plant defense responses via interacting with NtSKP1 to promote vector performance

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Abstract: Virus-plant-insect tripartite interaction is one of the important determinants of the population dynamics of both types of organisms in the field. The relevant literatures have identified patterns about plant-mediated interaction between whitefly MEAM 1 and Tomato yellow leaf curl China virus (TYLCCNV). Thereinto, the virulence factor ßC1 encoded by TYLCCNV betasatellite played a key role in this indirect mutualism. Here, we found ßC1 interacted with the tobacco protein SKP1 (S-phase kinase associated protein 1), and NtSKP1 regulated the survival rate and fecundity of whitefly on plants. NtSKP1 and ßC1 could impact the gene transcript level in jasmonic related pathway through degrading the JAZ1 protein. These results suggested that ßC1 inhibited the plant defense responses through interacting with NtSKP1, and enhance the performance of vectors on plants.

Biology and ecology of Lycorma delicatula in its home range in China

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Abstract: The spotted lanternfly, Lycorma delicatula, is a plant hopper that is invasive in the USA and South Korea but is native to China. Lycorma delicatula is not a serious pest in China, and its biology and host range are not well studied. The host dependence, oviposition substrates, and population differentiation were studied in the home range in China. From 2017-2019, eight species of host trees were caged to determine whether L. delicatula could complete its life history or not. The results showed that the tree-of-heaven (Ailanthus altissima), Chinese toon (Toona sinensis) and chinaberry (Melia azedarach) were the preferred hosts of the pest. The spotted lanternfly can develop into adults and produce egg masses feeding solely on each of these trees. The pest feeding on grapes developed into adults but never laid eggs. The nymphs feeding on kiwifruit and Sophora japonica died before the third instar. The oviposition behavior of L. delicatula is not aligned with what would be expected based on optimal oviposition theory; the pest can oviposit on host plants, non-host plants, and even some inorganic substrates such as stones, textile, etc. The pest probably prefers to oviposit on the substrates that are stable, sheltered from rain and wind, and with lower pressure from natural enemies. As we found both the morphology and population density among different regions were varying, the differentiation of geographical populations of spotted lanternfly was also analyzed by using molecular methods based on samples collected from all locations where the pest occurred naturally in China

Development of a biological control program against spotted lanternfly: preparing for the future

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Abstract: The spotted lanternfly (Lycorma delicatula) is an exotic invasive plant-hopper that was discovered in Berks County Pennsylvania in 2014 and has since spread to five additional counties, as well as to Virginia, Delaware, and New Jersey, indicating that populations of spotted lanternfly are on the move. It threatens the grape, tree fruit, plant nursery and timber industries, which in Pennsylvania are valued at over $12 billion. This insect causes direct damage by removing sap, but indirect damage also occurs because black sooty mold grows on the copious honeydew excreted by nymphs and adults. Quarantines have been put in place to restrict the movement of plant, wood and stone products, but unfortunately the spotted lanternfly is not finicky about oviposition sites. Egg masses are cryptic and it is difficult to regulate the movement of all items potentially harboring them. Recent research on host plant utilization indicates that spotted lanternfly may be able develop to the adult stage on plant species other than tree-of-heaven (Ailanthus altissima), which could confound the eradication effort based on using tree-of-heaven as trap trees. We propose that given the eradication challenges, we should be proactive and develop a biocontrol program against the spotted lanternfly. As pest densities decrease, natural enemies with good searching behavior can be used as a tool in the ongoing eradication effort, and if eradication becomes untenable, the groundwork will have been laid for a classical biological control program.

The goal of our research is to discover parasitoids attacking spotted lanternfly in China where these pests are not in outbreak and are not considered economic pests, with the hypothesis that these natural enemies are partly responsible for reducing pest population density. To date we have discovered two potential biocontrol agents: Anastatus orientalis (an egg parasitoid) and Dryinus sp., which attacks lanternfly nymphs. Anastatus orientalis is found throughout the range of spotted lanternfly in China and depending on the circumstances (host plant, lack of pesticide use, etc.) parasitism rates can be high. We have conducted quarantine studies on the biology and life-cycle of A. orientalis, and we have initiated host specificity testing against plant-hoppers native to the U.S. In 2018 we collected Dryinus individuals and brought them to quarantine in the U.S. to start a rearing colony. Research on the biology, rearing, and host specificity testing of Dryinus species is ongoing.

Recent advances in biological control of important native and invasive forest pests in China

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Abstract: In recent decades, China has suffered severe attacks by both native and invasive forest pests. We have carried out a series of research projects on biological control of these pests. The fall webworm, Hyphantria cunea (Drury) (Lepidoptera: Arctiidae) has been sustainably controlled by an effective gregarious pupal endoparasitoid, Chouioia cunea Yang (Chalcidoidea: Eulophidae), which is native to China, and spraying HcNPV virus against the pest's larval stage. Pine wilt disease, caused by the pine wood nematode (Bursaphelenchus xylophilus (Steiner et Buhrer) Nickle) (Aphelenchida: Aphelenchidae), is currently the number one pest in China. The strategy for controlling the disease is to manipulate the nematode's vector, Monochamus alternatus Hope (Coleoptera: Cerambycidae). We discovered that Dastarcus helophoroides (Fairmaire) (Coleoptera: Bothrideridae) is the most important natural enemy in China pine forests. Mass rearing and release techniques were studied and developed. By releasing the parasitoid, 92.6% of the M. alternatus were parasitized in the first year. Meanwhile, three elaterid beetle species were found to prey on the larva of M. alternatus. The red turpentine beetle, Dendroctonus valens (LeConte) (Coleoptera:Scolytidae) was suppressed by a predator, Rhizophagus grandis Gyllenhal (Coleoptera: Rhizophagidae) introduced from Belgium and a total 3334 ha. of pine forests were protected. The oak longhorned beetle, Massicus raddei (Blessig) (Coleoptera: Cerambycidae) is the number one pest in the northeast forests of China, where it damages trunk of oaks, mainly Quercus liaotungensis and Q. mongolicus. An integrated management technique was developed for controlling the longhorned beetle: a special black light was invented for trapping the adults; the parasitoid Sclerodermus pupariae Yang et Yao (Hymenoptera: Bethylidae) was released against young larvae; and the parasitoid Dastarcus helophoroides eggs and/or adults were released when the hosts were mature larvae and/or pupae. By applying the technique for five years in northeastern China oak forests, the oak longhorned beetle has been controlled to a large extent. The emerald ash borer, Agrilus planipennis Fairmaire (Coleoptera: Buprestidae), is native to eastern Asia, including China, and feeding by larvae damages ash trees. Natural enemies of the emerald ash borer were investigated and seven species were found in China, of which Spathius agrili Yang (Hymenoptera:Braconidae), Tetrastichus planipennisi Yang (Hymenoptera: Eulophiae), Sclerodermus pupariae Yang et Yao and Oobius agrili Zhang et Huang (Hymenoptera: Encyrtidae) are predominant and have high potential for biocontrol of the pest. The biology, behavior, ecology and mass rearing techniques of the parasitoids were studied.

Effects of rearing on the host specificity and performance of a potential biological control agent of the olive fruit fly

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Abstract: Psyttalia ponerophaga is a parasitoid of the olive fruit fly Bactrocera oleae that shows potential as a possible biological control agent against this invasive pest. This parasitoid has been reared for 9 years (75 generations) at EBCL USDA ARS on an alternative host, Ceratitis capitata. The present study was designed to test the hypothesis that rearing on an alternative host affected the performance and specificity of P. ponerophaga. To test this hypothesis, two populations of P. ponerophaga (rearing and wild) were compared in host specificity and performance trials under non-choice and choice conditions with two non-target Tephritidae species. Results showed that parasitoids of the two populations tested were able to successfully parasitize the two non-target species. The hypothesis that >75 generations of rearing on an alternative host decreased the specificity of the parasitoid was not supported by the data, which showed the opposite pattern: the wild population was more effective at successfully attacking non-target hosts than the rearing population under no-choice conditions. Parasitism of non-target hosts was significantly lower in choice-test settings, but was not totally absent. Genetic analyses of dead pupae of the two non-target species revealed several occurences of failed parasitism attempts on both species, particularly in trials involving the rearing population of P. ponerophaga. The wild P. ponerophaga population was more efficient than the rearing population at parasitizing B. oleae larvae: overall parasitism rate and progeny produced per female were higher, and sex ratio was more female-biased in the wild population. These results show that long-lasting rearing on an alternative host decreased the efficacy of P. ponerophaga at attacking its main host, which could have negative consequences for its foraging efficiency under realistic field conditions.

Post release monitoring of genetic diversity and Wolbachia infection of recovered Psyttalia lounsburyi, a biocontrol agent of the olive fruit fly in California

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Abstract: Introduced biocontrol agents are expected to experience a loss in genetic diversity as the result of severe bottlenecks at different stages of biocontrol programs. Moreover, released biocontrol agents have to face and adapt to new abiotic or biotic conditions. Hybridization between individuals from different origins may favour the adaptability of the released biocontrol agents by increasing the available genetic variability. However, hybridization can be prevented when the two parents are harbouring different reproductive manipulators, such as the cytoplasmic incompatibility-inducing Wolbachia symbiont. It is thus important to get a better understanding of genetic processes and host-microbe interactions that can affect the establishment of a biocontrol agent.

Bactrocera oleae (Diptera: Tephritidae), is the most serious pest of cultivated olives worldwide. The parasitoid wasp Psyttalia lounsburyi (Hymenoptera: Braconidae) collected in Kenya and South Africa, were evaluated in quarantine. At the onset of the biological control program, the two populations of P. lounsburyi mass reared in the quarantine were genetically characterized and it indicated that they belonged to two different mitochondrial lineages. In addition, Wolbachia infection statuses were assessed for both populations and revealed the presence of two genetically different Wolbachia variants, a double infection in 96% of Kenya population, and a single infection in 50% of the South Africa population. A preliminary study on the effects of Wolbachia on its host suggested that the two variants are able to induce cytoplasmic incompatibility and that they are incompatible one with another. It also indicated that Wolbachia infection was associated with a decrease of available mature eggs.

From 2005 to 2015, more than 60 000 individuals of P. lounsburyi have been released in different counties of California. P. lounsburyi was recovered from field samples and is now established in coastal regions. The goals of this study were to assess the genetic diversity of the recovered parasitoids to identify which populations of P. lounsburyi established and spread and to study the Wolbachia population dynamics in the released populations in term of prevalence, and spatial and temporal variation of Wolbachia variants. Questions about the role of Wolbachia in the success of population establishment and hybridization were also addressed by this study.

Whereas P. lounsburyi of Kenya origin represented more than 99% of the parasitoids released, genetic studies of specimens recovered in 2015 revealed that the predominant haplotype is of SA origin. In addition, almost all the tested individuals of SA origin harbor the Wolbachia variant II indicating the spread of this Wolbachia variant in SA population. P. lounsburyi of Kenya origin mostly harbors both Wolbachia variants. The fitness cost of Wolbachia coinfection might be considered as a factor limiting the establishment of Kenya population although other fact

Evolution of active tandem repeat arrays in the nuclear and mitochondrial genomes of the jewel wasp

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Abstract: In this study, we sequenced, assembled and annotated the genomes in four jewel wasp species in the Nasonia genus and an outgroup species Trichomalopsis sarcophagae. The mitochondrial (MT) genome ranges from 14 to 16 Kbp in four species, with length variations due to the AT-rich control region (CR). Strikingly, we identified an 8,876 bp repetitive region in the CR of Nasonia vitripennis (Nv) MT genome immediately after the Cyb gene, containing thirty-seven 217-bp tandem repeat units organized in a palindromic structure. Unlike the typical tandem repeats found in known MT genomes, these repeats are significantly longer and extremely GC-rich (51%). The Nv-specific repeats were confirmed in all strains with Nv MT background, including three laboratory Nv strains collected in the US, one lab strain in Europe, an European population reference panel, as well as an Nv-mitochondrial replacement strain, suggesting that they were acquired after the split from other Nasonia species. Furthermore, these tandem repeats are actively jumping into the protein-coding regions in a subset of Nv MT genes, resulting in heteroplasmy that likely disrupts function of a subset of mitochondria within individuals, perhaps contributing to mitochondrial mutational load. Extensive search in public databases only identified repeat arrays with >70% sequence similarity in Nv nuclear genome and its B-group Wolbachia wVitB. A total of 19 repeat regions were identified in the Nv nuclear genome, 14 of which have more than 10 repeat units. The largest repeat array consists of 147 repeat units. At least 5 of these repeat arrays are insertions from the MT genome, as they are located in the NuMTs (nuclear mitochondrial DNA) and encompass partial MT-Cyb pseudogene sequences. These sequences are molecular fossils of the ancient MT repeats. After inserted into the nuclear genome, they undergo significant expansion through an unknow mechanism. We also discovered four types of repeat units in the Nv Wolbachia strain wVitB genome, suggesting the MT copies could be derived from the Wolbachia genome. This 9Kb parasitic repeats can be highly deleterious in the Nv MT genome, and we hypothesize that it may serve as the replication origin in the MT and reached fixation in Nv. This type of repeat was not observed in any other insect. They have similar characteristics of alpha-satellite sequences in vertebrates but with no sequence homology. This tandem repeat family behaves like a mobile element within the mitochondrion and between nuclear and cytoplasmic genomes.

Circadian light entrainment in a hymenopteran insect (Nasonia vitripennis)

Authors: Wang Yifan, University of Groningen, Netherlands

Abstract: Earth experiences daily and seasonal variations in light intensity and temperature due to its rotation. As a consequence of this, organisms under selection pressure have evolved an endogenous system to optimally capitalize environmental resources and to adapt to frequent fluctuations in light and temperature (Allada and Chung, 2010). This endogenous circadian rhythm persists in constant conditions but is also entrained by external signals, with light being the most important stimuli (Ben-Shlomo and Kyriacou, 2002). The molecular mechanisms of how the daily and seasonal changes of day length are detected, measured, interpreted, and translated into physiological signals are under intensive investigation. Cryptochromes, sensitive to UV and blue light, are important photoreceptors involved in the circadian light entrainment in Drosophila and plants by inducing protein degradation (Katz and Minke, 2009). However, a non-light sensitive mammalian-like CRY is found in other insect orders forms part of the biological clock as the core transcriptional inhibitor (Chauhan et al., 2017). It remains unclear what mechanisms are used in circadian light entrainment in insects with only the non-photosensitive mammalian-like CRY (Lam and Chiu, 2017). The Hymenoptera is a major insect order, comprising of bees, wasps, and ants, that carries mammalian CRY only. Therefore, the aim of this project will be to elucidate the mechanism by which the circadian clock of Hymenopteran insects (using Nasonia vitripennis as a model) is used to synchronise to light and to find the molecular substrate for latitudinal selection pressures on variation in light sensitivity. The results expected include the qPCR measurements of light induction of circadian clock genes, an action spectrum for circadian light resetting, and CRISPR-CAS manipulation of candidate circadian light induction pathway genes. While the experiments are still ongoing, I will present current data on the effects of different light intensity on circadian phase shifts and future experiment designs.

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Circadian photoreception in a hymenopteran insect Nasonia vitripennis

Authors: Wang Yifan, University of Groningen, Netherlands

Abstract: Hymenopteran insects are crucial species of our ecosystems and fulfill valuable ecological roles in nature, as well as in agricultural and industrial sectors. With the global declines in their population sizes, it is necessary to understand their circadian system, since it is essential for orientation, foraging, and anticipation of the environment (Eban-Rothschild and Bloch, 2011).

A key component in circadian system regulation is light. Cryptochromes (CRY) is an important photoreceptor involved in the circadian light entrainment in Drosophila by inducing protein degradation (Katz and Minke, 2009). However, many other insects such as Nasonia vitripennis, are lacking such light-sensitive CRY and thus, the circadian photoreceptors and the mechanisms underlying circadian light entrainment remain unclear (Lam and Chiu, 2017).

By constructing a circadian action spectrum, the current results indicate that opsins are the major circadian photoreceptors in Nasonia, and more than one opsin is involved in the regulation of circadian responses. There are potential color contrast mechanisms between different opsins. These results provide insight into reducing the harmful effect of artificial light at night (ALAN), by using artificial light with a narrower bandwidth and specific wavelengths.

Genetic mechanisms underlying desiccation resistance across Drosophila species

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Abstract: One of the largest challenges for organisms living in terrestrial environments is water loss. Insects use cuticular hydrocarbons (CHCs), a lipid layer on the body surface, to prevent water from escaping from their body. Previous studies have shown that the presence of a subset of these CHCs, the methyl-branched CHCs (mbCHCs), contribute to desiccation resistance in some Drosophila species. Among Drosophila species possessing mbCHCs, a length variation of mbCHCs ranging from 24 to 32 carbons has been observed. The longer chain mbCHCs physically correlate with higher efficiency in preventing water evaporation. However, whether the length variation of mbCHCs accounts for different levels of desiccation resistance is unknown, along with the molecular mechanisms. In our study, we conducted a meta-analysis which showed Drosophila species with longer chain mbCHCs have higher desiccation resistance. Using a candidate gene approach, we identified a fatty acyl-CoA elongase gene in D. melanogaster, which we named mElo, responsible for elongating mbCHCs from 24 to 28 carbons. Drosophila mojavensis is a desert fly species with the highest desiccation resistance and the longest mbCHCs (28 – 32 carbons). In D. mojavensis, we identified its mElo ortholog (Dmoj/mElo) and showed that the transgenic overexpression of Dmoj/mElo in D. melanogaster led to longer chain mbCHCs and significantly higher desiccation resistance than the control flies. Phylogenetic analysis suggested that mElo is conserved across Drosophila species. Future studies will focus on understanding whether this fatty acyl-CoA elongase gene underlies the length variation of mbCHCs and different levels of desiccation resistance in Drosophila species.

Geographical variability of Messor arenarius ants from different regions in Northern and Central Israel

Authors: Warburg Ittai, Haifa, Israel

Abstract: In this work it was found, that lengths of Messor arenarius ants from southern parts of the Coastal Plain of Israel between Tel-Aviv and Ashkelon (12.32mm ± 1.68mm; N=37), are significantly bigger than lengths of those ants from northern and central parts of this Coastal Plain between Tel-Aviv and Rosh-Haniqra (11.46mm ± 1.83mm; N=63) (t=2.3463; S.E.=0.368; D.F.=98; P=0.0210 in a bilateral t-test). It was also found, that mandible widths of M. arenarius ants from southern parts of the Coastal Plain of Israel between Tel-Aviv and Ashkelon (2.216mm ± 0.630mm; N=37), are mostly significantly bigger than mandible widths of those ants from northern and central parts of this Coastal Plain between Tel-Aviv and Rosh-Haniqra (1.746mm ± 0.530mm; N=63) (t=3.9910; S.E.=0.118; D.F.=98; P=0.0001 in a bilateral t-test). These differences in sizes of M. arenarius ants between these northern and central regions and these southern regions are related to climatic differences between these areas. The southern parts of the Coastal Plain of Israel are hotter and have more arid conditions than the northern and central parts of this Coastal Plain.

A long and perilous crossing: the migratory trajectories and journey times of the Australian Bogong moth

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Abstract: Studies of the large-scale population dynamics and pathways of migratory insects are few due to the difficulty of observing and tracking such small animals. Entomological radars provide observations of high-altitude insect migration activity and have revealed many fascinating aspects of migration ecology and flight behavior. However, this technique can only provide information on migrations at particular locations. We report here a study of springtime migratory movements of Australian Bogong moths (Agrotis infusa; Lepidoptera: Noctuidae) from their breeding grounds on the inland plains of New South Wales to their aestivation sites in the Snowy Mountains, a journey of up to 1000 km towards the south or east. The study draws on long-term data from an entomological radar at Bourke, NSW, observations from weather surveillance radars at Namoi, NSW and Yarrawonga, VIC, and a modified trajectory simulation model, to assess the moths' migratory paths. We extracted events and seasonal patterns of migration activity across the 14-year study period and correlated these events with meteorological variables. We then assess the likelihood of a take-off (initiation of migration), based on the weather conditions at the time, and predict the trajectories the migrants would then have followed. We predict that migration will be most strongly influenced by synoptic-scale pressure patterns that bring higher temperatures and stronger winds in a favorable migratory direction, but that these conditions only occur intermittently (i.e. on a minority of nights), with the moths hiding, feeding or resting at other times. Consequently, trips from northwest NSW to the Snowy Mountains may take many weeks depending on how frequently favorable conditions occur in a particular season.

Spatial configuration and landscape context of wildflower areas determine their benefits to pollinator α- and β-diversity

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Abstract: Wildflower areas have become a staple tool within agro-environmental schemes (AES) to counteract pollinator declines. While their role in providing food resources to resident flower-visiting insects is unambiguous, the conservation effectiveness in a landscape context is less clear. Particularly, how multiple vs. single wildflower area utilization differs between simple and complex landscapes is understudied. We examined colonisation and community dynamics of wild bees and hoverflies in 33 newly established wildflower areas across a gradient of landscape complexity and connectivity during three consecutive years. We recorded more than 25% of the wild bee and hoverfly species of Hesse in an area of approx. 10 ha, substantiating the general benefit of wildflower areas to pollinators. While alpha-diversity increased with landscape complexity in isolated wildflower areas, the opposite pattern was observed for connected ones. The low alpha-diversity in complex landscapes indicated a dilution effect between connected sites. The inverse relationship between alpha and beta diversity among wildflower areas within landscapes suggests interspecific trade-offs between local resource conditions and landscape context. Accordingly, the establishment of multiple wildflower areas is advisable to increase connectivity of suitable habitats in simple landscapes. Moreover, adjusting local conditions to landscape context likely optimizes conservation effectiveness in modern agroecosystems.

Arthropod genomics for our planet: the i5k, Darwin Tree of Life, and Earth BioGenome projects

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Abstract: Arthropod genomes are critical for performing cutting-edge entomological research, from gaining key insights into basic animal biology, to finding new ways to limit the effects of damaging species or protect threatened ones, and to understand the evolution of arthropod diversity on Earth. The recent successes of the pilot phase of the 5’000 arthropod genome sequencing initiative (i5k, http://i5k.github.io), and the launching of the Darwin Tree of Life (www.darwintreeoflife.org) and Earth BioGenome (www.earthbiogenome.org) projects highlight the importance of insect genome biology as a tool to improve our knowledge of the millions of species with which we share our planet. The i5k initiative has been growing as a community of researchers focused on arthropod genomics that works towards improved sequencing, assembly, annotation, and data management standards, with the goal of facilitating the sequencing and analyses of the genomes of 5’000 arthropod species. The Darwin Tree of Life project, led by the Wellcome Sanger Institute, plans to sequence and assemble high-quality genomes of all known species of animals, plants, fungi and protists in the British Isles. These projects, along with other global partners including the Global Invertebrate Genomics Alliance and the Global Ant Genomics Alliance, form part of the larger Earth BioGenome project, which aims to sequence, catalogue and characterise the genomes of all of Earth’s eukaryotic biodiversity. Rapidly advancing technologies are making such ambitious projects possible, but scientific and organisational challenges will still need to be overcome in order to maximise the benefits to humanity. Here we present a brief overview and up-to-date progress report with contributions from leaders of each of these major arthropod genomics initiatives.

Effects of ground temperatures on survival and energy usage of overwintering queen bumblebees

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Abstract: Bumblebees are critical pollinators in serious decline, in part due to changing climate. Studies have primarily focused on effects of rising temperatures during the growing season, but most of a temperate bumble bee’s life cycle is spent overwintering underground. Queen bumble bees burrow underground in the fall and rely on energy stores to survive harsh conditions until the following spring. Fall and winter ground temperatures therefore determine energy use, overwintering survival, and potentially the spring nesting success of queens. However, little is known about ground temperatures experienced by overwintering bumble bees or how those temperatures determine success during this critical period. We combined measurements of lower lethal temperatures and the temperature dependence of metabolic rates for overwintering and active bumble bee queens with ground temperature data to estimate geographic variation in survival and energy use at different soil depths. Ground temperatures from throughout North America provided estimates of range-wide differences in optimal overwintering soil depth. This approach not only reveals optimal overwintering depths for bumble bees now, but also allows for predictions of how a warming climate might influence bumble bee overwintering survival in the future.

Can thermal plasticity improve insects’ resilience to climate change?

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Abstract: Extreme temperature events are increasing in frequency and intensity due to climate change. Insects are particularly vulnerable as, predominately, species are ectothermic. Insects can enhance their thermal limits through acclimation, yet evidence that plasticity is sufficient to aid survival under temperature extremes is limited. Here, using meta-analyses across 1,374 effect sizes, 72 studies and 94 species, we show that thermal limit plasticity is pervasive but generally weak: per 1°C rise in acclimation temperature, critical thermal maximum increased by 0.09°C and per 1°C decline, critical thermal minimum decreased by 0.15°C. Moreover, small but significant publication bias suggests that the magnitude of plasticity is marginally overestimated. Juvenile insects were more plastic than adults: thus, indicating a developmental window which elicits a larger response. Overall, critical thermal limit plasticity is likely of limited benefit to insects during extreme climatic events, yet we need more studies in under-represented taxa and geographic regions.

Biodiversity and evolution in fossil insects from the Eocene

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Abstract: Eocene climates around 50 Mio years ago provide possibly the best analogs for the world's near-future climates (Burke, Williams, Chandler et al. 2018). In the Early Eocene no ice was present even at the poles, and warm-adapted organisms had a wide diversity and unexpected biogeography. The high biodiversity and evolution of Eocene insects can be exemplified from the fossil Lagerstätten Messel and Green River. The Messel Pit Fossil site is a UNESCO world natural heritage site in Germany and its maar lake sediments preserve a highly diverse flora and fauna (e. g. Smith, Schaal & Habersetzer 2018). The Green River Formation was deposited in a large lake system located in Utah, Wyoming and Colorado (USA) (e.g. Smith, Carroll & Singer 2008, Grande 2013). Recently studied ichneumonid wasps (Hymenoptera) from Messel provide evidence that the extant genera Rhyssella and Xanthopimpla date as far back as the Early/Middle Eocene. Xanthopimpla is considered to indicate a warm climate. Five out of seven new species from Messel can be placed unequivocally in extant subfamilies and genera. A new species belonging to the subfamily Labeninae is the only record from Eurasia and suggests a formerly wide distribution of this group (Spasojevic, Wedmann, Klopfstein 2018). From Green River, two new, probably extinct genera and five new species have been described, and ten formerly described species were revised (Spasojewic, Broad, Bennett et al. 2018). Bugs (Heteroptera) have also been studied from both sites, and studies are still ongoing. For example, tingid bugs are present in both sites. Their diversity in Messel with more than four species is high, while from Green River only one species of tingid bugs has been described. The species from Green River displays strongly enlarged antennae, which are completely unknown in tingid bugs today. These distinctive modifications of the antennae got lost in the extant relatives (Wappler, Guilbert, Labandeira et al. 2015). Another peculiar, extinct genus of bugs belongs to Pentatomidae, and is present in both fossil sites. These bugs possess prominent humeral angles of the pronotum and a spinose pronotum and abdomen. A possible function of this extreme morphology might be defense against predators (Wedmann, Kment, Campos et al. 2021). Extinct giant ants belonging to the genus Titanomyrma (Formicidae, Hymenoptera) are present in Messel with two species and in Green River with one species. Giant ants were shown to be thermophilic and the distribution in North America and Europe implies that migration took place during a hyperthermal episode in the beginning of the Cenozoic (Archibald, Johnson, Mathewes et al. 2011).

Effectivenesses of the various exposure patterns of insecticides against the brown planthopper, Nilaparvata lugens (Stål)

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Abstract: Chemical pest control was still the dominant strategy in Asian rice production through the last decades, and therefore the precision-sprays of pesticides technologies for integrated high-tech crop protection were required, such as the use of drones. However, the cases of less than ideal insecticidal efficacies always appeared depending only on the drone-based system in the rice fields, especially for the brown planthopper (BPH), Nilaparvata lugens, a notorious pest damaging on the rice stems.

We supposed that the cause of failure might be related to the position differences between the BPH damage parts (rice stem base) and the distribution of pesticide deposition (rice canopy) after the drone sprayer operation. This present study focused on pesticide utilization rates under the conditions of the various exposure patterns of insecticides and their effectiveness against BPH at tillering growth stage of rice. For these three insecticides, dinotefuran, nitenpyram and pymetrozine, they had optimum controls (70.0 % - 87.5% against BPH) on day seven by the normal insecticide spraying (NIP) application (whole plant exposed to individual insecticide mentioned above), the range of corresponding pesticide residue (CPR) was 0.231 mg/kg - 0.693 mg/kg on day four; the second one was the spraying application covering the rice stem (56.7% - 75.0% against BPH), their CPR were accounting for 59.7% - 88.2% of the NIS application levels; the worst ones were the applications of directly adding the chemicals into water (depth: approximately 3.3 cm) and leave-only exposed to insecticide (25.5% - 55.4% against BPH), their CPR were accounting for 29.6% -57.6% of the NIS application levels. Taken together, under the conditions of the same amount of pesticide use, there were remarkable differences in utilization rates of insecticides among the various exposure patterns, which also could have immediate impacts for BPH control. This research provided the empirical evidences of normal BPH management decision-making, also could contribute to improve the operations of pesticides precision-sprays against the pests and diseases by innovative technology in the future.

Knockdown of the chromatin remodeling ATPase gene Brahma impairs the reproductive potential of the brown planthopper, Nilaparvata lugens

Authors: Wei Qi, China National Rice Research Institute, China

Abstract:

1. The full-length cDNA of the chromatin remodeling ATPase gene Brahma was cloned in N. lugens.
2. NlBRM transcripts was abundantly expressed in the egg and ovary.
3. Knockdown of NlBRM by RNAi could impair the ovarian development and fecundity of females.

Functional analysis of non-ATPase regulatory subunit genes in a rice pest, Nilaparvata lugens

Authors: Wei Wang, State Key Laboratory of Rice Biology and Ministry of Agriculture Key Lab of Molecular Biology of Crop Pathogens and Insect Pests, Institute of Insect Sciences, China

Abstract: The 26S proteasome is involved in the regulation of the process of degradation of ubiquitinated proteins in organisms. The 26S proteasome consists of the 20S core particle (CP) complex and the 19S regulatory particle (RP) complex. The composition of the 19S complex divided into ATPase regulatory subunit (Rpt) and non-ATPase regulatory subunit (Rpn). Here, we identified 14 Rpns through searching the transcriptome data of the brown planthopper, Nilaparvata lugens, a monophagous rice pest. The developmental stage-expression showed that Rpn transcripts were detected at high levels in egg and/or female adult, but at low levels in male adult. RNA interference via microinjection with double-stranded Rpns resulted in the abnormal ovary development in N. lugens female adults and inhibited oviposition or egg hatching from the rice seedlings (except dsRpn5), implying that Rpns were necessary for oocyte maturation in female adult. These findings improve our understanding of the reproductive and developmental strategies in insects and provides potential targets for the future management of rice pests.

Fast polypedal locomotion: Experiments and modelling approaches to explain the occurrence or absence of gait changes

Authors: Weihmann Tom, Dept. of Animal Physiology Institute of Zoology University of Cologne, Germany

Abstract: Legged locomotion is a main concern of integrative physiological research. Traditionally it is examined on various levels from a range of different perspectives including behaviour, control and biomechanics. For arthropods, much of this research is based on very few established laboratory species largely ignoring major anatomical differences while wider ranges of body size, running speed and behavioural adaptations are often available only for vertebrates. In legged terrestrial locomotion, different gaits and energetic economy are largely determined by the biomechanical characteristics of a locomotor apparatus defining the dynamics of the centre of mass (COM). However, COM dynamics are determined by the degree of leg synchronization, the single leg duty factors and the resulting overall vertical ground reaction forces. While slow locomotion in arthropods seems to lack much COM oscillation many insects employ alternating sets of diagonally adjacent legs when moving quickly, which can result in pronounced COM bouncing and might indicate elastic energy recovery within the legs. Apart from synchronized sets of legs, storage and recovery of movement energy also requires cyclical movements which are mostly restricted to relatively smooth, firm and reliable substrates. For small scale creatures like terrestrial arthropods, natural substrates rarely fulfil all three of these conditions, which might compromise the exploitation of COM oscillations in order to economize locomotion energetics. Accordingly, it has been shown recently, that some insect and arachnid species switch back to lower degrees of leg synchronization when running close to their top speed. By using simple model approaches, I will explain the impact of running speed, anatomy, leg coordination and temporal disturbances of the legs' touch-down and take-off on the gait choice at high running speeds in multilegged animals.

Microbiota of solitary pollinators - A moving target for priority effects

Authors: Weinhold Arne, Ludwig-Maximilians-Universität München, Germany

Abstract: Unlike social insects, solitary pollinators acquire their microbiota entirely from the environment, which makes them highly vulnerable to environmental influences. The timepoint of acquisition can be important for the microbial community assembly, known as priority effect, but depends largely on stochastic effects and random influences. Here, the influence of local habitat (e.g. local flower diversity or fragmentation of the habitat) can play a major role, as well as the movement pattern and foraging distance which definiens the microbial acquisition range. Host movement has contrasting effects on the gut-microbiota as it can either reduce or enlarge spatial scale (aggregating vs dispersing host). While aggregation could enhance inter-host transmissions and increase the uniformity among conspecifics or social groups, an increased dispersal movement could dissolve effects of the local environment and extends microbial dispersal limitations across plant-pollinator networks (comparing local foraging of mason bees vs. semi-migratory butterflies). Though host movement and migration distance and can directly influence major drivers of the host microbiota it has been little regarded within host-microbiota frameworks.

Evolution of oviposition strategies in Heteroptera

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Abstract: Ovipositor morphology has been shown to be associated with life history strategy in several groups of insects. Heteroptera include lineages with plate-like and laciniate ovipositors and oviposition sites range from leaf litter, soil, and surfaces of plants to eggs being inserted into plant tissue. The literature on both ovipositor morphology and oviposition sites of Heteroptera is dispersed. We here use a phylogenomic dataset covering ~80% of true bug families (Hemiptera: Heteroptera) and comprehensive literature searches to trace the evolution of ovipositor types and oviposition strategies across the suborder.

Evolution of raptorial legs in the assassin bugs (Hemiptera: Heteroptera: Reduvioidea)

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Abstract: Reduvioidea (Hemiptera: Heteroptera), or the assassin bugs, are one of the morphologically and ecologically most diverse lineages of hemimetabolous insects, with around 7000 described species, 2 families and 26 subfamilies. As predators, they have evolved a great variety of leg modifications to handle the prey. However, detailed assessment of the raptorial features has been done only for few specific groups within Reduvioidea, while broader analyses lacked comprehensive taxon sampling. Additionally, the investigation of evolutionary history of raptorial leg modifications has been hindered by a lack of comprehensive phylogenetic hypothesis of the group. Here we will show a recent progress on reevaluating morphological characters pertaining to raptorial behavior. A phylogenetic dataset with significantly improved taxon sampling and comprised of various data types will be used to provide a framework for reconstructing evolutionary history of raptorial characters.

Bacterial inhibition of trypanosome infection establishment in the tsetse fly midgut and its potential to enhance the efficacy of sterile insect technique-mediated population suppression

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Abstract: Tsetse flies (Glossina spp.) vector pathogenic trypanosomes in sub-Saharan Africa. These parasites cause human and animal African trypanosomiases, which are debilitating diseases that inflict an enormous socio-economic burden on inhabitants of endemic regions. Disease control currently relies largely on reducing tsetse population densities through the use of pesticides, traps and sterile insect technique (SIT). While these programs are effective, their high cost and intensive labor investment make them difficult to sustain. Additionally, SIT presents epidemiological risks because released (sterilized) male flies can transmit disease (male and female tsetse are obligate blood feeders). With respect to enhancing the efficacy of tsetse SIT programs, novel strategies aimed at reducing the vector competency of released males require development. With this goal in mind, we discovered that stable colonization of tsetse's midgut with the exogenous bacterium Kosakonia cowanii Zambiae (Kco_Z) inhibits the ability of trypanosomes to colonize the fly. This parasite refractory phenotype results from the fact that Kco_Z acidifies tsetse's midgut environment, which inhibits trypanosome growth and thus infection establishment. Importantly, Kco_Z infection does not impact the fecundity of male or female tsetse, nor the ability of male flies to compete with their wild-type counterparts for mates. We thus propose that Kco_Z could be used as one component of an integrated strategy aimed at improving tsetse SIT programs via the release of trypanosome-refractory flies.

Climate oscillations and nutrient dilution underlie insect herbivore cycles and declines

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Abstract: Parsing variation in animal abundances at multiple time scales, and assigning mechanism, is a fundamental challenge in an era of global change. Key drivers of insect herbivore abundances include climate, plants communities, and their interactions. Disentangling these signals sheds light on underlying drivers of abundance patterns and recent widespread reports of insect decline. We tested two time series (16 and 22 years) of annual grasshopper abundances for cyclicity using spectral analysis and then decomposed time series to disentangle cycle and trend. We asked if large-scale climate oscillations of El Niño Southern Oscillation (ENSO), North Atlantic Oscillation (NAO), and Pacific Decadal Oscillation (PDO) drive grasshopper abundances. We then examined changes in plant biomass and nutrient content as drivers of long-term trends in grasshopper abundances. Abundances exhibited a significant 5-year cycle and the presence of abundance cycles caused overestimation of grasshopper declines in the shorter time series. Climate cycle indices of spring ENSO, summer NAO, and winter PDO predicted grasshopper abundances in the 22-year time series, while summer NAO and spring PDO predicted grasshopper abundances in the 16-year time series. In addition to cycling, grasshopper abundances declined 2.2-2.7% annually resulting in a cumulative 37% decline in the 22-year time series. Local plant biomass in this system increased over time, diluting nutrient concentrations in plant tissues. Grasshopper abundances track plant nutrient concentrations, suggesting decreasing food quality in response to CO2 fertilization drives grasshopper abundance declines.

Mapping the distribution of coccinellids in Argentina through Citizen Science: goals and challenges

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Abstract: Native ladybird biodiversity is declining in many regions of the world mainly due to the effect of invasive species, habitat loss, and climate change. Argentina presents a very diverse landscape with about 160 reported ladybird species, from which 21% are endemic. However, because of the lack of researchers studying their biodiversity, the knowledge about ladybird abundance and distribution shows big gaps, making it impossible to evaluate their trends and to develop conservation strategies. In addition, deforestation, changes in land use, and the extended invasion of the harlequin ladybird (Harmonia axyridis) threatens native ladybird species and call for urgent national initiatives in the conservation of this group and other beneficial insects. The use of traditional techniques for biodiversity surveys in large countries like Argentina would be extremely expensive and time-consuming. Citizen Science is a powerful alternative to gather biodiversity data for wide geographical scales, and it is also a way of engaging people with science, increasing their awareness of environmental issues. Here, I will present preliminary data of a new long term Citizen Science Project aimed to map the distribution of conspicuous ladybirds across the country and to analyse their trends which will be the base for the development of conservation programs. I will also discuss the limitations and challenges of this kind of approach in South America.

Modality-specific circuits for skylight orientation in the fly visual system

Authors: Wernet Mathias, Free University Berlin Institute of Biology, Germany

Abstract: Different visual cues like celestial bodies, skylight polarization, and colour gradients are used by navigating insects. How the brain processes and integrates this information for navigational decisions (like a given flight heading), remains incompletely understood. On a cellular and synaptic level, little data exists on either (i) the specific differences between those circuits mediating polarization vision versus color discrimination, or (ii) at which level they are integrated. We use Drosophila as a model system for dissecting the pathways which connects the eye with the central brain, using a combination of molecular-genetic, ultrastructural, behavioral, and physiological techniques.

Like in other insects, the ommatidia of the fly compound eye fall into three subtypes, as defined by Rhodopsin expression in their long visual fiber photoreceptors (R7 and R8), connecting to an equal number of repetitive microcircuits within the optic lobes. While two stochastically distributed subtypes mediate color vision, morphologically and molecularly distinct ommatidia in the ‘dorsal rim area (DRA)’ detect skylight polarization and are necessary for mediating orientation responses. Using the Drosophila neuroanatomical toolkit, we have shown how DRA-specific differences in neural circuit architecture (cellular composition, morphology, synaptic distribution and connectivity) adapt DRA microcircuits to their modality-specific function, i.e. polarization instead of color vision.

We are now characterizing the circuits for skylight orientation using a combination of light-microscopic neuroanatomy tools and 3D reconstruction of electron microscopic data spanning the entire fly brain. The importance of modality-specific circuit elements are being characterized using different behavioral assays, like virtual flight arenas for tethered flies, as well as GCamp activity imaging. The circuit motifs we describe will add much-needed details to the connectivity diagram of the compass pathway of insects. More generally, our model system serves as a platform for understanding how a locally-restricted part of the visual system is adapted to a specific function.

Evaluating the impact of commonly used herbicides on African honey bee gut microbiota in Kenya

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Abstract: Honey bees play a crucial role in natural ecosystems and agricultural production. The honey bee harbors specific yet simple gut microbiota composed of about nine bacterial clusters. The gut microbiome are being implicated in food digestion, detoxification of harmful molecules, protection from opportunistic pathogens and parasites, providing essential nutrients, among other key roles. In the last decades, the honey bee population worldwide has drastically decreased and the causes are not yet fully understood. Aspects such as environmental stressors, low genetic diversity or invasive pests and pathogens might all be implicated. Another potential course is herbicide use which is known to have side effects in crops and/or beneficial insects that visit such crops. This detrimental effect could be sometimes direct (e.g. affecting the insect's natural system) or indirect (e.g. by affecting the beneficial microbes associated to the insect). We hypothesize that honey bees' health is compromised by usage of herbicides via their gut microbiota. Therefore, this study aims to evaluate the effects of paraquat and glyphosate herbicides on the adult honey bee gut microbiota. The study will also aim to determine if the gut microbiome, in short time scale, might develop resistance to such chemicals. Glyphosate and paraquat are herbicides are commonly used in Murang'a County, Kenya, where large scale of fruit farming e.g. avocado and cucurbits is practiced.

To achieve our goals, the toxicity level of glyphosate and paraquat on honey bees will be determined before evaluating their effects on the bee gut microbiota. We will also examine whether these compounds induce oxidative stress in the honey bee gut tissue. Lastly, a serial gut microbiota passages from bee to bee, chronically fed with the herbicide will be conducted until a potential resistance is observed.

We expect that the data and possible bacterial strains generated in this study will outline the impacts of pesticides in honey bee health and set up the basies for policy development in safe pesticide use/doses. In addition, if we find a resistance development against the herbicides, we will analyze this further with the aim of spreading such beneficial effect in the field.

Non-insecticidal Mosquito Bite-resistant Garments

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Abstract: Vector-borne diseases have had a devastating impact on human health through arthropods, especially mosquitoes. Garments may be used as a barrier to biting insects, and thereby are useful in preventing disease transmission. Commercially available insect protective clothing is either untreated or is treated with permethrin, an insecticide that kills or repels insects through contact with the treated surface. Widespread use of permethrin in both long-lasting insecticidal nets (LLINs) and as an agriculture insecticide has resulted in high levels of resistance, especially in Africa. Resistant mosquitoes may land on permethrin treated surfaces without experiencing adverse effects, and therefore, clothing treated with permethrin may not be effective at preventing bites in areas where resistant strains are dominant. Other concerns about insecticide treated textiles include a limited active period, potential adverse effects on human health and poor compatibility with synthetic fibers. Given the rise in insect-transmitted disease and the prevalence of resistance, there is a need to develop alternative safe and effective bite-resistant garments that are active against resistant mosquitoes and other arthropods and pose no possible hazard for human health. Prototype bite-resistant textiles were designed to provide a physical barrier to penetration while also maximizing thermal comfort and durability. A predictive model was developed based solely on mosquito morphometric analysis and describes combinations of textile structures that effectively prevent mosquitoes from biting. The bite-resistant capacities of the prototype fabrics were evaluated by an arm-in-cage bioassay and were used to validate the predictive model. Protective garments constructed from prototype fabrics were evaluated for bite resistance in walk-in cage experiments. thermal comfort was evaluated in tests using a sweating manikin under controlled conditions. The prototype garments provided 98% or higher protection from mosquito bites with air/moisture vapor permeability that was superior to chemically treated uniforms. Based on these results, this unique textile technology has enormous potential for mitigating the incidence of vector-borne diseases by preventing human-vector contact.

Landscape heterogeneity shapes functional community composition and can mitigate adverse effects of local land use intensification

Authors: Westphal Catrin, Functional Agrobiodiversity Department of Crop Sciences University of Goettingen, Göttingen, Germany

Abstract: Landscape composition (e.g. diversity of habitat types) and landscape configuration (e.g. number, size and arrangement of habitat patches) represent two components of landscape heterogeneity and can have different ecological implications for species diversity, community composition and provisioning of ecosystem services. Moreover, local habitat characteristics, such as the intensity of agricultural management, can interact with the two components of landscape heterogeneity and can also modify functional community composition. I will focus on the general research question how effects of local land use intensity and landscape heterogeneity interact in shaping the composition of arthropod communities in grasslands. First, I will examine how independent gradients of compositional and configurational landscape heterogeneity, across eight spatial scales, shape taxonomic and functional diversity of butterfly communities in 91 managed grasslands across Germany. Second, I will disentangle the effects of independent gradients of landscape composition (diversity of land cover types: measured using the Shannon diversity index) and configuration (average patch size within the surrounding landscape) and local land use intensity on the functional composition of grassland arthropod communities comprising six orders (i.e. Araneae, Coleoptera, Diptera, Hemiptera, Hymenoptera and Lepidoptera) and 599 species.

Instead of using land cover maps, functional maps were derived based on habitat preferences of individual butterfly species during different life stages. Landscape heterogeneity metrics were then calculated from these functional maps. While functional landscapes with high compositional heterogeneity promote butterfly communities with greater taxonomic diversity, high configurational heterogeneity enhances functional diversity of butterfly communities with increasing numbers of vulnerable species (e.g. feeding specialists).

A RLQ analysis was used to investigate the co-correlations between in-field management intensity and landscape-scale heterogeneity (R table) and species trait attributes (Q table), constrained by the relative abundance of each species (L table). The grassland arthropod communities showed a unified response to both landscape-scale heterogeneity and local land use intensity. Adults and larvae with specialized feeding habits, species with shorter activity periods and relatively small body sizes are selected against in simplified landscapes with intense in-field management.

The studies demonstrate that landscape-level effects determine functional community composition and can even buffer negative effects of in-field management. A decline in functional community composition can lead to functional homogenization, affecting the viability of the ecosystems by decreasing the variability in their responses to disturbance and altering their functioning and the provisioning of ecosystem services.

The role CABI plays in building trust for sustainable access and benefit-sharing of biological control genetic resources

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Abstract: CABI is a not-for-profit international organization with the mission of improving people's lives worldwide by solving problems in agriculture and the environment, while engendering trust, facilitating science and ensuring that benefits are shared. CABI is in a unique position in that it is both a provider and a user of biological control agents and often acts as an intermediary between provider and user countries. As a way of building trust between both sides, CABI has developed a publicly available access and benefit sharing (ABS) policy and ABS best practices built around the principles of the Nagoya protocol. CABI's ABS best practices aim to facilitate compliance with national legislation on ABS in the countries in which it works and in those that provide genetic resources for CABI's use. As an initial step CABI started to align its ABS best practices to comply with its host country requirements. In Switzerland for example, CABI is in discussion with the Swiss Competent National Authority to get CABI's ABS Best Practice officially recognized in a public register. The benefit of having a best practice recognized is that it is an accepted procedure that reduces the risk of non-compliance while at the same time building trust with the provider and user countries. In addition to this, CABI is working openly to negotiate agreements in provider countries such as China. Ultimately, CABI as an international, intergovernmental organization is committed to the Convention on Biological Diversity and the Nagoya protocol and its staff will ensure the compliant access and utilization of biological control agents in the countries where CABI works.

Understanding ladybirds – the "extinction of experience"

Authors: Weyman Gill[1], Butler Fidelma[3], Whelan Padraig[4] and McKeown Sean[2], [1]Fota Wildlife Park and University College Cork, Ireland, Ireland, [2]Fota Wildlife Park, Ireland, [3]University College Cork, School of Biological, Earth and Environmental Sciences, Ireland, [4]University College of Cork, School of Biological, Earth and Environmental Science, Ireland

Abstract: Ladybirds are often considered to be charismatic insects. Yet, what do people really know about them? Threats of urbanisation, habitat availability and disconnection of people from nature add up to what is termed the "extinction of experience". This lack of understanding of nature has been frequently highlighted and a loss of first-hand experience being during childhood is likely to have contributed to a decline in values of biodiversity held by humans. Research in the United Kingdom found that children often lack the ability to identify common species. The complexity of natural systems also makes it difficult for people to understand conservation issues. Life experiences can be very important and outdoor recreation, education, fieldwork, museum, and laboratory studies have the potential to provide young people with necessary close experiences of life. A questionnaire survey in 2018 found that 96% of participants recognised the shape of a ladybird when compared to other invertebrates and 60% agreed that ladybirds were important. A follow-up survey in 2019 investigated the origin of public attitudes and understanding of ladybird conservation, taking into account a range of factors including early childhood experience, gender, and age.

Mating Disruption as an integral part of the Integrative Pest Management of Row Crops

Authors: Wheeler Christopher[1], Srigiriraju Lakshmipathi[1], Serrano Miguel[1] and Galvan Tederson[1], [1]Provivi Inc.

Abstract: The Lepidopteran chemical communication system involved in mate finding was first manipulated in the 1970's with the area-wide application of synthetic female sex pheromones to control the economic infestations of P. gossypiella in cotton. Since the success of this novel pest control method, mating disruption technology has been developed and commercialized for some of the most economically important moth pests of the world. Mating disruption has been most popularly adopted in pome fruit & nut tree agricultural systems but has also had commercial success in the control of C. suppressalis in Spanish rice, and now S. frugiperda in Mexican corn. Mating disruption is a species-specific, non-lethal form of pest control that can reduce crop damage and pest populations to levels comparable with conventional insecticide approaches. The traditionally high cost of synthesizing lepidoptera sex pheromones have likely been a barrier to the adoption of this technology in low-cost, large hectarage row crops. Recent advancements in the syntheses of these pheromones, and the arrival of invasive species like the fall armyworm create a potential for more widespread adoption of mating disruption as a viable and economically-feasible pest control method in row crop agricultural systems like the corn and rice systems therein described.

Machine Learning Classification for Lidar-based Insect Detection

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Abstract: Lidar-based insect detection is of growing interest to the entomological community due to the noninvasive and nondestructive nature of lidar measurements. Unfortunately, the vast quantity of data collected by pulsed lidar systems makes it time consuming to identify data samples corresponding to insect data. This problem is compounded when lidar measurements are taken in the field, rather than in a controlled laboratory environment. In field measurements, it is quite common that less than 1% of the raw data includes information about flying insects. In this abstract, we show how machine learning algorithms can support manual inspection by quickly identifying possible insect-containing lidar field measurements, allowing scientists to avoid the tedious process of manually sifting through the collected data. Using supervised algorithms with modifications to account for high class imbalances, we automatically identify approximately 1% of the raw data as containing insects; this portion of the data contains over 50% of human-identified insects In addition, we propose advancements in algorithm development and hardware implementation that will lead to real-time insect detection. In addition to accelerating entomological decision-making processes, real-time insect detection may allow for higher quality data collection in field measurements. While still in its early stages, machine learning has the potential to accelerate lidar-based entomological research.

Probing molecular interactions between orthotospoviruses and thrips vectors for discovery of new targets for disrupting transmission.

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Abstract: Tomato spotted wilt virus (TSWV) and other thrips-transmitted orthotospoviruses are significant threats to production of food, fiber, and ornamental crops. There are limited effective control strategies for this virus due to the difficulty of controlling the thrips vector. We study the basic transmission biology of TSWV with the goal of developing new ways to disrupt the disease cycle. We have documented that the TSWV Gn protein is a viral attachment protein and capable of inhibiting virus acquisition and subsequent inoculation by thrips. We have also characterized thrips proteins that respond to and interact directly with virus during the transmission process. With this new knowledge, we aim to determine if TSWV-interacting proteins are determinants of vector competence and possible targets for reducing thrips vector transmission efficiency.

Ancient Enemies: Phylogenomics of the Culicidae Reveals Ancient Radiations

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Abstract: The Culicidae are among the deadliest animals on Earth, responsible for immense human suffering due to the numerous vector-borne diseases they transmit. Although there are more than 3500 described species of mosquitoes, the vast majority of research has focused on a handful of species responsible for epidemics of disease, such as Aedes aegypti and Anopheles gambiae. As such, our evolutionary understanding of mosquitoes lags behind many other important insect groups. This lack of knowledge prohibits analyses of key vector phenotypes, such as host association and vector competence, and complicates taxonomy and broader systematics. To date, there have been only limited studies utilizing molecular data in this family, and morphology has at times provided conflicting information on deeper relationships among genera in the Culicidae. Here, we present the results of the most comprehensive phylogenetic analysis of the Culicidae to date, based on genomic data. We leverage existing genomic resources and new sequence capture data from 200 species to reconstruct the evolutionary relationships of major genera in the family. Then, we use this phylogenomic dataset to date the key divergence times in this group, and evaluate those divergence in context with major vertebrate lineages to provide insight into the evolution of the world's deadliest animals.

Chemical and behavioural adaptations of Maculinea butterfly larvae to their Myrmica host ants on the example of the reintroduced and source population of Maculinea teleius

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Abstract: Ants of genus Myrmica hosts diverse myrmecophilous community including social parasites such as Maculinea butterflies, which larvae live inside host nests. The most crucial moments in the parasite life cycle are the infiltration of the butterfly larvae in the host ant nest and integration with host colony. Both steps are mediated mostly by chemical deception; Maculinea larvae synthesize a mixture of cuticular hydrocarbons (CHC) that mimic those of Myrmica ant species. Also Myrmica host ant populations can change their cuticular hydrocarbons in response to parasite pressure and become stricter in recognizing nest-mates. Chemical mimicry match of Maculinea larvae to their host ants can be reflected by ant behavior towards parasite larvae during adoption process as well as by larval survival inside host colony.

We study this co-evolution system on the population of Maculinea teleius that was reintroduced in the Netherlands in 1990 and the source butterfly population from Poland. Such difference of almost 30 butterfly generations between the source Polish and the reintroduced Dutch population offers unique opportunity to study the local adaptations of M. teleius butterflies to their host ants and to detect ongoing co-evolution processes between parasite and host populations. We will present results of CHC profiles of pre adoption M. teleius larvae as well as CHC profiles of Myrmica ants coming from the source and reintroduced populations. Moreover, we will also show results of cross-adoption experiment between Dutch and Polish M. teleius larvae and their main host ant, Myrmica scabrinodis coming from source and reintroduced population.

The distribution of viral natural enemies in fall armyworm (Spodoptera frugiperda) in Africa

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Abstract: The fall armyworm (FAW, Spodoptera frugiperda) is a highly invasive crop pest. Native to America, it was first reported in Africa in 2016 and rapidly spread throughout the continent causing devastation to crops, particularly maize (Zea mays) and rice (Oryza sativa). It has since spread to Asia, with countries including India, China and Japan all reporting that FAW is present. One mechanism for the control of fall armyworm is biocontrol using the virus Spodoptera frugiperda nucleopolyhedrovirus (SfMNPV). As well as being sprayed artificially, SfMNPV is also present naturally within FAW populations in the Americas. African armyworm (Spodotpera exempta) populations in Africa also have a nucleopolyhedrovirus present naturally, Spodoptera exempta nucleopolyhedrovirus (SpexNPV), which also has the potential to be used as biocontrol against the African armyworm. These viruses are ideal as biocontrol agents as they are highly species-specific meaning the risk to non-target species is minimal, are safer for farmers to use than chemicals and have relatively high success rates when sprayed in fields. It is not yet known whether either of these viruses are present within FAW populations in Africa. However, increasing our understanding of these viruses within FAW in Africa could provide insights into natural population control, and highlight the potential for biocontrol in Africa. To address this gap in our understanding, this study investigated the distribution and abundance of SfMNPV and SpexNPV within Africa. This study found that throughout Africa, both SfMNPV and SpexNPV were found to be present within FAW populations. Interestingly, the prevalence of both viruses varied between different African countries. Furthermore, virus distribution also varied between different sites within countries. Overall, this study provides a useful insight into the distribution of viral natural enemies within FAW in Africa, and how this varies between different countries and regions.

Developing and testing annual flowering seed mixes for wild pollinators in gardens and urban green spaces

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Abstract: The decline of pollen and nectar feeding insects is a cause for concern, given their vital contribution to pollination services. Multiple factors are attributed to their decline, with fragmentation and loss of floral resources considered one of the most important. As the wider landscape becomes more fragmented, gardens and urban green spaces can provide an important network of resources for wild pollinators. Public awareness of the plight of pollinators has led to an increase in wildlife friendly gardening, including the use of pollinator friendly seed mixes and recommendation lists to select suitable plants for pollinators. Whilst these lists are useful, there is evidence to suggest that many lack consistency and are based upon anecdotal evidence. The majority of studies investigating seed mixes for pollinators have been focused on agricultural landscapes, with few looking at seed mixes used in gardens and urban green spaces. Results of preliminary research carried out at the National Botanic Garden of Wales investigating commercially available, pollinator friendly seed mixes, found that only 20% of species included in a seed mix designed to attract bumblebees were visited by bumblebees. The results infer that there is potential to improve these seed mixes. The aim of this investigation was to develop and test annual flowering seed mixes to attract a diversity of wild pollinators, using plant-pollinator interaction data obtained systematically from published literature. Two annual flowering seed mix treatments, each consisting of twenty species were developed using data collated systematically from over 500 published, peer reviewed articles, selecting plant species that attracted a diversity of wild pollinator species and were horticulturally suitable. Seed mix treatments were compared to commercially available seed mixes by carrying out observational surveys of the pollinators visiting each seed mix treatment. Floral surveys were carried out both within the treatment plot and in the surrounding Botanic Garden to determine which species were available to pollinators compared to those they visited. Since observational surveys provide only a snapshot of information about foraging behaviour. DNA metabarcoding methods using ITS2 and rbcL markers were also used, to investigate the proportion of plant species used by wild pollinators within the seed mix treatments, compared to the surrounding Botanic Garden. This research will be used to improve seed mixes for the conservation of wild pollinators in gardens and urban green spaces.

Flight Dispersal Capabilities of Spotted Lanternflies

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Abstract: The spotted lanternfly, Lycorma delicatula (White), is an orchard and forest pest native to China. Since its detection in Pennsylvania, USA in 2014, it has spread to other US states as well. We conducted experiments to determine the flight capabilities of L. delicatula adults to assess the relative threat posed by each type with regard to expanding the infestation area through their natural flight behaviors. To understand the effect of mating status, females were collected from mating pairs, captured on plants, and netted during flights averaging 24 m, then dissected and examined for male spermatophores, a diagnostic character for determining mating status. The weight, amount of yellow area on the abdomen, wing area, and body length and abdominal width was recorded from these females. Sedentary females on plants were selectively collected for their large and swollen abdomen. They were capable of only flying ~4 m when forcibly launched and were significantly heavier than the in-flight-captured females. More than 93% of these large, sedentary females had mated whereas <5% of the flight-captured females had mated. Spontaneously flying females weighed significantly less, and had significantly smaller and less yellowed abdomens than sedentary females captured on plants. We concluded that nearly all the observed spontaneously flying L. delicatula females were unmated and therefore pose a lower threat to spread the infestation than previously thought. We then explored the upper limits of flight to help determine the capability of the insects to fly long distances and rapidly expand the infestation range. We observed the behavior of tethered spotted lanternflies to record the number of successive flight bouts, and for how long individuals can fly while tethered. Additionally, we recorded the flight distance and duration of spotted lanternflies in the field that had spontaneously taken flight or been manually launched. We found that females can perform at least 20 successive bouts with only 1 min between bouts when flight durations were limited to 20 s per bout. Bouts averaged 97.9 ± 11.4 s when bout durations were unlimited with some adults flying bouts that lasted over 400 s. If performed naturally, these bouts in quick succession could result in the female flying a distance of over 1000 m in less than half an hour. However, adults spontaneously taking flight in the field flew for an average of only ~13 s and traveled an average of ~29 m before landing on the ground or on nearby objects such as light lamp posts, grapevines, or trees. This information is key in determining how far a locally dispersing adult L. delicatula can fly before finding a suitable host to finish feeding and attain reproductive maturity. We also hypothesize that these thinner, spontaneously flying females embark on these 10–50-m-long flights because they need to find new trees on which to feed to complete their egg maturation in order to oviposit successfully.

Direct and delayed effects of exposure to a sublethal insecticide concentration on food consumption and reproduction of a leaf beetle

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Abstract: The global use of agrochemicals has increased dramatically and pesticides have become a serious source of environmental pollution. With the use of insecticides not only pests of crop plants are affected, but also non-target organisms. The toxic chemicals are present in varying concentrations in the environment and even in sublethal concentrations they can affect the development or behaviour of the exposed organisms. Next to detrimental effects caused by direct exposure to sublethal insecticide concentrations, organisms may also have to cope with delayed effects after exposure to this environmental stress. To elucidate such direct and delayed effects of exposure to a sublethal insecticide concentration within one generation, we chose the mustard leaf beetle, Phaedon cochleariae, which we considered as a non-target organism. Adult beetles were either non-exposed or exposed to a sublethal concentration of a pyrethroid and the effects on food consumption and reproduction were investigated at three time points, during, immediately after, and at a delayed time after insecticide exposure. We hypothesized that during insecticide exposure food consumption and reproduction will be reduced compared to non-exposed beetles, but that beetles may recover with time after ending the insecticide exposure. As expected, during the insecticide exposure food consumption and reproduction were lower than in control beetles. Directly after ending the insecticide exposure, beetles from both treatment groups showed a similar consumption rate, which kept comparable over time. The number of eggs was still lower directly after ending the insecticide exposure, but at a delayed time the initially exposed beetles had caught up with the reproduction of the non-exposed beetles. Likewise, at the delayed timepoint the hatching success of the two groups did not differ any longer. Thus, individuals may be able to recover from insecticide exposure after a certain time. In conclusion, our results highlight that both direct and delayed effects of environmental stressors on fitness-related traits need to be considered. Consequently, we provide evidence that organisms may recover from an exposure to a toxic chemical.

Of insects and decorations: behavior of insect pollinators on conspicuous sterile flowers of Hydrangea spp. (Hydrangeaceae)

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Abstract: Decorative flowers (sterile yet conspicuous flower) can be found in various angiosperm families. Adoxaceae and Hydrangeaceae have a unique flower arrangement: a cluster of small fertile flowers is surrounded by larger decorative flowers. These decorative flowers have been largely hypothesized to attract pollinators. To identify whether the decorative flowers have pollination related functions, we carried out field manipulation experiments in nine Hydrangea species, from which only one species does not present natural decorative flowers. The results showed that for most of the studied species, the presence of decorative flowers increased the frequency of visits and weakly increased the frequency of visits per unit area to inflorescences. Decorative flowers also appeared to act as landing-sites for three species that had a high ratio of the surface area of decorative-flowers to the total surface area of the inflorescence. The results suggest that the main function of decorative flowers of the studied Hydrangea species is to boost attractiveness to pollinators by increasing the inflorescence surface area, whereas the landing-site function was evident only in certain species. It is likely that species without natural decorative inflorescences use other attraction enhancing mechanisms, in the case of this study, coloration and odor cues for H. hirta.

Evaluation of acaricidal and antimicrobial activity of entomopathogenic fungal metabolites against the two-spotted spider mite, Tetranychus urticae

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Abstract: Entomopathogenic fungi are widely used for controlling various pests as representative biological control agents, and their metabolites have also reported various biological activities such as plant growth promotion, antioxidant activity and antibacterial activity. This study was conducted to evaluate the possibility of simultaneous control of pests and plant diseases using fungal metabolites. The acaricidal activity and antimicrobial activity against plant pathogens were evaluated for metabolites of entomopathogenic fungi with high virulence against the two-spotted spider mite, Tetranychus urticae. As a result, the fungal metabolites showed antibacterial and antifungal activity against various plant pathogens such as Botrytis cinerea and Colletotrichum acutatum along with acaricidal activity. These results showed that entomopathogenic fungal metabolites can be effectively used for simultaneous control of both plant diseases and the two-spotted spider mite.

Effects of drought stress on subcortical beetle assemblages may be mediated by fungal communities in beech

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Abstract: Severe droughts are likely to increase in coming decades with subsequent impacts on bark beetles, other subcortical insects and fungi. We exposed standardized beech logs and branches from trees affected by severe drought in 2018 at 9 sites located throughout the Ajoie region of Switzerland and reared beetles and assessed fungi (% cover) after one year. Beetle assemblages (18,500+ beetles and 60+ species) were dominated by Taphrorhycus bicolor (bark beetle) and Xylosandrus germanus (invasive ambrosia beetle) but also included a rich fauna of subcortical fungivores and predators. Fungal assemblages were dominated by Biscogniauxia nummularia (facultative pathogen induced by drought) and Hypoxylon fragiforme (common decay fungus) on bole sections and branches. We found colonization by fungi was strongly linked to both drought intensity and tree condition. We then compared beetle assemblages to drought severity, tree health and fungal abundance using multivariate regression trees to identify key factors determining composition of the subcortical beetle assemblages. We found that extensive colonization by fungi can in some instances supersede the importance of drought intensity or tree condition for determining beetle composition. This highlights an important, indirect role that secondary pathogens and decay fungi may play during droughts.

Detection of toxins in nectar by bees

Authors: Wright Geraldine, Department of Zoology, University of Oxford, United Kingdom

Abstract: Bee species forage for nectar offered by plant mutualists in return for pollination services. Though nectar is mainly composed of sugar, it can also contain compounds which are potential toxins for insects. Here I will show data that describes the detection range for several potential toxins, including pesticides, on the mouthparts of honeybees and bumblebees. I will show how the concentration and the nature of the sugars found in nectar affect the detection of compounds like pesticides.

Immune stimulation reduces the duration, frequency and transfer of trophallaxis in honeybees (Apis mellifera)

Authors: Wright Owen, University of Exeter, United Kingdom

Abstract: Group living social insects are at a greater risk of infectious diseases due to their close relatedness, high densities and frequent social contacts. One social behaviour of honeybees (Apis mellifera) is trophallaxis, which allows the transfer of nutrients and information between individuals and throughout the hive but poses a risk of disease transmission. To examine the effect of immune stimulation on trophallaxis, I used bacterial lipopolysaccharides to stimulate the immune system of harnessed honeybees in the laboratory and manipulated the satiation of the bees to produce donors and recipients. I then recorded and compared the behaviour of the bees during trophallaxis in dyads with an immune stimulated donor or recipient with a healthy partner bee, against dyads with a saline control. I found that the dyads with immune stimulated bees had a reduced duration of trophallaxis compared to that of control dyads. Fewer trophallactic events occurred and less trophallactic fluid was transferred in dyads with immune stimulated recipients. As hunger and motivation of immune stimulated bees was not found to be altered, I suggest this change in trophallactic behaviour is indeed a form of social immunity to prevent the transmission of disease between nestmates.

The evolution of insecticide resistance in the brown planthopper (Nilaparvata lugens Stål) and the rice stem borer (Chilo suppressalis) of China

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Abstract: The brown planthopper (BPH), Nilaparvata lugens, and the rice stem borer (RSB), Chilo suppressalis, are economically important pests on rice in Asia. Chemical control is still the most efficient primary way for these two pests control. However, due to the intensive use of insecticides to control these two pests over many years, resistance to most of the classes of chemical insecticides has been reported. We will talk on the status of insecticides resistance in BPH and RSB collected from China over the period 1996–2019 and 2001-2019. We also showed some case studies of the biochemical and molecular mechanisms underlying resistance in BPH and RSB. The insights study of this presentation has provided on how resistance evolves, and the selectivity of insecticides. These results will be beneficial for effective insecticide resistance management strategies to prevent or delay the development of insecticide resistance in BPH and RSB.

CRISPR-mediated Gene knockout reveals role of P450s in xenobiotic resistance and detoxification in Helicoverpa armigera and Spodoptera exigua

Authors: Wu Yidong[2], Wang Huidong[1], Zuo Yayun[1], Yang Yihua[1] and Shi Yu[1], [1]College of Plant Protection, Nanjing Agricultural University, China, [2]Nanjing Agricultural University, China

Abstract: The cotton bollworm (Helicoverpa armigera) and beet armyworm (Spodoptera exigua) are two major agricultural pests of global importance. Resistance cases to most insecticide classes have been reported for these two pests. Management of these two pests in agroecosystems relies on a better understanding of how it copes with phytochemical or synthetic toxins. We have developed a new strategy (gene cluster knockout), which can rapidly identify the contributions of insect P450s in xenobiotic detoxification and serve to identify candidate P450 genes for insecticide resistance.

For H. armigera, we deleted a 85 kb genomic fragment covering all nine P450 genes from the CYP6AE subfamily by the CRISPR-Cas9 method, and assayed toxicities of diverse phytochemicals and insecticides against both the background strain and the knockout strain. We then functionally expressed recombinant CYP6AE enzymes to identify the specific P450s involved in detoxifying xenobiotics. Several of CYP6AEs involved in detoxifying plant toxins and chemical insecticides were rapidly identified through the CRISPR-based reverse genetics approach in conjunction with in vitro metabolism.

For S. exigua, a genetic locus for abamectin resistance was mapped on 15.5-17.5 Mbp of Chr17. Conserved synteny in the Lepidoptera suggested that a CYP9A gene cluster in this location may harbor one or more P450 genes responsible for abamectin resistance. By large fragment knockouts, P450 gene sequence alignment and functional expression, we identified that a mutation (F116V) within substrate recognition site 1 (SRS1) region of CYP9A186 results in acquiring the capacity to detoxify abamectin and thus conferring resistance in S. exigua.

Current status and genetic basis of field evolved resistance to Bt cotton in cotton bollworm from China

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Abstract: Transgenic cotton expressing a single Bt protein Cry1Ac has been planted in China since 1997. Management of Cry1Ac resistance in the cotton bollworm, Helicoverpa armigera, has been largely dependent on the “natural refuge strategy” for more than two decades. The effective refuge percentage was estimated to be 56% during 2010-2013 based on non-Bt hosts (mainly corn, peanut and other legumes) in northern China. From 2010 to 2019, Bt cotton planting area decreased by 70% in northern China, which further increases the effective refuge size. Although the natural refuge delayed resistance evolution, the percentage of resistant individuals increased from 1% in 2010 to 8% in 2019. Further, the resistant individuals with non-recessive inheritance of resistance increased from 37% in 2010 to 86% in 2019. Genome-wide association studies (GWAS) was employed to screen diverse resistance loci to Cry1Ac in field-derived resistant individuals of H. armigera from northern China. The GWAS results showed the tetraspanin gene HaTSPAN1 with T92C mutation was the most abundant resistance gene conferring dominant resistance to Cry1Ac Bt cotton. Phylogenetic analysis reveals the HaTSPAN1 mutation arose from at least three independent origins in norther China. Considering current Cry1Ac resistance status, pyramided Bt cotton producing two or three Bt proteins is urgently needed for resistance management of H. armigera in northern China.

Global threats to Bt resistance management in Australia

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Abstract: Pathways to pest incursions can involve natural events (i.e., relating to climatic patterns), or human-mediated actions that relate to trade and/or human movements. Understanding the population genetics of targeted pests, especially of a cosmopolitan and widespread species, may distinguish introduced populations from local populations but do not enable pathways of introduction and associated biosecurity risks to be assessed. An example of this is the recent introduction of the Old World bollworm Helicoverpa armigera into Brazil, where genetic research was able to demonstrate multiple introductions but failed to establish factors that underpinned the catastrophic biosecurity breach. In Australia natural movements of insects including H. armigera, from Asia/South East Asia into northern Australia, have been detected using genetic markers, and represents the current recognized biosecurity risk to Australia’s agricultural industries including the cotton-growing sector. Although H. armigera have repeatedly evolved resistance to insecticidal chemistries used for their control and resistances to the Bt Cry toxins that are expressed in the Bollgard II cotton variety are also known, their management has nevertheless been successful in Australia through strict industry practices that incorporate a well-developed resistance pest management strategy. Successful management of Bt resistances is less well-established in some neighboring countries and movements of individuals carrying undesirable resistance traits into Australia would rapidly undo decades of robust scientific-based H. armigera management practices. Although biosecurity risks associated with natural incursion are difficult to control, research can identify appropriate pathways to target with actions to reduce accidental introductions due to trade. We integrated genetic data with information on international trade movements to assess biosecurity risks that are associated with accidental introduction of novel Bt resistance genes in H. armigera into Australia. We further considered the case of an incursion into Australia of the dominant Cry1Ac gene present in Chinese populations of H. armigera and the implications in terms of function of the existing pre-emptive resistance management plan for recessive resistance currently in place for Bt cotton.

Snellenius manilae bracovirus-encoded microRNAs as regulators in host immune responses

Authors: Wu Yueh-Lung[1], Tang Cheng-Kang[2], [1]Associate professor of the Department of Entomology in National Taiwan University, Taiwan, [2]Ph.D. candidate of the Department of Entomology in National Taiwan University, Taiwan

Abstract: Parasitoid wasp eggs are easily attacked by the immune systems of their insect hosts during parasitism. In response to this, parasitoid wasps have developed several mechanisms to inhibit the immune and physiological responses of the host, such as the production of venom and specialized wasp cells, and symbiosis with polydnaviruses (PDVs). These factors alter the host physiology to give the wasp offspring a greater chance of survival. However, the molecular mechanisms for most of these alterations remain unclear. Here, we found that the bracovirus of Snellenius manila (SmBV) encoded miRNAs into the host larvae, Spodoptera litura, during parasitism. Two of these miRNAs blocked the host's immune responses by regulating the signaling pathways, which enabled the survival of S. manilae larvae within the S. litura host. Microinjecting the inhibitors of these two miRNAs into parasitized S. litura restored their immune responses and significantly decreased the S. manilae pupation rate. These results show that these two SmBV-encoded miRNAs play an important role in regulating host immune responses. Overall, we demonstrate a cross-species regulation by miRNAs in animal parasitism and its possible function in the alteration of the host immune system during parasitism.

DiversityScanner 4K: A high resolution extended focus camera setup as an extension module for the DiversityScanner

Authors: Wuehrl Lorenz[1], Meier Rudolf[2], Giersch Matthias[1], [1]Karlsruhe Institute of Technology, [2]Leibniz Institute for Evolution and Biodiversity Science, Germany

Abstract: Manual investigation of invertebrate biodiversity and abundance in Malaise trap samples is a time-consuming and cost-intensive task that requires expert knowledge. New approaches have shown that automated solutions based on Artificial Intelligence can support experts in evaluating the large number of samples collected. Especially if the phenotype of individual species in a bulk sample has to be evaluated. Therefore, we presented the DiversityScanner as a robotic solution that offers the opportunity to automatically image, measure, and classify invertebrates (< 3 mm) and sort them into 96-well microplates for barcoding [Wührl et al. 2021]. To significantly improve image quality, an optimized camera system was integrated into the DiversityScanner 4K. Thanks to an extended focus system and a 12-megapixel camera, the image quality has been improved to such an extent that even the smallest structures, such as tiny bristles are now shown in detail. By using a focus tunable lens, extended focus images can be generated from several images with different focus planes. Therefore, an algorithm automatically aligns the images, recognizes sharp areas, and generates a high-resolution extended focus image. Finally, the object can be classified by a Neuronal Network and the biomass of the insect can be estimated from the image.

Genomics of the common pine sawfly (Diprion pini)

Authors: Wutke Saskia[1], [1]University of Eastern Finland, Finland

Abstract: Understanding outbreaks of forest pest insects has become increasingly important as mass outbreaks occur more and more frequently. With the help of constantly advancing genomic methods, we can now gain new insights into the adaptive mechanisms involved in insect outbreaks. During mass outbreaks larvae of the common pine sawfly (Diprion pini) cause severe defoliation of pine forests. Despite the impact of this species on forest ecosystems and economy, almost nothing is known about its genomic architecture. One particularly interesting aspect is its resistance to baculoviruses. These viruses can be used as biological control for other pine sawfly pests but are ineffective against the common pine sawfly. We sequenced the genome of the common pine sawfly based on a combination of sequencing technologies (Nanopore long-reads, Illumina short-reads, and 10X Genomics linked-reads). We used functional and comparative methods to investigate genomic innovations and the immunity to baculoviruses of this severe pest species. We present a high-quality genome assembly that extends our understanding of the evolution of sawflies and provides a resource for improved pest management and biological control strategies.

Automated Classification of Invertebrae Images by Neuronal Network based Algorithms

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Abstract: Automated image-based solutions for classification of invertebrae have become increasingly important for monitoring abundance and biomass [Høye et al, PNAS 2021]. Here we present different Convolutional Neuronal Network (CNN) based algortithms that are used for sorting and classification in the DiversityScanner [Wührl et al, MER 2021] and for classification of tic images taken with a smartphone. The image dataset consists of 8943 tic images and multiple data augmentation techniques were employed to increase the number of data. On the test dataset the CNN achieves an accuracy of 98% when predicting the developmental stage, 98% for the sex, and 94% for the genus. The distinction of the various species in the genus Amblyomma is particularly difficult.

How automation, machine learning, and DNA barcoding can accelerate species discovery in "dark taxa": Robotics and AI

Authors: Wührl Lorenz[1], Rettenberger Luca[1], Matthias Giersch[1] and Meier Rudolf[2], [1]Karlsruhe Instiute of Technology, Germany, [2]Leibniz Institute for Evolution and Biodiversity Science, Germany

Abstract: Robotics and artificial intelligence are two methods that are suitable for improving processes that are normally done manually. Therefore, these techniques also can be used when examining specimen-rich invertebrate samples, where traditional sorting methods are to slow and require expert knowledge. For that reason, we developed the DiversityScanner: a classification, sorting, and measurement robot for invertebrates. The 500 x 500 x 500 mm robot has three linear axes that enable a camera unit and an automated pipette to be moved over a square Petri dish, containing up to 150 specimens. After starting the DiversityScanner the image taken by an overview camera mounted directly above the Petri dish is utilised to calculate the position of the insects. Then the camera unit is moved over one specimen to capture high resolution detailed images. Convolutional neuronal networks (CNNs) are then used to classify the specimen into 14 different insect taxa (mostly families) and the specimen length and volume are estimated. In a final step the specimen is moved into a microplate using an automated pipette. In this talk we show how the DiversityScanner uses automation and artificial intelligence to take advantage of previously nearly untapped resources in the study of specimen-rich invertebrate samples.

Combining incompatible and sterile insect techniques to eliminate field populations of the mosquito Aedes albopictus

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Abstract: Release of artificially-reared radiation-sterilized males has successfully suppressed field populations of several insect pest species, but its impact on mosquito vector control has so far been limited. A related approach uses the endosymbiotic bacteria Wolbachia to generate condition-dependent sterilization, but may be undermined by the accidental release of females. Here, we show how a combined incompatible and sterile insect technique (IIT-SIT) approach successfully suppresses and effectively eliminates field populations of the world's most invasive mosquito species, Aedes albopictus. Following the creation of a mosquito line with a novel triple Wolbachia infection, millions of competitive factory-reared males of this line were released. When mated with wild-type females, the mating incompatibility generated by the novel triple Wolbachia infection resulted in embryonic death. Pupal irradiation of the released mosquitoes prevented unintentionally-released triply-infected females reproducing in the field, enabling near elimination of wild populations in two release sites across two years. Community support for the IIT-SIT approach strongly increased following mosquito releases, as nuisance biting decreased. This successful field trial demonstrates the feasibility of area-wide application of IIT-SIT for mosquito vector control.

Functional identification of the serpin genes involved in melanization in Plutella xylostella

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Abstract: Serine protease inhibitors (serpins) are widely distributed in animals, plants and prokaryotes, and participate in a broad spectrum of physiological processes. In the innate immune response of insects, serpins play a crucial role in the melanization reaction. In this study, two serpin genes, Pxserpin-3 and Pxserpin-6 from Plutella xylostella were cloned and identified. The ORFs of Pxserpin-3 and Pxserpin-6 encode 451 and 414 amino acid residues, respectively. The expression profiles of Pxserpin-3 and Pxserpin-6 genes at different developmental stages demonstrate that Pxserpin-3 has the highest expression at the adult stage, and Pxserpin-6 is highly expressed at the egg and pupal stages. We injected 4th instar larvae of P. xylostella with E. coli and S. aureus. The results showed that the mRNA levels of Pxserpin-3 have the highest expression after injection at 3 h and the highest expression of Pxserpin-6 was observed at 12 h after injection. PxSerpin-3 has a strong response to gram-negative bacteria, but the response of Pxserpin-6 to gram-positive bacteria was faster than gram-negative bacteria. RNAi analysis showed that the transcript levels of Pxserpin-3 was significantly decreased 6 h after injection, and Pxserpin-6 significantly decreased 24 h after injection. RNAi-mediated knockdown of Pxserpin-3 and Pxserpin-6 influences the expression of many genes involved in melanization, and antimicrobial peptides, as well as the Toll and Imd signal pathways. We further recombinant expressed the Pxserpin-3 and Pxserpin-6 in E. coli BL21. The UV CD spectrum shows that the different secondary structures of these two recombinant proteins which indicate their possible diverse functions. We then measured the inhibition activity of the purified recombinant proteins. PO activity was blocked after incubation of recombinant proteins PxSerpin-3 with the larval plasma of P. xylostella and E.coli, but activated by Pxserpin-6. Further transcriptome analysis suggest that the Pxserpin-3 and Pxserpin-6 were participated in the regulation of midgut immunity which response to Bacillus thuringiensis. Our results show that the important functions of Pxserpin-3 and Pxserpin-6 in P. xylostella immunity, especially in the regulation of prophenoloxidase activation.

The Movement and Spread of Oriental Fruit Fly (OFF), Bactrocera dorsalis (Hendel) (Insecta: Diptera: Tephritidae), in Asia – Need a Better Tool for Predicting the Invasion of the Pest

Authors: Xia Yulu, NSF Center for Integrated Pest Management, North Carolina State University, United States

Abstract: Abstract The Oriental Fruit Fly (OFF), Bactrocera dorsalis (Hendel) (Insecta: Diptera: Tephritidae), is an important quarantine pest worldwide. The pest damages more than 400 fruits and vegetables. Although OFF is regarded a tropical species, scientific reports suggest that the pest widely occurs in abundance in the temperate regions such as northern China. However, it is unclear whether the occurrences are due to migration and/or established populations. Authors tend to believe that the occurrences were migration populations which were introduced in the early season from the warm regions. Two primary factors might play key role here: 1) OFF is not on the list of quarantine pests in the major source countries such as China, it means that the host materials are free movement in large scale, 2) the emerging massive transportation systems were built in Asian countries in last decade or so. China’s Belt and Road Initiative (BRI) can facilitate the pest movement in the region. It presents more challenge to conduct risk analysis, and predict pest invasion. A new tool, which incorporates the population dynamics in the global scale, needs to be developed

Fly competitive ability and not temperature or species diversity determine population dynamics and stability on a Drosophila-parasitoid community

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Abstract: The role of diversity on the stability of communities is being debated for long in ecology. Communities with higher diversity are described to be more stable as they have lower population fluctuations reducing the risk of species lost. However, in a lot of ecological communities, the interaction dynamics of some species leads to an uneven distribution of species abundances with one dominating the others. Furthermore, this ecological dynamic can be affected by abiotic factors like temperature. To determine which of these factors (diversity, temperature or species interaction) determines the dynamics of drosophila-parasitoids communities we performed a microcosm laboratory experiment. During five months, we recorded the dynamics of twelve different food webs (different combinations of flies and parasitoid species with two diversity levels) at two temperature regimes. We didn´t observed any major effect of temperature or diversity on community stability, with parasitoids playing a minor role. In contrast, we observed an important fly species effect with a gradient on its competitive ability and dominance. Strong competitors exclude all the rest of the species while weaker ones allowed coexistence and increased diversity. We concluded that the presence of dominant species determines fly community composition and stability.

Molecular basis of response to (sub)lethal stresses

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Abstract: Tephritid fruit flies, including Queensland fruit fly (Qfly, Bactrocera tryoni) and Mediterranean fruit fly (Medfly, Ceratitis capitata) are destructive insect pests of fruits and vegetables, affecting world trade in horticultural products. With the discontinuation of chemical control options in Australia, such as Fenthion and Dimethoate for the treatment of commodities susceptible to fruit fly infestation, it has become urgent to understand how stress-based control techniques such as heat, cold and irradiation can be used to effectively kill fruit fly without affecting fruit quality or environmental health.

This project aimed to uncover the molecular-level response of fruit fly to stressors including heat and cold. This has never been done before in other insects except some basic work on Drosophila flies. We developed a molecular model system based on Medfly and Qfly that can be run in a controlled, molecular laboratory. We achieved that by developing highly controlled bioassays that induced a 75% fly mortality on third instar larvae. We further improved a method for acquiring gene expression data and used it to build the first atlas of stress-response in Tephritid fruit flies.

For example, in Medfly, our results showed that during heat treatment and recovery, 31 genes were differentially regulated.

Overall, we found that heat treatment had considerably less variance than cold treatment. These differentially regulated genes span a specific class of molecular functions related to protein biosynthesis, including heat-shock proteins (HSPs), metabolic enzymes, RNA-binding proteins, translation initiation factors, and transcription factors.

A pronounced feature of our data is the regulation of a panel of Heat Shock Proteins (HSPs) in both heat and cold treatments. Gene expression data is correlative. To investigate causality, we established the RNA interference (RNAi) technique and used it to study the function of HSP in the molecular response to stressors.

This project provides new knowledge on the disinfestation mechanisms for two of Australia’s most economically destructive horticultural pests. This understanding will enable more effective approaches to be trialled for pre-export treatment and assist in market access negotiations with trade partners. Ideally, this will benefit growers in the future with more efficient treatment alternatives for fruit fly control and reduced treatment costs. Less use of toxic chemicals is of direct benefit to both the environment and to people. The research underpins the development of next generation tools to safeguard fresh produce from fruit fly damage.

Unfolding the truth behind refolding of Odorant Binding Proteins

Authors: Xu Wei[2] and Zareie Reza[1], [1]Director, Proteowa Pty SABC, Murdoch University, Australia, [2]Food Futures Institute, Murdoch University, Australia

Abstract: Like many other organisms, insects use chemical stimuli to regulate behaviors including feeding, egg-laying, and mating. Odorant binding proteins (OBPs) are one of the crucial aspects of insect chemosensory system, which plays an essential role in transporting the hydrophobic volatile odorant molecules to the olfactory receptors. Most of these insect OBPs are expressed at large scale using bacterial host due to its relatively less complicated and high production mechanism. However, one of the major concerns of bacterial expression is that the protein is expressed in an unfolded state in inclusion bodies (IBs), which require further in-vitro protein refolding step to make the protein biologically active. While doing this, there are always high chances of protein misfolding which results in soluble or insoluble protein aggregation. Thus, it is highly important to confirm the efficiency of each refolding method, used for OBP refolding, in terms of getting the correctly folded structure of the target protein. Instead, it has been observed that many of the past insect OBP studies have shown insufficient results to confirm the success of their respective refolding method. This insufficiency of proof for validation of the refolded protein structure generates significant doubts on many of these functional studies of insect OBPs. In this study, we used four Helicoverpa armigera OBPs, HarmOBP2, HarmOBP5, HarmPBP1 and HarmGOBP2, as model proteins to compare the different protein refolding strategies and their success in resulting in correctly folded proteins. Along with that, we have developed a novel pH-dependent method of protein refolding which demonstrated as a better strategy for some of these HarmOBPs refolding compared to other used methods. Further, we compared and validated the binding patterns of these refolded OBPs with the reporter and natural ligands. Finally, we used a reverse chemical ecology methodology to isolate and identify the natural ligands for HarmOBP2 and HarmOBP5. This study points out a crucial but largely ignored step of insect OBP research, protein refolding and the loopholes associated with it in previous studies.

Challenging of Intergrated Management for Resurgent Aedes aegypti in St. Augustine, Florida

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Abstract: Aedes aegypti L. is a primary vector for Zika, Dengue, Chikungunya, and yellow fever viruses. The species of mosquitoes was a major container-inhabiting mosquitoes in Florida. Since 1986 Ae albopictus, the Asian Tiger Mosquitoes was found in Florida and Houston, Texas and the fast spread of the mosquitoes, Ae. aegypti gradually disappeared from North Florida. In 1992 Ae. aegypti totally disappeared from Northeastern Florida. In Feb 2016, Ae. aegypti was collected from downtown St. Augustine, Florida ad Anastasia Mosquito Control District (AMCD) collaborated with the County Department of Health (DOH) launched an eradication program. We divided the city into 5 routes and each route with 2 technicians (one from DOH for education and inspection and one from AMCD for inspection and making the necessary control action). The teams visited/inspected all residents through streets by streets and doors by doors to educate residences and inspect/make necessary treatment for the residential property where we found the adult or larval mosquitoes. We used the BTi and Altosid for larval control except for emptying containers and educating people how to prevent from breeding mosquitoes, and conducted adulticides with ULV, thermal, and barrier spraying of permethrin, sumithrin, and bifenthrin products based on justification with positive landing rate counts, ovitraps and other type of traps with collection of this species of mosquitoes. We conducted the inspection and control every Wednesday for about 2 years. During the 2 year efforts, there were No outbreak of Zika and Dengue even if there were several imported cases. However, the species of mosquitoes had not been limited for spread. Now we often collected and found the mosquitoes in south, west, and north areas. Based on our ovitraps and BG sentinel trap surveillance, the species of mosquitoes are still spreading to other areas. Also, the mosquitoes collected from different spots of St. Augustine showed different levels of resistance based on the cooperation study with the University of Florida/IFAS/Florida Medical Entomology Laboratory.

It is a big challenge for us to control the spread of the mosquitoes in north Florida. Since 2018 we've collaborated with University of Florida/Department of Entomology and Nematology and USDA/ARS/Center for Medical, Agricultural, and Veterinary Entomology, Gainesville, FL to study and evaluate the control efficacy by SIT (released male mosquitoes treated by radiation to the partial area of the city) and collaborated with MosquitoMate to release Wolbachia-infected male mosquitoes, and cooperated with SpringStar to mass deployment of the AGO traps in the city to control of Aedes mosquito population. Also, we hired more intern students and visiting scientists each year to join our team to study the basic biology, behavior, survival, sugar/plant feeding, and breeding habitants, especially bromide plants as one of major sites, and other novel control method and technology.

Sugar feeding ecology of Aedes aegypti in Mali and its control with Attractive Toxic Sugar Baits (ATSB)

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Abstract: It is common knowledge that Ae. aegypti can take blood and convert it to triglycerides and glycogen that provide energy, and this led to subsequent observations in the field that female Ae. aegypti were taking multiple blood meals within a single gonotrophic cycle. Accordingly, it was assumed that Ae. aegypti may be less dependent on sugar for energy than other mosquito species and presumably rarely feed on sugar. This assumption has changed in recent years and there is increasing evidence that Ae. aegypti are frequent sugar feeders, given the right environment.

In Urban Bamako, Mali, West Africa we determined the relative attraction of Ae. aegypti males and females to a variety of sugar sources including flowers, fruits, seedpods, and honeydew in the laboratory and using plant-baited traps in the field. We observed the rhythm of blood feeding versus sugar feeding activity of Ae. aegypti in vegetation and in open areas. Finally, we studied the effectiveness of spraying vegetation with ATSB on Ae. aegypti in sugar rich (lush vegetation) and in sugar poor (sparse vegetation) urban environments.

In urban Bamako, Ae. aegypti depend on environmental resources of sugar for feeding and survival. The demonstration that Ae. aegypti populations rapidly collapsed after ATSB treatment, in both sugar rich and sugar poor environments, is strong evidence that Ae. aegypti are sugar-feeding frequently. This study demonstrates that Ae. aegypti mosquitoes depend on natural sugar resources, and a promising new method for vector control, ATSB, can be highly effective in the fight against Aedes-transmitted diseases.

maintaining genetic structure of industrial mass reared beneficial insects

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Abstract: Mass rearing of beneficial insects for commercial use in agriculture and diseases control is limited to few dozens of species. Maintaining production stability or low variation, is a major challenge for the mass rearing facilities worldwide which face industrial and economic constrains. While high fitness for target organism is the main driving forces of the mass rearing facilities, other traits can be in favor for the application in sites. However, sustaining genetic variation within the mass rearing processes is crucial for both ideal aims. Usually, mass rearing facilities are managing stock culture, which harbor disease free colony in a relief conditions allowing sufficient population size. Such population should be reliable and post-adopt source tor the industrial production. Never the less, following changes in the genetic structure can be difficult, especially when production accelerate with scales. This paper present overview on applicable tools and measurements that can be use in the maintain of the genetic structure of industrial mass reared populations with special emphasis on Tephritidae.

Conservation of ladybirds: Malaysia insights

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Abstract: Ladybirds (Coleoptera: Coccinellidae) are predator species that prey on aphids and scale insects. In Malaysia, this family has not been actively studied using molecular phylogenetic methods even though many species have the potential to be applied as biological control agents. Therefore, inventory studies were conducted in several ecosystems. We surveyed both the ladybirds as well as their host plants that had been infested by aphids or scale insects. DNA barcode analysis (cytochrome c oxidase subunit I, COI) was to resolve identification problems due to morphological variability. We observed a total of 17 species of ladybirds. These are Cheilomenes sexmaculata, Chilochorus nigritus, Coccinella transversalis, Coelophora inaequalis, Henosepilachna pusillanima, Henosepilachna vigintioctopunctata, Henosepilachna kaszabi, Heteroneda reticulata, Illeis koebelei, Megalocaria dilatata, Rodolia rufopilosa, Micraspis discolor, Harmonia octomaculata, Cryptogonus orbiculus, Cryptogonus fractemaculatus, Nephus sp., and Scymnus posticalis. We also identified host plant species, which helps our understanding of which pest species infest which plants. From our study and previous work, it seems that the invasive alien species Harmonia axyridis has not (yet) arrived in Malaysia. As part of our surveys, we screened ladybirds for the presence of natural enemies such as fungal ectoparasites (Ascomycota: Laboulbeniales: Hesperomyces virescens sensu lato) and parasitoid wasps (Hymenoptera: Braconidae: Dinocampus coccinellae) prior to the potential arrival and spread of Ha. axyridis. We have thus far found He. virescens s.l. on three specimens of Coccinella transversalis.

Potential bio-molecules related to male reproductive physiology for bio rational pest suppression of Spodoptera litura(Fabricius) (Lepidoptera: Noctuidae)

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Abstract: Spodoptera litura (Fabr.) is a nocturnal tropical pest damaging a wide range of important agricultural crops. Ecologically sound strategies are required to control this pest due to its immense resistance against all conventional pesticides. In this study a novel strategy is discoursed for the development of bio-molecules to be integrated with other biorational pest control tactics. Here, we are intending to target male reproductive physiology for pest suppression approach.
In vitro-sperm activation assay was designed to test the presence of sperm activating biomolecules in different prostatic parts of male reproductive tract. This assay confirmed the higher concentration of activator molecules in the lower prostatic part of reproductive tract. The activator biomolecule was proteinaceous in nature and was identified as trypsin like serine protease. Proteome-profiling of prostatic part further confirmed the presence of trypsin like serine protease of molecular weight 27kDa with 254 amino acids. Sperm activation assay using trypsin enzyme (in lieu of prostatic activator) leads to sperm activation and trypsin inhibitor (ex. Soyabean) ceased motility in sperm in presence of its natural activator from the prostatic part. dsRNA of trypsin like serine protease, administered to larvae and pupae, affected the growth index and inhibited the sperm activation in the adult moths. Further, the feasible modalities regarding use of sperm activation inhibitors are being exploited for their use as potential bio-pesticides. The role of sperm activation inhibitors is discussed to act as potent environment friendly bio-molecules to be integrated in radio-genetic method (Inherited Sterility Technique) for an effective suppression of this serious polyphagous pest.

Regulation of dopamine neurons for proper valuation

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Abstract: During olfactory associative learning of Drosophila melanogaster, neurotransmission from the protocerebrum anterior medial (PAM) cluster dopamine neurons signal reward and drive appetitive memory. Precise activity regulation of the PAM neurons is therefore critical for proper reward values. Here we show that genetic disruption of GABA signaling in the PAM neurons causes cognitive bias. Disrupting the expression of a metabotropic GABA receptor, GABA-B-R3, in the PAM neurons enhanced appetitive memory. This memory increment was due to increased learning asymptote but not acquisition speed. In accordance, we observed augmented calcium responses of the PAM neurons to sugar ingestion, consistent with the increased subjective reward signals. We further identified that the anterior paired lateral (APL) neuron is a cellular source of GABA for the PAM neurons. Strikingly, PAM disinhibition involved not only increased appetitive learning but also broader generalization and cognitive judgment bias to reward predicting cues. We thus concluded that GABA signaling onto appetitive dopamine neurons are crucial for proper valuation, perturbation in which causes delusional optimism bias.

Brain insulin-producing neurons directly respond to light and temperature in controlling reproductive dormancy in Drosophila melanogaster females

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Abstract: In response to the combination of low temperature (~10°C), short-day photoperiod (10L:14D) and starvation (water only), D. melanogaster females exhibit reproductive dormancy, in which ovarian maturation is arrested without yolk accumulation in the oocyte. Insulin-producing cells (IPCs) in the brain play a pivotal role in the control of dormancy: reduced activity of IPCs promotes dormancy whereas increased activity stimulates ovarian maturation. We endeavor to unravel how environmental cues are integrated by IPCs for their regulation of dormancy by in vivo whole cell patch clamp recording. We find that IPCs hyperpolarize their membrane potential upon light-illumination even after the conduction block with tetrodotoxin (TTX), indicating that IPCs directly respond to light. A decrease of temperature from ~25°C to ~10°C depolarizes IPCs, which as a consequence generate action potentials, even in the presence of TTX, indicating that they also directly respond to temperature. We further show that a seven-pass gustatory receptor and two-pore-domain K+ channel represent integral components of the temperature sensing mechanism in IPCs, as deficits of these two proteins lead to impaired responsiveness of IPCs to temperature and concomitant disturbance of reproductive dormancy.

Finding indications of lag time, saturation, and trading inflow in the emergence record of exotic agricultural insect pests in Japan

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Abstract: Agricultural imports are the primary pathway for the introduction of exotic insect pests. The invasion records of exotic insect pests are also influenced by the lag time before detection and saturation caused by the limited species pool of potential invaders. We compiled an exhaustive list of exotic insect species in mainland Japan and tried to evaluate the connection between the commodity types (flowers, fruits, vegetables, cereals, and timber) and agricultural pests types (outdoor, stored product, greenhouse, forest, and timber pests), in addition to the effects of lag time and saturation. We found that lag time was prominent when all pest types were merged into one group, while saturation always existed when we divided the records into the four agricultural pest types. We suspect that the saturation effect was masked by admixture amongst pests with different saturation patterns. Our findings indicate that all commodities, i.e. flowers, fruits, vegetables, cereal, and timber, contributed to invasion of pest insects as potential pathways. However, it was unclear if certain items had comparatively greater significance in this process.

Comparing the performance to forecast pest outbreaking risks between statistical modelling and machine learning in the case of Japanese cucumber.

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Abstract: Forecasting the pest outbreaking risks has been primary important in modern pest management. Historically, the statistical modelling has long played a central role in the pest-risk forecasting, while an alternative approach, i.e., machine learning, recently is getting popular. A machine learning may be advantageous since it automatically produces plausible forecasts without any statistical assumptions while a statistical modelling generally has a theoretical structure and thus it allows us to interpret the forecasts logically. We compare the performance of these two different approaches by using survey records of cucumber diseases for 20 years in all Japanese prefectures which were collected in the national program for plant-pest monitoring, called “Prevalence Reconnaissance Business”. As for the statistical modelling and machine learning, we employed the state-space modelling and the neural network, respectively. Both approaches were challenging because the dataset has many missing records and the relative/categorical order of the visual infection rate and the actual infection rates are mixed up. Traditional statistical approaches will not be applied to such the type of data sets. Comparing the results from these two confronting modern approaches, we will discuss how the recent advantages in data-sciences can change methodologies and improve the accuracy in future pest management.

Plant-to-plant communication aboveground reduces root nodule symbiosis

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Abstract: Volatile organic compounds (VOCs) mediate plant-to-plant communications in many species. Injured plants release specific VOCs, such as methyl jasmonate and methyl salicylate, that induce defense and reduce herbivory in undamaged recipient plants. However, their effects on belowground responses have not been elucidated. We hypothesized that aboveground plant-to-plant communication reduces root nodule symbiosis via a resource-based trade-off with induced defense in leaves and shoot-root signaling. Soybeans were exposed to the volatile organic compounds (VOCs) of damaged leaves of Solidago canadensis var. scabra, and leaf defense traits (leaf mass per area (LMA), C/N ratio, total phenolics) and root nodule symbiosis (number and biomass of root nodules) were measured. LMA and total phenolics were not affected, however plants that received VOCs had higher C/N ratios and fewer root nodules than untreated plants. The number and dry weight of nodules was negatively correlated with the C/N ratio in leaves. Thus, plant-to-plant communication aboveground led not only to changes in leaf traits, but also to reductions in root nodule symbiosis in soybean for expression of induction defenses. Previous studies on aboveground plant-to-plant communication focused on changes in aboveground plant traits and associated communities. In this study, we found that aboveground plant-to-plant communication affected belowground root nodule symbiosis. Future studies of the effects of plant-to-plant communication on belowground plant tissues may find broader effects.

Development of Odorant Receptor Neurons in Ants

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Abstract: Animal behavior is based on the dynamic interpretation of sensory stimuli by the brain. Eusocial insect, including ants, display striking phenotypic differences between castes, including their behavioral responses to chemical stimuli. To precisely distinguish the social cues, ants evolved more complex chemosensory system, where odorant receptor genes (ORs) were dramatically expanded during social evolution. Using germline mutation in orco (OR co-receptor) in the ant Harpegnathos saltator, we found that OR functionality is essential for pheromone-induced social cooperation, reproductive physiology and proper development of odorant receptor neurons (ORNs). Interestingly, although male and female ants display striking differences in the OR expression pattern, most neurons die in the absence of orco. However, the survival of a small group of ORNs is likely independent of orco. This study may reveal how olfactory neural development is regulated in eusocial insects.

Nutritional stress negatively impacts life history traits and antiviral immunity but enhances susceptibility to dengue virus infection in Aedes aegypti

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Abstract: Diet-induced nutritional stress plays a key role in regulating health and disease outcomes, because of its interaction with the immune system. In mosquitoes, diet-induced nutritional stress may affect their vectorial capacity through its impact on phenotypic traits, infection susceptibility and immune performance. However, how these three factors are affected by larval and adult nutritional stress remains unclear. Here, we manipulated mosquito diet to create two levels of nutrition at both larval and adult stages and evaluated the effects of low nutrition (nutritional stress) on mosquito Aedes aegypti. We demonstrate that larval and adult nutritional stress negatively affects adult size and survival, respectively, and synergistically reduce the fecundity. Mosquitoes that experienced nutritional stress as adults, but not as larvae were more susceptible to becoming infected with dengue virus after ingesting an infectious blood meal, but developed lower viral titers than their unstressed counterparts. In addition, the mosquito immune response to dengue virus infection appears to be suppressed by both larval and adult nutritional stress with distinct involvement of key immune signaling pathways. Overall, our findings demonstrate a crucial role of nutritional stress in mosquito life history traits, infection outcome and immune response which in turn influence vectorial capacity for dengue virus.

Research on spotted wing drosophilia(swd) in northeast of China

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Abstract: 1. Occurrence of spotted wing drosophila (swd) in northeast of China, based on data collected from 16 locations (orchards), 7 cities, during 2016 to 2019. Including the host range and damage regularity. We found the population of adults reaching to the top from the middle of July to the end of August, depending on different fruits maturation periods, and there are 9-10 generations per year of swd in northeast of China.

2. Control management. The current control of swd in China is not very clear or standard, because of ignorance or less recognition of the pest. Local growers generally consider swd as a saprophytic fruit fly, and are lack of the knowledge of this unique fruit fly. By our research work, more and more growers recognize it is significant to monitor and control swd in their fields. Trapping is the most effective and safe management to control swd, according to our research these years. So new bait formula from raspberry and new style of trap container have been developed and applied in fields in Liaoning.

3. Phylogenetic analysis of Wolbachia in different geographical populations of swd. The genetic differences of different geographical swd are helpful to explore how does it spread and diffuse worldwide.

Resistance of Helicoverpa zea to Bt crops in the United States

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Abstract: The cotton bollworm or corn earworm, Helicoverpa zea, is a major target of Bt cotton and pyramided Bt corn in the U.S. In recent years, field-evolved resistance of H. zea to Cry1 and Cry2 proteins has been widely reported in the U.S., especially in the southern states. In addition, a recent study provided strong evidence that H. zea has developed field-evolved resistance to Vip3Aa protein in the southern U.S. that meets the criteria for early warning of resistance but not practical resistance. Currently, high dose/refuge and gene-pyramiding are the two main IRM strategies implemented for planting Bt crops in the U.S. Information on the susceptibility of the field populations, resistance allele frequency, genetic basis and cross-resistance of Cry and Vip3Aa resistance can help evaluate the risks associated with the resistance in the field. In this study, we evaluated the susceptibility of the field populations of H. zea against Cry and Vip3Aa proteins, estimated its resistance allele frequency, characterized the genetic basis of Cry2Ab and Vip3Aa resistance, and finally checked the cross-resistance patterns of Cry and Vip3Aa resistance in H. zea. These information are valuable for testing assumptions of IRM for resistance management of H. zea.

Vibrational communication of insects: the intra- and inter-specific communication

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Abstract: Vibrational communication is a primitive yet widespread mode of communication in insects. The vibrational signals are transmitted through solid substrates and usually inaudible to human, and hence attract limited attention to scientists in the past. Nowadays, more than 195,000 of insect species covering 17 orders have been reported to use this mode of signal, and many of which are hemipterans. Psyllids are one group of insects that utilize vibrational signals, especially during the course of reproductive behavior. These signals are species- and sex-specific, and usually characterized by more complex male signals that may have been driven by sexual selection. Closely related taxa tend to share a similar pattern of signals, indicating the vibrational signals is a promising systematic character with phylogenetic significance. Not only for the intra-specific communication, vibrational signals also have been found to be involved in communication at inter-species level such as ant and butterfly symbiosis. Larvae and pupae of myrmecophilous butterfly species produce vibrational signals to attract their attending ants in order to obtain care and protection from ants. Although the vibrational signals seem to be an effective communication mode, utilization of vibrational signals may be confronted to varied biotic and abiotic challenges. For examples, some signals may be eavesdropped by predators or conspecific competitors. The natural background noise including rain and wind can also interfere the signal transmission efficiency. To conclude, how these factors shape the evolution of vibrational communication and its application into systematics requires more empirical evidence and possibly represents a core issue in the field of biotremology, the study of organismal vibrational behavior, in the near future.

Evaluation of pest control efficiencies for different banker plant systems with a simple predator-prey model

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Abstract: In Japanese glasshouses, the banker plant system has been introduced for biological control of different pest species. To evaluate the effectiveness of such a continuous way of releasing predators from the banker plant for controlling pests on the crop, we developed a simple model for the interaction of the pest and predator in the crop. We parameterized the model for three different pest-predator systems, namely (1) Thrips palmi with its predator Gynaeseius liturivorus on sweet peppers, (2) Tetranychus urticae with its predator Neoseiulus californicus on peppers, and (3) Aphis gossypii with its predator Aphidoletes aphidimyza on eggplants. We used the parameterized models to predict under what conditions biological control in a banker plant system is successful. Therefore, we defined successful as keeping the pest below the economic injury level of the crop. Our main analytical result is that for successful control the maximum lifetime consumption of immigrating predators should exceed the daily prey growth at half saturation value. For practical purpose this translates into the fact that the immigration of predators when the initial pest density is low is crucial for successful control.

Release strategy of natural enemies in augmentative biological control in greenhouses

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Abstract: The release strategy of natural enemies is an important factor affecting the suppression of pests in augmentative biological control in greenhouses. Conventional methods to release natural enemies are to introduce natural enemies several times weekly or biweekly. The same number of natural enemies can be released once or can be divided into several releases. The predatory hemipteran bug Nesidiocoris tenuis (Reuter) is used to control the whitefly Bemisia tabaci (Gennadius) infesting tomatoes in greenhouses around the world. We developed a simple predator-prey model for the interaction of B. tabaci and N. tenuis on tomato crops in a greenhouse. We parameterised the model and performed numerical simulations using the model to predict under what conditions biological control is successful. A specific total amount of natural enemies was divided over 1 to 12 weekly releases at different initial numbers of B. tabaci. We defined that control was successful when the pest was below the economic injury level of the crop throughout the simulation that spanned a half year (182 days). The results of our simulations suggest that multiple, but not too many, introductions of N. tenuis are necessary for successful control. Moreover, the number of introductions of the predator should be increased for successful control when the total number of predators increased. This is due to the fact, that a certain kind of dilution will make that the predators do not overexploit the prey initially. Overexploitation causes the predators to go extinct, and the small number of prey that survives can thereafter grow freely exponentially. These findings indicate the importance of multiple introductions of natural enemies or their continuous release from the banker plant system for successful control of pests.

An automatic monitoring system for paddy light-trap pests based on machine vision and deep learning

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Abstract: Monitoring pest populations in paddy fields is important to effectively implement integrated pest management. In the world, current field pest monitoring practices involve manual field investigation, sweep nets, pheromones, sticky trapping boards, light traps or other insect traps.

Light trap can attract many species of pests by different optical spectrum. Light trap is widely used to monitor field pests all over the world. In China, some intelligent light traps of crop pests can automatically turn lights on and off, kill insects by far infrared light and automatically exchange insect recycling bags every day. In one week, technicians take the insect bags back and pick the target pests up from the trapped insects and count them . However, the manual approach of identifying and counting pests from lots of trapped insects is time-consuming, labor-intensive and error-prone, especially in pest peak periods.

In this paper, we developed an automatic monitoring system of paddy light-trap pests based on machine vision and deep learning. This system is composed of an intelligent light trap, PC or phone client platforms and a cloud server. The light trap firstly traps, kills and disperses insects, then collects images of trapped insects and sends each image to the cloud server. To avoid light-trap insects pile up, a vibration plate and a moving rotation convey belt are adopted to disperse these trapped insects. Two residential networks (ResNets) are loaded in server and used to automatically identify five target pests from lots of light-trap insects. One ResNet-50 has 4 output units corresponding to 4 categories (three species of moth pests and one category of non-target big insects), and the ResNet-18 has 3 output units corresponding to 3 categories (two species of rice planthopper pests and one category of non-target small insects). To compare with the identification performance of different CNNs for five pests, we trained other four state-of-the-art convolutional neural network architectures, namely CaffeNet, VGG-19, GoogleNet, ResNet-152 in big insect training sets, and also trained other four CNN, namely cifar10, VGG-6, ResNet-16 in small insect training sets. To evaluate the correlation of daily data between manual identification and image automatic identification of pests, their correlation coefficient was computed.

The moth identification results show that CaffeNet obtained small AP and mAP values of three pests and non-target-big insects. ResNet 50 and ResNet-152 gained higher AP values than CaffeNet, VGG-19 and GoogleNet. Although ResNet-152 obtained higher AP results of three big pests, the AP value of non-target big insects was only 65.8%. It means the ResNet-152 leaded to overfitting because of deeper net layers and many non-target big insects are misjudged. ResNet-50 achieved the highest AP value with 88.9%. So we chose the ResNet-50 to identify the big light-trap pests. The planthopper identification results show that Cifar model obtained

Sexual dimorphism in wing shape of the Dacus ciliatus Loew, 1862 (Diptera: Tephritidae): A geometric morphometric analysis

Authors: Yaran Mehmet, Gaziantep Universtiy

Abstract: Dacus ciliatus Loew, 1862 (Diptera: Tephritidae), lesser pumpkin fly, is a major pest of a wide range of Cucurbitaceae in many parts of Africa, some parts of Asia and the Middle East. D. ciliatus is a polyphagous fly, and damages crops in the Cucurbitaceae. D. ciliatus is classified as an A1 quarantine pest by the European and Mediterranean Plant Protection Organization (EPPO) and significant in terms of quarantine for CPPC (Caribbean Plant Protection Commission). The fly was recorded first time in cucumber cultivation areas of South-eastern Anatolia Region (Diyarbakır, Mardin, Siirt and Şırnak) in Turkey. This study contributes the literature in the field of sexual dimorphism by comparing wing shape. In the study fifty males and fifty females Dacus ciliatus specimens were used. Fifteen-homolog landmark used for geometric morphometric analysis of wings, which were modified from Schutze et al., 2012. MANOVA (multivariate analysis of variance) was performed in Morpheus to see differences in wing shape of sexes. In analyses, statistically significant differences were found among the wing shape of male and female specimens. Finally, results showed that landmark-based geometric morphometric analysis could be a powerful discriminator to determine sexual dimorphism of D. ciliatus.

Consequences of male- female fly ratios on reproductive potentiality and longevity of Blow fly, Lucilia cuprina (Diptera: Calliphoridae)

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Abstract: In Bangladesh, every year a huge amount of dried fish has been damaged due to the blow fly (Lucilia cuprina, Diptera: Calliphoridae) invasion which is responsible for both health and currency hazards. As a result, blow fly has been regarded as one of the most destructive pests for fish drying industries in Bangladesh. Keeping these issues in mind, we are focused to develop and apply Sterile Insect Technique (SIT) towards blow fly control/suppression. Optimizing the male and female fly ratio is an essential part of an effective SIT program. Different sexual proportion of flies have significant effect over the biotic potential and adult longevity. Hence, in this research we are trying to identify the best ratio of male and female blow flies which in turns will maximize the productivity and potentiality of the flies. With a view to produce a good number of potential blow flies for SIT program, a good proportion of male and female flies have been combined in laboratory condition. The combinations were listed (male: female) as 1:1, 1:2, 1:3, 1:4 and 1:5 respectively. The ratios of female flies have been combined per male to observe the reproductive potentiality and longevity for each ratio. The highest number of egg mass was revealed from 1:4 ratios of male and female flies. But there was no significant (p > 0.01) differences in egg mass number from 1:1 to 1:5 ratio. Whereas the weight of the total egg mass was significantly (p < 0.01) varied among the ratios. Female flies showed a more or less similar linear situation for longevity while male flies ended up with a short-lived phenomena. From this experiment it can be concluded that there must be at least four female per male for a mass production and a good number of potential progenies. In order to keep the mass rearing process upright and for a good number of potential flies we can prepare our laboratory cages with a good proportion of female flies per male fly (1:4) which in turn will surely put a positive feedback for our blow fly SIT program.

Selection on gustatory receptors at early stages of host plant specialization in an island Drosophila population: a genomic perspective

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Abstract: Most Drosophila species are generalists feeding on decaying plant materials. A peculiar case was the discovery of the specialization of Drosophila sechellia on toxic fruits of noni (Morinda citrifolia) on the Seychelles. Although genomic comparisons with its closest generalist species have revealed a rapid rate of evolution of chemosensory genes including olfactory and taste receptors, the possible order by which those changes occurred remains unknown. We have recently discovered another case of specialization on toxic noni implying a population of the generalist species Drosophila yakuba on the island of Mayotte. Behavioral assays confirmed the higher olfactory and taste preference of island flies for noni toxins compared to mainland D. yakuba. The close relationship between island and mainland population permits the fine dissection of the evolution of the chemosensory, highlighting a potential genetic parallel evolution between D. sechellia and D. yakuba during their independent specialization on the same toxic host.

Sexual dimorphism of wing coloration in Numenes moths as possible sex-limited mimicry

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Abstract: Theoretically, the following four patterns of relationships between mimicry and sexual dimorphism in coloration are distinguished; unimodal mimicry (both sexes of mimic species resemble the same model species), female-limited mimicry (females of mimic species resemble the model species, males do not), male-limited mimicry (males of mimic species resemble the model species, females do not), and dual mimicry (each sex of mimic species resembles a different species of model). Although unimodal mimicry and female-limited mimicry have been well studied, there were only a few descriptive studies about male-limited mimicry and dual mimicry, and there was no empirical research for the function and evolutionary process of these mimicries yet.

Two moths, Numenes albofascia and Numenes disparilis, belong to the genus Numenes (Lymantriidae) in Japan, have distinctive sexual dimorphism in their colorations. Male Numenes albofascia closely resembles Pidorus atratus (Zygaenidae) in its coloration, and female Numenes albofascia resembles Arctia caja (Arctiidae) and/or Pericallia matronula (Arctiidae). Likewise, male Numenes disparilis resembles Neochalcosia remota (Zygaenidae), and female Numenes albofascia resembles Arctia caja and/or Pericallia matronula. The emerging seasons also correspond between suspected mimic and model species. We examined them in wing color patterns in visible and ultraviolet light, wing size, daily activities both in the laboratory and field, and unpalatability.

As a result, coloration patterns of each species have no significant difference in visible and ultraviolet light. Both Numenes albofascia and Numenes disparilis have sexual dimorphism also in their wing sizes, and the differences of wing size are correspondent to those of suspected model species. The activity times of suspected mimic species and model species are overlapping, and Numenes albofascia and Numenes disparilis have also the difference in their activity times between sexes. Predation experiments show that Numenes albofascia and Numenes disparilis are palatable to predators, On the other hand, all suspected model species have repellent effects.

Numenes albofascia and Numenes disparilis have a possibility of rare example of Batesian dual mimicry (each sex of mimic species resembles a different species of model). The conspicuous sexual dimorphism in coloration of them may result from the difference in warning colors between the model species. In Lymantriidae, adult moths lack mouthparts in both sexes and do not fly for searching for their food. Therefore, the flight activity of males is limited to search for females expelling pheromones, and the flight activity of females is limited to the search for oviposition sites. Once the flight time differs between the sexes, it is possible that sexual dimorphism in coloration occurs due to invisibility and mimicry toward different models in each sex.

Rebooting the systematics of Australian Culex (Culex) mosquitoes (Diptera) using whole genome shotgun data and morphology

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Abstract: Australia is home to 12 described species of Culex (Culex) Linnaeus, 1758, including the common banded mosquito Culex (Culex) annulirostris Skuse, 1889 which is a known vector of Japanese Encephalitis virus, Ross River virus, Murray Valley encephalitis virus and Kunjin virus. Despite their medical importance, the taxonomy of Australian mosquitoes has waned since the passing of prominent mosquito taxonomist Dr Elizabeth ‘Pat’ Marks. She designated three unnamed species in the subgenus Culex, including species Culex “Marks No. 32”, a manuscript name that has since been used for decades by Australian mosquito workers. An additional two undescribed species and six proposed cryptic species have also been identified in the subgenus. Recent advances in whole genome shotgun sequencing technology has enabled sampling of mitochondrial genomes from historical pinned collections. We have digitised and sequenced mitochondrial genomes from authoritatively identified pinned mosquito specimens held in the CSIRO Australian National Insect Collection to reconstruct the phylogeny of Australian mosquitoes, with a focus on subgenus Culex. This data is being used to accurately identify freshly collected specimens, assign authoritative species names to molecular clades and inform the description of new species.

Transcriptomic effects of larval dietary conditions on adult Aedes aegypti and potential effects on vectorial capacity

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Abstract: The yellow fever mosquito, Aedes aegypti, is a major vector for several arboviruses including dengue, chickungunya, and zika, and can be found in many tropical regions around the world where its larvae develop in a wide variety of aquatic environments. The physiological state of individual adult Aedes mosquitoes can also clearly be expected to affect several parameters related to vectorial capacity. Therefore, it seems likely that highly variable larval environmental factors influencing adult mosquito physiological and immune systems, such as larval nutrition, are important for our understanding of vectorial capacity. In this study, two groups of Ae. aegypti larvae were reared in conditions supplied with either a nitrogen rich detritus or nitrogen poor detritus as their diet source. Total RNA was then extracted from multiple adults from each treatment group at days 1, 5 and 15 post emergence and Illumina based RNA-seq differential gene expression analyses were performed using a standard analytical pipeline. Along with significant lifelong changes seen in core cellular machinery, such as ribosomes and amino acid metabolism pathway components, important changes were also seen in certain immune genes, odorant receptor genes, and genes related to pesticide metabolism. An improved understanding of changes in mosquito physiology based on carbon:nitrogen levels in larval environments will form a framework for future studies investigating the relationship between larval environment, adult physiology and vector competence.

Wherefore art thou mosquito? The historical and contemporay distribution of Aedes aegypti in the United States.

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Abstract: The distribution of Aedes aegypti (L.), the yellow fever mosquito, has been difficult to map as data on the occurrence of this species is often absent across much of its United States range. This poses serious challenges for control efforts and for predicting where outbreaks of arboviruses like Zika and dengue could occur, both of which are transmitted by this species. Historically, yellow fever plagued the United States across the 18th to early 20th centuries, resulting in thousands of deaths and many more illnesses. Up until the discovery that Aedes aegypti (L.) was the causative agent of the disease, no records were kept on the distribution of this species, complicating our understanding of its historical distribution and the factors important for its contemporary locations within the U.S. To determine the historical range of Ae. aegypti within the U.S. we examined the range of yellow fever epidemics across time and space. We tested the hypothesis that the distribution of Ae. aegypti was driven by human population density. This was tested by compiling a list of all yellow fever incidence in the U. S., human population density for that time period based on U.S. census tracks (analyzed in ten year intervals from 1870-1910), the number of people infected at the census and city level, and the human mortality when data were available. We found no relationship between infected individuals and human population size during each decade at the census track level, however a strong positive relationship did exist between infected humans and population size when epidemics with human population data at the city level. To understand the current distribution of this species, we also examined the hypothesis that climate (mean maximum and minimum temperature, mean rainfall) and anthropogenic factors (human population density, average household income, and percent of abandoned properties in neighborhoods) would explain the current range of Ae. aegypti. These factors and occurrence data for both spring and summer months were incorporated into a machine learning species distribution model to predict habitat suitability for Ae. aegypti. We found that anthropogenic factors, specifically human population density, had a large effect on explaining the distribution of Ae. aegypti regardless of season. Thus, both historical examinations and contemporary data strongly suggest that the distribution of Ae. aegypti is based on human population density within the United States, a fact that has been generally overlooked until now. Such information is important as this species continues to experience range expansion under a rapidly changing climate.

Phylogenetic pattern of the mimicry within the genus Euploea (Lepidoptera: Nymphalidae, Danainae)

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Abstract: The alpha-taxonomy, mimicry, mating strategy, overwintering ecology and chemical defense of the butterfly genus Euploea have been studied extensively during the last decades. The wings pattern and unpalatability of them are known to be significant in driving the convergent evolution of colour-patterns of other butterflies and diurnal moths in Indo-Pacific region. Up to date about 61 species and numerous subspecies of Euploea are recognized. Although the genus is very often mentioned in studies on butterfly biology and mimicry, the majority of the studies confines to less a dozen of the species. The phylogenetic relationships within the genus was only studied once during the 1980s based on morphological characters and a Hennigian approach. The previous study, however, neither successfully resolve the phylogeny nor re-organize the classification. Meanwhile, morphological characters are not sufficient to distinguish species with extreme sexual dimorphism, polymorphism, internal mimicry and high individual variability. In order to evaluate the correlations between divergence times, clade age, speciation, biogeography and hostplant associations, we reconstructed the first Bayesian phylogenetic trees of Euploea butterflies using sequence data of 5 loci (COI, EF1a, RPS2, cytochrome b and wingless) from 40 species, and use this tree to assess the correlation between the diversity of mimicry ring and the landmass in SE Asian islands. Our phylogenetic analysis reveals that: (1) Euploea is a monophyletic group comprising at least 9 morphologically distinct and well-supported clades; (2) extreme sexual dimorphism has evolved only once in E. mulciber + E. configurata clades; (3) convergence in wing pattern appears in every clades with sympatric distribution; (4) the area of island correlates with diversity of mimicry rings, while this phenomenon is not detected in continent; and (5) species diversity of the genus is underestimated.

Toward a better understanding of the phylogeny of Epicopeiidae (Lepidoptera, Geometroidea), a small family with remarkable diversity in mimetic morphology and behavior

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Abstract: The family Epicopeiidae is a small moth group comprising xx species in 10 genera distributed throughout the eastern Palaearctic and Oriental regions. All the species exhibit remarkable variations in size, wing shape and wing patterns that involve various mimicry rings dominated by toxic butterflies and moths. Although the extraordinary mimicry of this family has attracted attention from lepidopterists since the 19th century, a robust phylogeny, on which the systematics is based, is still unavailable due to rarity of most taxa in both the field and museum collections. In the present study, we included 8 of the 10 known genera in the analysis and also included various samples to represent the phenotypic diversity of some polymorphic taxa for a more accurate inference of phenotypic evolution. We used 6 protein-coding genes and employed maximum likelihood and Bayesian inference to reconstruct the phylogeny. We also examined the morphological characters that were used to reconstruct the preliminary phylogeny by previous authors. Our results clearly show existence of polyphyly in two genera and the separation between genera is also supported by morphological characters. The “swallowtail butterfly wing shape” has evolved independents at least twice and this suggests that wing shape evolution is highly plastic in this family. Polymorphic mimicry is also confirmed in four species and is highly correlated with diversity of models. Our finding reveals that Epicopeiidae has demonstrated a remarkable evolutionary history that is accompanied with dramatic changes in morphology as well as adult and larval biology.

Performance Comparison of Population Modelling on Different Pest Scenarios

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Abstract: Over the past decades, the use of pest population modelling has been vast in Decision Support System (DSS) and Integrated Pest Management System (IPM). Various simulation models are designed in order to model the dynamic development of pest population. There are huge challenges in pest population dynamic simulation. However, this field of research contains high impact factor on greenhouse growers and the pest management industry. In order to understand the importance of this research, the knowledge of common practices in the greenhouse is crucial. These knowledge inclusive of observation methods used to estimate the overall pest population with larvae and adult counts gathered. Two typical circumstances are investigated in this paper, the accuracy, behavioral analysis, and computational performance of the designed models are evaluated.

The first circumstance is that unique pest stages that consists of both larvae and adult counts are used as initial simulation input into the simulation models, whereas the second circumstance is that balanced pest population is distributed with either the larvae or the adult counts across all the other stages as initial simulation input into the simulation models. In this research, two simulation methods are evaluated, namely, the boxcar train model and the simplified phenological degree-day model. The results from both of the evaluated models shows that the balanced pest population input provide a result closer predicted values as compared to the unique pest stages of larvae and adult counts. The outcome of these two circumstances is evaluated in the simulation models and the result obtained is able to operate as a guidance for simulation model developer of the future.

Testing and developing automated pheromone traps for forestry and crop protection

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Abstract: Pheromone traps are used for insect pest monitoring in crop protection, solving research questions and as early warning systems for emerging pests, either native or non-native. Traps that lure insects with synthetic pheromones come in different shapes and sizes, with or without glue papers, depending on the expected catch. However, the goal is the same: 1) identify the catch 2) time the catch and 3) count the catch. The major shortcoming of traditional traps is the need for manual checks at certain intervals. The Internet of Things (IoT) opens new opportunities for developing real-time insect monitoring on 4 and 5G networks with remote sensor devices globally.

In 2019, we firstly developed, automated pilot traps based on mobile phone technology to monitor the European spruce bark beetle, Ips typographus (Coleoptera: Curculionidae). Secondly, we tested commercially available traps (Trapview© and iScout Metos©) with pea moth, Cydia nigriana (Lepidoptera: Tortricidae) in a pea field of southwestern Finland. All the traps incorporated machine learning algorithms for image recognition.

For bark beetle monitoring two different traps “wet” and “dry” were assembled using field durable cell phones that were powered with 20W solar panels with external batteries for backup. The setup was in operation for over two months. The traps took three images per day that were stored in Amazon Web Services (AWS) cloud environment. The accuracy of the photos was inadequate in “wet” trap for counting the individual beetles. In “dry” trap the counting become only problematic when the beetles accumulated into the collection container. Image segmentation and counting process utilized the Unet convolutional neural network and the OpenCV library. A total of 42 images were manually annotated and the remaining images only processed. System performance was evaluated by using 10 non-annotated images as the test set. From 10 test images, error percentage was estimated to be <10 % based on manual counting.

During the June-July monitoring period of pea moth the commercial traps operated as expected and species identification succeeded at varying levels. The user also trained the system by identifying the pest monitored. The trap captures were comparable to manually checked delta traps. With the automatic monitoring the farmer would have been able to make his pest management decisions two days earlier than with manual traps. The commercially available traps, however, need modification regarding battery consumption, power generation of the solar panels and durability of the trap in Fennoscandian field conditions.

As a conclusion more research and development activities are needed to produce easily operable, reliable, durable and reasonably priced products. The results with the pilot remote monitoring funnel traps for the bark beetles indicate that a functioning prototype needs low-cost components and further development of the trap’s cleaning mechanism by com

Comprehensive collection and analysis of environmental DNA of arthropods remained on a plant

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Abstract: For community ecology of arthropods and pest control on plants, the survey of the arthropods on plants is a crucial step. However, its effectiveness is often hindered by many lines of problems in collecting small organisms on plants as well as high levels of skills required for species identification. In aquatic systems, to solve such problem, environmental DNA (eDNA) based techniques of metabarcording have been remarkably improved. However, application of eDNA-based metabarcording to terrestrial arthropod communities on plants remains rarely explored due to the difficulty of collecting eDNA of the organisms from plants tissues. To solve this problem, we developed a new eDNA collecting method for the arthropods on plants and crops using eggplant and cabbage as model systems. DNA barcode region, Cytochrome c oxidase subunit I (COI) gene, of the collected eDNA was comprehensively sequenced by a high-throughput sequencer after being extracted, purified, and amplified. As the result, more than 21 arthropod species were detected. It includes four parasitoid species and one predator species that were not observed by visual survey. This high coverage and sensitivity imply the effectiveness of the developed method despite of its simplicity. In this presentation, we are also going to show the results of monitoring arthropods and eDNA on rice plants in experimental rice field every two weeks for 5 months.

Seasonal adaptation of embryos and larvae of the Antarctic midge

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Abstract: The Antarctic midge, Belgica antarctica is the only insect endemic to the Antarctic Peninsula and its offshore islands. It has a 2-year life cycle and spends most of this period as a larva. Embryos, pupae, and adults are present only during the austral summer. Although its physiology has been extensively studied, there is little information on how they adapt to the Antarctic seasons. First, we investigated embryonic thermal tolerance and found that almost all embryos developed to the 1st instar larvae at temperatures ranging from 0 to 15 °C. These results indicate that immobile embryos have sufficient thermal tolerance to withstand fluctuating summer temperatures. Contrarily, the 1st instar larvae could develop to the 4th (final) instar larvae only at 4 °C. Mobile larvae may escape adverse temperatures behaviourally. The 1st instar larvae could develop to the 4th (final) instar stage, but the 4th instar larvae arrested their development and no pupae appeared. The observation revealed the 4th instar larvae enter obligatory diapause. In general, diapause can be terminated by winter cold. We found that the 4th instar larvae exposed to the simulated Antarctic winter conditions for 3 and 6 months successfully resume their development after cold exposure, whereas only a small portion of control larvae under Antarctic summer conditions resumed their development. The longer chilling treatment made more larvae resume their development. We found the Antarctic insect uses obligatory diapause to set the timing of the emergence of short-lived adults.

Peptidergic networks in circadian clock neurons regulate locomotor activity rhythms in Drosophila melanogaster

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Abstract: All lifeforms on our planet have been subjected to 24-h environmental changes caused by the earth's rotations. To cope with the dynamic changes of 24-h cycles, circadian clock has been evolved from a very ancient organism such as cyanobacteria. The fruit fly Drosophila melanogaster is an excellent model for studying the molecular mechanism and neural network of animal circadian clocks. One of the most successful examples is the discovery of the period gene in 1971 by Konopka and Benzer —the first clock gene. The period gene is expressed in about 150 neurons in the fly brain, and those neurons are supposed to be involved in behavioral rhythms. Among them, a cluster of four small neurons located in the lateral brain, so-called ventrally located small lateral neurons (s-LNv), has been proposed as master pacemaker neurons, which express a neuropeptide, Pigment-dispersing factor (PDF). A loss of PDF causes a diminished morning activity, a phase-shift of evening activity toward the midday and weak activity rhythms under free-running conditions. The s-LNv neurons send signals to other pacemaker neurons through the PDF-receptor. We recently found that a cluster of two pacemaker neurons located in the dorsal brain, so-called anteriorly located dorsal neuron 1 (DN1a), express a neuropeptide, CCHamide1 (CCHa1) and this signal goes to the s-LNv neurons through the CCHa1-receptor. A loss of CCHa1 reduces the overall activity level. The double knockout of PDF and CCHa1 causes an additive phase-shift of evening activity and this phenotype was even more pronounced under a long-day condition. These results suggest that s-LNv and DN1a are reciprocally coupled via a neuropeptidergic circuit, which delicately regulates the daily activity pattern.

Impact of radioactive Cs on freshwater biota by the Fukushima nuclear power plant accident

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Abstract: During the Fukushima Daiichi nuclear power plant accident, radioactive substances were emitted into the environment, which contaminated forest litter as well as algae, sand substrates, aquatic invertebrates, and fish in freshwater streams. Because these substances have substantial effects on stream ecology over many years, it is necessary to clarify the diffusion and decay mechanisms of radiocesium is needed. Radioactive Cs contaminations of aquatic insects in pools were consistently higher than those in stream riffles. Contamination by the radioactive Cs differed depend on species, location and stream velocity. Contamination of fishes, those are used by human for food, is considered to be occurred via dietary uptake, and consequently, the degree of fish contamination was diet-dependent. The ecological half-life of cesium and the transfer coefficient also differed among aquatic invertebrate groups and location. The radiocesium concentration in algae was related to stream current velocity. These trends would lead to a longer period of freshwater contamination. Radiocesium concentrations would continue to decrease in more highly contaminated areas, but it is difficult to reduce radiocesium concentrations in less-contaminated areas because different contamination mechanisms would be at work. Controlling the water flow is key to regulating radiocesium concentration in freshwater ecosystems.

Phylogeny and higher systematics of Psocodea

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Abstract: Long-recognized as two insect orders, Psocoptera (booklice and barklice) and Phthiraptera (chewing and sucking lice) have recently been integrated into a single order, Psocodea. Morphology, Sanger-sequence and NGS techniques have been adopted to elucidate the higher-level phylogeny of Psocodea and, overall, these data sets converge on common ground. Psocodea is divided into three monophyletic suborders, Trogiomorpha, Troctomorpha (in which Phthiraptera is embedded), and Psocomorpha, and the latter two suborders are sister taxa. Monophyly of Phthiraptera was once questioned but is now corroborated. Taxonomically, Phthiraptera should be treated as an infraorder within Troctomorpha, and the widely recognized four subgroups of parasitic lice (Amblycera, Ischnocera, Rhynchophthirina and Anoplura) can be maintained as “parvorders”, with establishment of an additional new parvorder for the mammal-parasitizing ischnocerans (family Trichodectidae) which is placed as the sister of Rhynchophthirina + Anoplura. A couple of uncertainties remain for the higher-level phylogeny even with genomic dataset and extensive taxon sampling: e.g., monophyly of the family Prionoglarididae is ambiguous, although the family retains the most primitive forms and thus is key to understand the origin and evolution of Psocodea; placement of the genus Lachesilla and the family Peripsocidae is highly unstable, which made monophyly of the infraorder Homilopsocidea ambiguous.

Control of North American Planthopper, Metcalfa pruinosa on Sesame Fields

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Abstract: Since Metcalfa pruinosa was first reported in Koera, it has continually caused damage to many crops. Metcafa pruinosa exist not only in farmland but also in forest areas, and are difficult to control due to the influx of individuals from near forest. M. pruinosa has been occurred in orchard and its surroundings because of various host range. Thus, it has been difficult to decide spatial range and control time for efficient management. In this study, occurrence and dispersal pattern of M. pruinosa in sesame field were surveyed using clear sticky traps, and spatial patterns were analyzed with SADIE(Spatial Analysis by Distance IndicEs), based on location information at sticky traps. Results showed that the population density of M. pruinosa began increasing in early June. M. pruinosa nymph mainly dispersed in mid July and in late July, emerging season of adult. The distribution of in early June in sesame field was aggregative pattern in the area adjacent to the mountain. Therefore, if the seeding time is delayed in areas that are not in contact with mountain-area, it may be possible to reduce the damage of M. pruinosa.

Multitrophic interactions among plants, insect pests and their natural enemies regulated by endophytic entomopathogenic fungi

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Abstract: Entomopathogenic fungi (EPF) are now known to act as endophytes and therefore EPF leaf sprays may lead to both direct effects on the insect pest via contact with the fungal spores and direct and indirect effects on the pest when it feeds on endophytically colonised leaves. However, knowledge is limited concerning the possible impact of this endophytic behaviour on the plant chemical ecology, on the relationship insect pest-plant and insect-pest-natural enemies. In this sense, our studies have addressed the efficacy of the natural enemies (predators and parasitoids), when offered both sap-sucking and chewing pests that had been feeding on melon plants endophytically-colonized by the entomopathogenic fungi. The lacewings, Chrysoperla carnea consumed the same number of aphid prey in the same time in treatments and control. In a choice bioassay, C. carnea larvae preferred to feed on aphids reared on B. bassiana colonized plants compared with control plants. From other hand, the number of aphids parasitized by Aphidius colemani and their sex ratio were not influenced by whether the aphids had been feeding on B. bassiana colonized plants or not. However, the reproductive potential of Hyposoter didymator was significantly reduced in Spodopetra littoralis larvae fed with colonized plants if compared with larvae fed with non-inoculated plants, with parasitisation percentages of 32.6 and 67.7%, respectively. Our findings support the use of endophytic entomopathogenic fungi in combination with other natural enemies, such as predators and parasitoids, in Integrated Pest Management programs, whereas their use should be evaluated on a case-by-case basis.

Role of entomopathogenic fungus Metarhizium brunneum (Ascomycota: Hypocreales) in integrated management of olive fruit fly Bactrocera oleae (Diptera: Tephritidae)

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Abstract: The olive fruit fly Bactrocera oleae (Rossi) (Diptera: Tephritidae) is the most destructive pest to the olive crops worldwide. The control of this monophagous tephritid fruit fly is now at a critical moment because of the resistance developed by this pest against the chemical insecticides hardly available for its control. Soil treatments with the Metarhizium brunneum (Petch) (Ascomycota: Hypocreales) strain EAMa 01/58-Su targeting third-instar larvae in the soil during autumn and emerging adults from the soil during spring, under different climatic conditions, is considered as a pioneer method that can reduce the B. oleae population density emerging from the soil during spring up to 70%. This fungus can be mixed with the herbicides in the atomizer tank to do a simultaneous application which reduces the application costs. From other hand, our studies have demonstrated the lack of negative direct or indirect impact of such treatments on both the soil-dwelling non-target arthropod population and the parasitoid Psyttalia concolor (Szépligeti) (Hymenoptera: Braconidae). In addition, soil application of this fungus to control B. oleae leaves no residues in olive oil, in contrast to the use of chemical insecticides. Our works highlight the adaptation of the olive fruit fly control method based on soil application of M. brunneum to the IPM approach.

Management strategies for almond pests in Australia

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Abstract: Australia's almond industry, valued at around AUD $1 billion, is threatened by two destructive insect pests that damage the almond kernel: Carpophilus truncatus (Coleoptera: Nitidulidae) and Apomyelois (=Ectomyelois) ceratoniae (Lepidoptera: Pyralidae). Presence of unharvested nuts (mummy nuts) in orchards is positively related to higher numbers of these pests and crop damage. A two-year field study was conducted to determine the spatial distribution and prevalence of these pests in almond orchards and their relationship to mummy nuts and crop damage. Targeting mummy nuts with orchard hygiene practices is expected to reduce pest damage.

Modified trapping systems are being developed for both pests as timely and accurate monitoring is critical for pest management. Field trials evaluating the response of adult carob moth to ten different coloured delta traps showed that clear traps were twice as effective as any of the coloured traps in trapping male moths, and that black traps were more effective for female moths. Pheromones and fungal odour attractants for the beetle have been identified and successfully tested in the field. These results will help almond growers monitor pest infestations more effectively.

Parasitism of Hypothenemus hampei adults by Phymastichus coffea (Hymenoptera: Eulophidae): effects of parasitoid diet, age, and temperature.

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Abstract: The coffee berry borer, Hypothenemus hampei (Ferrari), (Coleoptera: Scolytinae) is the most destructive insect pest of coffee globally. A biological control wasp, Phymastichus coffea LaSalle (Hymenoptera: Eulophidae) is a gregarious endoparasitoid of H. hampei adult females. It has been introduced to Central and South American countries for the biological control of H. hampei. To release the parasitoid in Hawaii, host specificity was tested by exposing P. coffea to a range of coleopteran beetles. The effect of different temperatures (20 °C, 23 °C, 25 °C, 28 °C and 30 °C) on the developmental time, adult longevity, and sex ratio of the progeny were determined. The effect of diet on the longevity and oviposition was also determined. Results showed that the parasitoid is restricted to the genus Hypothenemus only and did not parasitise any other beetle. The optimum temperature for development was 24-26 °C. Higher temperature was detrimental for the development. The diet of 50% honey solution increased the longevity and oviposition.

Volatile-mediated between-plant communication in Scots pine and the effects of elevated ozone

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Abstract: Herbivore-induced plant volatiles (HIPVs) convey information between damaged plants and their neighbors. Coniferous trees release substantial quantities of HIPVs upon bark-beetle attack, representing a strong indicator of herbivore presence. However, plant-plant interactions mediated by bark-feeding-induced volatiles have not been investigated. Importantly, elucidation of plant responses to HIPVs has focused on defense, whereas effects on primary metabolism are largely unknown, vastly limiting our understanding of this ecological phenomenon. Here, we show that HIPV-exposure induces and primes volatile emissions, increases stomatal conductance and net photosynthesis rate, alters resin duct traits, and ultimately reduces damage caused by herbivores. Elevated ozone, an important tropospheric pollutant and threat to volatile-mediated interactions, alters the plant responses. However, the final defense outcome was not significantly affected. These findings demonstrate that HIPVs modulate conifer metabolism through responses spanning photosynthesis and chemical defense. The responses are adjusted in the presence of ozone pollution, but the defense benefits remain intact.

Unravelling 150 million years of evolution between termites and their gut microbiome using metagenomics

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Abstract: Termites are amongst the most abundant terrestrial animals on earth largely due to their ability to digest lignocellulose, the most abundant organic molecule on earth. Lignocellulose is broken down in the termite gut with the help of symbiotic bacteria. Studies have shown that most termite gut microbes are found nowhere else than in termite guts, and that they are acquired by vertical transfer from parent to offspring, and horizontal transfer between colonies. Up to now, most studies have used 16S rRNA marker to determine the bacterial community composition, preventing any functional analyses. Additionally, most studies focused on distantly related species, preventing any attempt to analyze the interactions between termites and their microbiome at evolutionary timescale. To address these questions, I sequenced gut meta-genomes of 150 termites, selected to represent host diversity across the termite tree of life. In this talk, I will describe how bacterial communities and their function varies within and between termite species. I will also discuss how the gut bacterial community evolved across the termite tree of life.

Parasitic characteristics of Asobara japonica on alternate host and photoperiod for mass production

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Abstract: In General, pest infected with parasitoid was released when applying a parasitoid to a filed. In this case, there are concerns of artificially inoculating non-infected pests with parasitoid. To solve this problem, the technique of screening infected pests with natural enemies and alternate host that do not harm crops can be used. This study was carried out to confirm the parasitic features of A. japonica on alternate host: Drosophila melanogaster and photoperiod for mass production of natural enemies. A. japonica was parasitic on D. melanogaster larvae and the emergence of adults were observed from D. melanogaster pupae. Just like the D. suzukii, black spots(larvae) and white spots(pupae) were observed in D. melanogaster. The parasitic rate in D. melanogaster according to the evolution of generations was similar to that of D. suzukii up to the third generation. The parasitic rate of D. suzukii according to the generation progress of D. melanogaster as host was slightly decreased, but it was similar to that of D. suzukii as host. The effect on generation progression by photoperiod was not significant in short day and neutral day conditions.

The fauna of cerci-bearing apterygotes (Diplura, Archaeognatha and Zygentoma) from China

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Abstract: As the largest country in Asia and the third largest country in the world, China harbors nearly 20% of all known insect species on earth due to dramatic differences in topography, climate and vegetation across China. However, the species diversity of the apterygotes is highly underestimated so far, especially for the representatives equipped with leg-derived cerci classified in the taxa Diplura, Archaeognatha and Zygentoma. This study summarizes the current knowledge on Chinese records of Diplura (six families, about 50 species), Archaeognatha (two families, 31 species) and Zygentoma (three families, 10 species) and surveys their distribution and phylogenetic relationships. Further steps of our project on the biodiversity of basal hexapods from China will be outlined, including the application of modern information technologies currently promoted by the Specialized Information Service Biodiversity Research (BIOfid).

Phylogeny, taxonomic revision, and evolution of brachyptery in the New World leafhopper tribe Faltalini (Hemiptera: Cicadellidae: Deltocephalinae)

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Abstract: The deltocephaline leafhopper tribe Faltalini currently consists of 11 genera and 27 described species. The tribe occurs in the New World from the southwestern United States through Argentina and Chile. Existing records and observations indicate that most members are endemic to grasslands and live and feed on grasses (Poaceae), although some have been collected in or near tropical forests. Recent field work in South America, especially in Argentina, and examination of specimens from multiple institutions has revealed the existence of two new genera and 35 new species of the tribe. Many more are expected to be discovered with more field work, especially in understudied grassland regions of South America. In light of the discovery of the new taxa, the tribe is taxonomically revised, including an account of its taxonomic history, a key to the genera, defining morphological characters for the tribe and for generic groups, descriptions of all genera including two new genera, descriptions of 35 new species, and a phylogenetic analysis based on a dataset of 51 morphological characters scored 40 taxa.

The morphological phylogenetic analysis of members of the tribe and outgroup taxa resolved Faltalini as monophyletic, resolved three well-supported relationships among generic groups, and resolved all genera for which multiple taxa were included as monophyletic. The phylogeny suggests a stepwise reduction in wing length. Macroptery is the ancestral condition and sequential reduction in wing length culminated in a clade including seven genera which are completely brachypterous. The nature and morphology of brachyptery, especially of the hindwing, is explored using SEM imagery and instances of brachyptery in Faltalini are compared to other independently evolved instances in the subfamily Deltocephalinae.

Managing Helicoverpa armigera (Noctuidae) in Australian Grain Crops: Current Status and Future Prospects

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Abstract: Helicoverpa armigera Hübner (Lepidoptera: Noctuidae) is a major pest of broadacre crops in north-eastern Australia. Prior to the introduction of transgenic cotton in the 1990s, high levels of insecticide resistance in H. armigera almost caused the collapse of the Australian cotton industry.

The Australian Grains industry is still heavily reliant on conventional insecticides to control H. armigera. Subsequently, resistance of H. armigera to the frequently used insecticides is an ongoing challenge. In particular, the development of resistance to more selective options (e.g. indoxacarb and chlorantraniliprole) is closely monitored and managed.

Integrated Pest Management (IPM) can improve H. armigera control and help mitigate the threat of resistance. Several measures have been developed to provide better information and enhanced management tactics for growers:

1. Wide-scale pheromone trapping to detect mass moth movements.
2. Development of economic thresholds for H. armigera in several summer and winter grain crops.
3. Development of NPV (nuclear polyhedrosis virus) as a biological control.
4. Evaluation of improved control measures for other grain pests, the management of which affect H. armigera
5. Development and release of an insecticide resistance management strategy for H. armigera.

However, there are still major limitations to the adoption of IPM of H. armigera in Australian grain crops. The inexpensiveness of broad-spectrum insecticides and the difficulties associated with incorporating natural enemies into management decisions are particularly problematic. Moving forward, a promising avenue of research for some crops, for example the summer grain crop pigeonpea, is selecting crop varieties that are resistant or tolerant to injury from H. armigera and other pests.

Population regulation of caterpillars in northern hardwood forests

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Abstract: Interannual variation in caterpillar abundance can fluctuate by greater than 20-fold in northern hardwood forests; however, the broad-scale drivers of this variation are not well understood (Reynolds et al. 2007). We illustrate continuous large annual variation in caterpillar abundances at Hubbard Brook Experimental Forest, New Hampshire, USA from 1986 to 2019 and reapply a thermal sum model to explore how temperature influences caterpillar abundance. When observing the density dependence of caterpillar populations, we aim to see if the equilibrium abundance remains stable or changes between years. We observe if the equilibrium abundance varies between different host trees, American Beech (Fagus grandifolia) and Sugar Maple (Acer saccharum), to understand how changing species composition may influence the stability or instability of caterpillar populations. Finally, we hypothesize the role of 1) foliar Nitrogen, 2) phenology of leaves, 3) air temperature during leaf expansion, 4) snow depth, and 5) variation in Ichneumon wasp abundance in changing caterpillar abundance based on long-term correlating datasets. Understanding these drivers of variation in annual caterpillar abundance informs us about potential changes in host availability for parasitic insects such as wasps and the food availability to many birds, as well as contributing to our understand of global insect decline.

Demography and fitness of Anastatus japonicus reared from Antheraea pernyi as a biological control agent of Caligula japonica

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Abstract: Japanese giant silkworm (JGS), Caligula japonica Moore, is an emerging defoliator pest of forest and fruit trees in East Asia, causing severe economic losses. To develop a cost-effective biological control program against JGS, we used eggs of the Chinese oak silkworm (COS) Antheraea pernyi Guérin-Méneville as an alternative host to rear the most dominant JGS egg parasitoid Anastatus japonicus Ashmead. We compared the demographic parameters and total parasitism (killing) rates of A. japonicus parasitizing JGS and COS eggs using an age-stage, two-sex life table method. The results showed that A. japonicus performed differently on these two different hosts. Anastatus japonicus reared from COS eggs had a higher fecundity (369.7 eggs per female) and a longer oviposition period (35.9 days) on the COS than JGS eggs (180.9 eggs; 24.0 days). Consequently, A. japonicus parasitizing COS eggs had a higher intrinsic rate of increase ($r = 0.1466$ d–1), finite rate of increase ($\lambda = 1.1579$ d–1) and net reproductive rate ($R0 = 284.9$ offspring) than those parasitizing JGS eggs ($r = 0.1419$ d–1, $\lambda = 1.1525$ d–1, $R0 = 150.0$ offspring). The total net parasitism rate (the number of parasitized hosts in which the parasitoids successfully developed) of A. japonicus parasitizing COS eggs was 284.9, significantly higher than that of A. japonicus parasitizing JGS eggs (150.0), while the net non-effective parasitism rate (the number of parasitized hosts in which the parasitoids failed to develop) of the former (0.0) was significantly lower than that of the latter (9.6). These results suggest that A. japonicus can be efficiently reared on the alternative (or factitious) COS eggs, and the reared parasitoids have a high biological control potential against the target JGS.

Multiparasitism: an innovative mean for mass production of Trichogramma on the large eggs of Chinese silkworm, Antheraea pernyi

Authors: Zang Lian-Sheng, Institute of Biological Control, Jilin Agricultural University, China

Abstract: Trichogramma parasitoids are important biological control agents for insect pest management. However, efficient means for mass production of Trichogramma parasitoids are needed. Large eggs of the Chinese silkworm, Antheraea pernyi, have practical advantages as hosts for Trichogramma production such as the high parasitism rate, low cost, and easy storage and transport, which has been regarded as among the best factitious hosts for mass production of Trichogramma parasitoids. However, the thick and hard chorion of the large eggs is a limiting factor for some dominant parasitoids against insect pests, such as T. ostriniae and T. leucaniae, which are unable to normally form emergence holes to escape and consequently are fatally trapped. Recently, we found the feasibility of mass production of Trichogramma via multiparasitism with T. dendrolimi (or T. chilonis) on these originally nonpermissive host eggs of A. pernyi. The results indicate that T. ostriniae and T. leucaniae could be normally emerged from the large eggs through multiparasitizing with T. dendrolimi (or T. chilonis). Particularly, the outcome of multiparasitism between Trichogramma parasitoids is significantly impacted by factitious host species and parasitoid age. These findings encourage production of some dominant Trichogramma species on industrial scale for IPM programs.

Performance of two egg parasitoid species from Zambia and four indigenous Trichogramma species from northeastern China against fall armyworm, Spodoptera frugiperda

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Abstract: Fall armyworm Spodoptera frugiperda (Smith) (Lepidoptera: Noctuidae), is a new invasive pest causing serious damages in Asia and Africa. Trichogramma are the dominant biological control agents that has been applied to control lepidopteran pests worldwide. To prevent the outbreak of invasive S. frugiperda in China, performance of the two egg parasitoids collected from Zambia and four native species of Trichogramma egg parasitoids from northeastern China were studied. The two egg parasitoids from Zambia were identified as Trichogramma sp. nr. mwanzai and Trichogrammatoidea sp. by using combination of both molecular and morphological characters. The results showed that both parasitoid species from Zambia significantly preferred to 1-day-old age eggs of S. frugiperda. These two imported parasitoid species can be massively reproduced on Corcyra cephalonica eggs. In native species, all four Trichogramma species could accept S. frugiperda eggs and complete development successfully, but significant differences in fitness parameters were found among them. The parasitism of T. dendrolimi, T. ostriniae and T. leucaniae was higher than 80% on S. frugiperda egg masses, while only T. dendrolimi females offered to S. frugiperda eggs parasitized higher number of eggs among all the tested species. Finally, the performance of two parasitoid species from Zambia and four native Trichogramma species on S. frugiperda eggs were compared. The present study provides useful information on mass breeding and releases of indigenous egg parasitoids against the invading S. frugiperda in Africa and China in future.

Recent advances toward the sustainable Nesidiocoris tenuis exploitation in tomato crops

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Abstract: Generalist predators are often highly efficient biocontrol agents of various crop pests. Besides, they can also feed on various non-pest foods. The zoophytophagous mirid bug Nesidiocoris tenuis (Reuter) (Hemiptera: Miridae) is largely employed in biocontrol programs in tomato crops in Euroafroasia through augmentative releases and conservative strategies. Under certain circumstances, it can cause economic losses by its repeated feeding on tomato plants. Here we report recent experimentations on various aspects of potential N. tenuis exploitation in tomato crops, such as banker plants, variety susceptibility, induced plant defenses, insecticide selectivity. The results of our recent experiments provide new insight useful for optimizing Integrated Pest Management tomato packages.

BugMap: understanding the expansion of Halyomorpha halys with the support of citizens

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Abstract: Tracking the invasion of alien species requires the rapid gathering of a vast amount of data, a goal that can be achieved with the coordinated work of researchers and citizens. In this context, the application of citizen science programs to the monitoring of alien species is becoming particularly popular, although its efficacy should be object of more accurate evaluation through specifically designed experiments. BugMap is a smartphone app specifically designed to track the expansion of Halyomorpha halys, the brown marmorated stink bug (BMSB) in Trentino, Northern Italy. In the present study, we compare the BMSB distribution provided by data obtained with standard monitoring methods (i.e. attractive traps, visual sampling) and BugMap, in terms of time and spatial coverage.

From 2016, BugMap collected more than 3000 records, thanks to the contribution of technicians, farmers and citizens. The photographic validation associated with BugMap showed good accuracy since the vast majority of the records targeted the correct stink bug species. The heat maps generated with these records showed a reliable evolution of the areas with higher concentration of BMSB with time, coherent with the data obtained with the traditional monitoring. Furthermore, BugMap data has proved to be particularly useful to monitor both the BMSB phenology (e.g., first appearance of nymphs and eggs) and presence in different environments (e.g., cultivated areas, woods, parks), throughout the year. Our conclusion is that the real time information provided by BugMap could be employed as an instrument for timely decision-making and to support IPM strategies.

Managing Spider Mites, Banks grass mite (Oligonychus pratensis (Banks) and Two-spotted mite (Tetranychus urticae Koch) on Corn

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Abstract: Insecticide choice for controlling spider mites (Bank grass mite - BGM and Two-spotted mite - TSM) on corn is critical because most pyrethroid and organophosphate insecticides used have a disproportionately adverse effect on beneficial species which contributes to mite flare ups. During management decisions, producers must document the mite species and life stage proportions as available miticides have variable effects on these two species: TGM is less susceptible to most available products compared to BGM, and not all miticides are capable of killing adults (adulticidal) and eggs (ovicidal). Data from spider mite control studies in the US Southern Plains is sparse, and therefore, in an effort to provide producers with efficacy data that will inform their management decisions, we conducted two studies at OPREC (Oklahoma Panhandle Research and Extension Center) in Goodwell, OK during the summer of 2019. In the first replicated study, we evaluated the effectiveness of 5 available miticides with variable modes of action and predicted efficacy for controlling spider mites in corn. In the second study, we evaluated two miticide products ('Onager' and 'Zeal') that were predicted to conserve beneficial species. In both trials, the results clearly indicated that all miticides tested were effective at suppressing spider mites in corn and producers can reliably choose among these products dependent upon their management goals that may include conservation of beneficials.

Back to the origin: the importance of considering genetics and sources of natural enemies' populations in classical biological control programs

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Abstract: Classical biological control depends on the importation and successful rearing of natural enemies' populations, and many times when a successful program has been carried out in one region natural enemies are imported from this introduced area rather than from the area of origin. This often leads to populations experiencing strong founder effects, loss of genotypic variability and increased inbreeding. Here we show two biological control programs carried out in Chile, where evaluations lead to the decision that importations should be carried out from the area of origin. The first project deals with the importation of Trioxys pallidus (Hymenoptera: Braconidae) to control the walnut aphid, a pest detected in Chile in 2009. Initially, parasitoids were going to be imported from California (USA), but given the recent reports of a loss in effectiveness of biological control, the decision shifted to carry out foreign exploration in Iran, the area of origin, and made collections on the intended host. In 2011, mummified aphids were imported and in the 2012-2013 season they were released. Establishment and dispersal were confirmed, as well as a depression on the pest population. The second project deals with Mastrus ridens (Hymenoptera: Ichneumonidae) to control codling moth. In this case M. ridens had also been imported to California over 20 years ago, and from there laboratory populations were sent to other countries. We collected parasitoids in its area of origin, Kazakhstan, and imported insects from a laboratory colony in New Zealand, as well as samples from other laboratories. We found that this parasitoid presented complementary sex determination (CSD), and thus inbreeding could result in the generation of diploid males. Analyses revealed that populations in captivity had lower genetic diversity and a larger proportion of diploid males than those in the wild. In laboratory experiments we found no effects of inbreeding on several female life history traits, but in inbred lines females produced less daughters, male biased sex ratio and higher proportion of diploid males. Populations with lower initial genetic diversity, showed lower growth rate and less production of females. These projects highlight the importance of carrying out pre- and post-release population genetics and carefully considering the sources of natural enemies in classical biological control programs (Funding: FONDECYT 1181256).

Resistance mechanism of the brown planthopper, Nilaparvata lugens, to buprofezin

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Abstract: Buprofezin is an insect growth regulator that inhibits chitin biosynthesis. It has been applied extensively on rice for the control of brown planthopper (BPH), Nilaparvata lugens. However, BPH has developed high level of resistance to buprofezin in the field. In this study, the molecular basis of buprofezin resistance was investigated in a buprofezin resistant strain from Wuxi field (Bup-R). The genetics of resistance was investigated by reciprocally crossing strain Bup-R with a susceptible strain (Bup-S) and revealed an autosomal incompletely recessive mode of inheritance. A synergistic study in vivo and a biochemical study in vitro indicated that an enhanced detoxification mediated by P450s to some extent contributes to the buprofezin resistance in the Bup-R strain. These data suggested that the P450-mediated metabolic detoxification of xenobiotics might be an important mechanism for buprofezin resistance in the BPH. The implementation of appropriate resistance management strategies is strongly advised to delay the further spread of resistance.

Terpenoids mediate interactions of the guava-citrus-psyllid

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Abstract: Intercropping can reduce agricultural pest incidence, and shows great potential of an important sustainable alternative to conventional pest control means. Understanding the ecological mechanisms for intercropping could optimize its use, particularly in tropical systems which present a large number of potential intercropping possibilities. Citrus is threatened worldwide by greening disease (huanglongbing, HLB) vectored by the citrus psyllid, Diaphorina citri (Hemiptera: Psyllidae). Control of HLB/citrus psyllid can be partially achieved through intercropping with guava, Psidium guajava, but the mechanisms remain unclear. We tested the hypothesis that guava volatiles affect psyllid behavior by altering the attractiveness of citrus through plant-plant interactions. In choice and no-choice cage experiments, psyllid settlement was reduced on citrus shoots that had been exposed to guava shoots for at least 2h. In Y-tube olfactometer experiments, psyllids oriented to odors of unexposed, compared to guava–exposed, citrus shoots. Emission of volatile terpenoids was reduced in citrus shoots that had been enclosed with guava shoots, suggesting that citrus metabolically responds to the odors of neighboring guava plants. ß-caryophyllene was the most abundant and characteristic volatile terpenoid volatile compound of the flushing shoots from the tested ACP host-plant species. Tissue expression profiles of nine known DcitOBPs were analyzed based on the transcriptome database, DcitOBP3 and DcitOBP6 exhibited high expressions in the antennae of both sexes and the ovipositor of females, and qRT-PCR validated the result. The binding ability of two recombinant proteins to eight ligands was studied by competitive binding analysis, as a result, DcitOBP6 exhibited stronger binding ability to ß-caryophyllene. Behavioral trials indicated that the sexually mature female adult psyllids were significantly attracted to ß-caryophyllene at the concentration of 0.1µL/mL and 10µL/mL. RNAi analysis in female D. citri showed that the reduction of DcitOBP6 transcript abundance led to a decrease in behavioral responses to ß-caryophyllene. The results demonstrate that DcitOBP6 is involved in the perception of ß-caryophyllene. Further study is needed to reveal the semiochemicals emitted by guava plants which elicit citrus responds. Well understanding of the interaction of guava-citrus-psyllid could led to the development of sustainable and ecological pest management system.

Migration Processes and Patterns of Fall Armyworm in China: Comparing with the situation in the USA

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Abstract: In January 2019, the invasive fall armyworm (FAW), Spodoptera frugiperda, arrived in China. Then, the southern half of the mainland of China has been covered by FAW during the first half year. By mid September of 2019, 26 (/30) provinces in China were covered by the invasive pest. What will be happened to this invader in China when their colonization complete? We draw up the migration processes and patterns of FAW in China by comparative perspectives on migration arena in the New World and East Asia.

1. The Asian Monsoon systems will provide dominant wind direction during spring, summer and autumn to accelerate the northward and southward migration processes of FAW in East Asia, from Indochina Peninsula to Russia Far East, Korea Peninsula and Japan Islands.

2. In the tropical New World, the round-year easterly prevent the moths of FAW immigrate to North America from Central and South America, that make a very small overwintering population of FAW located the most southern parts of Texas and Florida. So, the outbreak frequency of FAW in North America is not high and the outbreak areas are limited to local scale.

3. But in East Asia, all over the Indochina Peninsula are suitable habitats of FAW and will form the permanent year-round breeding areas of FAW and Infinite source populations of FAW for China. Meanwhile, the vast planting areas of staple grain crops in China will provide unlimited food resources to the pest. Therefore the population size of FAW in mainland of China will be larger and larger and FAW will outbreak year after year on multi-crop system in all over China.

4. The southwest low-level jets over the Great Plains shape the north and eastward migration patterns of FAW in North America, that make the moths get out of the wheat belt in northwest USA and mainly damage the corn belt in USA and Canada. But in China, there are no dominant winds before the summer monsoon emerged and during the transition period between summer monsoon and winter monsoon in spring and early autumn. The FAW will show multidirectional migration patterns to establish vast spatial distribution across the mainland, especially the westward migration to colonize the western China. So, FAW will become a super pest soon in China.

Connectivity of aerial corridors of hopper vector and epidemics of southern rice black-streaked dwarf virus

Authors: Zhai Bao-Ping[1], Li Xijie[1], Lu Jiahao[1], Guo Jiawen[1], [1]Nanjing Agricultural University, China

Abstract: Southern rice black-streaked dwarf virus (SRBSDV) is a virus can only be transmitted by white-backed rice planthoppers (Sogatella furcifera, WBPH), a pest feed on rice. SRBSDV disease broke out several times in southern China and north Vietnam, but the outbreak mechanism is not clarified. Since there is no rice planting in southern China and north Vietnam. This area is like an ecological trap formed for both WBPH and SRBSDV. Then, how could the virus appear in southern China and north Vietnam next year? Among the adjoining areas, Hainan Island and central Vietnam have rice planting in winter. These are places where the virus conserves. In this research, we explored a method to use connectivity index to describe aerial corridor for WBPH. Meanwhile, seek for the reason SRBSDV outbreak degree fluctuating among different years. The connectivity of aerial corridors of WBPH make the insects return central southern Vietnam in late autumn and immigrate into southern China and north central Vietnam in Spring to re-colonize in the new planting rice fields. Besides, the connectivity of the Hainan-north central Vietnam corridor would support the viruliferous WBPH from Hainan immigrate into north central Vietnam by easterly during March and April or land on north central Vietnam with summer Typhoon during June and July, with triggering the SRBSDV outbreak and epidemic.

Attract-and-kill: A feasible approach to manage cocoa pod borer infestation in cocoa plantation

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Abstract: The cocoa pod borer (CPB) is an insect pest for cocoa production in Southeast Asia. It could cause crop loss more than 80%. Currently, application of synthetic pesticides is only effective method for growers to control CPB population in cocoa plantation. The sex attractants of CPB has been identified in the 1980s, however, application against CPB was halted in the early 1990s due to economic reasons and lack of commercial quantities of sex attractant. We have modified synthetic method for more economical production. Effectiveness of an attract-and-kill strategy was then evaluated for two years in Malaysia cocoa plantation. Our results demonstrated that the attract-and-kill strategy was as good as ongoing conventional synthetic pesticide application. In addition, the killing stations with lower dose loadings of sex attractant could significantly reduce the number infested cocoa pods caused by CPB. Our finding will help growers and scientists to develop a feasible approach using semiochemcials based on natural product to efficiently, safely, and environmentally friendly manage cocoa pod borer infestation in cocoa plantation.

New advances on the functional genomics of the brown planthopper

Authors: Zhang Chuan-Xi, 1.Institute of Plant Virology, Ningbo University, China; 2.Institute of Insect Science, Zhejiang University, Hangzhou, China

Abstract: The brown planthopper (BPH), Nilaparvata lugens (Stål) (Hemiptera: Delphacidae), is a serious migratory rice (Oryza sativa L.) pest, which causes a conservative estimation of more than US$300 million per year world wide. Our new advances on its functional genomics includes: (1) A chromosome-level of the genome was assembled. (2) Whole genome sequencing of 358 brown planthoppers uncovers the landscape of their migration and dispersal worldwide (3)A comprehensive omics analysis and functional survey of cuticular proteins was revealed in the hopper and compared with other insects. (4) Plastic development of wing morphs and body colors was found to be determined by two different neoropeptides, respectively. (5) Salivary proteomes of planthoppers and their interaction with planthoppers. (6) Two new female determinants were identified in the planthopper sex determination pathway.

Competing beetles attract egg-laying in hawkmoth

Authors: Zhang Jin, Raza Syed Ali Komail

Abstract: Nutrition is crucial for survival, but that is only one of the countless factors. It's the wild west in nature, so smart choices must be made. Blindly, but with time and ingenuity on its side, evolution has provided species with diverse strategies to help them defuse the Darwinian struggle. In our study, contrary to our assumption we found that tobacco hawkmoths (Manduca sexta) preferentially oviposit on Jimson weed (Datura wrightii) that is already infested by a specialist, the three-lined potato beetle (Lema daturaphila). The fitness advantage was not found to be direct, as larvae developed more slowly when feeding together with Lema beetles. In nature, the caterpillars of M. sexta are heavily predated by a parasitic wasp, Cotesia congregata. Plants infested by their food competitor, the beetle L. daturaphila, kept this parasitoid away. Consequently, moths preferred the beetle-infested plants despite the availability of better food sources. Over time this preference is conceivably embedded in M. sexta biology. We identified that the volatile α-copaene, emitted by beetle-infested Datura, plays a role in this preference. We demonstrate that odorant receptor (Or35) is involved in α-copaene detection by performing heterologous expression and single-sensillum recordings. What at first appeared to be a counterintuitive strategy turned out to be a cooperation that has been molded by multi-trophic interactions.

RNAi interference on the chitinase gene HcChi for the control of Hyphantria cunea (Lepidoptera: Arctiidae)

Authors: Zhang Sufang, Key Laboratory of Forest Protection of the National Forestry and Grassland Administration of China, Research Institute of Forest Ecology, Environment and Protection

Abstract: Hyphantria Cunea is an important forestry quarantine pest in China. They frequently outbreak in Northeast, North and Central China, which lead to serious threat to forest health and ecological safety. In this study we explore the application of RNAi to control H. cunea. The result show that the injection of 5th instar larvae with dsChi doses 2.5μg could reduce the gene expression up to 66.8%, while 0.5μg lead to the pupation and eclosion stage deformity with a pupation rate of 31.03%. It also caused malformation during molting process of 4th instar larvae and lead to a pupation rate of 53.8%~77.8%. The chitinase dsRNA expression system was constructed using E. coli HT115 strain. 2nd and 3rd instar larvae were started to feed on dsRNA expressed by HT115, and caused the weight decrease of 40.7% and 10.7%respectively.

Full-length cDNA of SID-1 was cloned from H. cunea larvae by RT-PCR and RACE. The ORF of HcSID-1 is 2613 bp and encodes 870 amino acids. It is predicted that the gene has typical SID protein domains such as a long extracellular N terminal and 11 transmembrane domains. Phylogenetic analysis revealed the homology between HcSID-1 and other SID genes. Temporal and spatial expression patterns analysis showed that the gene was expressed in all tissues and all development stages of H. cunea, with the highest expression level in midgut. The expression of HcSID-1 could be reduced to 53.5% by RNAi. The down regulation of HcSID-1 could reduce the interference efficiency of dsChi up to 7.32 times, suggesting that Hc SID-1 may be involved in the systematic RNAi process in H. cunea.

A distinct strain of Arsenophonus symbiont decreases insecticide resistance in its insect host

Authors: Zhang Wenqing, Sun Yat-sen University, China

Abstract: Symbiotic bacteria are important drivers of phenotypic diversity in insects. One of the widespread symbionts to have emerged belongs to the genus Arsenophonus, however, its biological functions in most host insects remain entirely unknown. Here we report two distinct Arsenophonus strains in the brown planthopper (BPH), Nilaparvata lugens, a major pest insect in Asian countries that causes significant economic damage through rice crop destruction. Genomic resequencing data suggested that one Arsenophonus strain (S-type) negatively affected the insecticide resistance of the host. Indeed, replacement of the resident Arsenophonus with the S-type Arsenophonus significantly decreased host insecticide resistance. Transcriptome and metabolome analysis revealed down-regulation of xenobiotic metabolism and increased amino acid accumulation in the S-type Arsenophonus infected host. This study demonstrates how a symbiont-mediated phenotypic change can occur. The results of this study will aid in developing strategies that work through imposing an ecological disadvantage on insect pests, which will be of great value for pest control in agricultural industry.

A saliva protein 7 of the brown planthopper Nilaparvata lugens functions as an effector for defense responses in rice

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Abstract: The brown planthopper (BPH), Nilaparvata lugens (Stål) (Hemiptera: Delphacidae), a major pest of rice in Asia, is able to successfully puncture sieve tubes in rice with its piercing stylet and then to ingest phloem sap. In this study, we investigated the potential role of saliva protein 7 (NlSP7) in N. lugens virulence and adaptation to host resistance. The results were showed that NlSP7 was highly expressed in the salivary glands of BPH, and it has two alternative splicing variants. Both of them are expressed at high levels during the adult stages. Simultaneously, knocking down the two NlSP7 variants by RNA interference inhibited salivary flange and resulted in a lethal phenotype within two days for BPH feeding on rice plants, indicating that the NlSP7 was essential for plant-associated feeding. Knocking down the expression of two NlSP7 variants resulted in reducing the intake of brown planthoppers. Furthermore, NlSP7 might help BPH deal with plant resistance, and altered gene expression was observed when BPHs were transferred from a susceptible rice variety to a resistant one. Infestation of rice by BPHs whose NlSP7 was knocked down elicited higher levels of tricin which a secondary insect-resistant substance of rice than did infestation by control insects. These results indicate that the salivary protein in BPH, NlSP7, functions as an effector and plays important roles in interactions between BPH and rice by mediating the plant's defense responses.

Ionotropic GABA receptor of Chilo suppressalis

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Abstract: Insect ?-aminobutyric acid (GABA) receptor (GABAR) is one of the major targets of insecticides. In our study, cDNAs (CsRDL1A and CsRDL2S) encoding the two isoforms of RDL subunits were cloned from the rice stem borer Chilo suppressalis. Transcripts of both genes demonstrated similar expression patterns in different tissues and developmental stages, although CsRDL2S was ~2-fold more abundant than CsRDL1A throughout all development stages. To investigate the function of channels formed by CsRDL subunits, both genes were expressed in Xenopus laevis oocytes singly or in combination in different ratios. Electrophysiological results using a two-electrode voltage clamp (TEVC) demonstrated that GABA activated currents in oocytes injected with both cRNAs. The EC50 value of GABA in activating currents was smaller in oocytes co-injected with CsRDL1A and CsRDL2S than in oocytes injected singly. The IC50 value of the insecticide fluralaner in inhibiting GABA responses was smaller in oocytes co-injected with different cRNAs than in oocytes injected singly. Co-injection also changed the potency of the insecticide dieldrin in oocytes injected singly. These findings suggested that heteromeric GABARs were formed by the co-injections of CsRDL1A and CsRDL2S in oocytes. Although the presence of Ser at the 2'-position in the second transmembrane segment was responsible for the insensitivity of GABARs to dieldrin, this amino acid did not affect the potencies of the insecticides fipronil and fluralaner. These results lead us to hypothesize that C. suppressalis may adapt to insecticide pressure by regulating the expression levels of CsRDL1A and CsRDL2S and the composition of both subunits in GABARs.

In addition, the insect RDL subunit is an attractive target of insecticides and fluralaner is a novel isoxazoline insecticide with a broad insecticidal spectrum that mainly acts on the insect GABA receptor with an unique binding action. However, its molecular interaction with GABA receptor remains unclear. Therefore, we screened 14 potential binding residues (I258T and L275I in the first transmembrane (TM1);V288I, M298N, G303N and A304S in TM2; G319M (G3'M) /S, A327S, G336N, M338I and A339F, in TM3; M473V and I477D in TM4) in CsRDL1 using molecular modeling and verified the binding site with site-directed mutagenesis method and the TEVC technique. Compared to the wild-type (WT)-RDL, the G3'M mutation completely abolished the binding of fluralaner and mostly to avermectin, but not to fipronil on RDL of several insects (Apis mellifera, C. suppressalis, Drosophila melanogaster, Laodelphax striatellus, and Tetranychus urticae) expressed in Xenopus oocytes. Our results contributed to the understanding of the molecular interaction of fluralaner with RDL homomers and may be used to guide future modification of isoxazolines to achieve higher selective control of pests with minimal effects on non-targeted organisms.

Ultrabithorax is a key regulator for the dimorphism of wings, a main cause for the outbreak of planthoppers in rice

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Abstract: Tremendous progress has been made on the understanding of body phan specification by the Homeobox-containing genes (Hox), since the appearance of the four-winged Drosphila Ultrabithorax (Ubx) mutant over forty years ago. In the current model of insect wing develpment, Ubx is expressed in hindwings but not in forewings. Rice planthoppers, the most devastating rice pests, occur in two wing forms: the short-wing form for rapid population growth and long-wing form for long-distance migration, which together devise the mechanism for outbreak. Here we show that Ubx is a key regulator for switching between the long- and short-wing forms of the rice planthoppers. Ubx is expressed in both forewing and hindwing pads, which is different from the canonical model of Ubx expression. In brown planthopper, expression of Ubx (NlUbx) is regulated by nutritional status of the rice host. High-quality young plants induce NlUbx expression leading to the short-wing form; low-quality ripe plants reduce NlUbx expression resulting in long-wing form. We also showed that NlUbx is regulatetd by the insulin receptors NlInRI and NlInR2. The default expression of NlInRI inhibits NlUbx resulting in long-wings, while high-quality host induces NlInR2 expression, which represses NlInRI thus promoting NlUbx expression to produce short-wings. We referred to these as the NlInRI/R2-NlUbx pathway of wing morph regulation in rice brown planthopper. It is likely that this pathway has evolved uriquely in the planthopper lineage, which facilitated the evolution of the wing polymorphism. Our findings raised a major question about the current conceptual models for wing development in insects.

An orphan gene is necessary for male sperm maturation and spem competence in diamondback moth

Authors: Zhao Qian[1], You Minsheng[1], Li Yaqing[1] and Li Yiying[1], [1]Fujian Agriculture and Forest University, China

Abstract: Novel genes, which are also named as orphan genes, are the gene with no homologous genes in other organsims. Here we identified 7 novel genes, which are highly expressed in male adult in diamondback moth. Further analysis showed that these genes were located in the male accessory gland, which suggested their role in male reproduction in diamondback moth. We knock out one gene named Tssor-1 using Crispr/Cas9 to reveal the molecular functions of this gene. The result showed that the mutant strain has less eggs and the hatch rate is significantly low comparing with the wild type. Furthermore, KEGG and GO analysis indicated that this novel gene maybe involved in pathways related with sperm development and maturation. Our sperm competence experiments further validates this result: the competitive of wild type is higher than the mutant type in diamondback. Our results give insights into the evolution and population expansion of diamondback moth.

Study of invading Aedes aegypti of Yunnan Province in China

Authors: Zhao Tong-Yan, State Key Laboratory of Pathogen and Biosecurity, Beijing Institute of Microbiology and Epidemiology, China

Abstract: Aedes aegypti, an important vector species of dengue, zika, distributed in Hainan, Guangdong provinces in China based on mosquito fauna. There was no distribution record of the species in Yunnan until 2002, Ae. aegypti is now continuously found in nine cities and counties in this province. It is important to study population genetics(including of invasion strategies, colonization and dispersal), vector competence to zika, and insecticide resistance, It was found continuous invasion contributes to maintenance of genetic diversity and different invasion accidents result in the genetic difference among populations of Ae. aegypti in Yunnan based on microsatellite DNA analysis, a strain of Ae. aegypti from Yunnan showed high level of midgut infection and highly disseminated infection of salivary glands and ovaries. It was found the evidence of transovarial transmission of the population to zika virus. Three sodium channel mutations were common in the Ae. aegypti strains sampled from Yunnan, the V1016G mutation appeared to be most important kdr mutation.

Heterogeneity of rice stripe virus from the vector insect and host plant

Authors: Zhao Wan, State Key Laboratory of Integrated Management of Pest Insects and Rodents, Institute of Zoology, Chinese Academy of Sciences, China

Abstract: As a persistent, propagative plant virus, rice stripe virus (RSV) is usually transmitted between the vector insect, small brown planthopper and the host rice plant. To adapt to these two different organisms, RSV shows distinct genomic replication or gene expression patterns, different pathogenicities, and different genetic variations under distinct selection pressures in the vector and host, and provoking distinct immune responses among these two organisms. These different survival strategies will enrich our understanding of why viruses leading distinct symptoms when adapt to vectors and hosts.

Global invasions: Dispersion patterns and processes of Bactrocera dorsalis

Authors: Zhao Zhao[1], Li Zhihong[1], [1]China Agricultural University, China

Abstract: Since the start of the 20th century, many invasive alien species (IAS) have spread rapidly around the world, causing serious threats to economies, societies and the environment. Bactrocera dorsalis (Hendel) (Diptera: Tephritidae) is an important quarantine insect pest in many countries that spread around the world over the last century. This review collected information on the global distribution of B. dorsalis to explore the patterns of its invasion expansion. We found B. dorsalis to be distributed in 75 countries (comprised of 124 geographical distribution regions: provinces or states) in Asia, Africa, North America, South America and Oceania up to 2017. Asia and Africa were the most represented regions, accounting for 86.3% of the total number of countries. Also, the South America has a large number of suitable habitats for colonization of the oriental fruit fly. Furthermore, the potential geographical distribution will significantly increase by 15% in 2050 and 20% in 2070, which indicate there is a great invasion pressure to South America. From 1910 to 1990, B. dorsalis was only found in 5 countries, but in the last three decades, it has experienced a sharp increase in its rate of spread, invading 70 more countries. Global temperature anomaly has significantly positive correlation with the spread of B. dorsalis. We proposed a conceptual framework of synergy model of climate change and transportation activities to illustrate invasion expansions of the oriental fruit fly. Also, our findings shed light on the spatial invasion dynamics of alien species, with potential implications for understanding the trajectories of biological invasions under changing future climates and transportation activities. The results of this work provide a theoretical basis for understanding and predicting the continued spread of B. dorsalis under global changes.

The occurrence of Mopane worm (Gonimbrasia belina) in north coastal region of KwaZulu Natal

Authors: Zharare Godfrey [2] and Buthelezi Makhosi[1], [1]Mangosuthu University of Technology, South Africa, [2]University of Zululand, South Africa

Abstract: The Emperor moth Gonimbrasia belina is an economically important insect consumed in central and southern African, where it is harvest from the wild. Generally, G. belina occurs within a tropic ecoregion feeding primarily on mopane trees (Colophospermum mopane). It has not been reported to occur in the sub-tropical region. Here, we report its occurrence in a subtropical region in KwaZulu-Natal province of South Africa. A phylogenetic analysis based on the CO1 gene indicated that the G. belina population in the northern coastal region of KwaZulu-Natal did not differ from that of the Mopane woodlands in the Limpopo province in the northern part of South Africa. This confirmed-that G. belina is indeed present in the northern coastal subtropical region of KwaZulu-Natal, this being so far the southernmost occurrence of G. belina. Sclerocarya birrea is its main host in this region, but was also observed feeding on Mangifera indica,Trema orientalis, Vochellia karoo, Sclerocroton intergerimus and Schotia brachypetala, Burkea Africana and Saba comorensis. This proved that G. belina is a polyphagous insect adapted to a wide range of climatic conditions, and does not seem to have host plant-related barriers than can impede its territorial colonization in southern Africa

The Northern Coastal Region of Kwazulu Natal is Identified as s Suitable Sanctuary Area for the Over Exploited Mopane Worm (Gonimbrasia belina

Authors: Zharare Godfrey [2], Buthelezi Makhosi[1], [1]Mangosuthu University Of Technology, South Africa, [2]University of Zululand, South Africa

Abstract: Gonimbrasia belina is a species of emperor moth whose edible larva is harvested from the wild for food in central and southern African tropical regions. It feeds primarily on Mopane tree (Colophospermum mopane). Hence, it is commercially harvested from Mopnane woodlands. Both over harvesting of its larvae and the destruction of the Mopane woodlands are threatening its biodiversity. This raises the need to create sanctuaries of G. belina that are safe from exploitation. The aim of this study was to evaluate the potential of the northern coastal region of KwaZulu Natal as a sanctuary for G. belina. The presence of G. belina in the subtropical biota along the northern coastal region of KwaZulu Natal was confirmed through Mitochondrion CO1 gene sequences. This being so far its southernmost occurrence. A survey revealed that it occurs over the entire Umkayakhude district, inclusive of the protected Ismamangaliso wetland Park and Hluhluwe game reserve. The survey further revealed there is currently very little utilization of G. belina by the local communities. A study of its biology revealed that its life-cycle is similar to those of G. belina populations elsewhere. It infests its plant hosts from the beginning of September to early November as does the populations in the Mopane woodlands, but differs from them by having one breakout per season instead of two. Marula (Sclerocarya birrea) is its main host, but was also observed feeding on seven other tree species. This proved that G. belina is polyphagous and adapted to a wide range of climatic conditions. Hence, there are no host plant-related barriers that can impede its territorial colonization in southern Africa. There is therefore scope to use northern KwaZulu Natal coastal region as a sanctuary for biodiversity conservation of G. belina. There are initiatives to cultivate Marula in the region for its fruits, which further increases the potential of the area as a sanctuary for G. belina by farming Marula for both its fruit and for G.belina. The protected nature reserves present in the region will ensure areas of non-exploitation by humans. To increase the genetic diversity, and hence biodiversity, of G. belina in the northern coastal region of KwaZulu Natal, it is suggested to import G. belina strains from other regions.

The potential contribution of inbreeding to the invasion success of a haplodiploid mite

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Abstract: Reproductive strategy (asexual and sexual reproduction) is associated with species' colonization because it helps to overcome the barrier of mate shortage at the invasion front. Haplodiploid females can reproduce asexually to generate sons and sexually to produce both daughters and sons. Mother-son and brother-sister matings may be common in these animals, which could be important for the colonization success of many haplodiploid species. We studied the mating modes of an invasive haplodiploid spider mite, Tetranychus ludeni, and examined whether inbreeding affected its reproductive fitness. We set up mother-son mating, sibling mating, and outbreeding treatments and recorded the mating success (the proportion of females that produced daughters), female fecundity, and the number of daughters produced for each of 11 generations. Our results show that the mating success of virgin females (around 75%) was similar in the three treatments. Inbred and outbred females produced similar number of eggs and daughters in every generation. We conclude that inbreeding may play an important role in establishment and colonization. In particular, the mother-son mating enables females, regardless of invasion stage, to establish a colony at a new site.

Genomic tales in the Asian honeybee: gene reuse facilitates rapid radiation and independent adaptation to diverse habitats

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Abstract: Background:

Understanding how honeybees adapt to diverse habitats during colonization may help to predict their chance of survival under changing environments and habitat loss. We used population genomics to identify genomic features facilitating rapid evolutionary radiation in the Asian honeybee, Apis cerana. We hypothesize that genes associated with adaptation following independent colonization of novel habitats are frequently reused, representing a key adaptive innovation in insects surviving environmental changes.

Results:

By analyzing 362 A. cerana genomes, we showed that multiple peripheral population groups radiated from the same central ancestry and adapted independently to diverse habitats. We identified dozens of genes under repeated selection across multiple peripheral groups with one gene, the Leucokinin receptor (Lkr), under selection in almost all peripheral groups. Suppression of Lkr by in vivo RNAi led to significant reduction in sucrose responsiveness, which could predetermine foraging task division. Furthermore, Lkr expression was elevated in foragers when compared to nurse bees and differed significantly between pollen and nectar foragers, indicating that both collective colony strategy and individual foraging decisions could be tailored through Lkr regulation. Selection peaks were exclusively found in Lkr intron-1, some of which overlapped with antisense lncRNAs, possibly regulating Lkr.

Conclusions:

Gene reuse is frequently employed by A. cerana colonizing populations to cope with diverse habitats, where genes associated with foraging play a critical role in response to dietary shifts. Our study suggests that gene reuse functions not only in parallel adaptation to similar environments, but also in exploring different habitats with high dietary diversity.

GPCRs- new targets for managing gypsy moth

Authors: Zhu Fang[1], Moural Timothy[1], [1]Pennsylvania State University, United States

Abstract: G-protein-coupled receptors (GPCRs) comprise one of the largest and most diverse family of membrane proteins, which transduce extracellular signals into cellular responses to hormones, neurotransmitters, and environmental stimulants. The ligands of GPCRs are extremely diverse, including chromophores, neuropeptides and hormones, acetylcholine, biogenic amines, nucleotides and nucleosides, lipids and eicosanoids, olfactory and taste substances, and so on. The ligand binding triggers GPCRs conformational changes, activing complex cytosolic signalling networks and causing the intracellular responses. Therefore, GPCRs play various important roles and draw the most attention for drug discovery. However, there is very few insecticides that target on GPCRs except the octopamine receptor agonists. Here, we identified and characterized physiological functions of two GPCRs from the transcriptome of gypsy moth. Specifically, with functional genomics and reverse genetic approaches, we investigated the potential roles of these GPCRs in regulation of xenobiotic detoxification.

Characterization of a serine protease inhibitor in Leptinotarsa decemlineata

Authors: Zhu Fang[1], Moural Timothy[1], [1]Pennsylvania State University, United States

Abstract: The Colorado potato beetle, Leptinotarsa decemlineata is a notorious agriculture pest feeding on plants of the Solanaceae family including potato, tomato, and eggplant. Rapid evolving resistance to pesticides has contributed to its success in establishing populations across North America, Europe, and parts of Asia. Many studies have been performed to reveal molecular mechanisms contributing to insecticide resistance; however, other mechanisms related to basic biological processes have yet to be understood completely. In this study, a novel serine protease inhibitor (serpin) gene was selected from the transcriptome of L. decemlineata with bioinformatics and functional genomics tools. Feeding RNA interference (RNAi) of our target genes showed systemic knockdown of this specific serpin and caused feeding inhibition in both larva and adult stages. We performed quantitative real-time PCR (qRT-PCR) to investigate the expression patterns of this gene in all developmental stages and multiple tissues. To investigate the function and structure of this serpin gene, recombinant protein was expressed in a genetically modified Escherichia coli strain and the three-dimensional structure of this protein has been uncovered. Potential roles of this novel protein and the significance of our study will be discussed.

Improved matting success in Hermetia illucens enabled by adults visual system

Authors: Zhu Fen[1], Wang Wanqiang[1], Liu Wen[1], Wang Xiao-Ping[1], Liu Xinhui[1] and Gao Zhenghui[1], [1]Huazhong Agricultural University, China

Abstract: When a substance reflects a light at a particular color, it often absorbs the light of its complementary colors. In Hermetia illucens, the relative reflectance of the dorsal side was the same in the head between the female and the male. The dorsal side of the male thorax had higher relative reflectance than that of the female. The abdomen of both sexes showed similar absorbed and reflected spectral signature. The ventral abdomen of the female thorax had higher relative reflectance than that of the male. The wings of the male had higher relative reflectance than that of the female. Females laid eggs under the light source at the wavelength of 375 nm, 420 nm, 465 nm, 505 nm, or 600 nm. We made a light with special wavelength. The light can help to improve the reproduction of H. illucens. Under this light, normal adults presented a high oviposit rate, which was about 90%. Adults with coated compound eyes showed a very low oviposit rate, which was less than 35%. In conclusions, visual system is very important for reproduction of H. illucens. The invented light can be used in mass production of H. illucens.

New repellent and deterrent for drosophilid and tephritid fruit flies

Authors: Zhu Junwei[3], Cha Dong[2], Loeb Gregory[1] and Roh Gwang-Hyun[2], [1]Cornell University Geneva, New York 14456, United States, [2]USDA-ARS Hilo, Hawaii, United States, [3]USDA-ARS Lincoln, Nebraska, United States

Abstract: Drosophilid and tephritid fruit flies are among the world's most destructive invasive pests. Frequent use of insecticides is generally necessary for effectively managing these flies. However, reliance on pesticides is costly and risky in terms of resistance development. To develop alternative control methods, we have been particularly interested in identifying chemicals that can repel flies from or deter oviposition on fruit. In this talk, we will report on experimental results from laboratory and field documenting significant reductions in infestation by spotted wing drosophila (Drosophila suzukii) and oriental fruit fly (Bactrocera dorsalis) in response to repellent and oviposition deterrent isolated and identified from microbial and plant sources. We will also discuss evolutionary context of fly avoidance on some of these chemicals.

Hypoxic Environment Protects Insects from Electron Beam Irradiation

Authors: Zhu-Salzman Keyan, Department of Entomology Texas A&M University, United States

Abstract: Ionizing irradiation, such as electron beam (eBeam), breaks nucleic acid strands by transferring energy directly to the molecules. Additionally, irradiation induces production of reactive oxygen species (ROS) that damages cellular structures, impairing multiple cellular pathways and processes. As a disinfesting technology to control storage pests, ionizing irradiation has expanded rapidly in recent years due to its detrimental effect on insects at all developmental stages. Modified atmospheres control storage pests by manipulating gas compositions in storage facilities. In a low O2 (hypoxia) environment, insects reduce their metabolic activities, and even cease to develop. Both eBeam irradiation and hermetic storage are safe and effective technologies to protect stored products. Although hypoxic environment improves performance of some irradiated insects, whether hypoxia affects irradiation of storage insects and impacts pest control efficacy remains to be investigated.

Using cowpea bruchid (Callosobruchus maculatus) larvae, we showed that, relative to eBeam irradiation under normoxia, the adult emergence rate increased substantially if they were exposed to hypoxia prior to and during eBeam treatment. Conversely, exposure to hypoxia only after eBeam irradiation did not have this protective effect. eBeam irradiation caused an increase in reactive oxygen species (ROS) in normoxic larvae but not in hypoxic larvae. The activity of citrate synthase, a pace-making enzyme in the citric acid cycle, was suppressed under hypoxia but resumed normal function within hours of reoxygenation, suggesting that reduced mitochondrial activity and thus less ROS production under hypoxia increased insect tolerance to irradiation. Furthermore, reoxygenation accelerated eBeam-induced glutathione S-transferase activation and potentiated eBeam-enhanced catalase activities. Faster and stronger detoxification capacity in eBeam-irradiated, hypoxic larvae may have protected them from oxidative damage. Taken together, hypoxic environment enhanced radiotolerance of bruchid larvae, presumably due to limited ROS production and elevated antioxidant enzymatic activities after reoxygenation. Therefore, as an important postharvest technology to protect stored grains, environmental factors must be taken into consideration when establishing irradiation doses. Information from this research is also useful in adopting irradiation technology in insect management in packaging, storing and shipping of commercial products, and in addressing concerns in international trade of agricultural products.

Phylogenetic relationships within the Cotesia ”tibialis” group and detection of potential new species (Hymenoptera: Braconidae: Microgastrinae)

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Abstract: The genus Cotesia includes koinobiont endoparasitoids of lepidopteran larvae. Most species are gregarious; the females superparasitize young caterpillars, usually first and the second instar, while parasitoid larvae emerge from mature ones. Upon the emergence Cotesia larvae spin their cocoons around or near the host, often connecting them into a unique ball-shaped mass cocoon. The way of cocoon spinning, its structure, colour and place of spinning relative to the host are, in addition to morphological differences between the specimens, also reliable characters for distinguishing species. In this study we selected a group of Cotesia species that form gregarious ball mass cocoons. Our goal was to analyse all specimens from this type of cocoons and to relate the results of their morphology, primarily the shape the forewings and the results of molecular analysis, thus revealing phylogenetic relationships of the studied taxa.

We compared several morphological characters of both males and females, while for the DNA analysis we used the barcoding gene COI. The sample analysed contained about 1000 individuals from seven countries. Six different taxa with European distribution are discovered within the tibialis group: Cotesia berberis (Nixon, 1974) – off-white ball cocoon; C. tibialis (Curtis, 1830) – cream ball cocoon; C. cf. tibialis – smoke white ball cocoon; C. ofella (Nixon, 1974) – yellowish ball cocoon; C. vanessae (Reinchard, 1980); – white ball cocoon and potentially new species, Cotesia sp. nov. – ivory elongated cocoon. Despite the extraction of the DNA from C. berberis, the sequencing failed, probably due to the oldness of the material. This species has been studied using only the cocoon structure and adult morphology. Cotesia berberis is very close to C. tibialis.

Presenting the results of geometric morphometrics of female forewings via CVA scatterplot, it is clearly visible that five distinct taxa occurred in the analysed sample. The CV1 strongly separates C. tibialis and C. cf. tibialis placed in the negative part of the CV1 while the rest of the taxa are placed in the positive part. Based on the general morphology of the wings, in the morphospace defined by the CV1 and the CV2, C. vanessae showed significantly different wing shape from the others, moving it away from the whole group.

According to molecular analysis C. vanessae is also positioned the farthest from the other species. Its genetic distance in relation to C. tibialis and C. cf. tibialis is 7.2% and 8% respectively, and it differs 8.5% from C. ofella. The genetic distance between C. vanessae and Cotesia sp. nov. is 7%. In the same time, Cotesia sp. nov. is genetically distant 2.5% form C. tibialis, 3.4% from C. cf. tibialis and 3.8% from C. ofella.

Investigating insecticide resistance in UK populations of cabbage stem flea beetle Psylliodes Chrysocephala

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Abstract: The cabbage stem flea beetle (CSFB) Psylliodes chrysocephala, is a major pest of winter oilseed rape (OSR) in the UK and Northern countries in mainland Europe including Germany, attacking emerging plants in the autumn and causing severe damage to the crop if left unchallenged. Prior to December 2013, control of CSFB relied on the protection of OSR seedlings by neonicotinoid seed treatments in conjunction with subsequent application of foliar pyrethroids sprays. However, the EU-imposed restriction on the use of neonicotinoids has left growers with just pyrethroids for CSFB control. The increased selection pressure, caused by a lack of alternative control agents with different modes of action, has led to the emergence of pyrethroid resistance in this pest. As CSFB resistance to pyrethroids can cause significant yield losses in OSR crops, and the continued use of these pesticides in their current format will only exacerbate this problem, there is a need to understand the mechanisms by which resistance has developed and is sustained within CSFB populations. Despite the presence of the target-site mutation kdr in UK populations, resistance does not completely correlate with kdr genotype, suggesting another mechanism of resistance is also present. The current study reports the extent and geographical spread of pyrethroid resistance in UK CSFB populations, the contribution of kdr (L1014F) and super-kdr (L925I) to this resistance phenotype and our efforts to identify the enzyme(s) involved in conferring the additional metabolic resistance component using next generation transcriptomic approaches.

Multiple functions of ETH receptor networks in the silkmoth Bombyx mori

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Abstract: Ecdysis triggering hormones (ETHs) from endocrine Inka cells act on target central neurons expressing two splice variants of ETH receptors (ETHR-A or ETHR-B) to activate the ecdysis sequence in insects. We detected expression of multiple excitatory and inhibitory neuropeptides in these receptor neurons using in situ hybridization and immunohistochemistry. Following activation of these neurons by ETHs, centrally released neuropeptides control the entire cascade of pre-ecdysis and ecdysis motor programs. Transgenic approaches using piggyBac vectors and electrophysiology techniques revealed specific roles of different neurons and neuropeptides during these processes. Careful examination of ETHR expression using in situ hybridization and qRT-PCR revealed expression of these receptors in specific cells of the corpora allata (CA), H-organ and Malpighian tubules (MT) prior to each ecdysis. In vivo and in vitro experiments indicate that ETHs are multifunctional hormones that act via ETHR-A/B to control various functions during the entire development; the ecdysis sequence and hindgut contractions by peptidergic neurons in the CNS, production of biogenic amines by H-organ, juvenile hormone production by the CA and water/ion balance by Malpighian tubules.

DNA metabarcoding in large scale insect diversity assessment

Authors: Zizka Vera[1], Schäffler Livia[1], Bourlat Sarah[1], Noll Niklas [1] and Kirse Ameli[1], [1]Leibnitz Institute for the Analysis of Biodiversity Change

Abstract: DNA metabarcoding is a promising tool for biodiversity monitoring, enabling the fast and high-resolution identification of insect communities from bulk samples. The method is based on the DNA extraction and simultaneous barcode amplification from samples containing a mixture of taxa and potentially also enables the analysis of intraspecific genetic diversity. This fast and cost-efficient approach enables taxonomic assignment of species hard to identify morphologically if those are listed in reference databases. To make metabarcoding applicable for upscaled biodiversity assessments, some challenges remain, which are tackled by testing and improving the laboratory and bioinformatic workflows. While comprehensive, high-resolution taxon lists can be achieved through DNA metabarcoding, there are still systematic biases within the workflow (e.g. taxonomic differences in primer efficiency, underrepresentation of small and rare taxa) while other issues arise when processing large numbers of samples for biodiversity monitoring (e.g. standardization of high-throughput protocols, lab and storage capacities). We have optimized critical steps in the molecular analysis within our projects (e.g. increased detection of low-biomass taxa) and continue to enhance the reliability of taxon identification from insect bulk samples and to improve the standardization of DNA metabarcoding methods for large-scale biodiversity monitoring.

Estimating species-abundance change with genomic tools

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Abstract: The key dimensions of ecological community structure are species composition and species abundances. Metabarcoding of mixed-species arthropod samples can provide reliable presence-absence information (composition), but abundance information is obscured by a combination of species-specific biases in DNA extraction and PCR and of stochasticity in data-file sizes after library prep, sequencing, and bioinformatic processing. I review recent advances in using genomic tools to extract abundance information. DNA-standard spike-ins recover within-species abundance changes across samples. Creating sample dilution series additionally allows recovery of across-species abundance differences within samples. In short, it is now possible to recover both composition and abundance information from mixed-species arthropod samples. Spike-ins and dilution series can be used in both metabarcoding and mitogenomic approaches. Finally, I describe a method that makes it possible carry out metabarcoding without PCR: the targeted assembly of barcode genes from shotgun-sequence datasets, using the software Kelpie, followed by read mapping to the extracted barcodes.

120 years of change in Arctic plant-pollinator interaction networks

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Abstract: The majority of the world´s plants rely on animal pollinators for reproduction, making pollination a key ecosystem service for the maintenance of natural and cultivated plant communities. However, pollinators are experiencing a severe global decline. Amongst other anthropogenic drivers, climate change is considered responsible for this decline. In arctic and mountainous regions, climate change is projected to be especially pronounced. Understanding the impact of climate change on ecosystems is challenging, since the effects may take decades to transpire. We aim to overcome that challenge by using a historical dataset collected by F. Silén in the summers of 1895-1900. Silén recorded flower visitors of 87 different plant species in the surroundings of Kittilä, Finland, providing us with a valuable insight on plant-pollinator interactions from over a century ago. For our project, we resampled plant-pollinator interaction networks in Kittilä and compared them with the historical data in order to explore the changes that occurred during the last century in plant-pollinator networks at high northern latitudes.

Vector Control Product Development in the US Department of Defense

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Abstract: The US Department of Defense (DoD) supports the research, development, testing, and evaluation of arthropod vector surveillance and control products to protect military personnel from vector-borne diseases. Diseases can significantly impact military readiness, and many vector-borne diseases have no vaccine or therapeutic treatment available. Therefore, the DoD uses vector control and bite protection technologies to prevent disease transmission. DoD laboratories around the world engage in research activities to develop new therapeutics, novel personal protective measures, and improved vector control tools. Several funding programs support product development from basic research through commercialization. The DoD frequently collaborates with other US Federal agencies, academic, and commercial partners to develop products that are useful both for military and civilian markets. This presentation will provide an overview of DoD research programs and priorities for vector control product development.

Identification and field verification of aggregation-sex pheromone from the predaceous bug, Arma chinensis, a natural enemy of the invasive fall armyworm Spodoptera frugiperda

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Abstract: Arma chinensis (Hemiptera: Pentatomidae) is a predaceous insect species that is native to China, Korean peninsula, and Mongolia. A. chinensis has received attention because of its ability to effectively suppress a wide range of agricultural and forest insect pests in the orders Lepidoptera, Coleoptera, Hymenoptera and Hemiptera. Both nymphs and adults of A. chinensis attack their insect prey, even when the prey are larger in size, and suck the body fluids from their prey with their proboscis. The fall armyworm Spodoptera frugiperda (Lepidoptera: Noctuidae) has currently become a new invasive species in China and recent outbreaks of this hungry caterpillar in Africa and southern Asia have resulted in maize yield losses as high as 50%. Preliminary tests indicate A. chinensis is able to control this voracious caterpillar in laboratory.

The pheromones are of two types: female produced sex pheromones which attract only males, and male-produced aggregation pheromones which typically attract both sexes. The latter type of pheromone has more recently been referred to as an aggregation-sex pheromone because its primary function is probably to bring the sexes together for mating. Adult A. chinensis males produce an aggregation-sex pheromone from dorsal abdominal glands and artificial aggregation-sex pheromone can attract adults of both sexes. The aggregation-sex pheromone consists of (E)-2-hexenal, (E)-2-hexen-1-ol, benzaldehyde and benzyl alcohol. Both antennae and proboscises of A. chinensis females and males responded to components from male dorsal abdominal gland extracts. (E)-2-hexenal and benzaldehyde elicited significantly higher EAG responses than those with (E)-2-hexen-1-ol and benzyl alcohol. Benzyl alcohol elicited the weakest EAG responses although benzyl alcohol was the most abundant of the four major components in male dorsal abdominal gland extracts. A field bioassay using trap catches demonstrated that (E)-2-hexenal and benzyl alcohol were key components of the pheromone for catching conspecific adults. Single pheromone components were the least attractive to A. chinensis in the field.

The successful application of augmentative biological control wherein natural enemies are released to control target pests requires colonization of the beneficial species. However, as we observed in field and forest land, many A. chinensis adults reared in laboratory disperse from release sites in a few days even though many prey were still present at the release site. Developing the aggregation-sex pheromone baits of A. chinensis to enhance the colonization of A. chinensis and the biological control of S. frugiperda seems to be a promising method in the future.

The amazing Maindronia species (Insecta: Zygentoma) and their evolution at the dry limit of the Atacama Desert

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Abstract: The silverfish family Maindroniidae (Insecta: Zygentoma) consists of three described species from desert biomes in Sudan, the Arabian Peninsula and Chile. This distribution is remarkable for closely related arthropods, suggesting a Gondwanan relict group. Extensive collecting efforts in Chile show a surprisingly widespread distribution in the Atacama. These insects were even found in hyperarid areas where no other metazoans could be observed. Maindronia can thus be considered as the most adapted desert animal in the Atacama, which in turn is one of the driest deserts in the world. The common habitat preference in the Chilean Atacama, and evidently also in Sudan, suggests that hyperarid environments have always been present, at least locally, in South America over the past 120 million years. Likely, Chilean Maindronia have evolved with and within the Atacama Desert. This scenario clearly differs from that shown for other animals or plants that have more recently migrated into suitable environments in the Atacama. Phylogenetic analyses show the presence of at least five clades derived from a single ancestor and diverging in the last 15 million years. The divergence times of the clades can be attributed to palaeoclimatic changes; mostly periods of extreme hyperaridity.

A comprehensive phylogeny of the species-rich Australian leafroller moths (Lepidoptera: Tortricidae) – the power of combining collection genomics and transcriptomics

Authors: Zwick Andreas[2], Sinclair Bronte[1], Hartley Diana[1], Nicholls James[1], Horak Marianne[1] and Bent Stephen[3], [1]Australian National Insect Collection, CSIRO, Australia, [2]Commonwealth Scientific and Industrial Research Organisation, Australia, [3]DATA61, CSIRO, Australia

Abstract: The Tortricidae are a species-rich family of moths with about 11,000 named species worldwide, and 1,200 named and unnamed species recognised in Australia. The group includes numerous economically important pest species (e.g., light brown apple moth, Epiphyas postvittana, and codling moth, Cydia pomonella), but relationships between these and between tribal groups are poorly understood. We present a phylogeny of all Australian tortricid species, robustly resolving tortricid relationships from the placement of the family to within species complexes. We demonstrate that the small subfamily Chlidanotinae is polyphyletic and that some Australian genera represent a further new subfamily that is sister to the diverse Tortricinae + Olethreutinae. With all but two recognised tribes occurring in Australia, our phylogeny also provides a well supported new working hypothesis for tribal relationships worldwide. Comprehensive taxon sampling and robust resolution across the entire depth of the phylogeny are achieved by combining collection genomics with transcriptomics. We developed a novel platform technology for low-cost, high-throughput collection genomics and used it to sequence old specimens of all identified named and unnamed tortricid species in the Australian National Insect Collection. To resolve deeper divergences we added transcriptomes for about 80 genera from freshly collected specimens. This approach offers a systematic and efficient way to revise the classification of the species-rich Tortricidae, and the model could be applied to many other mega-diverse groups of arthropods.

Effect of plant chemical variation and mutualistic ants on aphid herbivore populations

Authors: Zytynska Sharon, University of Liverpool, United Kingdom

Abstract: Plant within-species variation can alter direct and indirect interactions among species. In particular, host-plant genetic or chemical variation within a population creates a spatially heterogeneous habitat for specialized herbivores which can drive changes in the associated ecological community. Using a natural tansy plant (Tanacetum vulgare) population we showed that variation in plant volatiles, emitted from specialized storage structures on the plant surface, drive host selection of aphids (Metopeurum fuscoviride) in the early season when winged morphs have free choice among plants. Later in the season non-volatile metabolites in the plant were crucial for host selection by unwinged aphids. Host-choice by aphids was also driven by aphid genotype, with significant associations between plant chemotypes and aphid genotypes leading to non-random distribution of aphid genotypes across the plants in the field site. Furthermore, these associations were strengthened by interactions with ant mutualists, and had a cascading effect on aphid parasitic wasps. The approach used for plant chemical analysis allowed for the separation of the effects of volatile and non-volatile plant chemicals on the interacting species over the whole growing season. Follow-on empirical experiments were able to validate the field data to disentangle effects on aphid population growth, ant attendance of aphids, predation and parasitism across cloned plant chemotypes. Our work demonstrates how plant within-species chemical variation can structure the interacting community through direct and indirect multi-species interactions.

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Andrew Griffiths Design, supported by the RES

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