Sektion Chemische Ökologie & Verhalten / Section Chemical Ecology & Behaviour

Talks

sorted by category and main authors

Keynote

Insect pest management using new generation sex pheromones and innovative technologies

Konstantopoulou, M.

In recent years, the management of insect populations with significant public health or economic impacts has increasingly centered on biological and biotechnological approaches. Many chemical insecticides have been withdrawn from the market due to the significant risks they pose to human health, their detrimental impacts on ecosystems, and the increasing development of resistance among pest species. This transition highlights the escalating demand for eco-friendly pest management strategies, such as pheromone-based methods like mating disruption. In this context, the biological production of cost-effective pheromones represents a disruptive technology that paves the way for the rapid expansion of pheromone-based pest control products. Notably, biotechnological production of several insect pheromone components has already been successfully achieved using yeast systems and biocatalytic processes that rely on low-cost raw materials.
Yeast-derived pheromones for *Helicoverpa armigera* and *Plutella xylostella*, along with *Lobesia botrana* pheromone produced via a non-conventional metathesis-based method, demonstrate equivalent efficacy to their chemically synthesized counterparts in both monitoring and mating disruption applications. For field application, biologically derived pheromones formulated into plant protection products–primarily as flowable, biodegradable matrices–can be delivered via UAVs. This system is optimized for medium to large farmlands, encompassing both arable crops and orchards, and is implemented using precision agriculture practices. In addition, a hydrodegradable pheromone dispenser–designed to gradually dissolve and continuously release pheromone throughout the growing season–has been successfully tested in frequently irrigated fields, thereby eliminating the need for manual replenishment or removal.
These precise, time-efficient, and economically viable technologies are in line with European Commission initiatives such as the Green Deal's Farm to Fork Strategy and the Biodiversity Strategy, promoting food sustainability while preserving biodiversity.

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Keynote

Impact of air pollution on plant-pollinator chemical communication: Main effects and future perspectives

Proffit, M.

Since the beginning of the industrial era, ecosystems have been facing massive anthropogenic changes that may alter interspecific interactions, for instance the chemical communication between plants and pollinators. Among these changes, the increase in certain atmospheric pollutants can affect every step of such communication: a) the emission of volatile organic compounds (VOCs) by flowers (i.e., the emitter), b) VOCs lifetime in the atmosphere (i.e., the signal) and c) the sensory capabilities of pollinators (i.e., the receiver). We tested the potential effects of ozone (O_3), one of the major atmospheric pollutants, on two Mediterranean plant-pollinator interactions highly contrasted in terms of specificity and cognitive capacities of their pollinators. Under controlled conditions, we separately exposed plants, VOCs or insects to an acute O_3 concentration, mimicking an O_3 pollution peak characteristic in the Mediterranean basin. In addition, dose-response experiments were performed to determine the concentration thresholds at which O_3 altered pollinators' floral odor recognition. The results of our experiments confirm a generalized impact of O_3 exposure on each stage of plant-pollinator chemical communication, yet the thresholds at which these effects are observed differ between the two systems studied. The consequences of these multiple effects of O_3 and the current gaps in our understanding of the effects of atmospheric pollutants on plant-pollinator interactions will be discussed.

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Potential effects of multi-species pheromone combinations on the attraction of different stored product insect pests

Albrecht, C. & Fürstenau, B.

Protecting stored plant products from insect infestation is becoming increasingly important in times of growing crop instability due to climate change and global crisis. Successful

early detection of stored product pests at the various stages of food production can help to prevent food losses and ensure food safety. This is essential in order to take appropriate counter/control measures as quickly as possible to prevent greater losses and further spread of the insects. One possibility is to use commercially available trap systems baited with a mixture of pheromones from different target pests. It is thought that multi-species attractants could be advantageous for surveillance monitoring for a number of species simultaneously. However, knowledge of the effects of using pheromone combinations at a single site on the attraction of different stored product insects is limited.

In the AVoiD project (Abwehr von Vorratsschädlingen in Deutschland/Preventing stored product pests in Germany), three types of pheromone baited traps (one funnel and two floor traps) were installed at 11 grain storage and processing farms in Germany for a nationwide monitoring. The aim was to detect insect infestations on stored plant products at an early stage and to determine which (newly introduced) storage pest species might be present in the storage facilities and, in particular, outdoors in the field. Our results from 2023 and 2024 showed that some stored product insects whose pheromones were used in the traps were not caught or rather detected at any of the monitoring sites. This raised the question of whether these pest species were simply not present, or whether the use of multi-species pheromone combinations may have influenced their attraction due to a potential deterrent effect. The following experiments were carried out to answer this question.

In laboratory flight-cage bioassays, the long-term responses of various stored product beetles to floor traps (DomeTrap, Trécé Incorporated, Adair, Oklahoma, USA) equipped with different combinations of commercially available pheromones of different pest species and an additional kairomone oil were tested against a control floor trap (containing kairomone oil only) over a maximum of seven days per experiment. The short-term responses of the pest species to these attractants were investigated in a static 4-chamber olfactometer.

Key questions were whether (a) the attraction of test beetles/number of trap catches is affected (increased, reduced or prevented) by using multi-species pheromone combinations compared to single pheromone lures and (b) short- and long term responses to multi-component blends differ from each other.

The results of our study will be presented and discussed, indicating that the responses are variable and highly species-specific.

The “AVoiD” project is funded by the German Federal Ministry of Food and Agriculture (BMEL) as part of the Immediate Climate Action Programme 2022.

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The impact of endophytic communities on the volatile organic compound profile of sunflower *Helianthus annuus* and its detection by honey bees

Dumenil, C.; Favaro, R.; Angeli, S.; Braglia, C.; Alberoni, D.; Di Gioia, D. & Cappellin, L.

Plant Growth-Promoting Bacteria (PGPB) and Rhizobacteria (PGPR) are widely present in the rhizosphere and contribute to the health and performance of associated plants. Their effect can be extended to the volatile organic compounds (VOCs) released by plants and used in insect-plant communication. In recent decades, several anthropic factors have degraded the agroecosystem soil, thereby reducing the contribution of the microbial population to plant and ecosystem health and biodiversity. Enhancing the positive plant-microorganism interactions is thus a primary goal of crop management. However, evidence is lacking on the role that PGPB and PGPR exert on the chemical ecology of plants, notably in attracting pollinators. The hypothesis, at the basis of our project, is that PGPB and PGPR improve soil fertility and quality, and directly impact plant-pollinator interactions by modifying plant VOCs, nectar and pollen composition, thereby playing a key role in pollinator health and ecosystem functionality. One of our objectives is to measure the effects of these endophytic communities on the VOC profile of different sunflower cultivars and how these are detected by honey bees, Apis mellifera. Ancient and hybrid cultivars of sunflower were grown with different endophytic communities. VOCs were collected from the blooming flowers using closed-loop stripping analysis. Extracted VOCs were presented to the honey bee antenna in coupled gas chromatography-electroantennography experiment. Then, the antennally active compounds were identified using coupled gas chromatography-mass spectrometry.

This work is supported by the project “IMPLiCIT–Improving soil-plant-insect interactions to promote pollinators“ funded by the MIUR Progetti di Ricerca di Rilevante Interesse Nazionale (PRIN) Bando 2022- grant 2022NMAPEL.

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Chemical Ecology and Species Interactions in Agroecosystems affected by Agrochemical Pollution

Fuchs, B.

Sustainable insect pest management in crop production relies on specialized metabolites for bottom-up control and predatory insect abundance for top-down control. The immense use of glyphosate-based herbicides in weed control caused a persistent pollution of agroecosystems at soil level exposing the rhizosphere. Glyphosate disrupts the shikimate pathway, which is the biosynthetic basis for several metabolite groups produced by plants and a majority of microbes but the effects of glyphosate residues in soil on crop metabolism and species interactions is largely unexplored.
In a long-term common garden study, we studied the impact of herbicide soil legacy on plant biochemistry, symbiotic relations to microbes, defense against herbivores and beneficial insect behaviour. Plant responses to herbicide legacy in soil include altered phytohormone concentrations, specialized metabolite biosynthesis and volatile organic compound (VOC) emissions. Aphid herbivory increased on crop plants growing in herbicide polluted soil and altered VOC emission which caused behavioral changes of predatory insect.
Our results indicate that herbicide residues in soil have multifaceted consequences on crop plants by modulating plant metabolite concentrations with disruptive effects on plant protection and plant-insect interactions. Our results indicate that the exaggerated use of pesticides in recent decades created a soil legacy which reduces the effectivity of plant traits essential for sustainable crop protection and ecosystem functionality.

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Influence of primary and secondary plant metabolites on the migration and feeding behavior of *Cacopsylla pruni*, vector of the European Stone Fruit Yellows phytoplasma

Gallinger, J. & Gross, J.

The plum psyllid *Cacopsylla pruni* is a univoltine herbivore, specialized on *Prunus* and coniferous tree species. During their lifetime, plum psyllids are alternating twice between their deciduous and evergreen hosts. For reproduction, *C*. *pruni* adults migrate to stone fruit orchards in spring, where they lay their eggs exclusively on several *Prunus* species. Young adults emigrate to conifers in higher regions soon after emergence. Plum psyllids transmit the Phytoplasma '*Candidatus* Phytoplasma prunorum' and are therefore of significant importance for fruit growers. In host plants, the cell wall-less bacterium is restricted to the phloem and causes the European Stone Fruit Yellows (ESFY). ESFY is one of the most serious plant diseases in European fruit production, causing severe plant damage leading to a poor harvest and high economic losses. The impact of plant-borne volatiles and phloem chemistry on the behavior of *C*. *pruni* was investigated in search of potential infochemicals that can be used to manipulate the psyllid behaviour to prevent the spread of the vector insects and the phytoplasma.
The ability to find suitable hosts is crucial for the successful survival and reproduction of insects. Due to their migrational behavior, *C*. *pruni* needs to locate two divergent host plants, indicating a sophisticated identification based on several chemical cues. In field studies *C*. *pruni* preferred specific *Prunus* species for feeding and oviposition. Therefore, characteristic host plant volatiles (from *Prunus* and conifers) detectable by the psyllid antenna were identified. Olfactory preference indicated that preferences for different host plants are not only based on olfactory cues. Therefore, gustatory cues (phloem sap composition) from different hosts were analysed and their role in the host acceptance and development of *C*. *pruni* investigated, showing a great impact of specific plant sap compositions on the feeding and survival of *C*. *pruni*.

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Reducing aphid infestation by optical manipulation using a biodegradable mulch cover

Gruppe, B.; Niemann, J.-U. & von Hörsten, D.

Environmental pollution by plastic is a severe problem. It accumulates in ecosystems where it harms animals and human beings in various ways. However, plastic mulch cover has been used successfully in horticulture and agriculture production systems, as these foils prevent water from evaporating from the soil, regulate the soil temperature and suppress weed growth. Furthermore, plant growth can be regulated by the use of different plastic mulches. A biodegradable mulch cover providing these attributes as well could, therefore, replace common plastic mulch cover and prevent environmental pollution and damage. In order to do so, a project aims to develop a sustainable and fully biodegradable mulch cover (DIN EN 17033), called VliesFilm. Mo-

reover, these components have the advantage that they do not compete for food such as starch-based mulch cover products. The main objective of the project is to reduce the infestation of lettuce by the currant lettuce aphid, *Nasonovia ribisnigri* (Mosley) (Hemiptera: Aphididae), which is going to be investigated through field studies. The idea is to colour the product VliesFilm in different colours to manipulate the pest insect´s vision and consequently, its landing behaviour. This manipulation could contribute to the integrated pest management (IPM) system by a reduced or delayed infestation and is going to be evaluated in combination with flowering strips, too. As part of the project, VliesFilm is going to be specifically designed for common application techniques such as foil laying machines in the field.

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How does *Halyomorpha halys* select its host? Investigations on potential kairomones

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The Brown Marmorated Stink bug, *Halyomorpha halys* (Hemiptera: Pentatomidae), causes considerable damage especially in fruit crops. A host range of over 200 different plants belonging to several plant families shows the polyphagous feeding behaviour of the stink bug. As an invasive species native to Eastern Asia no efficient natural enemies occur in the newly invaded regions. This can lead to a high occurrence in orchard areas with subsequent severe damages. The feeding behaviour on fruit and vegetables leads to deformations and corky brown tissue that makes it unmarketable.
Currently, for organic farming there is no plant protection strategy against *H. halys*. To solve this problem, the cooperative project BIOBUG aims to develop an eco-friendly, push & pull and attract & kill plant protection strategy. To develop such a strategy it is important to understand how *H. halys* finds suitable host plants. This study focuses on the investigation of the volatile organic compounds, which are decisive for the host plant selection behaviour of the bug. To detect attractive, volatile organic compounds, we monitored the abundance of *H. halys* on different fruit crops in a commercial orchard and an experimental field station. When high numbers of *H. halys* on one crop were observed, volatiles of fruit and leaves were collected through headspace sampling. Volatile samples were then analysed after thermodesorption, followed by gas chromatography coupled with mass spectrometry.
The analyses show that there were both differences and similarities in the volatile composition of the different host plants. The volatile perception of the insect antenna shared among fruits and main compounds were tested using electroantennography. Studying the behavioural response to perceptive compounds provided information on possible attractive or repellent effects on the stink bugs, which can be used for the plant protection strategy. Here, the results of the field monitoring, chemical analysis of plants, and laboratory biotests will be presented.

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Biocontrol plants altered behavioural response of whitefly (*Bemisia tabaci*) on tomato: How to discriminate between a barrier and a repellent effect?

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The whitefly, *Bemisia tabaci*, is a significant pest in tomato production, causing extensive damage and economic losses. In the pursuit of sustainable pest management strategies, this study investigates the deterrent effects of *Tagetes* species (*T. erecta*, *T. patula*, and *T. minuta*) and *Crotalaria juncea* on *B. tabaci* settlement and oviposition on tomato plants. Two dual-choice experimental set-ups were conducted in a climate-controlled chamber with eight replicates per treatment. The study confirmed the efficacy of the experimental setup, with similar *B. tabaci* dispersion and oviposition on the sides with tomato plants alone. When *Tagetes* or *C. juncea* were introduced, a significant reduction in *B. tabaci* settlement and oviposition was observed compared to tomato alone side (control). *Crotalaria juncea* acted as a sinkhole trapping the whiteflies. In order to identify the modes of action of the companion plants on *B. tabaci*, a follow-up experiment, modifying the spatial arrangement of the plants, reinforced was set-up to discriminate between a physical barrier effect and a chemical the repellent action of *Tagetes* species, independent of physical barriers. The findings suggest a potential synergycrossing between repellence and barrier effects for Tagetes species. when *C. juncea* acted as a sinkhole trapping the whiteflies. A GC-MS analysis revealed that the repellent effect is not linked to the intensity of the blend

but seems more associated to the composition. Some already known repellent volatiles such as limonene were identified but the major ketones compounds have also to be tested. Further, a GC-MS analysis revealed repellent volatiles from the *Tagetes* species.

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Insights into the chemical ecology of a wood-boring beetle and its mutualistic fungus

Lehenberger, M.

Fungus-farming bark and ambrosia beetles are associated with a diversity of microbes such as filamentous fungi, yeasts, and bacteria. Filamentous fungi, especially, are often thought to act as mutualists fulfilling crucial functions in beetle-fungus symbioses and are thus believed to be a key to beetle survival. However, the evidence for such a striking role is usually anecdotal as detailed studies focusing on fungal associates are mostly missing. Here, I studied the native ship-timber beetle *Elateroides dermestoides*, one of the few fungus-farming but non-social ambrosia beetles. This large ambrosia beetle colonizes both hardwood and softwood trees such as beech or spruce. It is described to have a mutualistic relationship with the vertically transmitted yeast-like fungus *Alloascoidea hylecoeti*, which is inoculated by the solitary beetle larvae in tunnels drilled into the nutrient-poor sapwood of weakened and recently dead trees. To date, it remains unclear how these large larvae with their long generation times (~2y) survive in such a challenging low nutrient environment. Further, sapwood of dead trees is a preferred habitat for various competing wood-degrading fungi, which have the potential to overgrow larvae of *E. dermestoides*.
In my presentation, I will highlight the essential role of *A. hylecoeti* as a valuable food source for *E. dermestoides* and a suppressor of antagonistic microorganisms. I will present nutritional analyses showing that the high content of free amino acids, soluble sugars, B vitamins, fatty acids, and ergosterol in the fungus is of great value to its beetle host. Moreover, I will show that *A. hylecoeti* utilizes multiple chemical compounds, including monoterpene alcohols and acetic acid, as well as phenolic compounds accumulated from host tree tissues, to efficiently outcompete antagonistic fungi. The nutritional value and competitive ability of *A. hylecoeti* described here likely make a decisive contribution to the success of its insect partner, the ship-timber beetle.

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Integrated push and pull strategy for optimised plant protection against flying insects in energy-optimised Greenhouses

Niemann, J.-U.; Stukenberg, N. &
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Young plant production in greenhouses is relatively energy-intensive and usually involves the preventive use of pesticides. The FuturLights project aims to produce resilient ornamental young plants under glass with significantly reduced carbon equivalent (CO_2e) emissions compared to current production systems. In order to achieve these resource savings, the ‘young plant cultivation system’ is being energetically optimised at various points. The holistic approach combines the aspects of plant cultivation, plant protection, product development, sensor technology and automation as well as enterprise accounting and consulting with a focus on reducing CO_2e.
With regard to plant protection, a push and pull strategy against insect pests will be investigated/used. A patented LED system emitting repellent (push) light from the crop is combined with attractive LED traps (pull) to keep the crop free of infestation. The basis for the push and the pull effect is the so-called blue-green antagonism, which influences host finding in many herbivorous insects and is utilised here for plant protection purposes. In this project, whiteflies and aphids serve as model organisms.
The overall FuturLights concept also includes physiological and plant cultivation aspects. Analogous to the LED system for insect defence, the LED lighting of the young plants is being optimised in a further work package. The aim of this work package is to produce resilient plants with an economically optimised radiation spectrum while minimising energy consumption. Furthermore, in order to demonstrate the limits and synergies of the techniques both systems will ultimately be combined with each other. The experiments are overlaid by the ‘virtual operation’ approach

developed in-house. The power requirement for the LED technology is determined analogue to the experiments. These data are used to calculate the power required for self-sufficient operation of the lighting system. In this way, an energy balance for different operating sizes, structures and contribution margins can be drawn up. Thereby, information on a possible investment in more modern technology can be offered to small and big companies. Moreover, a company's own regenerative energy supply can be included in the modelling as well.

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Visual ecology of herbivorous insects: An underestimated field of research

Stukenberg, N. & Niemann J.-U.

The visual ecology and physiology of insects is generally well understood for some model organisms such as honey bees and butterflies, but knowledge is still relatively limited for economically important herbivorous insects. With a view to developing tailored optical manipulation measures for integrated pest management, it is important to understand and expand research on the visual ecology and physiology of relevant herbivorous insects. By combining basic and applied research, we have the opportunity to take a step forward today. The general key features of the visual ecology of herbivorous insects are outlined.
Visually guided host plant finding is generally accepted as a binding link between potential olfactory orientation, which provides insufficient directional information, and suitability selection upon host contact by herbivorous insects. The colour choice behaviour of herbivorous insects is a well-known example of an innate response that cannot be modified by experience or learning. Visual acuity in insects is determined by the properties of the compound eye, which include the number and size of the ommatidia and, most importantly, the interommatidial angle. The physiological basis for the visual perception of light is provided by the photoreceptor cells in the insect compound eye, which contain the visual pigments. If the spectral sensitivity of a photoreceptor is known, the photon catch from a stimulus light of known spectral distribution can be calculated. Combined with behavioural data from colour choice experiments, the photoreceptor excitations can be used to model potential chromatic interactions of photoreceptors. An important mechanism for colour perception is colour opponency, where the outputs of multiple photoreceptors are compared by antagonistic neural processing. The attractiveness and detectability of an object is determined not only by its colour, but specifically by the contrast between the target and its background. Therefore, the photon catch of the target is usually calculated relative to the background, i.e. both reflectance spectra are included in the modelling. The underlying mechanism is photoreceptor adaptation, which is the relative adjustment of the receptor signal to the perceived light of the target versus the background.

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Decoding Chemical Communication: Insights into Cuticular Hydrocarbon Profiles of the Termite *Anacanthotermes turkestanicus*

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Cuticular hydrocarbons (CHCs) are vital chemical signatures that underpin termite communication, mediating behaviors such as nestmate recognition, caste differentiation, and colony defense. This study deciphers the CHC profiles of *Anacanthotermes turkestanicus*, a key pest species in Central Asia, to unveil their role in colony dynamics and chemical communication. Using Gas Chromatography-Mass Spectrometry (GC-MS), we characterized CHC compositions across castes (workers, soldiers, reproductives) and explored age-dependent variations in colonies at different developmental stages. Our findings reveal pronounced heterogeneity in CHC profiles in younger colonies, transitioning to more homogeneous patterns in mature colonies. These insights not only enhance our understanding of termite chemical ecology but also pave the way for innovative pest management strategies, including synthetic CHC-based baiting and disruption of colony cohesion. This research offers a novel perspective on leveraging chemical ecology to mitigate the economic and ecological impact of *A. turkestanicus* infestations.

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Sektion Biogeographie und Faunistik / Section Biogeography and Faunistics

Talks

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Keynote

Terrestrial arthropod species and community responses to climate change in the Arctic

Høye, T.T.

The harsh climate, limited human infrastructures, and basic autecological knowledge gaps represent substantial challenges for studying arthropods in the Arctic. At the same time, rapid climate change, low species diversity, and strong collaborative networks provide unique and underexploited Arctic opportunities for understanding species responses to environmental change and testing ecological theory. Here, I provide an overview of individual, population, and ecosystem level responses to climate change in Arctic arthropods. I focus on thermal performance, life history variation, population dynamics, community composition, diversity, and biotic interactions. The species-poor Arctic represents a unique opportunity for testing novel, automated arthropod monitoring methods. The Arctic can also potentially provide insights to further understand and mitigate the effects of climate change on arthropods worldwide.

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Building an insect macrogenetics database

Dovydaitis, E.; Gerth, M. & Schmidt, C.

Genetic diversity is a fundamental component of biodiversity that contributes to the capacity of populations to cope with environmental change. Understanding the extent to which population genetic processes are consistently associated with environmental factors across species is a powerful way to examine the processes maintaining patterns of biodiversity. The field of macrogenetics addresses these types of questions by synthesizing publicly available data to study population genetics at broad spatial and taxonomic scales. Macrogenetics research predominantly focuses on vertebrates, particularly mammals, and rarely features invertebrates. We therefore know little about the broad scale spatial distribution of insect genetic diversity across species or how such patterns covary with drivers of global change, such as urbanization and agriculture.
To address this issue, we are harvesting publicly available genetic data from non-laboratory insect populations to build a macrogenetic database. Most macrogenetic studies utilize mitochondrial DNA (mtDNA); however, our database is built using nuclear DNA (nuDNA). We selected microsatellites, which are highly polymorphic and neutrally evolving, from population genetics studies. Using a list of over 50,000 insect genera and common names, we queried the Dryad data repository for microsatellite genetic data. We then selected data to include based on a priori inclusion criteria. This presentation will showcase the database building process and provide some preliminary analytical results on Bombus. Thus far, we compiled data from 4620 individuals across 243 populations and 14 *Bombus* species. We estimated two measures of genetic diversity (allelic richness and gene diversity). We then used mixed effects linear regression models to test the effects of human-driven land use change, such as urbanization and agriculture, on the genetics of *Bombus* populations. In areas with a higher human footprint, some species, such as *B. hypnorum* and *B. ruderatus* tended to have lower levels of genetic diversity. On the contrary, other species such as *B. occidentalis* and *B. terrestris* had higher levels of genetic diversity in areas with a higher human footprint. This pattern may be influenced by their role as commercial pollinators in fields and greenhouses. Using such analyses can elucidate how land use changes impact populations and their genetic diversity, which can in turn be used to inform conservation efforts.

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First Record of *Megaselia scalaris* in Southern Kazakhstan

Dulat, B.; Makhambetov, A.; Dairbekova, Z.; Yanin, K.; Yegorov, P. & Gritsenko, D.

Phytopathogens and pests that cause diseases in apple trees pose significant threats to agriculture, adversely affecting both yield and fruit quality. This makes their study a critical issue. In Kazakhstan and other countries with advanced horticultural practices, the identification of phytopathogens, their natural vectors, and pests is essential for the development of effective disease control and prevention strategies. Among such pests, *Megaselia scalaris* is officially classified as a quarantine pest absent in Kazakhstan, yet it is recognized as

having quarantine significance. This report marks the first documented occurrence of *M. scalaris* in Kazakhstan, highlighting the urgent need for ongoing monitoring and a comprehensive evaluation of its potential impacts on agriculture and local ecosystems.
In the present study, four apple orchards were monitored in September and October of 2024. A total of 100 apple samples showing signs of pest damage were analyzed, revealing three puparia in one sample, while other samples contained traces of larvae. The puparia were carefully placed on moistened cotton in Petri dishes for incubation. After the flies emerged, morphological characteristics were observed and analyzed.
DNA barcoding of the flies was performed using universal primers targeting the cytochrome c oxidase subunit I (5'-TCCACTAATCACAARGATATTGGTAC-3' & 5'-GAAAATCATAATGAAGGCATGAGC-3') and 16S rRNA (5'-TARTYCAACATCGRGGTC-3' & 5'-CYGTRCDAAGGTAGCATA-3') genes, with sequencing conducted using Nanopore technology. Morphological characteristics confirmed the assignment to the Phoridae family, based on the analysis of puparial form, the structural features of the flies' bodies, and the distinctive wing venation patterns.
The sequences of 16S rRNA and cytochrome c oxidase subunit I were concatenated and aligned against a database comprising available insect sequences from NCBI. The alignment yielded 53,390 reads, of which 48,906 (91.60%) successfully mapped to the reference sequence of *Megaselia* species. Coverage analysis revealed variable depth across different *Megaselia* species, with *M. scalaris* exhibiting notably higher coverage and a stable length distribution compared to other species in the reference database. Mapping quality scores of 60 were observed for reads aligning to *M. scalaris*.
This study provides the first documented occurrence of *M. scalaris* in Kazakhstan, offering valuable insights into the taxonomy and geographical distribution of this genus. The findings underscore the importance of continued surveillance and targeted research to assess the agricultural and ecological implications of this species.

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The Year of the Microhymenoptera– Insights from Malaise trapping on Parasitoid Wasps and Insect Decline

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Microhymenoptera, which mostly include parasitoid wasps, play an important role as natural enemies of their hosts in terrestrial ecosystems, but are mostly overlooked in insect monitoring studies as they are small-sized and experts are often rare. Therefore, it is unclear to what extent microhymenoptera are affected by insect decline. This knowledge gap needs to be filled, because microhymenoptera are essential for the resilience of an ecosystem. We used Malaise trap samples and insect biomass data from the LUBW insect monitoring project from three study sites to learn more about the relationship of insect biomass, and abundance and diversity of microhymenoptera. Malaise traps were used from March to November in 2019 and emptied every two weeks. Samples were size-fractionated and Hymenoptera specimens from the micro fractions were sorted out, counted and identified at least to family level. We used statistical models to test, how total microhymenoptera abundance and diversity on family level relate to total insect biomass. In total, we counted 90,452 microhymenoptera specimens that we could assign to 26 families in 10 superfamilies. We found a significant relationship between microhymenoptera abundance and insect biomass, as well as between diversity of microhymenoptera families and insect biomass. This indicates that insect biomass can be a valuable proxy for insect abundancy trends even for microhymenoptera. Thus, the decline of insect biomass highly likely also affects microhymenoptera. Overall, microhymenoptera numbers peaked twice during the year, first between June and July and second between July and August, although number of peaks, and timing varied between families and sites. This data set forms a baseline for microhymenoptera occurrence in low-intensity managed meadows in south-western Germany. Our study also highlights the value of mass samples to study microhymenoptera in the context of insect decline.

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Revised Checklist of Serbian Orthoptera: Updates and Insights After Five Decades

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Although the first studies on Orthoptera in Serbia were published in the mid-19th century, limited research efforts in subsequent years left Serbia among the least studied countries in Europe regarding Orthoptera fauna. In recent years, however, systematic investigations have significantly enhanced orthopterological knowledge in the country. Nevertheless, the distribution of many species remains poorly understood.
Currently, the Orthoptera fauna of Serbia comprises 179 species, including 103 species of Ensifera and 76 species of Caelifera, with two species represented by two subspecies.
An updated checklist of Orthoptera species in Serbia is presented, highlighting the changes based on comparisons with previously published data. The primary aim of this checklist is to consolidate and present the findings from publications and surveys on Serbia's Orthoptera fauna up to the year 2024.
While the current understanding of Orthoptera in Serbia remains incomplete, this checklist will serve as a valuable foundation for future research and aims to foster greater interest in Orthoptera studies within the country. The dataset incorporates records from 1861 to 2024 available in published literature, field data collected during our own expeditions, and citizen science platforms such as iNaturalist (inaturalist.org), Observation.org (observation.org), Alciphron (alciphron.habiprot.org.rs), and Biologer (biologer.rs).

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Bodenparameter in Biotopen Madagaskars für den Trichterbau und Wasserhaushalt von Ameisenlöwen (Neuroptera, Myrmeleontidae)

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Untersuchungen zum Baugrund und an Baustoffen dienen der Bestimmung ihrer Festigkeit und der Beurteilung der mechanischen Eigenschaften des Materials. Technische Verfahren zur Ermittlung der Wasserdurchlässigkeit, der Verteilung von Korngrößen und anderer Eigenschaften basieren auf DIN- bzw. EN-Vorschriften. Diese Verfahren werden von uns erstmals auf Bodenproben angewendet, in denen Ameisenlöwen ihre Fangtrichter errichten.
Der Erstautor und eine Science Community konnten auf Madagaskar 32 verschiedene Habitate mit diesen Larven nachweisen. Aus 12 dieser Habitate wurden Bodenparameter analysiert, deren Eigenschaften mit dem Körperbau, der Anlage von Fangtrichtern und dem Wasserhaushalt der Larven korrelieren.
Auf Madagaskar sind nach Penny (2003) mindestens 72 Arten der Myrmeleontidae nachgewiesen (vgl. Abraham & Dobosz 2011). Sie kommen dort in Küstensanden und Halbwüsten, in Waldregionen, in Lavahöhlen und in erodierenden Felsgebieten vor. Auf den Inselbergen der vor 138 Mio Jahren abgetrennten Gondwana-Landmasse sind Neuroptera bzw. Myrmeleontidae wohl noch nicht gesucht worden. Dazu gehören alte Faunenelemente, die sich von Ost-Gondwana herleiten, aber auch später eingewanderte oder vor Ort neu entwickelte Formen (Engel et al. 2018, Krivokhatsky 2021).
Schluff (<0,063 mm) und Grobsand (0,63 bis 2,00 mm) liefern in den Proben die geringsten Anteile. Rieselfähiger Fein- und Mittelsand (0,063 bis 0,63 mm) ist zu ca. 85% enthalten. Bei allen 3 homomorphen Larvenstadien entspricht die Form des Abdomens einem spitzwinkligen Dreieck. Zum Trichterbau gleiten die Löwen mit ruckartigen Bewegungen und gleichzeitigen Sandwürfen rückwärts auf einer Spiralbahn durch das Substrat, so schnell, dass 132 Fangtrichter von L_3-Larven im Mittel in 25:13 errichtet sind. Mit x=366 Wurfbewegungen/Trichter werden dabei 2.550 mg Sand bewegt, das ist z.B. das 60-fache der Biomasse. Das Porenvolumen ist sowohl für die Atmung als auch für die Wasserführung im Boden wesentlich. Als Regen ist Wasser in der Dornensteppe im Süden Madagaskars unregelmäßig und über Monate nicht verfügbar. Zu den spezialisierten Anpassungen gehört, dass Ameisenlöwen, wenn Wasser in den oberen Bodenhorizont eindringt, innerhalb von 60 min bis zu 40 Gew.% ihrer Biomasse über die Haut und die Greifzangen gewinnen.

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Structural and functional shifts in caterpillar communities from rainforest to plantation systems in Sumatra, Indonesia

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Caterpillars are herbivorous insects that live in canopy plants in various ecosystems. The conversion of rainforests to agricultural land results in population decline and biodiversity loss; this likely also applies to caterpillars. We studied caterpillar responses to rainforest transformation into agricultural systems in four land-use systems: rainforest, jungle rubber (agroforestry), and rubber and oil palm (monoculture) plantations in Sumatra, Indonesia. In 2013/14, we collected approximately 2000 caterpillars in an eightfold replicated plot design using canopy fogging. We identified 22 caterpillar families, followed by an analysis of abundance, richness, and community composition. We also classified families that contributed ≥80% of abundance in each plot and selected 1–3 individuals for stable isotope analysis. Caterpillar abundance was higher in rainforests compared to other land uses. Conversely, the caterpillar richness of rainforest and jungle rubber surpasses that of rubber and oil palm. The composition of caterpillar families in the rainforest was more comparable to jungle rubber and rubber than oil palm, indicating shared community traits. Therefore, converting rainforests to plantation systems results in a strong decline in caterpillar abundance and richness. Isotopic positions in rainforest and jungle rubber communities overlapped; that is also observed in rubber and oil palm plantations. Rainforests support more unique ecological niches and trophic dynamics than agricultural systems. Jungle rubber, rubber, and oil palm highlight potential transitional or disturbed isotopic indications, showing ecosystem degradation or mixed contributions of basal resources. Overall, the results allow a deeper understanding of the relationship between changes in lepidopteran community structure and changes in their functioning due to the conversion of rainforests into plantation systems.

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Effects of local and landscape factors on alpha and beta diversity of urban wild bees and derived conservation suggestions

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Urbanisation is one of the most severe modifications of landscapes. Therefore, cities are often regarded as detrimental for biodiversity, including wild bees. Conditions within urban areas are considered to act as environmental filters, which result in biotic homogenisation. In contrast, cities are also discussed to be potential refuges for wild bees. In this study, responses of wild bees and bee communities to urban land use and other potential environmental filters were analysed.
In Braunschweig, Lower Saxony, Germany wild bees were sampled with pan traps at 49 sampling points, which were spread across the entire administrative area of the city. Effects of different land-use types on wild bee alpha-diversity were examined at 12 radii ranging from 50 to 1500 m around each sampling point. To account for species-specific requirements, bees were grouped according to their traits. Effects of potential environmental filters on wild bee beta-diversity were analysed using multiple matrix regression. Dissimilarities in wild bee community composition between sampling points were compared with respect to geographic distances, distance to the city centre, nearby land use, soil characteristics and community composition of locally flowering plants.
An increasing proportion of anthropogenically managed flower-rich areas, i.e., long-term allotments and cemeteries, increased total abundance and species richness of wild bees, as well as abundance of most wild bee groups, whereby the most relevant radius varied between bee groups. Only some bee groups were affected by impervious surface, mainly within a 100 m radius and in a non-linear unimodal manner. Community compositions of wild bees differed markedly between sampling points and depended on nearby soil texture and the local community of flowering plants. However, community compositions of flowering plants themselves depended on nearby land use, which suggests an indirect effect of urban land use on wild bees.
Consequently, conservation measures to support wild bees in urban areas should consider the species-specific dependencies of wild bees on the composition and accessibility of nutritional and nesting resources. The value of cities as habitats for a heterogeneous set of wild bee communities may increase with preservation and creation of heterogeneous flowering plant communities throughout the city. Flower-rich anthropogenically managed areas like long-term allotments and cemeteries should be maintained and preserved.

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Sektion Biologische Schädlingsbekämpfung / Section Biological Control

Talks

sorted by sections and main authors

Keynote

Why clearer rules make sense: The importance of a regulation for invertebrate biological control agents in Germany

Herz, A.

Biological control, the use of (invertebrate) antagonists of pests to protect plants, regulate invasive organisms or control nuisance pests, is an indispensable option for sustainable agriculture. In addition to efforts to promote conservation biological control through the consistent application of the principles of integrated pest management and the appropriate design of agroecosystems, the production and use of invertebrate biological control agents (IBCA) for augmentative biological control has a long tradition in Germany. This method has already reduced the use of chemical pesticides by farmers for decades, especially under protected conditions. Less common is the so-called classical (importation) biological control, i.e. the introduction of specific natural enemies of invasive organisms from their area of origin, which was only carried out in a few cases in Germany more than 70 years ago. This method has gained new interest in recent years in the face of highly destructive, invasive plant pests and attempts of other European countries to introduce efficient IBCA to control them. Nevertheless, the introduction and release of IBCA can pose environmental risks if there are unacceptable effects on non-target organisms. For more than 20 years, and particularly since the arrival of the invasive Asian lady beetle, *Harmonia axyridis*, in Europe, the scientific community, stakeholders in the biocontrol industry, and national and international authorities have been elaborating and implementing procedures for the safe use of IBCA. There are tools for environmental risk assessment and decision support that are constantly being developed, for example, by the Joint EPPO/IOBC Panel for Biological Control Agents. These EPPO PM 6 Standards have also been adopted by many European countries to establish a legal framework and registration process for IBCAs. In Germany, however, no specific regulatory provision for the authorization and registration of IBCA has yet come into force. We propose developing a regulatory procedure that takes into account an environmental impact assessment (risks and benefits) for IBCA species that do not occur naturally in Germany and need to be introduced from other regions. Such a procedure can help to increase safety when using IBCA and thus promote the ecological and environmental advantages of biological control. Furthermore, it would help to harmonize decisions at the European level and also enable research into the natural enemies of invasive pests as part of a preventive approach. The presentation gives an overview of the history and success of the use of IBCA in Germany, the changes in the legal framework and ideas for a legally secure practice using illustrative examples.

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Integrated management of fruit fly (*Bactrocera dorsalis*) by using Nanoparticles additive with combination of entomopathogenic fungi

Ahmad S.

Entomopathogens play an important for the pest management, due to their effectiveness against different fruitfly species, including *Bactrocera dorsalis*, *B*. *zonata* and *Ceratitis capitata*. For the sustainable management of *B*. *dorsalis*, we observed the effects of three EPF strains (*M*. *anisopliae*, *B*. *bassiana*, and *A*. *niger*) with combination of nanoparticles Zno and Ag. We examined four concentrations of EPF strains (1x102, 1x104, 1x106, and 1x108 cfu/ml) with nanoparticles by using topical and direct application. The data of EPF was collected after 4, 6, 8 and 10 days and the effect of nanoparticle analyzed. The concentration of *B*. *bassiana* showed highest mortality 90.47% trailed by *M*. *anisopliae* 85.71% and *Aspergillus* spp. 66.79%. The mortality rates of zinc oxide and silver were 86.74% and 95.56%. The results showed that EPF high mortality rates as compared to the nanoparticles. It is concluded that combination of nanoparticles and EPF is very effective approach for the sustainable management of *B*. *dorsalis*.

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Einsatz von Offene-Zucht-Systemen und maßgeschneiderten Blühstreifen zur Bekämpfung von *Aleyrodes proletella* im Rosenkohlanbau

Bertels, N. & Meyhöfer, R.

Zur Förderung eines nachhaltigen biologischen Pflanzenschutzes im Kohlanbau sind

strategische Kombinationen verschiedener Maßnahmen zur Nützlingsförderung entscheidend. Effektive Gegenspieler lassen sich gezielt mithilfe von Offene-Zucht-Systemen direkt am Feld ansiedeln. Maßgeschneiderte Blühstreifen fördern durch eine reichhaltige Umgebung mit einem großen Pollen- und Nektarreservoir sowie zusätzlichen Alternativwirten die funktionelle Biodiversität. Ziel dieses Freilandversuchs war es, herauszufinden, ob die gezielte Kombination von Offene-Zucht-Systemen und maßgeschneiderten Blühstreifen einen Einfluss auf die Population der Kohlmottenschildlaus *Aleyrodes proletella* und den Verschmutzungsgrad der Röschen hat. Dafür wurden entlang eines Rosenkohlfeldes ein weiterentwickeltes Offene-Zucht-System (Wirtspflanze: Sonnenblume) und ein maßgeschneiderter Blühstreifen („Hannover Mix“) separat und kombiniert miteinander angelegt. Sowohl die Wirtspflanze als auch die Anbaumethode des Offene-Zucht-Systems wurden in den vergangenen Versuchsjahren weiterentwickelt. Während der Etablierungsphase mit dem Alternativwirt, der Gewächshausweißen Fliege *Trialeurodes vaporariorum*, und dem Gegenspieler *Encarsia tricolor*, einem wichtigen Parasitoiden von *A*. *proletella*, wurde das Offene-Zucht-System mit einem Vlies abgedeckt. Der maßgeschneiderte Blühstreifen und das Offene-Zucht-System wurden nebeneinander an der dem Wind zugewandten Seite angelegt, um eine gezielte Verdriftung der Nützlinge in die Kultur zu ermöglichen. Neben regelmäßigen visuellen Bonituren wurde mit Fangpflanzen, Gelbschalen und Bodenfallen die Nütz- und Schädlingsaktivitäten erfasst. Im Vergleich zum Vorjahr zeigte sich, dass in den Offene-Zucht-Varianten sieben Wochen früher dreimal so viele adulte *E*. *tricolor* im Rosenkohl aktiv waren. Die Parasitierungsrate durch *E*. *tricolor* betrug 52% und war damit am höchsten in der kombinierten Variante. Dabei konnte die Population von *A*. *proletella* um 43% gesenkt werden, verglichen mit der unbehandelten Kontrolle. Die Aktivität der Parasitoiden stieg in den Offene-Zucht-Varianten früher im Jahr an und war im Verlauf der Erhebung doppelt so hoch wie in der Kontrolle. Die Ernteanalyse ergab, dass der Verschmutzungsgrad der Röschen aus der kombinierten Variante um 28,92% geringer war als Röschen der Kontrollvariante. Die Ergebnisse zeigen, dass maßgeschneiderte Blühstreifen und Offene-Zucht-Systeme die Population von *A*. *proletella* senken können. Besonders die kombinierte Anwendung führte zu einer deutlichen Steigerung der Parasitierungsrate und einer Senkung der Schädlingspopulation. Darüber hinaus konnte der Verschmutzungsgrad der Röschen verringert werden, was die potenziellen Vorteile dieser Methode für den Kohlanbau unterstreicht. In diesem Jahr sind Praxisversuche zur Optimierung und Integration in die betrieblichen Arbeitsabläufe geplant.

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Dual action of the endemic entomopathogenic fungi *Beauveria bassiana* GxABT-1 against *Myzus persicae* and the Beet mild yellowing virus

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Investigating new biocontrol agents to overcome the use of neonicotinoid insecticides is of great importance to control *Myzus persicae*, the main vector of Beet Mild Yellow Virus (BMYV). Herein, we studied the direct and endophytic potential of two strains of Beauveria bassiana GHA from BotaniGard and the endemic one GxABT-1 against *Myzus persicae*-Sugar BMYV pathosystem. Eight days post fungal treatment, GHA and GxABT-1 caused more than 90% mortality among treated aphids. To assess the endophytic potential, sugar beet seeds were treated, and fungal colonization in the plant tissues was assessed. The endophytic potential of both strains was correlated with several aphid-related factors, including life cycle, attraction to the treated plants, and ability to transmit BMYV. Both fungi successfully colonized the treated sugar beet plants, with GxABT-1 notably disrupted *M*. *persicae* life cycle. Regarding the behavioural experiments, aphids were more attracted to leaf discs from untreated plants than to the fungal-treated ones. However, when the choice was between fungal-treated plants, aphids showed a significant preference towards GxABT-1-treated leaves over those with GHA. While there was a slight reduction in viral load in GxABT-1-treated plants, no significant effect on BMYV transmission was observed. These findings provide a baseline for further research concerning the performance of endemic fungal species with an entomopathogenic potential in more diverse agricultural systems using alternative application strategies.

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Alternierendes Mulchen zur Förderung heimischer Nützlinge und zur Reduktion des Birnenblattsaugers

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In zwei Feldversuchen wurde die Wirkung alternierend gemulchter Fahrgassen auf heimische Nützlinge und die Kontrolle des Birnenblattsaugers im Birnenanbau untersucht. Alternierendes Mulchen führte zu einer deutlichen Förderung der Blumenwanzen im Vergleich zu dauerhaft gemulchten Fahrgassen. Die erhöhte Populationsdichte der Blumenwanzen trug maßgeblich zur effektiven Reduktion der Birnenblattsauger bei. Die Ergebnisse zeigen, dass habitatfördernde Maßnahmen wie alternierendes Mulchen eine vielversprechende Strategie zur Stärkung der biologischen Schädlingskontrolle im Obstbau darstellen.

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The digger wasp *Pemphredon lethifer*–The key to a clean and effective aphid control?

Furtwengler, J. & Böckmann, E.

Aphids are a common problem in many crops. The use of biocontrol agents can be an alternative to plant protection products. However, the biocontrol agents available to date such as parasitic wasps or gall midges leave aphid mummies or their larvae on the plants. These leftovers are often not accepted by food retailers or consumers. *Pemphredon lethifer* (Shuckard, 1837) is a species of digger wasp that is native and widespread in Europe. Digger wasps of this genus are specialised on aphids. In contrast to other biocontrol agents, they prey on the aphid and transport it to their nest, leaving no leftovers on the plant. *Pemphredon lethifer* could therefore be a potential biocontrol agent for aphid control, especially in crops were aphids attack the marketed plant parts directly. However, the species has not yet been reared or commercialised, nor is there any knowledge of its efficacy in aphid control.
To test the efficacy of *P. lethifer* in aphid control we carried out cage trials in the greenhouse. Each cage contained six broad bean plants, which were previously inoculated with *Aphis fabae* aphids. Three treatments with densities of two, four or six female wasps were carried out. The aphid infestation was measured twice a week for a total of three weeks.
Even a small number of digger wasps achieved a significant reduction in aphid infestation. The effect lasted until the end of the trial. Initial results are presented and discussed. The results provide first insights into the potential of a possible use of *P. lethifer* for aphid control.

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Film: Trauermücken vorbeugen und regulieren mit Nützlingen

Kühne, S.; Kabakeris T.; Schorpp, Q.; Zange, B.; Lohr D. & Baron A.

Trauermücken gehören im Topfpflanzenbau zu den häufigsten Schädlingen und besiedeln die Gewächshäuser ganzjährig. In dem 6-minütigen Dokumentarfilm werden die Biologie und Verhaltensweise der Schädlinge gezeigt sowie neue Methoden des Monitorings und der Regulierung mit Nützlingen vorgestellt.

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Experimental evaluation of host specificity of the generalist parasitoid *Pachycrepoideus vindemmiae*

Martin, J.; Schetelig, M.F. & Herz, A.

Host specificity is an important criterion for the success of augmentative biological control using parasitoids. In Germany, two native parasitoid species are currently available for the biological control of *Drosophila suzukii* (Diptera: Drosophilidae), an invasive pest affecting soft-skinned fruit. One candidate is the cosmopolitan pupal parasitoid *Pachycrepoideus vindemmiae* (Hymenoptera: Pteromalidae). A literature review indicates that this species was reared from hosts belonging to at least 14 Diptera families, including pollinating and aphidophagous hoverflies (Syrphidae). If these findings represent the realized host range, augmentative releases might bear the risk for unwanted non-target effects and may suffer from low efficacy on the target host, *D. suzukii*.
To gain a better understanding of the host range of a German population of *P. vindemmiae*, we selected eight species from seven Diptera families and one Lepidoptera, relevant for the potential release habitat. In no-choice parasitism tests using single naïve *P. vindemmiae* females, six species from five Diptera families were parasitized at least once. As the next step, parasitism was determined on pupae of these species in comparison to *D. suzukii* pupae in a choice situation. The first hour was filmed for behavioral analy-

sis, followed by another 23 hours of incubation. Under choice conditions, *P. vindemmiae* parasitized *Ophyra aenescens* (Muscidae), *Sphaerophoria rueppellii* (Syrphidae), and *Lucilia sericata* (Calliphoridae) in 40%, 30%, and 6.7% of observations (n=30), respectively. No offspring developed from the remaining three non-target species. Overall, *D. suzukii* pupae were preferred in comparison to non-target species tested.
This suggests that this strain, which had been originally isolated from Drosophilidae, has probably preference for *D. suzukii*, being therefore a suitable candidate for the biological control of this pest. Especially, since habitat structure and temporal overlap further decrease the number of potentially affected non-target species in the targeted release conditions (mainly protected berry crops), even such parasitism can be rated to be limited and transient. Our study raises new questions about the difference between the potential and realized host range and the degree of specialization in generalist parasitoid populations.

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Tyria jacobaeae as a potential biological control agent of *Jacobaea vulgaris* and other ragwort species

Müller, S.; Shin, Y.E. & Herz, A.

Jacobaea vulgaris (tansy ragwort) is a native plant in Germany and toxic for grazing animals, as well as related ragwort species are. Due to the increase of *J. vulgaris* in grasslands under low-intensity management which famers use for hey production or grazing, *J. vulgaris* became a threat for farmer's livelihood and the wellbeing of their livestock. Therefore, the development of suitable biological control methods is in need to match farm's needs, safety of grazing livestock and nature conservation standards. Hence, we were looking for *Tyria jacobaeae* (cinnabar moth), a native and herbivorous insect and specialized feeding on *J. vulgaris*, and its potential to act as a biological control agent against this poisonous weed and related species in its native range. To investigate the acceptance of alternative host plants for *T. jacobaeae* adults, we conducted single choice oviposition experiments with *T. jacobaeae* females on *J. vulgaris* and two related species, *Jacobaea aquatica* and the invasive *Senecio inaequidens*. Likewise, we placed seven day old *T. jacobaeae* larvae (2nd instar) on the same three ragwort species to gain knowledge about the ability of the larvae to develop successfully on these plants measured by their weight and pupation success. As expected, we found that the highest percentage of females laying their eggs on leaves was with *J. vulgaris* (93%) followed by *J. aquatica* (75%), while it was lowest with *S. inaequidens* (53%). For the larval development, we found no significant differences between the larvae exclusively fed with *J. vulgaris* or *J. aquaticus*, whereas the weight of the larvae on *S. inaequidens* was already one week after experiment start significantly lower compared to *J. vulgaris*. Furthermore, no larvae on *S. inaequidens* were able to survive. As a next step, we wanted to evaluate the regulation potential of *T. jacobaeae* on *J. vulgaris*. Hence, we conducted a semi-natural field trial with mesh cages in the Westerwald, where we tested two densities of larvae on 18 *J. vulgaris* plants respectively. The results showed strong differences in defoliation pattern of *J. vulgaris* plants depending on the site. Responsible factor (larval density, plant differences, etc.) are currently tested in ongoing statistical data analysis. However, our results already state that *S. inaequidens* is not suitable as an alternative host plant for *T. jacobaeae*, whereas *J. aquatica* could be. Additionally, observations of our field trials showed that under the right circumstances, there seem to be potential for the biological control of *J. vulgaris* wit *T. jacobaeae*.

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Distribution and severity of white mango scale, *Aulacaspis tubercularis* (Hemiptera: Diaspididae) and its associated natural enemies in Kenya: New insights into options for its biocontrol

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The horticultural sector in Africa faces various biotic and abiotic constraints, which threaten the sustainability of this important sector to millions of smallholder farmers in the continent. The threat of alien invasive insects such as the white mango scale *Aulacaspis tubercularis* (Hemiptera: Diaspididae) further compounds the challenges of sustainable and safe production of horticultural crops in many ways. Globally, *A. tubercularis* is one of the key mango pests, thus, there is the need for continued monitoring of its distribution and severity on its preferred host plant, mangoes, as well as the associated natural enemies with the aim of improving management strategies. In the context of developing classical and augmentative biocontrol of this pest in East Africa, this study forms the basis for understanding

the ecology and potentially empty ecological niches for the introduction of its co-evolved efficient natural enemies.
Methods: A field survey was conducted in selected mango orchards within the mango growing agroecological zones in Central, Eastern and Coastal regions of Kenya, between May and August 2024. Farmer orchards were purposively sampled based on three criteria: (1) number of mango trees (N≥20); (2) diversity of mango varieties (at least two different varieties); and (3) distance between sampling points (≥4km). In each mango orchard, 20 mango trees were randomly selected and marked for sample and data collection. A wooden quadrat (30 x 30 x 30cm) was placed on each of the four-compass directions of the lowest branches of the mango trees, after which, leaves infested with *A*. *tubercularis* were picked and placed in 4-litres transparent buckets. Additionally, predators that were observed on any other mango leaf within the tree sampled, were collected and placed in sterile unused Petri dishes (Citotest®; 90 x 15mm). From the collected mango leaves, sections of leaves with *A*. *tubercularis* were cut and placed in the Petri dishes, covered, labelled, and wrapped with rubber-bands. After every two days post-sampling, the number of male and female *A*. *tubercularis* from each mango tree was counted. Moreover, parasitoids and predators that were recovered, were transferred into separate 2-litre plastic boxes, based on their tentative morphological similarities. In the laboratory, all the suspected parasitoids and predators were reared on *A*. *tubercularis* for at least two generations to confirm their association with the host insect. Furthermore, a morphological identification of the natural enemies was conducted.
Results: *Aulacaspis tubercularis* is becoming a serious pest of mangoes in Kenya, unlike the earlier reports that the insect does not cause any significant effect on mangoes. The pest is widely distributed across all the sampled mango growing regions in Kenya. However, the severity of *A*. *tubercularis* varied with altitude, where the highest populations of the pest per orchard were recorded in altitudes between 800 and 1500 m above the sea level, and the lowest populations recorded in altitudes above 1500 m. Additionally, the population of the pest varied with the mango variety, being severe in some of the improved varieties (Tommy Atknis, Ngowe) and all local varieties (Doddo), while the lowest proportions were recorded on Apple and Kent mango varieties. Several Coccinelid beetles belonging to *Chilocorus* spp. and *Rhyzobius* spp. were recorded as the associated predators. Furthermore, two parasitoid species belonging to the genus *Aphytis* and *Arrhenophagus* were recovered.
Conclusion: In light of these findings, laboratory assessment of the biology and population dynamics, host range, and mass-rearing strategies for efficient biocontrol agents are currently undertaken. Moreover, the implications of the findings will be discussed in the context of biocontrol of invasive armoured scale insects in horticultural crops.

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Application of pupal parasitoids for the biological control of *Drosophila suzukii* (Diptera: Drosophilidae) in berry fruit production

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Drosophila suzukii, the spotted wing drosophila, has become a serious pest in the production of soft fruits and sheltered berry crops in Europe. Its ability to damage ripe fruit makes it a significant concern for commercial and organic fruit growers. The native pupal parasitoids *Trichopria drosophilae* (TD) (Hymenoptera: Diapriidae) and *Pachycrepoideus vindemiae* (PV) (Hymenoptera: Pteromalidae) are promising biological control agents parasitizing pupae of this pest insect and can supplement current measures in both integrated and organic production.
The research project „ParaDrosu," initiated in 2021, explores various aspects with the final aim of developing a product for the application of the two pupal parasitoids in berry fruit production. Emphasis is put on the application device, which is important to ensure optimal protection during transport and release and is critical for sufficient dispersal in the crop. Factors such as release times, intervals, and parasitoid numbers are assessed. Semi-field and field trials in Southern Germany are performed to characterize the parasitoids' efficiency in controlling *D*. *suzukii* in berry fruit cultivation.
The effectiveness of the pupal parasitoids TD and PV was tested in raspberry foil tunnels in 2023, including three closed raspberry foil tunnels of 425 m each and using bait stations to assess dispersal and parasitization efficiency. Weekly applications by release of parasitoid adults in the tunnel at two different densities (2.5 TD + 2.5 PV and 5 TD + 2.5 PV) showed good parasitization activity of D. suzukii pupae contained in the bait stations only by TD. Additionally, semi-field dispersal trials in 2022 and 2023 showed that TD could move up to 15 meters along a raspberry row

in a netted tunnel and can also find and parasitize pupae in bait stations two rows further on.
An assessment of four warm temperature scenarios in climatic chambers indicated a significant reduction in TD lifespan under the high-temperature scenario, while PV showed no signs of susceptibility. Furthermore, the impact of commonly used plant protection products in soft production was evaluated in glass Petri dishes. The results demonstrated that insecticides and acaricides, particularly Spinosad and Maltodextrin, when applied as fresh coatings, caused significant mortality in both TD and PV.
In the end, the project will provide new biological control agents suitable for mass production, along with comprehensive guidelines for the integration of both parasitoids in berry fruit cultivation, aiming to effectively manage *D. suzukii* under the climatic conditions of Central Europe.

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Flowering fields: Companion planting to promote natural pest control in potato

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By diversifying farm landscape, pest control can be promoted and a more resilient cultivation system can be developed. While diversification measures in time such as crop rotation or cover crops are already well-established in agriculture, in-field diversification measures, such as companion plants, remain largely unused due to economic concerns or technical aspects of integrating them into common cultivation practices. In this study we therefore planted buckwheat and faba beans as companion plants in between the potato plants to increase arthropod diversity. Our focus was on generalist predators to improve the control of the most important aboveground insect pest, the Colorado potato beetle (CPB). In two years of field trials we were able to successfully establish faba bean and buckwheat as companion plants. We monitored ground- and leaf dwelling generalist arthropod predators as well predation rates on CPB egg clusters. In this talk we will show the positive benefits of companion plants and that this could be an effective measure that requires low-investments for farmers and is thus likely to increase acceptance.

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Kommerzieller Nützlingseinsatz in Deutschland: Vergangenheit – Gegenwart – Zukunft

Wührer, B. & Zimmermann, O.

Während in China schon vor über 2000 Jahren Ameisen zur Bekämpfung von Schädlingen in Mandarinen und Orangenplantagen eingesetzt wurden, blicken wir in Deutschland auf eine fast hundertjährige Geschichte zurück. In den 1920er Jahren wurden Zehrwespen gegen die Blutlaus eingesetzt und in den 1950er Jahren entsprechend Erzwespen gegen die San-José-Schildlaus. In beiden Fällen fand eine „klassische biologische Bekämpfung“ in Form einer Nachführung fehlender Gegenspieler gegen neue Schadorganismen statt („classical biocontrol“). Diese Aktivitäten der Pflanzenschutzbehörden in Baden-Württemberg gingen als historische Beispiele für den biologischen Pflanzenschutz in Europa in die Lehrbücher ein. Durch die Entwicklung von Massenzuchtmethoden und die Ressortforschung der Landes- und Bundesbehörden, insbesondere der Landesanstalt für Pflanzenbau (nun Abtl. 3 des LTZ Augustenberg) und des Instituts für Biologischen Pflanzenschutz der Biologischen Bundesanstalt (umbenannt in Julius-Kühn-Instituts), wurde die wiederholte Freisetzung von nützlichen Arthropoden, als „Überschwemmungsmethode“ (inundativ) oder als saisonale Etablierung (inokulativ) entwickelt. Die erfolgreichste Methode im Freiland ist die biologische Bekämpfung des Maiszünslers durch Schlupfwespen der Gattung *Trichogramma*. Eine maschinelle Produktion von Ausbringungseinheiten sowie die Applikation durch Drohnen ermöglichen einen Einsatz auf ca. 100.000 ha.
Nützlingseinsatz im Gewächshaus wurde vor allem aufgrund von Resistenzen der Weißen Fliege gegen Pflanzenschutzmittel propagiert. Mit der Folge, dass auch gegen andere Schadorganismen, wie z. B. Spinnmilben, Blattläuse und Thripse biologische Lösungen in die Bekämpfungsstrategie eingebaut wurden. So entwickelten sich Blattlaus-Schlupfwespen, Florfliegen und Raubmilben zu ökonomisch bedeutenden Nützlingen. Aktuell werden ca. 100 Nützlinge kommerziell angeboten. Die biologische Bekämpfung im Gemüse hat sich auf den Bereich Zierpflanzen ausgeweitet und wird auch im geschützten Tunnelanbau bei Strauchbeeren (z. B. Erdbeeren, Himbeeren, Heidelbeeren) angewandt. Neben der Freisetzung von Nutzarthropoden im Freiland, im geschützten Anbau und der Lagerung, ist die Anwendung nützlicher Fadenwürmer, entomopathogener Nematoden z. B. auf Sportrasen gegen die Engerlinge des Junikäfers, gegen Raupen des Eichenprozessionsspin-

ners und im Einsatz gegen überwinternden Apfelwickler etabliert.
Ein weiterer Schritt wäre es nun, den Freilandeinsatz zu erhöhen. In der Regel geht es hier noch vorrangig um die Schonung vorhandener natürlicher Gegenspieler durch die Reduktion von Pflanzenschutzmitteln und das Anlegen von Saumstrukturen als Habitate und Blühangebote. Es gibt aber inzwischen Ansätze heimische Nützlinge zu vermehren und zusätzlich freizusetzen, um ihre Ansiedlung und Ausbreitung im Agrarbereich zu beschleunigen. Bezüglich der Nachführung von Gegenspielern invasiver Arten, die vor 100 Jahren noch ein Aushängeschild innovativer Pflanzenschutzmethoden in Deutschland war, stehen die Aktivitäten weitgehend still, weil eine erforderliche Verordnung für die Freisetzung von Nutzarthropoden im Zuständigkeitsbereich des Bundesministeriums für Landwirtschaft, Ernährung und Verbraucherschutz (BMEL) fehlt. Das dadurch rechtlich zuständige Bundesamt für Naturschutz (BfN) unter dem Bundesumweltministerium (BMU) nimmt eine strikte Haltung gegen jegliche Freisetzung nicht-heimischer Arten ein, selbst wenn wissenschaftliche Daten eine geringe Umweltwirkung nachweisen. In unseren Nachbarländern und Südeuropa werden solche Freisetzungen nach EPPO-Standards und Prüfung des Kosten-Nutzen-Verhältnisses, sowie der Umweltwirkungen durchgeführt.
Beispiele sind Schlupfwespen gegen die Maden der Kirschessigfliege und die Samuraiwespe gegen die Marmorierte Baumwanze, aber auch laufende Untersuchungen am CABI zu einer parasitischen Fliege gegen den unmittelbar vor der Grenze aktiven Japankäfer, der den Obst- und Weinbau in Deutschland bedroht.
Den langjährigen Erfolgen, immer mit dem Ziel der Reduktion der Anwendung von chemisch-synthetischen Pflanzenschutzmitteln, steht nun aufgrund fehlender rechtlicher Rahmenbedingungen eine Handlungsunfähigkeit bei der biologischen Bekämpfung invasiver Schadorgansimen gegenüber.

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Sektion Wald-/Forstentomologie / Section Forest Entomology

Talks

sorted by category and main authors

Keynote

Seasonal adaptations of forest insects– Why diapause matters

Schebeck, M.; Lehmann, P.; Laparie, M.; Bentz, B.J.; Ragland, G.J.; Battisti, A. & Hahn, D.A.

Life histories of forest insects are affected by various abiotic environmental factors. Aside from direct temperature effects, dormancy is a key regulator of forest insect life cycles. Numerous species enter diapause to time their seasonal occurrence, in order to exploit favorable environmental conditions as efficient as possible and to mitigate harmful effects of seasonal stress. Diapause expression of various forest insects is highly diverse and affects different parts of their life histories, like survival, reproductive success, the number of generations per year (voltinism), or timing with critical resources. Here, we give insights into diapause expression of species belonging to key functional groups in forest ecosystems, i.e. leaf/needle-feeding species, bark/xylem-dwelling insects, and litter/soil-dwelling species. By comparing different forms of dormancy expression of species of various systematic and functional groups, we aim to find similarities of seasonal adaptations in forest insects, which helps us to understand life cycle regulation in ecologically relevant species of temperate forest ecosystems. Furthermore, we will emphasize on diapause-related effects on central life-history traits, like survival, voltinism, resource management or phenological timing with crucial resources, and discuss those under current and future climatic conditions. Finally, we will also show how specific habitat traits of forest ecosystems can affect diapause expression and seasonal performance. This will not only help us to get a better understanding of insect seasonality of widespread species, it will also be the basis to infer management strategies for certain forest pests.

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Bark gouging as a viable alternative to therapeutic debarking during larval development of *Ips typographus*

Frühbrodt, T.; Sikora, C.; Lemme, H. & Hahn, A.

Ips typographus is the most relevant forest pest in Europe. Exhibiting irregular decadal outbreaks, it has caused enormous amounts of timber loss in *Picea abies* forests in the recent years. Integrated management comprises silvicultural measures and intensive monitoring, both serving as preventive measures. The direct control of this pest mainly relies on the timely detection and removal of damaged or already infested trees, with the objective of preventing *I. typographus* reproduction and dispersal. Despite being simple in theory, this strategy is often challenging in practice due to logistic and structural constraints. Particularly small numbers of scattered, infested trees, as may occur after snow breakage or windthrow, are not easily integrated in harvesting schemes. Yet these trees play a pivotal role in the propagation of *I. typographus*. Mechanical bark treatments represent an insecticide-free alternative for bark beetle control. Preventive bark gouging had previously been shown to be a more efficient substitute for complete debarking, thereby preserving other bark and wood boring insects, and with a higher societal acceptance in respect to the recreational use of forests. However, it was unclear whether and for how long after colonisation bark gouging also serves as a therapeutic measure against *I. typographus*. Here, we conducted a two-year time series with cut logs to investigate whether bark gouging is also effective in reducing *I. typographus* reproduction during offspring development. Therapeutic bark gouging was achieved through the utilisation of an add-on device designed for use with conventional chainsaws. The treatment was conducted at different stages of *I. typographus* development: early oviposition, late larval stage, pupation. The number of offspring per bark area was compared to that of control logs with untreated bark, and to that of completely debarked logs. Therapeutic bark gouging significantly reduced the emergence of *I. typographus* offspring at all developmental stages. The overall effectiveness was significantly greater for earlier stages, suggesting that bark gouging should be conducted as soon as possible after the onset of colonisation. After swarming of the overwintering generation in spring, different generations and their sister-broods typically start to overlap in late spring and early summer, which makes it impossible to ascertain the predominant developmental stage of the brood inside a tree. Because of

the comparatively low effectiveness of bark gouging at the time of pupation, it should therefore be employed preferentially at the begin of a season before overlapping generations occur. Given the low investment costs for the device and the high efficacy at the early stages of *I. typographus* colonisation, we think that bark gouging can be a valuable complement to current management approaches. We see its greatest potential of implementation i) for private forest owners with only small to very small patches of forest, a structure commonly found in many Central European countries, and ii) in case of difficult terrain where the use of heavy machines is impeded. A lower, but significant treatment effect was also observed for the sympatric *Pityogenes chalcographus*, emphasising the broader potential of bark gouging for bark beetle control. In addition, the comparatively positive consequences of bark gouging on non-target organisms compared to complete debarking may contribute to its overall efficacy. Further research is necessary to investigate whether populations of natural antagonists of *I. typographus* can also be fostered.

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The Bark Beetle Dashboard–A novel information platform for an Austria-wide support of bark beetle management

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Climate change-driven outbreaks of bark beetles (Coleoptera: Curculionidae, Scolytinae) have caused tremendous tree mortality around the globe, with severe ecological and economic consequences. In Central European forests, the European spruce bark beetle [*Ips typographus* (L., 1758)] is the most important biotic disturbance agent, whose proportion of damage has doubled in the last two decades. In Austria, *I. typographus* infestations also severely impacted forestry, with 4 million m³ of damaged timber in 2023. With almost 18 m³ damaged timber per hectare the amounts were unprecedented high in the region of Eastern Tyrol, exceeding the annual wood increment in the forests by a multiple in 2023. This situation shows that not only in secondary spruce forests at lower elevations, but also in near-natural spruce forests at montane and high montane/subalpine altitudes, bark beetle outbreaks can occur on a large scale. Effective measures and tools to support forest management in preventing and mitigating bark beetle damage are therefore urgently needed.
For this reason, we developed the practice-oriented Bark Beetle Dashboard in a joint project of BOKU University and the Austrian Research Centre for Forests (BFW). The dashboard provides important information for *I. typographus* management in several maps with high spatial and temporal resolution for the whole of Austria and has been online since May 2024. In addition to the daily updated *I. typographus* development status based on the well-established PHENIPS model, the dashboard provides information on the current water supply of the forests based on the SPEI index, the site- and stand-related predisposition (= susceptibility) of the forests to bark beetle infestation, and the amount of damaged timber in recent years. The development of the dashboard has been supported by recent advances in remote sensing based on Sentinel-2 time series, which allow the detection of tree species proportions and forest disturbances on an annual time scale with a high spatial resolution of 10 m.
The new Bark Beetle Dashboard provides an innovative decision-support for deriving forestry measures and adaptation strategies at different scales in the face of anthropogenic climate change:
- Identify hotspots of high site-specific susceptibility and acute infestation risk due to current forest cover and stand characteristics
- Improve of early detection and sanitation of bark beetle infestations, e.g. through knowledge of the current beetle development stages and drought stress conditions
- Encourage medium to long-term forest conversion towards climate-adapted mixed forests in areas with high infestation risk
- Inform decision makers responsible for the development of nationwide forest adaptation and mitigation strategies
The bark beetle dashboard will be continuously advanced and can be used on laptops and computers as well as on tablets and smartphones. The layout automatically adapts to the screen size of the end device. The larger the screen, the more functions are enabled. For large screen devices, there is the option to view two synchronized maps, which allows for a direct comparison of different maps side-by-side.
Access the dashboard:
https://ifff-riskanalyses.boku.ac.at/barkbeetle_dashboard.htm

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Effects of climate-change induced disturbance sites on moth communities in Central European mixed mountain forests

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Climate change has significant impacts on Central European forests: In recent years, Norway spruce (*Picea abies*) has experienced large-scale dieback within a short amount of time due to drought and bark beetle infestations. This dieback causes economic damage, but it could also have positive effects on forest biodiversity, as disturbed areas–if not salvage logged–can increase structural diversity at stand-scale, particularly by providing sunny patches with deadwood. These structures are beneficial for many insect taxa but are generally lacking in commercial forests. In this study, we investigated whether sparing areas affected by drought and bark beetle disturbances from logging influences taxonomic diversity and community composition of moths. Moths were chosen as they represent a mobile insect group with diverse habitat requirements. Moth data were collected using light traps from May to August 2023 at 10 recently disturbed (2018–2020) mixed mountain forest sites where deadwood had been retained, and 10 managed control sites without natural disturbance in the Black Forest, Southwestern Germany. At each site, forest structure and ground vegetation were mapped. We tested for differences in moth species richness and composition and related them to differences in forest structure, climatic parameters, as well as herbaceous plant and tree composition. While moth abundance was similar between treatments, species richness was significantly higher in disturbed forest sites, showing an extension, but not a turnover of the community composition. Analyses of Red-Listed moth species revealed a positive effect of increasing soil moisture on these species. Our results highlight the importance of structural diversity within forest stands for insect diversity. Further investigations of habitat guilds shall elucidate how the retention of disturbance sites can contribute to moth conservation in temperate mountain forest ecosystems.

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Seasonality of *Ips typographus* in a changing climate

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Diapause is a common strategy in insects to cope with seasonally re-occurring adverse conditions, affecting multiple life-history traits, including reproduction, survival, and voltinism. The spruce bark beetle *Ips typographus* is a major disturbance agent in spruce-dominated forests of Eurasia. It enters reproductive diapause to survive harsh winters and resumes activity in spring under favourable conditions. However, we lack precise information on the effects of environmental factors, such as photoperiod and temperature, on diapause induction and spring swarming, which can result in changes in seasonality in a warming climate. Knowledge of seasonal adaptations is essential to calibrate phenology and risk assessment models to guide management measures and silvicultural planning in order to mitigate eruptive outbreaks. We therefore conducted a series of comprehensive field and laboratory studies to quantify the effects of environmental factors on diapause expression in *I. typographus* under a wide range of photoperiod and temperature conditions.
Our experiments on diapause induction revealed a great variation in responses to photoperiodic and temperature cues. While most individuals entered diapause in response to short daylengths in August, a fraction of individuals reproduced at any daylength, as long as temperatures exceeded critical values. The high within-population variability in the timing of diapause induction is an effective strategy to cope with inter-seasonal variation in climatic conditions, but may also help to rapidly adapt in a changing climate. Spring swarming was mainly influenced by post-diapause temperature sums and modified by daily maximum temperatures, while photoperiod had only a small and ambiguous effect, indicating that spring swarming can potentially start immediately after cold temperatures have terminated diapause in mid-winter.
Ongoing climate warming will consequently extend the reproductive season of *I. typographus*, likely increasing its voltinism and population densities, which subsequently affects management measures and silvicultural planning. As a study system, our findings on *I. typographus* hence contribute to our understanding of seasonality in insects, and conserving structure and functionality of ecosystems.

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Analysing arthropod communities in the canopies of native and non-native tree species using eDNA

Mahla, L.

Forests in Central Europe are exposed to an increasing number of heat waves and droughts due to climate change. To support the

resilience of forests, tree species that are considered to be more resistant to changing climate conditions are increasingly being planted in many areas. The natural range of many of these species lies outside of Central Europe (non-native tree species, e.g. Douglas fir or red oak from North America). Forests and their individual trees are important habitats for numerous animal species. Arthropods in particular are often specialists, adapted to a single plant species or genus. This study investigated whether the diversity of arthropods in the canopy of native tree species differs from that of non-native tree species. Species communities were analysed by eDNA metabarcoding of leaf wash-off from 13 different tree species across 8 different sites. Results show differences between native and non-native tree species on a community level. Interestingly, a clear separation of arthropod communities was found between coniferous and broad-leaved tree species and further even each tree species showed its own arthropod community. Those community differentiations between tree species were less pronounced between non-native species. This study provides a first indication of the effects of the cultivation of non-native tree species on biodiversity in native forests.

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Eine neue Sicht auf Populationsdichte und Beutegewinn: Modell-Ameisen testen die Räuber-Beute-Beziehung im Habitat (Neuroptera, Myrmeleontidae)

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Ameisenlöwen, die Larven der Myrmeleontidae, sind Wartejäger, die nach der Anlage eines Fangtrichters oder unter der Bodenoberfläche inaktiv auf Beute warten. Bei der Erfassung der Populationsgröße mit der Wegfangmethode (Meissner et al. 2015) zeigte sich, dass in einer Population von *Euroleon nostras* Fourcroy die Biomasse der Larven extrem verschieden ist. Sie reicht z. B. im Juni am selben Tage von 1,0 mg bis 144,8 mg (n=469). In dieser Zeit sind alle drei Larvenstadien vorhanden, aber ihre Biomasse variiert im Verhältnis 1:145.
Die Hypothese, dass dem ein individuell verschiedener Beutegewinn vorausgeht, wurde im Habitat Nossentiner-Schwinzer Heide (Mecklenburg-Vorpommern) geprüft. Die Daten lieferten zufällig ausgewählte Habitatflächen gleicher Größe und Orientierung. Anzahl und Größe der Fangtrichter und ihre Lage zueinander wurden fotografisch dokumentiert und nach Bearbeitung am PC mit einem Gitternetz unterlegt (Meissner et al. 2012). Orientiert am Verhalten von Waldameisen (*Formica rufa* L., *Formica polyctena* Först.) bei der Nahrungssuche liefen so über die Kreuzungspunkte der Gitterlinien bis zu 80 Modell-Ameisen auf individuell verschiedenen Wegen aus maximal vier Richtungen ein. Sie durchquerten die Habitatflächen oder gelangten in die Trichter, allerdings mit unterschiedlicher Häufigkeit, dies in Beziehung zur Lage der Trichter und zu ihrer Dimension. Wie sich zeigte, beeinflusst die Räuberdichte/Habitatfläche den Beutegewinn gesetzmäßig. Laborversuche und die Reduktion der Anzahl von Trichtern per Zufallsprogramm brachten vergleichbare Ergebnisse.

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Wie die Taxonomie von Borkenkäfern durch KI und Automatisierung unterstützt werden kann

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In den letzten Jahrzehnten haben immer größere Borkenkäferpopulationen zur Schädigung großer Waldflächen auf der Nordhalbkugel geführt. Aufgrund des Klimawandels und anderer Faktoren kommen ständig neue invasive Arten zu den bereits vorhandenen hinzu, was die Waldbewirtschaftung noch schwieriger macht. Die Klassifizierung von Borkenkäfern durch Taxonomen auf der Grundlage morphologischer Merkmale und DNA-Barcoding ist begrenzt und zeitaufwendig. Daher wird ein Verfahren zur automatisierten Klassifizierung verschiedener Borkenkäferarten entwickelt. In einem ersten Schritt werden standardisierte Bilder verschiedener Borkenkäfer mit einem Entomoskop aufgenommen – einem Open-Source-Mikroskop, das für die Bildgebung von Invertebraten entwickelt wurde. Diese Bilder werden dann verwendet, um ein neuronales Netz für die Klassifizierung verschiedener Arten von Borkenkäfern und Nicht-Borkenkäfern zu trainieren. Die Genauigkeit der Klassifizierung ist hoch >90%) und unabhängig von der Ausrichtung der Borkenkäfer, was eine Auswertung mit hohem

Durchsatz ermöglicht. Bei Bedarf kann der Klassifizierungsalgorithmus auf den DiversityScanner übertragen werden – ein automatisiertes System zum Sortieren spezifischer Proben (identifizierte Borkenkäfer oder unbekannte Objekte) auf eine 96er Mikrotiterlatte für weitere DNA-Barcoding-Analysen. Diese Informationen können sowohl zur Bestimmung der Häufigkeit von Borkenkäferarten als auch zur Entwicklung effektiverer Schädlingsbekämpfungsstrategien verwendet werden.

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The nematode community of *Ips typographus* during an ongoing outbreak

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The spruce bark beetle *Ips typographus* (L.) is a major forest pest in Europe. Rising temperatures and prolonged dry periods put its host, the Norway Spruce *Picea abies* (L.), under stress. This allows the beetles to attack healthy trees and proliferate rapidly leading to significant economic losses and ecological disturbances each year. The Southern Alps experienced rather low damage caused by *I. typographus* until 2018 when the storm Vaia hit the region. Heavy snowfalls and droughts in the following years led to a massive and ongoing bark beetle outbreak in South Tyrol and Eastern Tyrol. Natural antagonists that co-occur with the beetle are an important factor in controlling the beetle population. A variety of organisms including bacteria and fungi are associated with the spruce bark beetle. However, even if nematodes are described to be commonly associated with bark beetles, their diversity and role on the bark beetle are currently understudied. In our project, we study the nematode community of *I. typographus* during the current outbreak in South Tyrol by performing metabarcoding of whole beetles. We aimed to determine which nematode species are living on and within the beetle and to identify potential antagonists and symbionts. We used DNA from adult beetles that were collected in South Tyrol across several years and at two different altitudes. Two genes (18S, 28S) were amplified and sequenced with a metabarcoding approach. The comparison of sampling years and altitudes will allow us to characterize the core nematode community and determine its stability. As some nematode species might have negative consequences for the host a deeper understanding of the associated nematodes is important to understand their role in the outbreaking dynamics of *I. typographus*.

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Impact of temperature on the development of the pine bark beetle *Ips* acuminatus, its most common fungal associates, and their symbiotic relationship under a changing climate

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Bark beetles are among the most destructive forest insects worldwide, and climate change increases the predisposition of coniferous forests to bark beetle mass outbreaks. In addition, the rise in temperature affects the voltinism of bark beetles, as insects are ectothermic and many parts of their life cycle (e.g. development and reproduction) are directly dependent on the ambient temperature. The effects of rising ambient temperatures, extreme weather events (e.g. storms, heavy snowfall) and unfavorable precipitation distribution on the occurrence of bark beetles can be observed globally and will become even more important in the future.
Bark beetles are associated with a variety of microorganisms whose development is also strongly influenced by environmental conditions. Many of these microorganisms fulfill important functions and can have a positive, negative or neutral influence on the development of bark beetles. A particularly close symbiosis has developed between some representatives of blue stain fungi and bark beetles. Some blue stain fungi serve as an additional food source, help the bark beetles to overcome the host tree's defenses and influence the colonization behavior of the beetles by producing volatile organic compounds. Blue stain fungi benefit from this symbiosis by dispersing into new habitats and the special microclimatic conditions in the breeding systems, which provide an optimal environment for growth. So far, the effects of rising temperatures due to climate change on the symbioses between fungi and beetles have hardly been researched. In the long term, however, there could be a decoupling of the symbiosis and detrimental effects on the fitness of both symbiotic partners, especially in bark beetle species that have an obligate symbiosis with fungi.
The pine bark beetle *Ips acuminatus*, a significant pest in European pine-dominated forests is an intermediate form between bark and ambrosia beetles, and has a phloeomycetophagous lifestyle, i.e. it feeds not only on phloem but also on fungal structures. In order to assess the influence of changing environmental conditions on the symbiotic partners,

knowledge of the influence of temperature on *I*. *acuminatus* and its associated fungi is essential. This can be determined through laboratory experiments and the application of mathematical models. In this study, the total development time of an *I*. *acuminatus* generation was determined at different constant temperatures under controlled conditions. Linear and non-linear models were used to describe the relationship between temperature and development. Due to the close symbiosis between *I*. *acuminatus* and its associated blue stain fungi, the influence of temperature on the growth of the most common fungal species associated with *I*. *acuminatus* was analyzed in addition to the temperature-dependent development of the beetles. These findings provide a deeper understanding of how climate change may alter the dynamics of this economically and ecologically relevant bark beetle species.

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Tissue and life-stage specific gene expression dynamics in the drywood termite, *Incisitermes schwarzi* (Isoptera: Kalotermitidae)

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Termites are eusocial keystone insect species that feed on wood matter and plants to obtain cellular energy. Certain invasive wood-feeding isopteran termite pests such as *Coptotermes* (Rhinotermitidae), *Macrotermes*, *Odontotermes* and *Microtermes* species (Termitidae) have caused immense damage to eucalyptus forests in Malaysia, Australia, India, China and Africa, due to increased wood decomposition sensitivity to warming temperatures, leading to global economic losses. Traditional forest pest management strategies have failed to curb these termite infestations, thereby urgently calling for the deployment of novel methods. A detailed understanding of the termite adaptation and physiology at the molecular level shall aid in development of future management measures utilizing molecular tools such as RNA interference (RNAi). In this study, we have selected the drywood termite, *Incisitermes schwarzi*, (Isoptera: Kalotermitidae) to investigate how these specific termites survive during their voracious feeding on spruce and birch deadwood in a drywood habitat. To understand their wood digestion response and detoxification behavior of the natural toxins present in deadwood, we have conducted gene expression analysis in different life stages and different tissues. Differential gene expression (DGE) analysis across developmental stages and tissue types, have revealed multiple gene families related to wood detoxification, wood digestion, growth and development of the termites, their eusocial behavior, and, adaptation to biotic and abiotic stress causing agents. Further, to understand the RNAi susceptibility/resistance of the termites, we have identified RNAi machinery genes and explored their expression dynamics across the different life stages and tissues in the drywood termites. The differentially expressed genes identified through this study could help in improving our understanding of termite adaptation to their lignocellulosic habitats and could serve as excellent putative targets for RNAi-based termite management.

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Entwicklung automatisierter Pheromonfallen für die Überwachung von Schadinsekten und Quarantäneschädlingen (DiMoTrap)

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Die aktuellen Klimaänderungen begünstigen u.a. die massenhafte Vermehrung von forstschädlichen Schmetterlingsarten, wobei in betroffenen Wäldern enorme wirtschaftliche und ökologische Schäden entstehen können. Die Dauerüberwachung von Schadinsekten im Wald ist unerlässlich, um steigende Reproduktionsraten bei einer Massenvermehrung rechtzeitig zu erkennen und die betroffenen Waldflächen durch geeignete Gegenmaßnahmen vor größeren Schäden zu bewahren. Eine der effektivsten Methoden zur Überwachung von forstschädlichen Schmetterlingsarten basiert auf dem Einsatz von Pheromonfallen.
Die bisher eingesetzten Fallensysteme erschweren wesentlich die Reaktionsfähigkeit von Managementmaßnahmen während der Progradationsphase einer Massenvermehrung, da die zeitliche Datenauflösung bis zu mehreren Wochen beträgt. Herkömmliche Monitoringverfahren, die auf manuell betriebenen Pheromonfallen basieren, zeigen allerdings erhebliche Schwächen, insbesondere im Hinblick auf den erforderlichen Arbeits- und Kostenaufwand. Diese Systeme erfordern regelmäßige Kontrollen vor Ort und manuelle Auszählungen, was nicht nur zeit- und arbeitsintensiv ist, sondern auch die Effizienz und Flexibilität des Monitorings einschränkt. Darüber hinaus schwankt die Abgaberate der Pheromonköder während des Überwachungszeitraums, was die Fangzahlen ebenfalls stark

beeinflussen kann. Daraus ergibt sich ein deutliches Optimierungspotential, das durch den Einsatz moderner, automatisierter Fallensysteme besser genutzt werden könnte.
Das Ziel des von der Fachagentur für Nachwachsende Rohstoffe (FNR) geförderten Verbundvorhabens (Förderkennzeichen: 2220WK38A4) liegt in der Modernisierung etablierter Pheromonfallen durch innovative, technische Lösungen hin zu einem modular aufgebauten, digital steuerbaren und anwenderfreundlichen System. Das Fallensystem soll während der Flugzeiten der zu überwachenden Schmetterlingsarten in der Lage sein, die gewünschten Funktionen des Anlockens, Fangens und Zählens der Zielarten autark auszuführen („Automatisches Fallensystem“). Im Fokus der Entwicklung stehen Fallensysteme für die häufigsten forstschädlichen Schmetterlingsarten in Kiefern- (Forleule, Nonne, Kiefernspinner) und Eichenbeständen (Schwammspinner). Das Forschungsprojekt wird von der Nordwestdeutschen Forstlichen Versuchsanstalt (NW-FVA) in Zusammenarbeit mit dem Fraunhofer-Institut für Fabrikbetrieb und -automatisierung (IFF) durchgeführt. Im Zuge der technischen Entwicklungsarbeit wurden im Förderzeitraum in einem ersten Schritt wesentliche funktionelle Komponenten eines digitalen Pheromonfallensystems identifiziert. Die angestrebten Fallenfunktionen wurden daraufhin technisch-konstruktiv zu konkreten Versuchsmustern, welche mit den aktuell genutzten VARI-OTRAP-Trichterfallen kompatibel sind, umgesetzt. Die automatische Falle ist so aufgebaut, dass die gewünschten Funktionsmodule je nach Bedarf zusammengestellt werden können. Eine zentrale technische Herausforderung des Vorhabens liegt in der automatisierten Erfassung der Zielorganismen, um diese systemseitig von den Beifängen zu unterscheiden.
In einer angestrebten Folgeförderperiode steht die Umsetzung einer technisch optimierten Datenfernübertragung unter Berücksichtigung aktueller Praxisanforderungen im Vordergrund. Das Ziel liegt dabei in der automatisierten Übermittlung von plausibilisierten Monitoringdaten an die Waldbesitzenden bzw. an die Waldschutzmeldesysteme der Länder. Schließlich ist die Entwicklung eines Moduls zur automatischen Entleerung des Fallensystems vorgesehen, um die Notwendigkeit von Vor-Ort-Kontrollen der Fallenstandorte zu minimieren und die Lockwirkung der gefangenen Organismen auf Aasfresser zu reduzieren.

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Parasitization by a braconid wasp affects diapause induction and termination of its imperfect host *Leucoma salicis* (Lep.: Erebidae)

Zankl, T. & Schafellner, C.

Glyptapanteles porthetriae (Hym.: Braconidae) is a major natural enemy of the spongy moth, *Lymantria dispar* (Lep.: Erebidae). For overwintering, the endoparasitic wasp larvae depend on alternative host species that have not yet been identified. As a co-member of the subfamily Lymantriinae with similar habitats, the satin moth, *Leucoma salicis* (Lep.: Erebidae), was considered a promising overwintering host. However, laboratory experiments showed that *G. porthetriae* only develops successfully in a low proportion of *L. salicis* host individuals. Nevertheless, significant impacts on the hosts physiology were observed in individuals that did not allow successful emergence of the parasitoid. Here we describe the effects of parasitism on the initiation and termination of diapause in *L. salicis* larvae.
According to the literature, *L. salicis* larvae undergo a facultative diapause. Since the critical values for suppressing diapause are photoperiods above 18 hours daylight or constant temperatures around 30°C, this largely corresponds to an obligate diapause under natural conditions. In our study, we compared the prediapause and postdiapause development of *L. salicis* larvae under different photoperiods and the influence of parasitization by *G. porthetriae*.
While 40 individuals remained unparasitized, 50 *L. salicis* larvae (first premolt or first day of second instar) were offered to *G. porthetriae* females for oviposition using a fine brush. The larvae were then divided to 16 hours daylight (LD) or 12 hours (SD) daylight at constant 20°C. The insects were maintained in groups of five individuals, fed fresh poplar (*Populus nigra*) leaves, weighed regularly, and all molts were recorded. Respiratory activity was measured with a volumetric respirometer 9, 15, and 21 days after parasitization. At least eight individuals per group were measured at each time point. Diapause manifestation was considered to occur when no feeding or weight gain was observed for 21 days. Diapausing individuals were maintained at 5°C and 8 hours of daylight for 30 days. After cold exposure, all individuals were transferred to long day conditions at 20°C. They were weighed weekly and feeding activity was recorded based on the presence of feces and feeding damage to leaves.
Mature wasp larvae successfully emerged from one host individual at 16 hours daylight

and two individuals at 12 hours daylight, exclusively before the manifestation of diapause. At no time was a significant influence of photoperiod or parasitization on the respiratory activity observed. While photoperiod also had no effect on *L*. *salicis* weight gain, parasitized larvae were significantly heavier starting two weeks after parasitization, weighing 86% (LD) and 81% (SD) more than individuals of the corresponding control groups. While the manifestation of diapause began with the third instar in 98% of all unparasitized larvae, the onset was delayed in a high proportion of the parasitized individuals. In 42% of parasitized LD individuals and 22% of SD individuals, the manifestation of diapause shifted to the fourth instar. Three parasitized larvae (6%) developed into adult moths without any developmental delay.

After cold exposure, diapause termination occurred significantly earlier in parasitized individuals of both photoperiod regimes. While 31% (LD) and 25% (SD) of the parasitized individuals resumed feeding within four days, no feeding was observed in unparasitized larvae within the first two weeks. This difference is almost exclusively attributable to individuals that showed diapause manifestation in the fourth instar. The termination of diapause in third instars was very similar in parasitized and unparasitized individuals, and most individuals resumed feeding between three and four weeks after cold exposure.

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Sektion / Section
Global Change Entomology

Talks
sorted by category and main authors

Keynote
The evolution of plasticity during anthropogenic change: Cue-environment mismatches and diapause

Nielsen, M.

Adaptive plasticity relies on a variety of cues to predict the future environment in which the plastic trait must function. For example, seasonal plasticity often uses photoperiod to predict future seasonal environments and produce appropriate phenotypic responses, such as diapause. If anthropogenic changes, however, alter either the cue or the environment, this can create a mismatch between them. Previously adaptive plasticity can become maladaptive unless evolution can correct for these mismatches. Climate change and urbanization are two potential causes of these mismatches for seasonal plasticity. Both change temperature independently from photoperiod, so insects which use photoperiod as a cue for traits like diapause will produce the wrong response for the new seasonal cycle. To test if evolution can correct this mismatch, I conducted work on diapause in two species of butterflies which use photoperiod as a primary cue. For *Pararge aegeria*, I tested if the response to photoperiod has evolved over the last 35 years of climate change by recreating historic experiments on diapause induction. For *Pieris napi*, I tested for urban evolution of responses to photoperiod by conducting a common garden experiment comparing diapause induction of populations from urban and rural environments. Both studies found evidence for evolution of the plastic reaction norms, but not always in the same way, showing that the evolutionary impacts of anthropogenic change on seasonal plasticity will depend on the species' natural history and the details of anthropogenic change.

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Surviving the heat: The Heat Shock Response under natural conditions in two paper wasp species

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One of the most important environmental factors to small ectotherms like insects is ambient temperature. Because of this, mechanisms that allow an organism to cope with temperature extremes are of great importance. With climate change comes an increased significance of those coping mechanisms related to heat stress. One mechanism like this is the Heat Shock Response which aids in recovery from and resistance towards heat stress. The Heat Shock Response has been shown to be active in the primitively eusocial paper wasps (*Polistes* spp.) under artificially induced heat stress conditions. Paper wasps build open-faced combs, which leaves the brood exposed to environmental temperatures and dependent on thermoregulating behavior of the adults. We sought to determine whether the Heat Shock Response is only induced under the extreme thermal conditions used in laboratory experiments or if it plays a role in coping with daily fluctuating temperatures under natural conditions. To do this, we collected pupae and larvae from wild nests of two paper wasp species (*P. dominula* and *P. nimpha*) in the morning, when temperature conditions were cool, and in the afternoon, when ambient temperature had been at its maximum for a few hours. The samples were frozen immediately after collection, and then at a later point used for qPCR, where we measured the expression of three heat shock proteins (hsp70, hsp83, and hsc70). To be able to relate the expression results to microclimatic conditions, we measured the temperature at each nest, starting the day before the morning collection and ending after the afternoon collection. We found that of the three genes examined, hsp83 generally had the highest expression in both larvae and pupae while hsp70 had the lowest. In *P. dominula*, heat shock protein expression was found to vary based on time of day, with the expression being highest in the afternoon. The difference was not as clear in *P. nimpha*. Furthermore, we found that expression varied between life stages (larvae and pupae) and between certain nests, indicating the importance of genetic and microclimatic differences. We did not find a large upregulation of hsp70 expression in the afternoon, where the temperature was highest, which is characteristic for Heat Shock Response induction under laboratory conditions. This highlights the importance for studies under natural conditions, as conclusions drawn based upon laboratory studies may not be directly applicable in nature.

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Reciprocal Role of Two Trehalose Transporters in Aestivating Cabbage Stem Flea Beetle and their Possible Relevance in a Changing Climate

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The cabbage stem flea beetle (*Psylliodes chrysocephala*, CSFB) is a significant pest of winter oilseed rape crops across northern Europe. Adapted to cooler climates, adults undergo obligatory aestivation during the summer to protect themselves from heat and desiccation stress. However, rising summer temperatures driven by climate change could potentially alter the physiological processes underlying insect aestivation. Gaining insights into the molecular and physiological mechanisms of aestivation is therefore essential for predicting the impacts of climate change on economically significant agricultural pests like CSFB. Trehalose, the primary hemolymph sugar, has been linked to energy homeostasis and stress resilience, but its regulation and function during aestivation remain poorly understood. Here, we investigated the roles of two trehalose transporters, Tret-1 and Tret-2, in modulating trehalose dynamics across different adult stages in CSFB. Through spatio-temporal transcript profiling, we found that Tret-1 was predominantly expressed in the fat body, where it facilitates trehalose export to the hemolymph, whereas Tret-2 expression was higher in the Malpighian tubules, mediating trehalose uptake from the hemolymph. RNA interference experiments revealed that Tret-1 is involved in transporting trehalose from the fat body into the hemolymph, while Tret-2 works reciprocally to transport trehalose into the Malpighian tubules. The disruption of trehalose transportation resulted in excess glucose, glycogen, and triglyceride levels, mainly in pre-aestivation beetles. Furthermore, the knockdown of either trehalose transporter caused a compensatory increase in feeding activity in pre-aestivation beetles, while the knockdown of Tret-2 compromised resilience to heat stress. Our findings uncover the reciprocal functions of Tret-1 and Tret-2 in regulating trehalose distribution and maintaining metabolic stability during aestivation. These functions are likely to be increasingly important as climate change imposes harsher environmental conditions, making the study of their regulation and adaptation vital for predicting and managing pest survival.

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Climate warming drives range expansion in the pine processionary moth, *Thaumetopoea pityocampa*, (Lepidoptera, Notodontidae) in Austria

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Warming temperatures pave the way for forest pests to spread into new territories. The pine processionary moth (PPM) *Thaumetopoea pityocampa*, primarily native to the Mediterranean, demonstrates this phenomenon.
Recently, concerns have been raised about the potential occurrence of PPM in recreational areas beyond its native habitat. A mass outbreak at the Dobratsch mountain in Carinthia (Austria) in 2016/17 indicates that the moth expands north and to higher elevations. Further nests have been recorded in surrounding areas, such as the popular vacation spot Faakersee.
Late-instar larvae of PPM pose a threat to human and animal health, as its utricating hairs can cause severe allergic reactions. The unique biology of PPM is characterized by specific conditions: Larvae feed in the cold season and leave their nests at night, when night temperatures rise above 0°C and temperatures in the nest reached +9°C the previous day.
Based on a mechanistic model, we reconstructed hypothetical nest temperatures of various regions in Carinthia to calculate potential PPM feeding activity of past decades and estimate the moths' expansion range.
Our results show that feeding conditions of PPM were met at an increasing frequency from 1999 onwards, proving clear impacts of a warming climate. Additionally, we found that nests can maintain temperatures above 0°C despite ambient temperatures dropping below -12°C. Hence, PPM larvae can tackle cold stress more efficiently than previously assumed and thereby ensure colony survival despite low winter temperatures.
Taken together, climate warming likely aids PPM expansion towards northern habitats and we report various regions in Carinthia with suitable conditions for PPM establishment and spread. To contain defoliation of pine trees and the medical risk presented by its larvae, it is crucial to monitor range expansion of this forest pest.

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Which traits determine how social insects can cope with climate change, and in particular with desiccation?

Menzel F.; Huthmacher, S. & Abou, B.

Climate change is a challenge for all species, but which traits determine whether a species is a winner or a loser? Here, we provide results from a Biology Letters special issue that we edited, but also from own research. Generally, climate change seems to favour generalists over specialists. Studies also indicate differential effects depending on trophic level. All this will result in drastic alterations of community composition. A main problem of climate change is elevated desiccation risk. Hence, drought resistance becomes a vital trait. It is mediated by the cuticular hydrocarbon (CHC) layer, which acts as physical barrier against water loss. However, its waterproofing capacity depends on its phase behaviour, which changes with temperature. Insects can affect phase behaviour through altering CHC composition, e.g. during acclimation. Our studies indicate that *Myrmica* ants change CHC composition depending on climate regime, which results in a homeostatic maintenance of phase behaviour, and is linked to drought survival. However, not all species or even conspecific colonies can acclimate equally well. Such differences seem to be linked to species- or population-specific CHC profiles, which differ in temperature-dependent phase behaviour. Hence, depending on CHC profile, species may differ in their ability to cope with drought.

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Harnessing Genomics and Machine Learning to Uncover Diapause Mechanisms and Predict Outbreak Risks in *Ips typographus*

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Diapause–a genetically programmed suppression of development–is a critical adaptation that enables insects to synchronize their life cycles with seasonal changes. This mechanism enhances population fitness and resilience by increasing survival chances during harsh periods. In *Ips typographus* (Curculionidae: Scolytinae), the Eurasian spruce bark beetle, facultative and obligate diapause strategies show varying geographic distribution, influencing voltinism, population dynamics, and outbreak propensity. Under climate change with milder winters, selection on facultative diapause and multivoltinism might be relaxed, promoting an increased reproductive output in many insect populations. This will likely lead to a higher prevalence of facultative diapausing beetles, particularly in populations traditionally dominated by obligate diapause and hence univoltinism. Understanding the genetic mechanisms underpinning diapause and its ecological drivers is therefore vital for predicting and mitigating outbreak risks. This study aims to investigate the genetic architecture underlying facultative and obligate diapause phenotypes and explore their geographic distribution and ecological significance in *I. typographus*.
We employed double-digest restriction site-associated DNA sequencing (ddRADSeq) to compare univoltine versus polyvoltine populations. Individuals with well-defined ecophysiological traits were reared under controlled photoperiod and temperature conditions to distinguish diapause phenotypes. Genome-wide association studies (GWAS) and supervised machine learning (ML) approaches were used to identify and rank single nucleotide polymorphisms (SNPs) associated with diapause traits. Population-specific ratios of diapause and non-diapause phenotypes in wild populations were then used to characterize outbreak risks across diverse environmental gradients.
Our analyses revealed significant geographic variation in diapause phenotypes. Obligate diapause predominated in univoltine northern populations, whereas facultative diapause was more common in multivoltine central populations. GWAS and ML approaches identified key SNPs linked to diapause phenotypes, providing genetic markers with predictive value for diapause in wild populations.
This study advances our understanding of the genetic and ecological mechanisms governing diapause evolution in *I. typographus* and highlights its adaptive significance in a changing climate. By integrating genomic and ecological data, we provide novel insights into pest dynamics and the potential for future outbreak predictions. The identified genetic markers represent valuable tools for monitoring population status and informing forest management strategies aimed at mitigating climate-driven risks.

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Interactions between land-use change and climate warming drive long-term wild bee declines

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Long-term data on species dynamics are scarce, limiting our understanding of biodiversity changes. We analysed over 17,500 museum records of 342 wild bee species collected between 1910 and 2021 at eight sites. Linking temporal distributions to land-use and climatic data, we show that continuous species turnover has reduced diversity over time. Early 20th-century landscape alterations primarily drove local extinctions of habitat-specialist species, initiating declines before global warming began. Subsequent climate warming has exacerbated these losses by reducing habitat suitability for already fragmented populations. While rising temperatures facilitate the immigration of thermophilic generalist species, land-use changes hinder this process; immigration would be faster in less altered landscapes. Habitat generalists with broad climatic niches show greater resilience, contributing to the observed species turnover and functional homogenization as their proportion increases. Climatic traits strongly influence species turnover, and the combined impacts of warming and land-use change further reduce species richness and functional diversity. Improving habitat connectivity and quality can enhance resilience to climate change, providing a clear target for conservation and policy.

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The range expansion of the Southern Small White butterfly *Pieris mannii*–A case of cryptic biodiversity loss due to urbanization

Wiemers, Martin; Blattner, L.A.; Kulanek, D.; Ruffener, S.; Ziegler, H.; Wymann, H.-P.; Michalik, P. & Berner, D.

Human-induced environmental change and globalization facilitate biological invasions, which can lead to the displacement of native species by non-native ones. Analogously, biodiversity loss may occur within species when habitat modifications facilitate the expansion of a specific population's range, leading to genetic admixture with native local populations. We demonstrate such intraspecific loss in population-level diversity in the Southern Small White (*Pieris mannii*), an originally sedentary butterfly that recently expanded its range across Central Europe due to urbanization. Using genome-wide markers from historical museum specimens and contemporary samples, we identify a distinct population initiating this expansion and reveal the genetic homogenization of native local populations by admixture with the expansive one. Our study illustrates how human-made environmental change can simultaneously benefit a species by permitting range expansion and drive cryptic biodiversity loss through the genetic homogenization of conspecific populations.

Blattner, L.A.; Kulanek, D.; Ruffener, S.; Ziegler, H.; Wymann, H.-P.; Wiemers, M.; Michalik, P. & Berner, D. (2024): Urbanization-associated range expansion genetically homogenizes a butterfly species. – Current Biology, 34(19), 4589–4595.e4.

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Hidden Impact of Drought: Tritrophic Dynamics in the Sugar Beet–Aphid–Parasitoid System

Rahman, S.; Vosteen, I. & Rostás, M.

Climate change leads to more frequent droughts and thus to abiotic stress in crops. Consequently, drought stress may alter tritrophic interactions in agroecosystems by changing bottom-up and top-down effects on herbivorous insects. However, how drought influences tritrophic systems remains poorly understood. This study explores the effects of two drought intensities on the sugar beet (*Beta vulgaris*)–black bean aphid (*Aphis fabae*)–parasitoid (*Aphidius colemani*) system, focusing on trophic-level performance shifts and herbivore-induced plant volatile (HIPV)-mediated parasitoid attraction. Experiments on drought-stressed sugar beet revealed that *Aphis fabae* benefitted from severe drought conditions, with faster development and higher reproduction rates in the first generation. However, over multiple generations, aphid population dynamics shifted, with initial increases on severe drought-stressed plants transitioning to significantly higher growth on moderately drought-stressed plants by the third generation. In severe drought conditions, aphid body length was significantly reduced. Primary metabolome analysis revealed that drought increased the concentrations of amino acids, organic acids, fatty acids, and sugar metabolites in the plants. Drought-stressed plants emitted significantly fewer HIPVs, leading to diminished attraction of *A. colemani* to aphid-infested plants. Parasitoid performance further declined, as evidenced by lower emergence rates, smaller body sizes, and fewer female progeny on drought-stressed plants. These combined effects may weaken

top-down regulation, promoting aphid outbreaks under drought conditions and exacerbating stress on sugar beet plants. Our findings underscore the complexity of drought-mediated multitrophic interactions, emphasizing the need to evaluate HIPV-mediated parasitoid attraction alongside primary metabolite-driven aphid responses to understand the interplay of abiotic and biotic stresses in crops.

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Sektion Biotremologie & Kommunikation bei Insekten / Section Insect Biotremology & Communication

Talks

sorted by category and main authors

Keynote

Innovations and new Terminology in Biotremology

Mazzoni, V.

In a world dominated by visual and chemical communication, vibrational signals transmitted through substrates represent a largely hidden yet fundamental mode of interaction in the living world. Biotremology, the emerging discipline that studies these mechanical signals, has revealed how insects, plants, and other organisms rely on vibrations to communicate, coordinate behaviors, and respond to environmental cues. Despite their ecological significance, vibrational signals have lacked a standardized terminology comparable to that used in chemical ecology. To address this gap, we propose a novel classification system, introducing terms such as ferodones and allelodones to describe vibrational intraspecific and interspecific interactions in a way analogous to pheromones and allelochemicals. This conceptual advancement lays the groundwork for interdisciplinary research and innovation, particularly in sustainable pest management.
By integrating vibrational and chemical signaling, we have developed innovative applications such as bimodal traps that combine pheromones with vibrational cues to enhance insect capture rates, and vibrational mating disruption techniques that reduce pest reproduction without pesticides. Beyond agriculture, vibrational ecology holds promise for monitoring biodiversity and detecting ecosystem stress by analyzing environmental vibrational patterns, collectively referred to as 'vibroscape'. The convergence of biotremology and chemical ecology represents a paradigm shift, offering novel tools for precision agriculture, conservation, and environmental monitoring. Establishing a shared scientific language for these multimodal interactions is crucial for fostering collaboration across disciplines and addressing global challenges related to climate change, food security, and biodiversity conservation. Furthermore, it facilitates dialogue with stakeholders, policymakers, and the general public, promoting greater interest in biotremology, enhancing access to public funding, and opening new opportunities for collaboration with the private sector.

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Chatter in the crypt–Insights into communication in burying beetles

Conrad, T.; Akassou, I.; Mangold, S. & Steiger, S.

Acoustic and vibrational signaling play a crucial role in behaviors such as mating, defense, and parental care–key aspects of cooperative behavior. Burying beetles, renowned for their elaborate biparental care and basic family structures, are valuable model organisms in behavioural ecology. Although it has been known since Darwin that both parents stridulate, the function of these signals remains unclear.
In this study, we investigated the role of stridulatory signals during family life across several burying beetle species. By recording biparental and uniparental parents throughout brood care, we tracked their stridulation activity and analyzed signal parameters. Additionally, we examined how offspring performance is affected in silenced parental pairs.
Our findings reveal that stridulation activity increases significantly after larval hatching, with no differences between uniparental and biparental contexts, indicating that post-hatching communication is primarily directed toward offspring. Importantly, offspring performance, including survival and weight gain, is strongly influenced by the parents' ability to communicate via stridulations. Through cross-over experiments, we were able to show that parental care differs between silenced and non-silenced parents.
These findings provide evidence for complex parent-offspring communication, previously thought to be exclusive to vertebrates, highlighting its critical role in offspring development and survival.

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What can beetle larvae tell us about soil greenhouse gas fluxes? Stridulation estimators as proxis for carbon cycle models

Görres, C.-M.

The diverse insect fauna in soils contributes directly and indirectly to greenhouse gas (GHG) emissions via their respiratory and metabolic activities, and their impacts on physical, chemical and biological soil properties. It has the potential to substantially influence the spatial and temporal variability of soil greenhouse gas (GHG) sinks and sources. However, the overall effect of soil-inhabiting insects on soil GHG fluxes still remains poorly quantified and studies have been limited to only a few regions and species, e.g. some soil-inhabiting larvae of the Scarabaeidae family. Two huge barriers preventing the quantification of soil faunal GHG emissions is the lack of suitable non-invasive methods for spatial and temporal soil fauna monitoring and a lack of ecological knowledge on species groups, especially at the larval stage. In this presentation, I will make the case that collaborations of GHG flux researchers and researchers studying insect biotremology and insect communication has a huge potential in further illuminating the “black box” soil and to open up a new research avenue by incorporating stridulation estimators as proxies into carbon cycle models. For example, we are testing a new fractal dimension-based data analysis method to automatically detect stridulations of root-feeding Scarabaeidae larvae in soil audio recordings and to calculate a semi-quantitative estimator of stridulation activity. It is the first data analysis method specifically targeting Scarabaeidae larvae stridulations in soils, enabling for the first time non-invasive species-specific monitoring, which is crucial for studying their GHG emissions at field scale. However, since the biodiversity crisis also affects belowground communities, time is of the essence for this new approach and interdisciplinary research: We might already be losing soil fauna species before we are able to understand their role in soil GHG flux dynamics and their communication patterns! Biotremology research has to go further into soils!

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Eavesdropping on psyllids: Vibrational signals of *Cacopsylla* species (Hemiptera: Psylloidea)

Kvinikadze, E. & Malenovský, I.

Insects communicate via different modalities, including olfactory, visual, tactile, acoustic and vibrational signals. While acoustic (air-borne sound) communication is well-known in groups such as crickets and cicadas, substrate-borne vibrational communication is much more widespread, observed in 18 of 26 orders of winged insects. Vibrational communication is most commonly associated with courtship, where the signals are used to locate a suitable mate. These signals are subject to various evolutionary constraints. Firstly, they must convey information about the identity of the species and at the same time be distinct from the signals of species that occur in the same environment. In sympatric species, the vibrational signals often show greater differences than in allopatric species. In addition, insects adapt their substrate-borne signals to the heterogeneous environments in which they communicate, such as complex plant structures. The phylogenetic signal in vibrational courtship calls remains a debated topic. These calls are important prezygotic barriers and affect mate choice and speciation, but their plasticity often leads to convergent evolution, especially in species inhabiting similar environments, as has been observed in bush crickets or lacewings. Psyllids (Hemiptera: Sternorrhyncha: Psylloidea) are a group of narrowly host-specific phytophagous insects that feed on phloem sap and are known to mate after vibrational duet-based courtship. Their signals are species- and sex-specific, with males actively searching for stationary, responding females. Several psyllid species are significant agricultural pests, and their vibrational signals hold promise for pest control strategies, including population density monitoring and disruption of mating behaviour through call playback. The production of vibrational signals in psyllids has long been attributed to stridulation, i.e. the rubbing of their wings against the thorax. However, our high-speed video camera recordings have recently shown that psyllids generate vibrations by simple wing-buzzing, i.e. tremulation and not by stridulation (Polajnar et al. 2024). Here we focus on vibrational signals in *Cacopsylla*, the largest genus of Psylloidea with 465 described species worldwide, which also includes important pests of fruit trees, but of which vibrational signals have only been recorded in 13 species. We were able to record the male calls of six Central European *Cacopsylla* species: *C. crataegi*, *C. hippophaes*, *C. ledi*, *C.*

pruni, *C*. *pyricola*, and *C*. *pyrisuga*. All known male calls of *Cacopsylla* spp. have the same basic structure: a series of short „chirps“ followed by a single long „trill“, a pattern not observed in other psyllids. At the same time, these calls differ between species in many traits, such as the number and duration of chirps, the trend of prolongation of successive chirps within a signal, the repetition time of chirps, the trill duration, and the pulse (the most fundamental structural element of a signal) rate. The combination of conservative and species-specific characters in the signals and the sympatric occurrence of closely related monophagous species on the same or different host plants makes *Cacopsylla* spp. an excellent model for studying the evolution of vibrational behaviour in both phylogenetic and ecological contexts. Investigating these relationships and testing the associated hypotheses will be the focus of our future research.

Polajnar, J.; Kvinikadze, E.; Harley, A.W. & Malenovský, I. (2024): Wing buzzing as a mechanism for generating vibrational signals in psyllids (Hemiptera: Psylloidea). – Insect Science, 31, 1466–1476.

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Ecomorphology of vibration receptor organs in orthopteroid insects

Strauß, J.

In insects, vibration receptor organs show an intriguing diversity of structures and locations on the body plan. Across different insect taxa, they can occur on the body surface (such as sensory hairs) and as internal chordotonal organs. The chordotonal organs also show variation in their structural complexity including the number of sensilla, groups of sensilla within specific organs, and distinct organs in different locations of the body. This indicates complex physiological mechanisms involved in the detection and processing of vibrational stimuli. Sensory organs can be investigated physiologically for the neuroanatomy and functional morphology, and for the ecomorphology relating to ecological adaptations and different signalling behaviours. Ecomorphology generally addresses variations in the organismic structures for performances and adaptations in relation to their ecology.
The relevance of such morphological and neuroanatomical variation is here considered for their role in detecting substrate vibrations in orthopteroid insects. In most insects, the subgenual organ in the tibia is the vibration receptor organ with highest sensitivity to vibrational stimuli. In orthopteroid insects, the subgenual organ together with additional chordotonal organs forms the subgenual organ complex. Here, the different adaptations in the subgenual organ as a broadly tuned vibration receptor and the accessory organ, a low-frequency receptor organ, are discussed with respect to the habitats and communication systems. The subgenual organs shows a consistent morphology in most orthopteroid taxa, but variation in the number of sensilla. The organ is placed in the hemolymph channel, and detects substrate vibrations transferred internally through the hemolymph. The accessory organ is a small chordotonal organ located at the posterior side of the subgenual organ with a close position at the hypodermis. It likely detects mechanical stimuli transferred over the leg cuticle. The accessory organ was recently found in several taxa of Ensifera, including some taxa with intraspecific acoustic signalling. There is no obvious match for an increase of mechanosensory organs or the numbers of sensilla in a specific organ of the subgenual organ complex to signalling behaviours using substrate vibrations. However, the accessory organ always occurs with the subgenual organ and at least one further organ, indicating the differentiation of the sensory complex. For further taxa of Ensifera where the accessory occurs occurs, vibrational signalling is identified (Stenopelmatidae, Anostostomatidae, Tettigoniidae, Rhaphidophoridae,). The presence of an elaborate sensory complex may also support behavioural studies in taxa with tympanal hearing organs, to reveal the importance of substrate vibrations in these groups. Ecomorphology of vibroreceptor organs thus links the physical parameters of signals, signalling distances, and substrate types to the adaptation of vibration receptor organs, and can provide valuable insights into vibrational behaviours of insects.

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Vibrational signals complement sound in the hearing Ensifera–Novel insights from model species

Stritih-Peljhan, N.; Žunič-Kosi, A.; Cillov, A. & Stumpner, A.

Communication by airborne sound emitted through stridulation has long been a primary focus in the study of Ensifera (Orthoptera). Vibrational signals as by-products of such signalling have also been recognized and investigated in several species. However, vibrational signalling by additional mechanisms that may complement stridulation is also present across various Ensifera groups but received little attention in experimental research. Crickets (Gryllidae) and bushcri-

ckets (Tettigoniidae) are generally considered highly specialized acoustic signallers, and their vibrational signals are mostly regarded as a functional backup for sound or a reversal to substrate vibration in response to predators eavesdropping on airborne signals. However, given the widespread presence of vibrational behaviours across Ensifera and their presumed ancestral condition relative to acoustic signalling, they may be much more prevalent than currently recognised. Here, we confirm that hypothesis with two behavioural case studies: one cricket and one bushcricket species, both used as models for acoustic communication. Our research uncovered vibrational signals that were unnoticed during decades of acoustic studies. In the house cricket, Acheta domesticus, we revealed vibrational signals produced by males during close-range courtship by swinging the body and drumming the legs on the substrate, in synchrony with stridulation. The resulting complex signal has the potential to mediate much more honest information about male quality then stridulation alone and may explain current ambiguities about the role of the courtship song in this species. Furthermore, in *Acistrura nigrovitatta*, a Phaneropterinae bushcricket, we found body tremulation signals that complement sound in both sexes, playing a role in both pair formation and lengthy courtship. As in crickets, their vibrational movements are hardly visible to an observer but produce substrate signals with amplitudes exceeding those induced by stridulation by an order of magnitude. Our results prompt a re-evaluation of communication in hearing Ensifera, challenging the general perception that sound is often the only non-contact mechanical signal in their sexual behaviour.

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Towards biological pest management: Analysis of vibrational signaling of *Pentastiridius leporinus*

Therhaag, E. & Gross, J.

About 200,000 insect species are estimated to use vibrational signals as a means of communication. The presented study focuses on the pattern of vibrational signals of the mating behavior of the planthopper *Pentastiridius leporinus*. *Pentastiridius leporinus* is known as a vector of two bacterial plant pathogens '*Candidatus* Phytoplasma solani' and '*Candidatus* Arsenophonus phytopathogenicus'. In Germany, affected crops are mainly sugar beet and potato, where infections lead to substantial losses. Recently, also infections in vegetables, i.e. onion, carrots or red beet, have been reported. Playing the right vibration pattern in the field would present a means of biological control to disrupt the mating of the vector, and thus could lead to a lower population.

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Sektion Schädlingsbekämpfung im Pflanzen- und Vorratsschutz / Section Insect Control in Plants and Stored Products

Talks

sorted by category and main authors

Keynote

Multiple approaches to pest control in fruit crops; plugging the gap of pesticide withdrawals

Fountain, M.T.

The fruit industry is entering a new era of fruit growing, with a continual need for research and development in the sector to address challenges such as 1) reduced availability of approved Plant Protection Products causing resurgence of pests and diseases not previously a major threat, 2) increasing consumer concern about residues on food, 3) pests and diseases overcoming resistant varieties/rootstocks and developing resistance to PPPs, 4) consequences of climate change, 5) increasing risk from alien pests and diseases, and 6) pressure to achieve Net Zero emissions and reduce the carbon footprint.
This talk will focus on the development of a novel semiochemical approach to control mirid bugs in fruit crops. The strategy includes attraction of mirids with the use of sex pheromones and plant volatile organic compounds–the Pull; and an insect produced compound which deters mirids feeding and damaging fruit–the Push. Combined, these create a Push-Pull approach that reduces feeding damage to the crop. The second topic will cover the year-round control of the invasive fruit pest, *Drosophila suzukii*. This insect lays eggs in soft and stone fruit and is difficult to control through conventional methods. However, combing approaches such at biocontrol, exclusion, sterile insect technique and bait sprays and help keep economic damage to an acceptable level.
It is increasing important that future pest control strategies work to defend crops all year round and target all life stages of the pest where possible.
All future strategies for controlling key pests and diseases of fruit crops should minimise environmental impact, protecting soil, air and water and aim to recover biodiversity, and futureproof pest and disease control through the minimisation of resistance.

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A case study on the potential of the earwig (*Forficula auricularia* L.) as biocontrol agent in pome fruits

Bischoff, R.

Earwigs are omnivorous insects that can be important biocontrol agents in permanent crops such as pome fruits, but their feeding habits can also make them important pests in soft-skinned stone fruits, for example. We investigated the management and potential of earwigs in apples and pears in a series of trials to understand their use as biocontrol agents. Our trials have shown that earwigs can be a viable alternative to chemical pesticides for the control of the woolly apple aphid and pear psylla. The provision of earwig shelters also reduced earwig faeces on fruit, a common complaint from growers about the use of this animal. A mark-recapture experiment showed that earwigs exhibit intermediate mobility, which is important if earwigs are to be released to colonise orchards with low earwig populations. Taken together, these studies show how a common native insect can be managed and integrated into pest management systems, helping to further reduce reliance on chemical pesticides.

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Modellierung der Populationsdynamik von Lepidopteren mit dem Tool „PhenoLogit“

Briem, F.; Bauer, S.; Schieler, M.; Schmitt, J.; Winkler, A. & Kleinhenz, B.

Die Prognose des räumlichen und zeitlichen Auftretens von Insekten in der Schädlingsbekämpfung einerseits und im Naturschutz andererseits ist eine große Herausforderung. Prognosemodelle und Entscheidungshilfesysteme (EHS) stellen in diesem Kontext effektive Instrumente dar, um Entscheidungen bei der Planung von Maßnahmen zur Bekämpfung oder Regulierung einzelner Schadinsekten bzw. zum Schutz von seltenen Arten zu unterstützen.
Die bei der Zentralstelle der Länder für EDV-gestützte Entscheidungshilfen und Programme im Pflanzenschutz (ZEPP) entwickelten und durch ISIP e.V. online bereitgestellten EHS ermöglichen es der landwirtschaftlichen Praxis, die Entwicklung vulnerabler Stadien der Insekten zu prognostizieren und chemische oder ökologische Pflanzenschutzmaßnahmen zu terminieren. Dadurch können unwirksame Behandlungen vermieden und der Einsatz von Insektiziden auf das notwendige Maß begrenzt werden. Ebenso ist es möglich Nützlinge effizienter einzusetzen oder Neben-

effekte auf schützenswerte Arten zu reduzieren.
Im Rahmen des Verbundvorhabens EntoProg (Entwicklung digitaler Prognosemodelle und Entscheidungshilfen im Pflanzenschutz zur Abschätzung des Befalls von Schadinsekten in Raps, Zuckerrübe und Mais) wird der Maiszünsler, *Ostrinia nubilalis*, als weltweit bedeutendster Schädling im Maisanbau modelliert.
Um berechnen zu können, ab wann und wie lange sich Individuen von *O. nubilalis* in einem bekämpfbaren Entwicklungsstadium befinden und der Einsatz von Nützlingen, wie z.B. *Trichogramma brassicae*, möglichst effektiv ist, wird der bei der ZEPP entwickelte Insektenmodellbaukasten „PhenoLogit“ verwendet. Durch diesen Algorithmus ist es möglich, das Befallsrisiko zu prognostizieren. Er basiert auf Temperatursummenberechnungen aktueller Wetterdaten und den spezifischen Kardinalwerten eines Entwicklungsstadiums von *O. nubilalis*. Durch die Verknüpfung verschiedener logistischer Funktionen kann sowohl das Populationswachstum, als auch der prozentuale Anteil eines jeden Stadiums von *O. nubilalis* an dessen Gesamtpopulation täglich berechnet werden. Das Modell wurde mit unabhängigen Daten validiert.
Der Algorithmus ist für viele Insektenarten nutzbar. Neben *O. nubilalis* wurde er bei der ZEPP bereits erfolgreich für weitere Lepidopteren wie bspw. den Apfelwickler, *Cydia pomonella*, den Fruchtschalenwickler, *Adoxophyes orana*, und den Erbsenwickler, *Cydia nigricana*, verwendet.
Neben der Prognose des Auftretens von Schadinsekten können EHS auch für den Erhalt schützenswerter Arten sinnvoll eingesetzt werden. So wird an der ZEPP aktuell ein EHS zum Schutz des Mosel-Apollofalters, *Parnassius apollo* ssp. *vinningensis*, mit dem Ziel entwickelt, während des Auftretens der vulnerablen Stadien schädigende Pflanzenschutzmaßnahmen zu vermeiden.

Die Förderung von EntoProg erfolgt aus Mitteln des Bundesministeriums für Ernährung und Landwirtschaft (BMEL) aufgrund eines Beschlusses des deutschen Bundestages. Die Projektträgerschaft erfolgt über die Bundesanstalt für Landwirtschaft und Ernährung (BLE) im Rahmen des Programms zur Innovationsförderung, Förderkennzeichen: 2821ABS030.

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Investigation of uncharacterized small RNA associated with summer diapause in the cabbage stem flea beetle

Cedden, D.; Güney, G.; Rostás, M. & Scholten, S.

Diapause is a dormancy state that enables insects to endure adverse seasonal conditions and involves complex gene regulatory mechanisms, many of which remain poorly understood. Small RNAs, including microRNAs (miRNAs), Piwi-interacting RNAs (piRNAs), and other non-coding RNA fragments, play critical roles in regulating gene expression and defending against viruses and transposons. In this study, we investigated the expression of small RNAs during summer diapause (aestivation), characterized by metabolic suppression and resilience to high temperatures, in the cabbage stem flea beetle (*Psylliodes chrysocephala*). Our focus was on small RNAs that had not been characterized in previous studies, which primarily examined dsRNA-derived siRNAs and endogenous miRNAs, which was shown to regulate summer diapause in this species. To achieve this, we isolated RNA-induced silencing complexes (RISC) and sequenced RISC-bound small RNAs. We then compared the expression profiles of RISC-bound small RNAs between aestivating beetles and other adult stages. We identified 26 RISC-bound small RNAs longer than typical miRNAs >24 nt) that were differentially expressed in aestivating beetles. Notably, these differentially expressed small RNAs included a potential spliceosome U1 fragment. Interestingly, these expression changes were observed only when comparing summer diapause with two non-diapausing adult stages and not between the two non-diapausing stages, suggesting these changes are specific to summer diapause. This study provides a preliminary step toward understanding the potential role of previously uncharacterized small RNAs in summer diapause.

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Optimizing dsRNA sequences for RNAi-based pest control with the dsRIP Web-Platform

Cedden, D.; Güney, G.; Rostás, M. & Bucher, G.

RNA interference (RNAi) is a tool for studying gene function and has emerged as a promising eco-friendly alternative to chemical pesticides. RNAi relies on delivering double-stranded RNA (dsRNA), which is processed into small interfering RNA (siRNA) to silence genes. However, so far, knowledge and tools for optimizing the dsRNA sequences for maximum efficacy are based on human data, which might not be optimal for insects and pest control. Here, we systematically tested different siRNA sequences in the red flour beetle *Tribolium castaneum* to identify se-

quence features that correlated with high efficacy using pest control as study case. Thermodynamic asymmetry, the absence of secondary structures, and Adenine at the 10th position in antisense siRNA were most predictive of insecticidal efficacy. Interestingly, we also found that in contrast to results from human data, high, rather than low GC content from the 9th to 14th nucleotides of antisense was associated with high efficacy. Consideration of these features for the design of insecticidal dsRNAs targeting essential genes in three insect species improved the efficacy of the treatment. The improvement was associated with a higher ratio of the antisense, rather than sense, siRNA strand bound to the RNA-induced silencing complex. Finally, we developed a web-platform named dsRIP (https://dsrip.uni-goettingen.de), which offers tools for optimizing dsRNA sequences, identifying effective RNAi target genes for pest control, and minimizing risk to non-target species. The identified sequence features and the dsRIP web-platform allow optimizing dsRNA sequences for both application of RNAi for pest control and research.

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Stored product insects outside storages in German fields–Climate induced or long standing?

Fürstenau, B. & Albrecht, C.

In Germany, little or no detailed data are available on the occurrence and distribution of stored product insect pests and the damage they cause to stored plant products. Not only endemic or established species, but also new (non-endemic) ones that migrate naturally or are introduced by trade and tourism pose a major threat. In addition, as the climate warms, heat-loving stored product pest species may move further north. The rice weevil *Sitophilus oryzae*, the maize weevil *S. zeamais*, the lesser grain borer *Rhyzopertha dominica* or the Angoumois grain moth *Sitotroga cerealella* are potential candidates to become increasingly established in Germany.
In addition, there will be a shift towards optimum development conditions for stored product insects due to higher mean annual temperatures. As a result, there is a risk that they may survive in the field, build up wild populations and infest grain already ripening in the field (and from there move into storage), as is common in tropical and subtropical countries. Successful early detection of storage pests must therefore start in the field, allowing targeted (counter-) measures to be taken before they can spread and infest neighboring storage facilities, and represents a future and important way of stored product protection.
The AVoiD project (Abwehr von Vorratsschädlingen in Deutschland), funded by the Federal Ministry of Food and Agriculture (BMEL) as part of the Immediate Climate Protection Programme 2022, investigates environmentally friendly strategies for the prevention and early detection of pest infestations on stored plant products. In addition to the study of climate-optimised (hermetic) storage techniques, a Germany-wide monitoring of stored product insects inside storages, but especially outside in the field, was established, to collect data on the occurrence and spread of (new) pests and correlations with climatic and regional factors from 2023–2025. To this end, various commercially available trap systems with pheromones and attractants were set up at 11 grain storage/processing farms (five of which were organic) in Baden-Württemberg, Bavaria, Brandenburg, North Rhine-Westphalia, Saxony and Schleswig-Holstein. Funnel traps (for flying insects) and two types of ground traps (mainly for walking insects) were placed in the grain stores and in nearby grain fields.
During the first two years of the project (2023 and 2024), a large number of storage pests of different species were caught inside and outside the storage facilities. In 2023, more than 3000 specimens were counted, including 11 moth and 19 beetle species, all of which have already been described or established in Germany. In addition to the Indian meal moth Plodia interpunctella, the European grain moth *Nemapogon granella* and various *Ephestia* species (e.g. the Mediterranean flour moth *E. kuehniella*), large numbers >100 specimens) of the sawtoothed grain beetle *Oryzaephilus surinamensis* and, above all, the lesser grain borer *R. dominica* were recorded. In 2024, a similar range of species was trapped, but in some cases at much higher abundances. Most pests occurred indoors, but interestingly a few species, in particular *R. dominica*, were found in high numbers outdoors on almost all test sites. This beetle, originally native to the tropics and subtropics, is a thermophilic species that is now distributed worldwide. In Germany, it was previously known to be largely synanthropic in grain stores, and only isolated occurrences in the field have been described. However, it is known that *R. dominica* can reproduce in various fruits of native trees, so that the occurrence of wild populations in Germany and a connection between

them and the landscape structure is possible. Ultimately, a key question is whether the high abundance in the field observed in this study is a new, climate-related phenomenon or whether it has remained largely undetected due to a lack of research in the past.

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Deadly synergism: Effects of pesticide mixtures on the seed bug *Oncopeltus fasciatus*

Gamer, E.L.; Sedlmeier, J.E. &
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An alarming decline in insect diversity and abundance has been observed in recent years. In addition to climate change and intensification of agricultural practices, the use of pesticides is often cited as a major contributor to this decline. Conventional agriculture uses synthetic chemical pesticides to protect crops from fungal infections, weeds, and pests. Residues of these pesticides are widely distributed in nature, where they can come into contact with a wide range of non-target insects. Despite growing concern, little research has been done on the effects of pesticide mixtures on non-target insects.
Here, we investigated the effects of three different pesticides–the insecticide acetamiprid, the fungicide fluopyram, and the herbicide terbuthylazin–on the non-target insect *Oncopeltus fasciatus* (Dallas, 1852). Dose-response assays were conducted to evaluate the toxicity of the individual active ingredients and their combinations.
We found that the neonicotinoid acetamiprid is almost 500 times more toxic to *Oncopeltus fasciatus* (LD_{50} value 24 h after application= 16.47 ng/µl) than to the honeybee (*Apis mellifera*). Notably, the combined application of all three pesticides resulted in significantly higher toxicity compared to acetamiprid alone. This finding suggests that complex pesticide mixtures can result in synergistic toxicity effects on non-target insects.
Our study suggests that other non-target insect species may experience similar effects when exposed to combinations of different pesticide active ingredients. In the context of the ongoing biodiversity crisis, our findings underscore the critical need for further research into the combined effects of pesticides. Such research is essential for understanding the broader impacts of intensive agricultural practices and pesticide use on insect populations and biodiversity as a whole.

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Die Ausbreitungsfähigkeit von *Xylocoris flavipes* innerhalb verschiedener Lagergüter

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Xylocoris flavipes (Reuter) (Hemiptera: Anthocoridae), the warehouse pirate bug is an omnivorous predator that attacks many warehouse pests like moths and beetles. There for it is a good tool for pest management. One main indicator of effectiveness is the capability of the beneficials to enter and distribute into the substrates. *Xylocoris flavipes* is not able to fly so the focus of our trials was on the ability to enter and move into different kind of substrates. Three different kinds of kernels (Sunflower seeds, Cashews, Bird seed) were placed into a vertical tube system, divided into three sectors (0–54 cm, 54–108 cm, 108–162 cm) and 500 *X*. *flavipes* (Adults and fifth Instars) were released on the top. After seven days the presence of *X*. *flavipes* was documented in the different sectors. *X*. *flavipes* dispersed over all three sectors and also eggs and first Instars could be observed in the three depths. The results indicated that *X*. *flavipes* reaches depth about 160 cm. Egg deposition and the hatching of first Instars enhance the treatment and its effectiveness. Further trails are necessary to evaluate the maximum depth *X*. *flavipes* could reach.

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Monitoring of western flower thrips *Frankliniella occidentalis* with checkpot yellow sticky traps in verbena

Polreich, M. & Stukenberg, N.

Yellow sticky traps (YST) are used to monitor insect pests in ornamental crops in greenhouses. An automatic monitoring and data management system is being developed in a joint project funded by the Federal Office for Agriculture and Food. This is intended to enable the detection and evaluation of insect pests in potted ornamental crops in greenhouses with the help of mobile monitoring swarms that move with the crops. These monitoring swarms will consist of several plastic pots,

'Smart Checkpots', in which small YST (12.5 cm x 5 cm) are integrated together with digital image evaluation, climate sensors and a transmission function.
The effectiveness and informative value of monitoring the western flower thrips (WFT) *Frankliniella occidentalis* with YST in the checkpot design was investigated in greenhouse trials with verbena plants. The correlation between the thrips caught on the checkpot YST and the thrips density on the verbena plants, which is necessary for accurate and reliable thrips monitoring, was determined. Two trials were carried out in spring/summer 2023 and 2024 with 270 and 1010 verbena plants respectively. The assessments were carried out weekly in the first trial and twice a week in the second trial. The number of thrips was recorded using the tapping method and counting the thrips on the YST of the checkpots. A destructive method was carried out in the first trial, whereby the verbenas were cut off and the total number of thrips was counted in the laboratory. Leaf and flower damage was recorded in both trials using a damage scale.
The results show that the number of thrips caught on the YST of the checkpots correlated positively with the number of thrips on verbena. Leaf and flower damage were positively correlated with the thrips population density. The critical number of thrips on YST causing severe plant damage was determined. The sex ratio on the YST was also assessed. At low densities, most of the adult thrips were male. As the density of thrips within the greenhouse increased the proportion of females on the traps also increased by the end of our trial. This change in the sex ratio of adults may have important consequences with respect to the potential for thrips outbreaks and damage to greenhouse ornamental plants.
In conclusion, it can be stated that YST in checkpot design have the potential to be used as a monitoring tool to support decisions in plant protection.

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Evaluation of different insecticidal schedules against pod borers in pigeonpea at Pantnagar, Uttarakhand, India

Rawat, D. & Tiwari, R.

Pigeonpea, scientifically known as *Cajanus cajan* (Linnaeus) Millspaugh, is a widely cultivated pulse crop in India during the kharif season. It is commonly referred to as 'Red gram', 'Tur,' or 'Arhar'. The crop is attacked by more than 250 insect pests but the damage caused by *Helicoverpa armigera*, *Melanagromyza obtusa*, *Maruca vitrata*, and *Clavigralla gibbosa* results in major reduction to the grain yield. However, improved cultivation practices along with location specific integrated management approaches may result in enhancement of yield. A field experiment on different insecticidal schedules was conducted in pantnagar during two consecutive kharif crop seasons (from 2022 to 2024) to evaluate their efficacy against *Maruca vitrata* and *Helicoverpa armigera* on pigeon pea. The different insecticidal schedules were Btk 0.5% WP – Chlorantraniliprole 18.5 SC, Btk 0.5% WP – Flubendiamide 480 SC, NSKE 5% – Chlorantraniliprole 18.5 SC, NSKE 5% – Flubendiamide 480 SC, Indoxacarb 14.5 SC – Chlorantraniliprole 18.5 SC, Indoxacarb 14.5 SC – Flubendiamide 480 SC, Lambda Cyhalothrin 5 EC – Chlorantraniliprole 18.5 SC, Lambda Cyhalothrin 5 EC – Flubendiamide 480 SC, Untreated control. Among the different insecticidal schedules, the cumulative overall mean for two sprays showed the least larval population of *H. armigera* (1.39) per plant and Maruca vitrata (3.11) larvae per plant in treatment Indoxacarb 14.5 SC @ 60g a.i./ha – Chlorantraniliprole 18.5 SC @ 30 g a.i./ha in comparison to the highest larval population of 8.50 *Helicoverpa* larvae per plant and 15.06 *Maruca* larvae per plant in untreated control for the year 2022–2023. For the year 2023–2024, the cumulative overall mean for two sprays showed the least larval population of *H. armigera* (1.26) larvae per plant and least larval population of *Maruca vitrata* (3.04) per plant in the same treatment the highest larval population of 8.44 *Helicoverpa* larvae per plant and 14.93 *Maruca* larvae per plant in untreated control. During the two consecutive years, grain yield of 1229 kg/ha and 1320 kg/ha respectively was observed for the same treatment.

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Climate change effects on mealybug honeydew composition and natural enemy fitness

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Biological control agents are essential in sustainable agriculture, relying on plant-derived food sources as an indispensable diet component. In some crops, such as grapevine (*Vitis vinifera*), food sources like extrafloral

nectar, or plant guttation are often scarce. The mealybug *Planococcus ficus* (Hemiptera: Pseudococcidae), an important grapevine pest, secretes honeydew that becomes a primary carbohydrate source for natural enemies. However, the nutritional value of mealybug honeydew is highly variable and remains poorly understood. Climate change, for instance, can influence host plant quality, potentially triggering plant- and insect host-mediated bottom-up effects on honeydew feeders. To bridge this knowledge gap, we investigated the composition of *P. ficus* honeydew and its potential alterations under climate change. Honeydew was collected from mealybugs feeding on grapevines cultivated in climate chambers with ambient or elevated CO_2 concentrations (400 and 800 ppm, respectively) and ample or limited water availability (water potential: -0.27 to -2.04 MPa). Metabolite profiling of the honeydew was performed using gas chromatography coupled with-mass spectrometry. We also evaluated the biological effects of these different treatments on honeydew as a food source for *Anagyrus vladimiri* (Hymenoptera: Encyrtidae), a crucial natural enemy of *P. ficus*. Our results revealed that specific metabolites, such as raffinose, increased under water-limited conditions, whereas other sugars decreased under elevated CO_2 and were unaffected by water stress. These changes in food quality were reflected in the longevity and fecundity of *A. vladimiri* females. Our findings highlight that climate-driven changes in honeydew quality can have cascading effects on natural enemies, underscoring potential challenges for pest management strategies in vineyard ecosystems under future climate scenarios.

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Mealworm frass as bio-fertilizer: Its impact on the growth of maize plant and feeding of fall armyworm, *Spodoptera frugiperda* (J.E. Smith)

Ullah, M.I.; Sajid, E.; Arshad, M. & Adnan, M.

Frass and vermicompost have garnered attention as potential biofertilizers due to their nutrient-rich composition, including organic matter, and ability to enhance plant resilience in adverse environmental conditions while improving resistance to insect pests and diseases. This study investigated the effects of mealworm frass and vermicompost applications compared to conventional fertilizers on maize growth and infestation by *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae).
After one month, maize plants treated with mealworm frass exhibited a significant height increase, reaching 131.7 cm compared to 87.9 cm in control plants. The average number of unfolded leaves was highest in the mealworm frass treatment at 8.05 per plant. Total leaf count also increased, with 9.05 leaves per plant in mealworm frass-treated plants versus 6.7 leaves in the control group. The leaf length under mealworm frass treatment measured 44.6 cm, more than double the 24.5 cm observed in the control plants.
Moreover, feeding damage caused by *S. frugiperda* was significantly reduced in mealworm frass-treated plants, with leaf consumption dropping to 40.0 cm compared to 66.2 cm in control plants. Larval mortality was also notably higher in mealworm frass-treated plants, reaching 55.3%, compared to 48.8% in vermicompost-treated plants and just 15.4% in NPK fertilizer-treated plants.
These findings highlight the remarkable potential of mealworm frass as an effective, sustainable biofertilizer that enhances crop productivity and supports pest management strategies, offering a dual-benefit approach to integrated pest management in maize cultivation.

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Diversifying maize with undersown crops: biodiversity benefits at the expense of yield?

Wersebeckmann, V.; Höppner, F. &
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Diversification of cropping systems can be a promising strategy to mitigate the negative impacts of agricultural intensification. Diversification through multiple crops grown on the same field increases spatio-temporal crop diversity and may enhance biodiversity and agricultural productivity. Maize (*Zea mays* L.) is an economically important and profitable crop, but its productivity is associated with high environmental costs and low biodiversity. Undersowing maize may be a promising approach to diversifying maize. Undersowing can increase habitat structure and may support arthropods and associated pest control services. Flowering undersown species can provide additional food sources for pollinating insects. However, farmers' acceptance of undersown species in maize is low because its competition with maize can significantly reduce yields.

In two studies, we investigated how diversification of a highly productive maize system affects the relationship between biodiversity and ecosystem functions with yield and asked whether the biodiversity-yield trade-off can be balanced.

In a first study, we tested six different flowering and non-flowering undersown species (fescue, cress, clover, vetch, mallow, marigold) in maize to investigate their effects on biodiversity, ecosystem functions (EF) and yield compared to mono maize stands and mono undersown species. We recorded agronomic (plant development, yield) and biodiversity and EF indicators (pollinator individuals and visits, arthropod activity density, pest predation). Maize yields were 15 to 65% lower for undersown maize than for mono maize, depending on the undersown species. Tall undersown species (e.g. mallow) were highly competitive, inhibiting maize growth and thus reducing yields more strongly, whereas small-growing legumes and fescue were less competitive leading to lower yield reductions. Pollinators benefited from the increased flower availability of most undersown species, while results for arthropods and EF were mixed. There was a significant trade-off between pollinating insects and yield, while pest predation was stable across the observed yield gradient.

In a second study, we asked whether yield losses could be further reduced and benefits for biodiversity and EF maintained by adjusting the configuration and composition of undersown species in the field. On five locations, we randomly assigned four treatments with increasing share of an undersown clover mixture: mono maize (0%), headland (6%), strips (48%) and full field (100%) to each plot. We recorded agronomic (plant development, yield), biodiversity and EF indicators (arthropod activity-density, pest predation) in undersown and pure maize parts of each plot and calculated total indicator values for each treatment. Yield losses increased with the proportion of undersown area from headland (-8%) to strips (-12%) to full field (-15%) compared to mono maize. The effects on arthropods and pest predation were again contrasting. Rove beetle activity density and seed predation increased with higher share of undersowing, while ground beetle activity density decreased. Spider activity density and predation on fly pupae remained unaffected.

Taken these results together: there is no ‘one fits all’ solution for all target organisms. Pollinators benefitted strongly from flowering undersown species, but given the high yield trade-off other measures such as flower strips may be more effective. Still, small-growing legumes or grasses can favor predatory arthropods and associated services while causing little yield reduction, and reducing their total area within the field by sowing them only at the headland or in strips might be a further strategy to balance yield and increase farmers’ acceptance.

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Sektion Insekten-Mikroorganismen Interaktionen / Section Insect-Microorganism Interactions

Talks

sorted by category and main authors

Keynote

Host-microbiome interactions in the Anthropocene (stories from honey bees and bark beetles)

Kowallik, V.

In recent decades our environment has been experiencing drastic, human-made changes. The consequences, especially regarding insects, range from steady declines/extinctions of species on the one hand, to outbreaks/"invasions" on the other. As most insects live in intimate relationships with microbial symbionts, these biotic interactions are undoubtedly disturbed by anthropogenic change such as chemicals, habitat modification, or climate change. In this talk, I will look at some of these effects on microbial symbioses in honey bees and bark beetles, two systems that show rather contrasting responses to environmental change.
The microbiome of honey bees (*Apis mellifera*) is well defined, socially transmitted and experimentally tractable. Leveraging these facts, we tested whether a chemically perturbed microbiome, as well as associated effects on host phenotypes, are transmitted across adult worker "generations".
In aggressive bark beetles (such as *Ips typographus*), which are known for their increasing mass outbreaks, host-microbiome relationships are much less understood. I will present our current work on protective functions, symbiont mediated effects on beetle behavior, and our plans to investigate how the microbiome may be affected by climate change.

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Beneficial yeast associates of the ground nesting bee *Andrena vaga*: The key to oligolecty?

Gardein, H.; Erler, S.; Greil, H. & Yurkov, A.

To understand fundamental questions of the bee's biology and ecology, it is essential to gain knowledge about their associated (micro-)organisms. Currently, functional descriptions of bee-fungi-interactions of solitary bee species, particularly ground-nesting bees, are scarce; so far most studies were conducted with managed social bees and their bacterial associates. In our study, we characterise the yeast community composition associated with the oligolectic mining bee *Andrena vaga*. We examined seven matrices of the early nest stage, using both classical cultivation and ITS2 DNA-metabarcoding. Remarkably, the only cultivated yeast from all egg samples was *Triodiomyces crassus*, a smut-related dimorphic yeast species. It assimilates salicin and produces antimicrobial glycolipids, potentially used for pollen detoxification and brood cell disinfection. This suggests that yeast associates might be a key factor enabling oligolectic bees to specialise on toxic pollen sources. The ecology and functionality of other identified yeasts like *Starmerella bombicola* are discussed here. In accordance with recent research, our findings suggest that solitary bees can possess core microbiomes and provide initial indications of vertical symbiont transmission for solitary bees, a phenomenon previously documented only in social bees. Our study sheds light on to the critical role of associated microorganisms and may serve as the missing link to unravel the uncertainties regarding the origin of oligolecty.

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Potential impact of climate change on the transmission of ToLCNDV mediated by *Bemisia tabaci*

Ripamonti, M.; Eickermann, M.;
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Bemisia tabaci, a globally significant agricultural pest, transmits hundreds of plant viruses, including tomato leaf curl New Delhi virus (ToLCNDV), which has recently caused severe outbreaks in cucurbits in Europe. Its adaptability, high reproductive rate, and insecticide resistance make it a key threat to food security, with climate change further exacerbating its impact. Within the VIRTIGATION project, we investigated how projected future climate could affect the *B. tabaci*–ToLCNDV–zucchini system, focusing on virus acquisition and inoculation efficiency. To evaluate virus acquisition, *B. tabaci* adults were exposed to ToLCNDV-infected plants under two climate scenarios. Acquisition efficiency was tested across three acquisition access periods (AAP: 2, 24, and 48 hours). The results indicated a marked increase in virus acquisition efficiency under future climate conditions, with longer exposure periods amplifying this effect. In a second experiment, inoculation efficiency was assessed by placing infectious *B. tabaci* on healthy zucchini plants for varying inoculation

access periods (IAP: 2, 24, and 48 hours). The findings showed higher inoculation success under warmer conditions, highlighting the potential for climate change to acceleratvirus transmission. Overall, these experiments show that future climate scenarios may significantly enhance both virus acquisition and inoculation efficiencies in *B. tabaci*, suggesting more dynamic transmission of ToLCNDV. These findings underscore the importance of developing climate-resilient pest management strategies to address the increasing risks posed by *B. tabaci* and its associated viruses in evolving agricultural systems.

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Keep or lose? Evolutionary dynamics of obligate endosymbiosis in the psyllid genus *Cacopsylla*

Schuler, H.; Corretto, E.; Štarhová Serbina, L.; Dittmer, J. & Michalik, A.

Symbiotic relationships play a critical role in the nutrition of insects. Especially most hemipterans, evolved intimate associations with microbial symbionts that provide essential nutrients lacking in their unbalanced diets, such as plant sap. These symbionts, primarily bacteria, often reside in specialized host cells called bacteriocytes, forming an obligate association critical for the host's survival. The evolutionary history of the insect host is marked by frequent events of symbiont acquisition, replacement, and loss. While some groups retain ancient, highly co-evolved primary symbionts, others supplement or replace them with secondary symbionts, which may confer adaptive benefits such as resistance to environmental stressors or pathogens.
Psyllids are phloem-sucking hemipterans that maintain on obligate relationships with the primary symbiont *Carsonella*. Here, we present a genomic characterization of the endosymbiont community of *Cacopsylla* species. We show that *Cacopsylla* species are dependent not only on one but on two primary symbionts. While *Carsonella* is widespread among different psyllid species, highlighting a long-standing association with this symbiont, a novel endosymbiont '*Candidatus* Psyllophila symbiotica' appears to be present only in *Cacopsylla* species. Unlike co-primary endosymbionts in other insects, the genome of *Psyllophila* is almost as small as the one of *Carsonella*, suggesting an ancient co-obligate endosymbiosis rather than a recent association. However, the association with the additional partner is more dynamic as *Psyllophila* was replaced by a Sodalis-like bacterium in at least one case. We present the evolutionary history of several *Cacopsylla* species and their symbionts and discuss the gain and loss of symbionts within these lineages.

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The spread of the *Wolbachia* strain wCer2 in *Rhagoletis cerasi* in the Czech Republic

Stauch, J.; Fiaschi, L.; Schebeck, M.; Schuler, H.; Lecic, S. & Stauffer, C.

The bacterial endosymbiont *Wolbachia* has been used to control insect pests due to its ability to manipulate their reproductive biology. Therefore, knowledge of *Wolbachia* dynamics in natural populations is fundamental. The European cherry fruit fly, *Rhagoletis cerasi*, is infected with the *Wolbachia* strain wCer2, mainly present in southern and central European populations, which is currently spreading into wCer2-uninfected populations driven by high unidirectional cytoplasmic incompatibility. Previous fine-scale sampling of populations along a transect in the Czech Republic, named T2, showed a smooth decrease of wCer2 infection frequencies from south to north within a distance of less than 20 km.
In this study, we present results focusing on the samples from the "core area" of the T2 transect, as well as populations collected along a parallel transect 30 km west of the T2. Results from the T2 core area generally followed the clinal pattern observed previously but revealed fluctuations from low to high in wCer2 infection frequency over small distances. The wCer2 infection frequencies at the parallel transect followed a similar clinal pattern of decrease from the south to the north, however, less steep compared to T2. These discrepancies will be discussed in the light of environmental factors, long-distance dispersal and temporal effects.

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New kid on the block: Cytoplasmic incompatibility is not only induced by *Wolbachia*, but also by *Spiroplasma*

Steidle, J.L.M.; Pollmann,; M.; Reinisch, R.; von Berg, L.; Hasselmann, M. & Gottlieb, Y.

Many arthropods carry endosymbiotic bacteria which manipulate their hosts' reproduction to promote their own spread. One such manipulation strategy is cytoplasmic incompatibility (CI), which causes the failure of fertilization after mating between host males infected with specific bacteria and uninfected females, leading to the absence of diploid offspring. While

the most well-known CI inducer is the bacterium *Wolbachia*, CI has also been shown to be caused by *Candidatus* Cardinium hertigii, *Candidatus* Mesenet longicola, *Rickettsiella*, and *Rickettsia*. *Lariophagus distinguendus* (Hymenoptera: Chalcidoidea: Pteromalidae) is a parasitoid of coleopteran larvae. It has been shown to be a complex of at least three species which are separated by different reproductive barriers including bacterial-induced CI. Remarkably, *L*. *distinguendus* is not infected by *Wolbachia* or any other of the described CI-inducers. Instead, PCR screening of the available *L*. *distinguendus* strains detected *Spiroplasma* infections in all three members of the species complex. *Spiroplasma* is a widespread bacterium even infecting vertebrates and plants. So far, it is not known to act as CI inducer. We investigated the relationship of *Spiroplasma* within the *L*. *distinguendus* complex using MLST. *Spiroplasma* in all species seem to be identical, which suggests a single infection event in a common ancestor of the *L*. *distinguendus* species. Interestingly, two species do not exhibit CI despite being infected with *Spiroplasma*. Obviously, they are resistant. In summary, CI can not only be induced by *Wolbachia*, but also by other endosymbionts including *Spiroplasma*. It causes CI in one species of the parasitoid *L*. *distinguendus* but not in others and might have contributed to speciation in this group.

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Sektion Invasive Arthropoden / Section Invasive Arthropods

Talks

sorted by category and main authors

Keynote

The cicada *Pentastiridius leporinus* (Linné) as a vector of various pathogens in sugar beet and potatoes

Rostás, M.; Gross, J.; Balakrishnan, K.; Kais, B.; Bruno, P.; Rahman, S. & Koffi, D.

Pentastiridius leporinus, a planthopper belonging to the large family Cixiidae (Hemiptera: Fulgoromorpha), has emerged as a significant agricultural pest. Adults feed on phloem sap from leaves, while nymphs develop in the soil, feeding on the roots of host plants for several months. Crucially, this insect vectors two plant pathogens: the gamma-proteobacterium *Candidatus* Arsenophonus phytopathogenicus and the phytoplasma *Ca*. Phytoplasma solani. These pathogens are the causal agents of the diseases Syndrome “Basses Richesses” (SBR) and Stolbur, which have caused severe economic losses in sugar beet and potato crops in Germany and Switzerland in recent years. These impacts have been caused by the periodic mass invasions of adult *P*. *leporinus* into fields during summer and the continuous food supply for nymphs feeding on winter wheat as a crop that follows sugar beet in crop rotation. Despite being native to the Palaearctic region, the biology and ecology of this invasive planthopper remain poorly understood, and effective management strategies are lacking. With its range continuing to expand, developing sustainable control measures is critical. This presentation will provide a comprehensive overview of recent research on *P*. *leporinus*, including its biology, host plant preferences, chemical ecology, and the development of potential biological control and agronomic strategies.

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Der Japankäfer *Popillia japonica* in Bayern – Aktuelle Situation

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Der Japankäfer *Popillia japonica* (Scarabaeidae, Coleoptera) wird in der EU als prioritärer Schadorganismus geführt und ist meldepflichtig. Über internationale Transporte und Tourismus gab es mehrmals vereinzelte Einschleppungen, die aber zunächst keine Etablierung des Schädlings auf dem europäischen Festland zur Folge hatten. 2014 wurde der Japankäfer in Italien (Lombardei) und 2017 an der schweizerisch-italienischen Grenze durch Fallenfänge nachgewiesen. 2020 ist erstmals ein Befallsherd im Kanton Tessin in der Schweiz festgestellt worden. Diese Population versucht man seit 2021 durch Eindämmungsmaßnahmen wieder in den Griff zu bekommen, eine Tilgung erscheint nicht mehr möglich. Über LKW-Transporte und Fahrzeuge von heimkehrenden Touristen, die der Japankäfer als versteckter „Hitchhiker“ nutzt, war eine Ausbreitung in Richtung Norden vorhersehbar. Bereits im Sommer 2021 ist ein Käfer in Basel in wenigen Kilometern Entfernung zu Baden-Württemberg aufgetaucht und im November 2021 fiel ein Exemplar bei der Endreinigung einer Pheromonfalle in Freiburg auf. In Bayern wurden bereits seit 2019 vermeintliche Funde von Japankäfern dem Institut für Pflanzenschutz der Bayerischen Landesanstalt für Landwirtschaft (LfL), welches gleichzeitig der Amtliche Pflanzenschutzdienst Bayerns ist, gemeldet. Sie stellten sich in den meisten Fällen jedoch als der Gartenlaubkäfer *Phyllopertha horticola* heraus. Dieser stellt aufgrund seines ähnlichen Aussehens die häufigste Verwechslungsmöglichkeit dar. Als ein weiteres Exemplar unter mehreren Gartenlaubkäfern wurde auch der tatsächliche Erstfund eines Japankäfers 2018 im Raum Oberstdorf in Bayern durch einen Urlauber aus Nordrhein-Westfalen eingestuft. Als Japankäfer fiel er erst einem Bekannten, einem Bielefelder Entomologen, auf. In dessen Sammlung befindet sich auch das Belegexemplar. Die Nachmeldung des Fundes 2019 führte leider zu keinem konkreten Fundort. Im Rahmen des Nationalen Monitoringprogramms auf Quarantäneschaderreger wird in Bayern dem Japankäfer über Pheromonfallen gezielt nachgestellt. Die Fallen wurden an vielbefahrenen Straßen sowie Grenzübergängen nach Österreich und anderen prädestinierten Eintrittsstellen am Bodensee und in Richtung Baden-Württemberg platziert. In den Jahren von 2021 bis 2023 wurden keine Positivfunde gemacht. Im August 2024 konnte dann an zwei Standorten in der Nähe von Lindau je ein Männchen des Japankäfers nachgewiesen werden. Zwei weitere Männchen gingen fast zeitgleich in Kiefersfelden in Fallen. Als bei Ortsbegehungen auf einem Sportplatz in Kiefersfelden Fehlstellen im Rasen entdeckt wurden, lag der Verdacht nahe, dass sich bereits eine Freiland-Population entwickelt haben könnte. Bei Grabungen auf dem Sportplatz wurden auch Engerlinge unter der Grasnarbe gefunden. Es handelte sich dabei jedoch um Larven des Junikäfers *Am-*

phimallon solstitiale und des Rotbraunen Laubkäfers *Serica brunnea*. In beiden Fällen – Lindau und Kiefersfelden – wird deshalb noch von einzelnen Einschleppungen ausgegangen, entsprechende phytosanitäre Maßnahmen laufen weiter.

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Diversity and new records of Rhizoecidae (Hemiptera: Coccomorpha) in Germany

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The family Rhizoecidae (Hemiptera: Coccomorpha) comprises 226 species with a cosmopolitan distribution. Rhizoecid species are exclusively hypogeal, feeding on plant roots. At the genus level, their distribution is concentrated in tropical regions, primarily within the Neotropics and Oriental areas. German botanical gardens, which regularly import plants from diverse regions worldwide to enhance or renew their collections, inadvertently facilitate the spread of non-native scale insects. This presents potential phytosanitary risks to local vegetation.
Currently, six Rhizoecidae species from two genera are recorded in Germany: *Rhizoecus albidus* Goux, *R. cacticans* (Hambleton), *R. franconiae* Schmutterer, *Ripersiella caesii* (Schmutterer), *Ri. halophila* (Hardy), and *Ri. hibisci* (Kawai & Takagi). To monitor changes in Rhizoecidae diversity within the country, 39 samples were collected from potted plants in the botanical gardens of Berlin, Bonn, Frankfurt, Hamburg, and Munich. Species identifications were performed using morphological analysis of microscope slide preparations and molecular data from the COI and 28S DNA regions.
The samples corresponded to 39 plant species, including 19 species of *Pelargonium* (Geraniaceae), seven species of *Begonia* (Begoniaceae), two species each of *Aphelandra* (Acanthaceae) and *Ruellia* (Acanthaceae), and one species from the genera *Balanites* (Zygophyllaceae), *Brachyglottis* (Asteraceae), *Ceratozamia*, and *Lepidozamia* (Zamiaceae), *Dalbergia* (Fabaceae), *Erythroxylum* (Erythroxylaceae), *Morinda* (Rubiaceae), *Salvadora* (Salvadoraceae), and *Salvia* (Lamiaceae).
Seven scale insect species were identified: *Geococcus coffeae* Green, 1933; *Rhizoecus arabicus* Hambleton, 1976; *R. cacticans*; *R. dianthi* Green, 1926; *R. nemoralis* (Hambleton, 1946); *R. falcifer* Kunckel d'Herculais, 1878; and *R. simplex* (Hambleton, 1946). Except for *R. cacticans*, all species are newly recorded for Germany.
Rhizoecus nemoralis was the most common species, found on 18 plant species in the botanical gardens of Frankfurt, Bonn, and Munich. *Rhizoecus dianthi* was associated with 14 plant species but occurred only in Munich. *Rhizoecus cacticans* was identified on 10 plant species in the botanical gardens of Bonn, Hamburg, and Munich. *Rhizoecus simplex* was found on eight plant species in Frankfurt and Munich. *Geococcus coffeae* was recorded on four plant species in Berlin and Bonn, while *R. arabicus* was associated with three plant hosts and observed only in Berlin. The least frequent species, *R. falcifer*, was associated with a single plant species in Munich.
Morphological redescriptions are provided for *R. arabicus*, *R. cacticans*, *R. falcifer*, *R. franconiae*, *R. simplex*, and *Ripersiella caesii*, along with intraspecific variations observed in *G. coffeae*, *R. dianthi*, and *R. nemoralis*. These findings support the hypothesis of underrecorded invasive Rhizoecidae species in Germany, underscoring their potential threat to the country's phytosanitary security.

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From Plant Volatiles to Nutritional Dynamics: Insights into BMSB Feeding Behavior and Control Strategies

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The Brown Marmorated Stink Bug (BMSB), *Halyomorpha halys* (Stål) (Hemiptera: Pentatomidae), is a highly adaptable pest that feeds on a wide range of plants, with a particular preference for fruits. As this invasive species continues to spread rapidly across Europe, its expanding host range poses a serious threat to fruit crops, leading to significant economic losses in agriculture.
Addressing the challenges posed by invasive insect herbivores requires a thorough understanding of their interactions with host plants. While advancements in pest management are ongoing, it remains unclear whether feeding by *H. halys* on various hosts triggers changes in plant volatile emissions that could be leveraged to disrupt its feeding behavior.
This study focuses on unraveling the interactions between BMSB and one of its host plants, the broad bean (*Vicia faba*, Fabaceae). Specifically, we examined how volatile compound emissions differ in bean pods exposed directly and systemically to BMSB feeding.

Volatile compounds were collected from damaged and undamaged bean pods (fresh or exposed to ambient conditions) and analyzed using gas chromatography-mass spectrometry. Additionally, adult BMSB feeding preferences for these pods were evaluated.
In parallel, the direct impact of BMSB feeding on bean pods was investigated through biochemical analyses of proteins, carbohydrates, and lipids. These studies aimed to quantify changes in macronutrient content resulting from feeding damage, providing insights into how BMSB feeding affects the nutritional profile of the host plant. The findings highlight the physiological toll of herbivory on the plant and its potential implications for pest preference and plant resistance.
Our findings reveal that BMSB feeding induces distinct alterations in the amounts and profiles of volatile compounds emitted by bean pods, alongside measurable changes in macronutrient composition. These results suggest that both volatile signaling and nutritional alterations influence the insect's food choices. Moving forward, these altered volatile blends will be tested as potential attractants or repellents in field trials, offering a pathway to develop more effective and sustainable control strategies against BMSB.

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Integration of Molecular Analysis Methods for Monitoring and Control of the Spread of Brown Marmorated Stink Bug (*Halyomorpha halys*) in Agroecosystems of Kazakhstan

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The brown marmorated stink bug (*Halyomorpha halys*) is an invasive insect species that poses a serious threat to agriculture ecosystems. Native to East Asia, this pest has spread globally, including to Europe, North America, and Kazakhstan, driven by its adaptability, ecological plasticity, and lack of natural enemies. For example, in 2010, *H. halys* caused $37 million in apple crop losses in the eastern United States (Leskey et al. 2012). Identifying the brown marmorated stink bug is challenging due to its similarity to other stink bugs, with morphological features often insufficient, especially in early developmental stages. In this regard, molecular analysis methods such as DNA sequencing are becoming increasingly important, providing high accuracy and reliability of species identification.
The brown marmorated stink bug was first recorded in Kazakhstan in 2016 (Yesenbekova 2017). However, at that time, identification was carried out solely on the basis of morphological features, which limited the possibilities for further study and control of the population. The lack of systematic monitoring and special measures to combat this pest contributed to its active expansion in various regions of the country. This makes the brown marmorated stink bug one of the significant invasive species that pose a threat to agroecosystems in Kazakhstan.
As part of our study, the brown marmorated stink bug was recorded in the Almaty region. For its identification, a molecular analysis method was used based on sequencing of the DNA region encoding subunit I of cytochrome c oxidase (COI) by primers 5'-TCCACTAATCACAARGATATTGGTAC-3' & 5'-GAAAATCATAATGAAGGCATGAGC-3' using Oxford Nanopore technology. For subsequent analysis, the sequencing data was compared with reference gene COI of the brown marmorated stink bug using the Mini-Map2 tool.
The first screen of sequencing data using basic local alignment search tool (BLAST) revealed the best matches to sequences of *H. halys*. The next analysis against reference COI revealed consistently high sequence identity across all samples, ranging from 86.2% to 96.7% (mean identity). The majority of samples demonstrated sequence identity exceeding 90%, with notably high values observed in three samples (all >96%). These particular samples also yielded the highest number of matching sequences >2000 hits each), providing robust support for the identification. The reliability of the molecular identification is further strengthened by the low standard deviations (0.615–4.57%) in sequence identity across all samples, indicating consistent sequence matching. Mean alignment lengths ranged from 70.4 to 123 base pairs, which is consistent with the expected amplicon size for the utilized COI primers. This molecular analysis, characterized by high sequence conservation and robust alignment statistics, strongly validates the morphological identification and confirms the presence of *H. halys* in the analyzed material.
This study highlights the importance of integrating molecular methods into invasive insect research in Kazakhstan, emphasizing the need for systematic monitoring and national programs to mitigate agricultural damage and environmental risks from invasive pests.

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Kultureller Ursprung sprachinvasiver Schadinsekten – Ein Beitrag zur Kulturellen Entomologie

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Unsere Alltagssprache bedient sich so manchem Vorbild aus der Welt der Insekten. In Sinnsprüchen, Sprichwörtern, Redewendungen und Zitaten finden dabei Schadinsekten besonders häufig Verwendung und dies meist in Form der Allegorie als wichtiges rhetorisches Gestaltungsmittel. Redensarten sind ein sprachliches Spiegelbild gelebter Kultur, was den Vergleich mit anderen Sprachen interessant macht. So hat jede Sprache ein charakteristisches Portfolio von ihnen, die sinnverwandt sein, aber auch zu Missverständnissen führen können. Die eng mit uns Menschen verbundenen Lebensweisen von Vorrats- und Materialschädlingen einschließlich der lästigen Fliegen bieten dafür die geschichtliche und kulturelle Basis.

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Aromia bungii (Coleoptera: Cerambycidae): Emerging global invader or localized concern?

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Aromia bungii is an invasive cerambycid beetle native to China, the Korean Peninsula, Mongolia, Vietnam, and the Russian Far East, with established populations in Japan, Germany, and Italy. This species represents a major phytosanitary threat due to its severe impact on Rosaceae. Predicting its spread in invaded regions and identifying globally suitable areas is essential for designing effective management practices and optimizing monitoring and early detection strategies. Species distribution models (SDMs) are indispensable tools in invasion biology for forecasting the potential distribution of invasive species across spatial and temporal scales. To improve predictive accuracy, we developed a modeling pipeline centered on three key principles: 1) Scale-dependent modeling–Our SDM employs two complementary models, both relying on presence-only data from repositories and additional original data. The habitat suitability model (HSM) assesses the effects of land-use covariates, including host plant availability and elevation, while the bioclimatic suitability model (BSM) evaluates bioclimatic covariates. This approach ensures an accurate evaluation of covariates acting at different spatial scales, with bioclimatic variables acting on a broad (continental) scale, while habitat variables acting on a finer (local) scale. Combining these two groups of variables in a single model could result in overemphasizing one group over the other. 2) Strategic allocation of background points (pseudo-absences, PAs)–The pattern of PA allocation is critical for disentangling the effects of the two groups of scale-related variables, enhancing model robustness. 3) Calibration on native range–A reliable SDM requires presence points derived from populations in equilibrium, where suitable, moderately suitable, and unsuitable areas reflect occurrence densities corresponding to resource availability. Thus, we calibrated the two models using data from the native range of *A*. *bungii*. According to the HSM, host plants were the most influential and positively correlated variable. In the BSM, the mean temperature of the wettest quarter and precipitation during the warmest quarter positively impacted the species' probability of presence, whereas isothermality was identified as a negative predictor. The specie overall suitability maps, from native to global scale, were obtained by multiplying the map of probability of presence obtained from the projection of the HSM with that obtained from BSM. Given the BSM map, the range of *A*. *bungii* was substantially limited by the bioclimate, while habitat conditions acted as limiting factors in the species' distribution. Host plants were the most important variable that positively influenced habitat suitability. Bioclimatic suitability improved as rainfall in the warmest quarter and average temperatures in the wettest quarter increased and as isothermality decreased. The widespread invasion of *A*. *bungii* in Japan is attributed to the coexistence of favourable bioclimatic and habitat conditions. Although Japan is geographically close to the species' mainland range, the sea acted as a barrier preventing natural colonization. Unlike other invasive species, *A*. *bungii* in Japan likely did not undergo ecological niche shifts, as the invaded area already provided optimal conditions, avoiding selection pressures during the invasion process. Globally, no ideal regions for the species exist outside SE Asia. In the Western Palaearctic, despite abundant suitable habitat, the species' natural spread appears limited by insufficient bioclimatic conditions, making significant range expansion in Europe unlikely. However, areas in North America

present minimal but notable suitability, warranting attention. Overall, *A. bungii* populations are unlikely to expand significantly without a bioclimatic niche shift, which appears improbable based on models calibrated on the native range and projected in SE Asia.

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Bacterial diseases in sugar beet transmitted by planthoppers–New challenges for breeding

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Two new sugar beet diseases, 'Syndrome des Basses Richesses' (SBR) and 'Rubbery Taproot Disease' (RTD), are spreading in certain regions of southern and eastern Germany, Switzerland as well as south-east European countries. Both diseases are transmitted by planthoppers, e.g. *Pentastiridius leporinus*, *Reptalus quinquecostatus* or *Hyalesthes obsoletus*, whose distribution varies across Europe. They serve as vectors for two bacterial pathogens, the proteobacterium '*Candidatus* Arsenophonus phytopathogenicus' and/or the phytoplasma '*Candidatus* Phytoplasma solani'. Currently, the proteobacterium is assumed to be the main causal agent of SBR, while RTD-expressing sugar beets are infected predominately with phytoplasma.
Both diseases must be brought under control by plant breeding through developing SBR- and RTD-tolerant or resistant varieties. In addition, monitoring programs are in place to understand the spread and composition of pathogens, and the flight activity of planthoppers better. Furthermore, agronomic approaches are evaluated such as the influence of the time of planthopper immigration on yield. This information can help to determine the optimal time for the application of agronomic measures to reduce planthopper populations. All these measures, combined with tolerant varieties aim towards an integrated control of the planthopper populations and the SBR/RTD diseases.

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Ausbreitung der invasiven Ameise *Tapinoma magnum* in Baden-Württemberg

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Relativ unbemerkt hat sich vermutlich seit über 20 Jahren eine invasive Ameisenart aus dem westlichen Mittelmeergebiet im Südwesten Deutschlands ausgebreitet: *Tapinoma magnum* Mayr 1861, eine Drüsenameise (Unterfamilie Dolichoderinae). Die ersten im Nachhinein als zu dieser Art zugehörig bestimmten Kolonien wurden 2009 in der Pfalz entdeckt (Heller 2011 als *Tapinoma nigerrimum*). Seifert et al. (2017) konnten die Taxonomie des *nigerrimum*-Komplexes klären. Er umfasst vier Arten, von denen drei aufgrund ihrer Bildung von polgynen, polydomen Superkolonien hohes invasives Potential haben. In Deutschland wurde bisher mit einer Ausnahme alle Vorkommen als *T. magnum* bestimmt. Die bisher bekannte Verbreitung dieses Neozoon liegt hauptsächlich in der Südpfalz und in Baden-Württemberg. In diesem Bundesland sind derzeit überwiegend Gemeinden entlang des wärmebegünstigten Rheintales betroffen von Südbaden über die Ortenau bis Nordbaden. Vermutlich gibt es Nester an weiteren Standorten als den bislang bekannten, prinzipiell muss im gesamten Oberrheingebiet mit Vorkommen gerechnet werden. Darauf deutet auch das Vorhandensein im benachbarten Rheinland-Pfalz, Hessen und im Elsass hin. Es gibt aber auch bereits Vorkommen in weiterer Entfernung von Baden-Württemberg: z. B. Burgdorf bei Hannover, in den Niederlanden, Belgien, der Schweiz (Seifert 2020).
Solange die Kolonien klein sind, werden sie offensichtlich nicht als problematisch erkannt. Dies ändert sich im Laufe der Jahre, wenn die Kolonien sehr volkreich geworden sind, große Areale als Superkolonie besiedeln (bis zu mehreren Hektar) und im Siedlungsbereich den Menschen durch ihre schiere Menge lästig werden oder weil sie ins Haus oder in Stromverteilerkästen eindringen und durch ihre Grabtätigkeit Pflasterungen lockern. Bekämpfungsmaßnahmen stellen sich als außerordentlich schwierig da und führen zu hohen Kosten bei gleichzeitig unsicherem Erfolg.

Betroffene Anwohner und kommunale Amtsträger fordern deshalb zunehmend öffentlich geförderte Forschungsansätze und Unterstützung bei der Bekämpfung. Der Landtag von Baden-Württemberg hat deshalb für zwei Jahre ein Forschungsprojekt bewilligt, um unser Wissen über die beteiligten Arten, ihre Ausbreitung und die Biologie von Arten aus dem nigerrimum-Komplex zu erweitern. Außerdem soll es Wissenschaftler, betroffene Kommunen und Schädlingsbekämpfer in Austausch bringen, um eine effektive Bekämpfung zu ermöglichen.

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PHID-Coleo II – Diagnosemethoden für Holz schädigende Käferarten bei Importkontrollen im Vergleich

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Zur Diagnose von Schaderregern stehen verschiedene Methoden zur Verfügung, die im nun abgeschlossenen Forschungsvorhaben untersucht und verglichen wurden. Zielorganismen waren bei Importen potentiell invasive Prachtkäfer (Buprestidae) und Borkenkäfer (Scolytinae), wie z. B. der Eschenprachtkäfer *Agrilus planipennis* und *Euwallacea fornicatus* und von den Borkenkäfern insbesondere *Aromia bungii*, der Asiatische Moschusbock. Neben klassischen bebilderten Bestimmungsschlüsseln wurden molekulargenetische Methoden (LAMP, COI-Sequenzierung, Metabarcoding von Mischproben) und KI-unterstützte Bilderkennung in Form einer App getestet. Die Vor- und Nachteile der Methoden werden vorgestellt und diskutiert.

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Sektion Funktionelle Biodiversität in Dauerkulturen / Section Functional Biodiversity in Permanent Crops

Talks

sorted by category and main authors

Keynote

Functional insect biodiversity in the vineyard environment

Hoffmann, C. & Kaczmarek, M.

Vineyards are mosaic-like ecosystems that simultaneously contain biotope components of a field, a pasture and a wooded area. The cultivation of vineyards represents an intervention in the succession towards a forest ecosystem and guarantees the preservation of a more or less species-rich steppe vegetation, which would not occur in the forest, on which a large number of insects can develop. In contrast to arable crops, the conditions for insects in viticulture have improved significantly in Germany in recent decades as a result of mechanization. Vegetated vineyards are a must wherever a tractor or harvester has to be used in wet conditions, as they help to avoid soil compaction. Our own studies with Malaise traps have shown that the species diversity of this vegetation is decisive for the species diversity and biomass of the insects caught in it.
The different types of greening in the vine row, in the understock area and on the canopy of the vine create a spatial and temporal mosaic of different small habitats that can make vineyards rich in insect species if no other disturbances occur. One potential disturbance is plant protection or the management system. Insecticides have been replaced by pheromones on over 90% of vineyards in Germany and Austria. This means that a previously significant bottleneck in biodiversity has been eliminated. In recent decades, this has led to the reappearance of previously extinct pests and rare species. The high use of fungicides, which is necessary for a grape harvest due to introduced diseases, can be reduced by using fungus-resistant grape varieties. However, these so-called PIWI vines can also be used to measure the role of fungicide use for biodiversity and mechanisms of natural pest regulation.
This showed that the global effect of the management system and plant protection on species diversity, trophic level composition and insect biomass in German viticulture tends to be overestimated in the public perception. In contrast, green cover inside and semi-natural habitats outside the vineyards have a beneficial effect on these parameters. By changing the vineyard geometry from fall line to horizontal terraces, the number of Red List species of Hymenoptera and Lepidoptera can be doubled despite plant protection.
When considering individual taxa or close multitrophic relationships between diseases, pests and beneficial organisms, plant protection can have a more differentiated influence, as some examples show.

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Erstnachweis von *Scaphoideus titanus* in Deutschland – Daten zur Phänologie und zum Infektionsgrad mit Flavescence dorée Phytoplasmen 2024

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Im Rahmen eines nationalen Monitorings wurden seit 2015 in Deutschland Erhebungen zum Vorkommen von *Scaphoideus titanus*, dem Überträger der Quarantänekrankheit Flavescence dorée (FD) im Wein, durchgeführt. Während es in Südeuropa durch *S. titanus* zu einer epidemischen Ausbreitung von FD kommt, ist Deutschland bislang frei von der Krankheit. In 2024 wurden nun erstmals Individuen von *S. titanus* in Deutschland gefunden. Da eine Einschleppung von *S. titanus* über den Transitverkehr in Süddeutschland erwartet wurde, wurden im südbadischen Rheintal Gelbtafeln in verschiedenen Weinbergen in der Nähe von Autobahn-Rastplätzen und Gewerbegebieten ausgehängt. Die Fallen wurden von Juli bis Oktober 2024 im zweiwöchigen Rhythmus gewechselt. Anfang August wurden die ersten Exemplare von *S. titanus* entdeckt und morphologisch und molekular bestimmt. Das Untersuchungsgebiet wurde daraufhin auf insgesamt 62 Fallenstandorte erweitert, von denen 49 dauerhaft kontrolliert wurden. Bis Mitte Oktober wurden in einer Befallszone von 182 ha über 450 Individuen von *S. titanus* in den Fallen gesammelt. Diese Ergebnisse deuten auf eine seit Längeren bestehende Population hin. Der Peak der Fänge war im August, aber Einzeltiere wurden bis Ende Oktober gefangen. In verwilderten Reben waren die Fangzahlen deutlich erhöht. Die Insekten wurden von den Gelbtafeln abgelöst und mit verschiedenen molekularen Methoden auf Phytoplasma-Infektionen untersucht. Es wurde eine PCR-Teststrategie etabliert, zu der auch ein Qualitätstest der Insekten-DNA-Extrakte gehört.

Hierzu wurden neue Primer im COII-Gen von *S. titanus* entwickelt und zur Normalisierung der PCR Ergebnisse eingesetzt. Insgesamt wurden 436 Individuen getestet, jedoch konnte keine Infektion mit FD-Phytoplasmen nachgewiesen werden.

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Flower reservoirs or flower boxes? Seeking the best low input strategy to promote biodiversity and pest control in modern stone fruit orchards

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Flower reservoirs' or 'flower boxes'? What would be the best low input strategy to promote biodiversity and efficient pest control in modern stone fruit orchards? Flower strips are a known management strategy used in orchards and vegetable production which provide habitat for beneficial insects increasing biocontrol of pests and pollination of crop plants. Flowers strips between tree-rows however, are not widely implemented in fruit production because of logistical challenges such as additional machinery, and high efforts needed for establishing and maintenance of flowers strips. Table cherry in particular could benefit from flowering habitats within the orchards. The majority of table cherry in Switzerland are equipped with a rain-protection roof and lateral insect nets. The nets hinder pests like fruit flies from entering and at the same time the natural enemies of most pests. Particularly the build-up of colonies of aphids is facilitated by the insect nets and the lack of nectar, pollen source and habitat for reproduction. Consequently, natural predation is low and pre-flower and post flower insecticide applications are the standard in organic and integrated production. Farmers need therefore support in developing insecticide-reducing and practically feasible management strategies. In this project, we exploit our large experience in Agroecology, to promote biodiversity and natural pest control in modern orchards by testing two low input strategies. The overall goal of this research project is to test the use of either 1) perennial 'flower reservoirs' installed in areas adjacent to the tree-rows where tractors etc. do not transit or 2) pre-planted 'flower boxes' distributed within the orchard in places where they do not disturb the management. We are carrying out field trials on commercial organic cherry orchards with flower reservoirs or flower boxes. We expect to increase pollinator visitation and biocontrol of aphids in orchards where flower reservoirs have been implemented. In this talk, we will introduce you to the designs, and to our challenges and findings so far. We expect that by the end of the project we will be able to show that these two strategies can provide similar or even more benefits than those provided by flower strips between tree-rows, while reducing the logistical challenges and maintenance efforts needed from farmers, and therefore, increasing its acceptance and implementation.

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Creating synergies: Companion plantings fostering biodiversity and pest control in organic strawberry fields

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Organic berry farming faces significant challenges in managing insect pests like the Southern Green Stink Bug *Nezara viridula* (Heteroptera: Pentatomidae) while adhering to sustainable and pesticide-free practices. Conservation biological control, which promotes natural enemies through habitat management, can offer a promising solution. At Hochschule Geisenheim University (Germany), an organically managed strawberry field was set up using a holistic habitat management approach to increase the overall resilience of the strawberry crops in the framework of the EU-project "ResBerry". Our primary aim was to increase functional insect diversity by implementing different plant species, including flower strips to provide additional food sources for beneficial insects and trap plants to distract insect pests from the strawberries. To evaluate the effectiveness of this habitat modification, systematic sampling was carried out during the 2023 and 2024 growing seasons using a Vortis insect suction sampler. Subsequently, collected insects were counted and taxonomically sorted resulting in a total of almost 19,000 individuals. The results demonstrate a successful colonization of predators such as Anthocoridae (Heteroptera) and Nabidae (Heteroptera), along with parasitoid Hymenoptera, within a short time period. Additional visual inspections of selected target insects on strawberry plants lead to findings of parasitism of *N. viridula* by a non-native tachinid fly *Trichopoda pictipennis*. Our study

reveals the effectiveness of companion plantings for a surprisingly fast establishment of functional insect diversity and will support recommendations for growers on practical implementation of respective plants in their cropping systems.

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Terracing in steep slope viticulture and its potential to promote biodiversity in vineyard ecosystems

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Viticulture on steep slopes has shaped some of Germany's most biodiverse cultural landscapes. However, the area under vines has declined sharply in recent decades due to insufficient profitability. Changing the type of cultivation from vertical to modern terraced vineyards could help to reduce the further abandonment of steep slope vineyards by keeping them economically viable. In addition, a significant area of modern terraced vineyards consists of embankments that remain uncultivated and extensively managed and may provide valuable habitats within the viticultural system, but little is known about the effects of changing the type of vineyard management on biodiversity.
Over a three-year period, we investigated the effects of vineyard management type (vertical vs. terraced) compared to abandonment, local conditions and the surrounding landscape on plant, orthopteran, wild bee, carabid and spider diversity at 45 study sites along the Upper Middle Rhine Valley (UMRV) in Germany.
The small-structured landscape of the UMRV supported a high species diversity, high numbers of rare and threatened species and diverse species communities across vineyard management types and abandoned vineyards. There was no uniform positive effect of a vineyard type on all groups studied. Rather, responses were group and taxon specific, driven by different vineyard management intensities, local vegetation structures, local soil conditions and the surrounding landscape.
In summary, plant species richness and composition were determined by management derived disturbance intensities. Extensively managed terraces had a distinct plant community and the highest plant species richness with more perennials and herbs. In contrast, highly disturbed vineyard inter-rows showed plant communities associated with annuals, ruderals and grasses, while abandoned vineyard plant communities were completely different with woody species and overall low plant diversity.
Orthoptera diversity was favoured by active vineyard management. Heat-adapted Caelifera species were abundant in open inter-rows with a high proportion of bare ground, while taller vegetation on terraces favoured Ensifera species. Abandoned vineyards substantially reduced Orthoptera species diversity.
Wild bees responded more strongly to the availability of nesting sites than to floral resources. Ground nesting bees were determined by the suitability of soil properties for nesting regardless of vineyard management type, whereas above-ground and cavity nesting bees were favoured by the woody structures of abandoned vineyards and the availability of semi-natural habitats (SNH) in the surrounding landscape.
Carabid diversity benefited from active vineyard management and responded positively to high levels of bare ground and high levels of vineyards in the surrounding landscape. In particular, xerophilous and thermophilous species decreased in abandoned vineyards.
Spiders diversity benefited from high landscape complexity. Abandoned vineyards supported very diverse spider communities, including some late-successional species, whereas cultivated sites and especially terraced vineyards were dominated by xerophilous species adapted to open habitat structures.
In summary, heterogeneous landscapes, including actively managed and abandoned vineyards and natural elements providing complementary resources, were critical to meeting the many specific needs. However, active vineyard management is essential to maintain the characteristic flora and fauna of steep slope viticultural landscapes. Terraced vineyards, especially when revegetated with regional seed mixes, have a high biodiversity potential and can help to combine economically viable steep slope viticulture with nature conservation objectives in a land-sharing approach.

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Sektion Landschaftsökologie und Naturschutz / Section Landscape Ecology and Nature Conservation

Talks

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Keynote

Reintroduction of butterflies with a parasitic life cycle: How to survive in the new home

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Interactions between species play a crucial role when it comes to successfully reintroducing animals after they have been lost. Reintroduction of species is used more and more to compensate for these losses, however, most of them are unsuccessful. Butterflies are often translocated to sites where their host plants occur, but without detailed knowledge about the ecology of the species, it is even difficult to survive only one winter. Translocating butterflies also provides a great opportunity to study evolutionary processes. Even if the conditions for success are given, the new habitat is never the same as the old one. So the translocated species has to adapt to new surroundings and conditions. In the case of parasitic butterflies, like *Maculinea* (*Phengaris*) *teleius*, the scarce large blue, not only the host plant *Sanguisorba officinalis* is important but also the host ant *Myrmica scabrinodis*. The caterpillars are adopted by the worker ants and brought to the nest. Here, caterpillars feed on the ant brood and hibernate. The communication between the caterpillar and the host ant plays an important role for successful adoption and survival in the ant nest and is thus a key factor for a possibly successful translocation.

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Insect decline–Evaluation of potential drivers of a complex phenomenon

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Insect decline is a complex phenomenon influenced by various causal factors acting at different spatial and temporal scales, affecting different insect groups. Large-scale effects, such as landscape changes, are assumed to be significant drivers, but comprehensive datasets directly linking factors to insect decline are largely lacking. Here, we provide a detailed analysis of potential drivers of insect decline in Germany over the last decades, where insect biomass has been measured in previous studies. We examined landscape structure, land use changes, grassland management, cropping practices, pesticide use, climate, and light pollution on federal state level in an exemplary region.
The results of the analysis suggest that habitat loss, changes in land cover, land use or land-use intensification are factors consistently correlating with declining tendencies in insects in Germany. Especially grassland faced transformation and/or management intensification by dairy farming and bioenergy plant cultivation, leading to a habitat quality degradation for insects.
This study represents one of the first comprehensive retrospective investigation of these factors. With this extensive dataset, we can link habitat drivers (landscape changes, agricultural uniformity, loss of fragmented structures) to insect decline trends, in conjunction with various potential causal factors (pesticides, urbanization, nightlight), contributing to a better understanding of insect friendly landscapes.

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What do they feed on? Identifying pollen from hoverfly guts using metabarcoding

Jaich, A. & Herz, A.

In the course of the worldwide decline in local insect populations, agricultural practices are one important factor due to changes in the landscape and the use of pesticides. To counteract this trend, the FInAL project (https://www.final-project.de/en/) is working with farmers to establish various measures and investigate whether these have a supportive effect on insects in order to establish a more sustainable agriculture. In the course of this project, hoverflies are also studied, because they play an important role both for biological control and pollination. The adults act as pollinators in important crops such as fruit production, while many hoverfly larvae are known to control pests such as aphids.
A simple action to support hoverflies is to increase the supply of flower resources throughout the year by flower strips or flowering crops. To assess whether these introduced flower resources are used, we can observe the insects in the field when they visit the flowers or, instead, we need to catch them and examine their gut contents, especially if we want to confirm the actual consumption of the flower resources. The subsequent morphological identification of pollen is possible, but

time-consuming and dependent on high-quality reference material. Alternatively, we tested a metabarcoding approach to examine the gut contents of hoverflies and gain insights into which plants they had really fed on. We developed a protocol for obtaining samples from different hoverfly preparations (whole insects, gut preparations, fecal samples) for metabarcoding and were able to show that the method works in principle. It was possible to identify pollen from plants that had been offered to the hoverflies in the laboratory and also to assess the relative amount in the diet. We then caught hoverflies in FInAL-fields with and without implemented biodiversity measures to obtain their pollen profiles by metabarcoding. The results will help to assess the impact of the measures on local hoverfly populations.

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Insektenrückgang und Aktivitäten im Naturschutz in Deutschland

Kuemmerlen, M. & Balzer, S.

Die aktuellen Roten Listen Deutschlands, stufen etwa die Hälfte der bewerteten Insektenarten als gefährdet, extrem selten oder als Teil der Vorwarnliste ein. Fast jede Zweite der bewerteten Arten weist rückläufige Bestandstrends auf, entweder kurzfristig, langfristig oder beides. Mit der ‚Krefelder Studie' von 2017 wurde zudem deutlich, dass auch die Biomasse der Insekten in deutschen Schutzgebieten, über eine relativ kurze Zeitspanne, sehr stark abgenommen hat.
Vor diesem Hintergrund, gab es ein erhöhtes Interesse der Politik am Thema Insektenschutz, was zur Verabschiedung des Aktionsprogramm Insektenschutz 2019 durch die Bundesregierung führte. Es folgten zahlreiche Forschungsinitiativen und -projekte in Deutschland sowie die Veröffentlichung vieler wissenschaftlichen Publikationen von hoher Relevanz. Auch auf der Ebene der Bundesländer, Kommunen und Gemeinden entstanden durch Bürger:innen angestoßene Initiativen. Zudem wurden Mittel aus unterschiedlichen Förderprogrammen auf Bundes- und Landesebene bereitgestellt.
Am Beispiel einiger Vorhaben des BfN, zeigen wir wichtige methodische und inhaltliche Ansätze zur Untersuchung des Insektenrückgangs. Diese beinhalten beispielsweise Einblicke in die Expositionspfade von Insekten zu Pflanzenschutzmittel und in die Verwendung ökologischer Merkmale von Insektengruppen. Auch die Öffentlichkeitsarbeit und Naturbewußtseinsbildung z. B. in und mit Kommunen steht im Fokus zahlreicher Vorhaben.
Um das Momentum von 2019 aufrecht zu erhalten und um die aktiven Forschungsgruppen zu einer koordinierten Zusammenarbeit zu motivieren, hat das BfN das Netzwerk Insektenexpert:innen ins Leben gerufen. Wir geben einen ersten Überblick zu den Aktivitäten und skizzieren die Forschungsfragen für die Zukunft.

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Agrivoltaic–An opportunity to enhance functional biodiversity in agriculture?

Lemanski, K. & Herz, A.

In order to mitigate climate change, a considerable expansion of renewable energy sources, including photovoltaics, is required. To prevent land-use conflicts between agriculture and energy production, agrivoltaic systems offer a promising solution. In these systems, the modules are either installed elevated above the crop itself or vertically adjacent to the crop, so that the area below or between the modules can still be used agriculturally. Currently, research is focusing primarily on energy production and agricultural yield. However, there is still a substantial knowledge gap regarding the potential impact of agrivoltaic systems on functional biodiversity.
Therefore, the aims of the interconnected research projects Solarnützlinge and VAckerBio 2 are to investigate the impact of agrivoltaic systems on insects. The projects focus on functional biodiversity, aiming to provide knowledge about how agrivoltaic systems can be designed in an environmentally friendly way, whereby insects provide additional benefits to agriculture through pest control and pollination. Project partners are the Fraunhofer Institute for Solar Energy Systems, the University of Hohenheim and Next2Sun Technology GmbH.
In order to address these questions, our work has deployed yellow-pan traps to monitor the insect biomass in two different agrivoltaic systems. In an elevated agrivoltaic system over a vineyard in Baden-Württemberg (Germany) traps were used in two consecutive years. Results show that the total biomass was higher in the control area without modules compared to the area with modules. A vegetation survey in the vineyard alleys indicated a differentiation in the plant community composition over the course of the growing season. This was combined with a higher percentage of bare soil underneath the modules. Together, this suggests that the decline of resources for insects in terms of food (pollen and nectar)

and shelter is one potential reason for the observed decline in insect biomass under the modules.
In order to promote functional biodiversity in a vertical agrivoltaic system in Saarland (Germany) in an oat field, perennial flower strips were sown below half of the modules. Below the other half of the modules established grass strips served as control. Results showed that insect biomass interacted between the submodule usages (flower vs. grass strips) and time. The emergence of the flowering plants on the submodule strips during summer, resulted in a higher insect biomass than in the control with grass strips. This effect diminished in autumn as temperature decreased. This suggests that establishing flower strips under modules can increase insect biomass in vertical agrivoltaic systems, presumably including beneficial insects.
The diversity of agrivoltaic systems reflects rapid advancements in this field, with a strong focus on optimizing energy generation and agricultural productivity. However, designing agrivoltaic systems concerning biodiversity can introduce new structures to agricultural landscapes that enhance ecosystem services. Therefore, integrating promotion of biodiversity from the early stages of system design is crucial. Furthermore, the findings in these projects highlight the need for further system-specific studies to address biodiversity impacts.

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Arthropod abundance is most strongly driven by crop and semi-natural habitat type rather than management in an intensive agricultural landscape in the Netherlands

Litovska, I.; Kleijn, D. & van der Plas, F.

The intensification of agriculture has been identified as one of the main causes of arthropod declines. To halt the decline of arthropods, changes in farming practices and management of surrounding habitats may therefore be needed. A key challenge is to identify which changes in management approaches are most effective in restoring biodiversity. Therefore, this study examines arthropod abundance and diversity in different agricultural and semi-natural habitats, and among different management types. Arthropods were sampled three times in spring and summer of 2022 and 2023 with emergence traps in 128 unique sites in an intensively farmed area in Western Netherlands. These sites included a variety of crops as well as semi-natural habitats. Our study showed that on average the abundance and diversity of arthropods of several taxa was lower in crop habitats compared to semi-natural habitats. However, these effects strongly varied among crop species. For instance, alfalfa, spelt, spring and winter wheat fields (that often had a high plant cover) supported similar arthropod diversity and abundance levels as semi-natural habitats. Interestingly, in crop fields most variables related to field management, such as herbicide applications or amount of nitrogen fertilizers, did not show any significant relationship with arthropod abundances or diversity. The number of days after cultivation was an exception, and was positively related to total arthropod abundance, Hymenoptera and Collembola abundances, and Coleoptera family diversity. Within semi-natural habitats, number of days after mowing was positively related to total arthropod abundance, Diptera, Hemiptera and Hymenoptera abundances, and Hemiptera family diversity. Additionally, plant cover was positively related to total arthropod abundance. Overall, our findings suggest that crop species and management practices that increase plant cover in spring and early summer are increasing arthropod abundance and, to a lesser extent, higher-taxa diversity in intensively farmed agricultural landscapes.

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Urban Flora and Its Effect on Insect Diversity

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Urbanization significantly impacts pollinator populations by reducing the availability of suitable habitats and floral resources. Flower visitors, including wild bees, are essential for maintaining ecosystem health, but they face challenges in urban environments where ornamental plants often dominate green spaces. To address this problem, this study, conducted in collaboration with the gardening department of the City of Regensburg, examines the attractiveness of ten plant species to flower visitors across eight locations in Regensburg, Germany, encompassing urban and semi-urban areas. Five plant species were pre-selected for their high attractiveness to pollinators, while the other five represent commonly used ornamental plants. Data collection involved recording flower visitors and identifying them into categories, measuring flower and environmental parameters, and analyzing flower area. The statistical analysis investigates species-specific attractiveness, diversity patterns, and potential environmental

influences on flower visitation. First findings suggest that *Salvia farinacea* and *Eryngium planum* attract both a high number and wide variety of pollinators, particularly wild bees, which were the focus of this study. Others, such as *Salvia splendens*, attracted a considerable number of visitors, but only a narrow range of diversity, or exhibited limited appeal in total, such as *Begonia semperflorens*. The findings aim to guide urban gardening practices, enabling the City of Regensburg to design pollinator-friendly green spaces and enhance urban biodiversity conservation.

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DNA barcoding-based approaches to investigate larval food resources of cavity-nesting bees and wasps

Sann, M.; Timm, L.; Prudnikow, L.; Wünschiers, R.; Fornoff, F. & Klein, A.-M.

Artificial nesting resources, also known as trap nests, have proven to be an ideal method for monitoring cavity-nesting bees and wasps, their collected food resources, and natural enemies. Nowadays, trap nests are frequently used to assess responses to environmental and biodiversity changes based on multi-trophic interaction networks. Here we present multi-trophic interaction networks of common apoid wasp and bee species that are generated by analyzing their collected larval food resources. Particularly, we applied a traditional DNA barcoding and a MinION-based metabarcoding approach. We recovered highly resolved bi- and tripartite networks including bee-plant pollen, natural enemy-bee-plant pollen, wasp-arthropod host, and natural enemy-wasp-arthropod host associations. The sampling of wasp nests during the construction period allowed us to give an accurate count and identification of the provided larvae food items, here different arthropod species. The latter include species that are known as agricultural and forest pests. The quantitative sampling of nests entails increased time costs but enables high-quality DNA barcoding and the reconstruction of quantitative interaction networks. Thus, our approach is a highly promising monitoring tool for gaining deeper knowledge on the ecology, habitat requirements and the impact of environmental and biodiversity change on cavity-nesting bees and wasps.

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Wie geht insektenfreundliche Mahd an Straßenrändern?

Sauter, M. & Steidle, J.L.M.

Das Insektensterben stellt als Teil des allgemeinen Rückgangs der Biodiversität und des damit einhergehenden Verlustes von Ökosystemdienstleistungen eine der großen Bedrohungen der Zukunft dar. Angesichts der Schwierigkeiten, auf politischem Wege einen verstärkten Schutz von Insekten zu erreichen, ist es wichtig, potenzielle Habitate zu identifizieren, um das Aussterben von Insekten zu verhindern. Für Insekten und Arthropoden des Grünlandes können Straßenrandstreifen und Bankette solche Habitate darstellen. Auch wenn die negativen Effekte der angrenzenden Straßen für diese Insekten noch unklar sind, so wird der Nutzen von Straßenbegleitflächen für die Biodiversität immer stärker diskutiert. Sie machen in Deutschland etwa 1.9% der Gesamtfläche aus, unterliegen keinen ökonomischen Zwängen und werden daher weder mit Pestiziden behandelt noch gedüngt. Sie können daher einen Lebensraum für zahlreiche Pflanzen und Tiere darstellen und als Korridor für die Vernetzung und den genetischen Austausch von Populationen dienen. Allerdings müssen auch Straßenrandstreifen und Bankette regelmäßig gemäht werden. Dabei werden meist konventionelle Schlegelmulcher eingesetzt, die hohe Mortalitätsraten bei Insekten und anderen Arthropoden verursachen. Verschiedene technische Modifikationen an den Mähgeräten können dazu beitragen, die Mortalität bei der Pflege von Straßenbegleitgrün zu reduzieren. Dazu gehören die Reduktion der Sogwirkung, ein nach unten geschlossener Gehäuseboden, verkleinerte Abrollwalzen, die Möglichkeit, die Schnitthöhe zu verändern und Insektenscheuchen. Darüber hinaus kann eine Aufnahme des Mahdgutes zur Aushagerung der Standorte und damit einer höheren Diversität der Pflanzen betragen. In dem Beitrag werden neueste Forschungsergebnisse zur Wirksamkeit dieser Maßnahmen vorgestellt und der aktuelle Stand bewertet.

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The Unseen Victims of Neonicotinoids: The Severe Impact of Acetamiprid on Non-Target Grassland Plant Bugs

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While pesticides have long been proposed as a major driver of insect decline, studies evalu-

ating their impacts on non-target species under realistic field conditions remain limited. Our research focused on the neonicotinoid insecticide Mospilan®SG (active ingredient: acetamiprid) and its effects on non-target plant bugs (Heteroptera: Miridae), a dominant and ecologically important group in European grassland ecosystems. A controlled field experiment found that the abundance of three key plant bug species declined by up to 92% within two days of exposure to concentrations representative of those expected at field margins, with marked differences in response between species.
Subsequent greenhouse feeding trials using insecticide-treated host plants, as well as controlled laboratory dose-response experiments, confirmed the substantial negative impacts of Mospilan®SG on these non-target species. Strikingly, a comparison of lethal dose 50 (LD50) values derived from Mospilan®SG with published LD50 for honeybees treated with a comparable acetamiprid formulation revealed that the insecticide was over 11,000 times more toxic to plant bugs than to honeybees. In addition, significant sex-specific sensitivity was observed: males of two tested species were more than 20 times more sensitive to the insecticide than females.
These findings indicate that prolonged exposure to this neonicotinoid could severely reduce wild plant bug populations, potentially favouring insecticide-resistant species and ultimately causing shifts in community composition. Our results suggest that sex-specific sensitivity should be considered in pesticide risk assessment and highlight that the true risk to non-target insects may currently be significantly underestimated.

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Trap types and capture characteristics– Insights from the MonViA project

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Reports of global declines have highlighted the need for reliable long-term estimates of insect populations to identify potential drivers of declines, perform taxa-specific risk assessments, and to measure potential effects of implemented conservation strategies. In this context, data on taxonomic groups providing important ecosystem services is of particular interest. The MonViA* project, aims to address this by establishing a comprehensive long-term monitoring in agricultural landscapes in Germany.
As part of this project the long-term monitoring of hoverfly populations (“nützLINK”) will serve as an indicator for the condition of agricultural management on a wider spatial scale. While adult hoverflies are important pollinators, the larvae of many species are effective predators of various field crop pests. In this study, a monitoring approach for hoverflies was developed and tested using orchard meadows as stable habitats embedded in the agricultural landscape as spatial matrix. These extensively managed agroforestry systems provide temporary refugia and resources for many insect groups. Using mainly conventional insect traps, we found that the different trapping systems had a significant impact on the captured hoverfly community. Pan traps and Malaise traps differed in both capture rate and species composition. Overall, Malaise traps caught more individuals (71%) and more species (60%) than standard yellow pan traps, although some species were exclusively caught by one trap type and not the other. In addition, the effectiveness of the standard yellow pan trap was also compared to a frequently used trap system with three coloured bowls (blue, white and yellow) last field season.
The concept of this monitoring program and the comparison of the capture characteristics of the trap types based on the data from the 5-year pilot phase (2020–2024) are presented in this paper.
* The MonViA project: https://www.agrarmonitoring-monvia.de/en/

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InsectMow–Development and Evaluation of insect- and spider-friendly mowing technique

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In Central Europe, species-rich grasslands are threatened by intensive agriculture with frequent mowing contributing to the reduction of arthropods such as insects and spiders. The interdisciplinary project “InsectMow” investigates the negative effects of mowing on grassland ecosystems and how they can be reduced by technical modifications. Therefore, we aimed to develop (1) a modified disc mower that causes less arthropod losses and (2) an effective insect flushing bar that allows insects to escape. In a three-year experiment, we have investigated the direct and medium-term effects of mowing with various mowing techniques and flushing bars on eight abundant arthropod groups in grassland,

covering two seasonal mowing events each year.
Our results show that mobile insects such as dipterans or cicadas are able to escape from the mower when a flushing bar and mower are tested together at low operating speeds. We have also shown that, contrary to previous assumptions, bar mowers affect the arthropod fauna in a similar way to disc mowers. Immediately after mowing, the average number of arthropods was about 35% lower for both mowing techniques compared to the unmown control plots. In addition, we found medium-term effects of mowing (two to four weeks after mowing) regardless of the mowing technique, with 27 to 90% fewer individuals on mown plots compared to untreated controls, depending on the taxonomic group. Our findings suggest that mowing in general has a negative impact on abundant arthropod groups in grassland and that tractor-driven double-blade bar mowers do not appear to be a truly insect-friendly alternative to a conventional disc mower. Therefore, other factors such as cutting height, refugial areas, and mowing regimes should be seriously considered to protect spiders and insects from the negative effects of mowing.

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Sektion Medizinische Entomologie / Section Medical Entomology

Talks

sorted by category and main authors

Keynote

Water management of terrestrial arthropods: challenges and solutions using the example of two endemic tick species

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Most terrestrial arthropods are confronted with a dehydrating environment, i.e. their passive water losses, e.g. cuticular transpiration, surpass their passive water gains. Moreover, basic physiological activities such as breathing, defaecation etc. lead to further unavoidable net water losses. Important ways of water gain are drinking, food intake, oxidative metabolism, and in some taxa also active water vapour uptake from the unsaturated atmosphere at relative humidities <99%. This contribution outlines the principles of water management in the postembryonic stages of *Ixodes ricinus* and *Dermacentor marginatus*, two hard tick species with an overlapping distribution in parts of Europe but with differing microhabitat preferences and a different life cycle timing. The former species occurs in and near forests or forest-like habitats (parks, cemeteries etc.), whereas *D. marginatus* prefers steppe-like, more open landscapes with a mix of trees, bushes and grassy terrain. Each postembryonic stage of *I. ricinus* and the adult stage of *D. marginatus* are long-lived, but the larval and nymphal stages of *D. marginatus* are comparatively short-lived. A typical feature of hard ticks is that they feed only once per life stage and may spend extended periods fasting in the unfed as well as in the engorged state. Emphasis in the present talk will be on water gains, in particular on the capability of active water vapour uptake in different developmental phases of these ticks, but also the significance of drinking and metabolic water for their water balance will be dealt with. For the interpretation of the findings, it is essential to consider the seasonal timing of the life cycles of both species, especially their longevity between the bloodmeals. The different life cycle strategies are clearly reflected in distinct differences in the water management of both species

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Keynote

About the others–Those not in your bed. Phylogeny, Evolution and Ecology of bed bugs (Heteroptera, Cimicidae)

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The two human bedbug species, *Cimex lectularius* and *C. hemipterus* are in the focus of the medical entomology. To understand their interaction with its human host better, information about their closest relatives will be provided: the members of the bed bug family Cimicidae. An overview of species diversity, distribution and morphological variation will be given. Patterns and evolution of host-cimicid will be discussed using phylogenic trees as a backbone. Ecological aspects of bed bugs species with their host will be exemplified through studies on birds and bats. Finally, a recent analysis about the mating system is presented.

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What determines the nest-dwelling ectoparasitic community of Great tit and Blue tit nests? Thinking outside and inside the (nest) box.

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Bird nests, particularly those built in cavities, are stable environments representing the habitat of numerous and diverse arthropods. Among other nest-dwelling arthropods, nests harbour several ectoparasites which may impact nestling development and survival. The composition and dynamics of ectoparasite populations can be influenced by various factors, including those inherent to the nest and external environmental factors. We evaluated the prevalence and abundance of nest-dwelling arthropod ectoparasites in nests of great tits (*Parus major*) and blue tits (*Cyanistes caeruleus*) breeding in nest boxes in central Portugal during two consecutive breeding seasons. We quantified the number of blowflies (*Protocalliphora azurea*), fleas, obligatory (Dermanyssidae and Macronyssidae) and facultative (Laelapidae) parasitic mites and other non-parasitic arthropods, and assessed the presence of louse flies (Hippoboscidae) in each nest. We examined how the relative quantity of anthropogenic nest materials influenced ectoparasite presence and numbers, and diversity and composition of non-parasitic nest-dwelling arthropod community. We also explored correlations between parasitic and

non-parasitic arthropod communities, and evaluated whether re-used nest boxes and breeding time were associated with ectoparasite prevalence and numbers in the two tit species. We found that great tit nests were more frequently infested with both obligatory and facultative parasitic mites than blue tit nests. In great tit nests, anthropogenic nest materials were negatively correlated with flea and booklice (Psocoptera) abundance. This effect seemed to be indirectly modulated by the abundance of some arthropod predators, such as hister beetles (Histeridae), which were positively correlated with anthropogenic nest materials. In nests of both tit species, obligatory parasitic mites were negatively correlated with the abundance of rove beetles (Staphylinidae), also predators of small arthropods. The nest box re-use increased the probability of infestation by louse flies and obligatory parasitic mites. In both tit species, broods reared later in the season had higher intensity of blowflies in their nests; however, prevalence and abundance of louse flies and facultative parasitic mites, respectively, decreased along the breeding season in great tit nests. Overall, our study highlights the complex interactions between species-specific breeding biology, nest design, and environmental factors in shaping ectoparasitic infestations and arthropod community dynamics in nest boxes.

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Citizen Science as a tool to study bed bug distribution? Experiences from a project in Germany, 2023–2025

Hartung, V.

Distribution of bed bugs is insufficiently known, especially on the regional and local scale. In Germany, no central authority collects or publishes such data. In October 2023, we have started a citizen science project to test if citizen science could provide sufficient data on bed bug distribution. Another objective of the study was an educational one, to promote knowledge about bed bugs in the population. While the media attention to the initiative was high, the feedback from the people was limited to only 70 reports between the 30th of October 2023 and end of January 2025. In these reports, bed bugs constituted only about 23%, the rest being other household pests or nuisances. The analysis of the feedback parameters and their comparison with likely infestation rates implies that the project failed to reach the target group, despite the broad media coverage. Still, the results indicate that such projects might be necessary in the future to reduce the social stigma that is still associated with bed bug infestation and thus encourage people to report the insects.

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Gnitzen (Diptera: Ceratopogonidae) als Vektoren des Oropouche-Virus in Europa?

Kampen, H. & Werner, D.

In vielen Regionen der Erde spielen Gnitzen der Gattung *Culicoides* (Latreille, 1809) eine wichtige Rolle als Überträger von tierpathogenen Viren, Protozoen und Filarien. Es ist aber nur ein einziger von Gnitzen übertragener Krankheitserreger bekannt, der für den Menschen pathogen ist: das in Mittel- und dem nördlichen Südamerika sowie der Karibik endemische Oropouche-Virus (OROV). Als Hauptüberträger gilt *Culicoides paraensis* (Goeldi, 1905), während Faultiere, nichthumane Primaten und Vögel als natürliche Reservoirwirte angesehen werden.
In den Verbreitungsgebieten der Neuen Welt treten OROV-Ausbrüche seit Jahrzehnten plötzlich auf und betreffen zumeist gleichzeitig tausende Menschen der lokalen Bevölkerung. Infektionen präsentieren sich i.d.R. mit Grippe-ähnlichen Symptomen. Obwohl auch Meningitiden gelegentlich vorkommen, ging man lange davon aus, dass erkrankte Personen wieder komplett gesunden. Todesfälle sind nicht bekannt geworden.
Im Jahr 2024 wurde von Todesfällen beim Menschen in Brasilien berichtet, die durch das OROV verursacht worden waren. Gleichzeitig kursierten in den Medien Meldungen über Fälle von OROV-Infektionen bei Reiserückkehrern in Südeuropa. Auch wenn davon auszugehen ist, dass Eintragungen des Virus aus Lateinamerika seit vielen Jahren regelmäßig vorkommen, ohne dass es hier zu einer Weiterverbreitung kam, lässt sich die Frage, ob in Mitteleuropa vektorkompetente Gnitzenarten vorkommen, nicht mit Gewissheit beantworten. Bis zum erstmaligen Ausbruch der Blauzungenkrankheit im Jahr 2006 ging man immerhin auch davon aus, dass native Gnitzenarten das Blauzungenvirus nicht übertragen könnten. Experimentelle Vektorkompetenzversuche sind leider nicht möglich, da sich die heimischen Gnitzenarten nicht im Labor züchten lassen.

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Tachinaephagus zealandicus Ashmead, 1904 (Hymenoptera: Chalcidoidea: Encyrtidae)–A new forensic indicator for Germany

Lutz, L.; Stock, B.; Lammers, M. & Amendt, J.

Forensic entomology analyses insect evidence to draw conclusions on legal matters. It is mainly applied for estimating the minimum postmortem interval (PMI_{min}), i.e. the time since the first insect colonization, by determining the age of insect stages developing on the human remains and analyzing the successive patterns, pre-appearance, arrival, residency and departure of insects from a carcass. Blowflies are the most important dipterans, as they are typical first colonizers, often occur dominantly on a corpse and are often well researched with regard to their development time. An insect group that has received little attention so far are parasitoid wasps (Hymenoptera: Chalcidoidea). Depending on their biology, they parasitize the larvae or pupae of blowflies and kill them during development (shortly after the attack or delayed, depending on the strategy used). Hence, they do not begin to develop until days or weeks after the initial colonization of the carcass by the fly host. Moreover, they often have a longer development period than the host itself. Knowing the parasitism strategy and developmental period of the parasitoid, extends the predictable PMI_{min} compared to using only the host development time. *Tachinaephagus zealandicus* is a chalcid wasp originally native to the southern hemisphere, but now also established in Europe and North America after its release for the purpose of biological pest control. It develops gregarious as an endoparasit on various forensically relevant fly species. The first discovery of *T*. *zealandicus* on a human corpse inside a puparia of the blowfly *Phormia regina* (Meigen, 1826) (Diptera: Calliphoridae) in Germany is described and the potential of this species and other parasitoids for forensic casework is discussed.

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Die Überschwemmungsmücke *Aedes vexans* (Diptera: Culicidae) – Biologie und Ökologie unter besonderer Berücksichtigung der potenziellen Blutwirte

Nehls, H.; Kampen, H. & Werner, D.

Die Stechmückenart *Aedes vexans* kommt nicht nur deutschlandweit vor, sondern nimmt auch in ihrer weltweiten Verbreitung immer mehr zu. Kenntnisse über die Biologie und Ökologie dieser Art sind für Vorhersagen zu ihrem Verhalten und ihrer Verbreitung von essenzieller Relevanz.
Die Bezeichnung „Überschwemmungsmücke“ verweist auf die Wahl der Bruthabitate und den Ort der Entwicklung der Mücke. Die Eier werden auf feuchtem Untergrund meist in Auebereichen oder Wiesengebieten entlang von Flüssen, Bächen oder Seen abgelegt. Erst nach der Embryogenese, deren Dauer temperaturabhängig ist, und Flutung der Flächen, z. B. durch ein Regen- oder Überschwemmungsereignis, schlüpfen die Larven. Während der Großteil der Larven nach dem ersten Überschwemmungsereignis schlüpft, wartet ein kleinerer Teil in den Eiern auf nachfolgende Flutungen.
Besonders als Folge eines Massenaufkommens können die weiblichen *Ae*. *vexans*-Weibchen auf der Suche nach Blutwirten sehr große Flugdistanzen zurücklegen. Dabei dringen sie oft in Siedlungsbereiche ein, wo sie zu einer Plage für Menschen und Tiere werden können.
Das Spektrum der Blutwirte wird sehr unterschiedlich beschrieben. Während in der Fachliteratur meistens eine ausschließliche Blutaufnahme an Säugetieren genannt wird, gibt es auch Untersuchen, nach denen Vögel als Blutwirte akzeptiert werden. Im letzteren Fall könnte *Ae*. *vexans* als Brückenvektor für Krankheitserreger dienen, für die Vögel Reservoir- oder Transportwirte sind. Aus Wildfängen von *Ae*. *vexans* wurden bereits diverse Viren, *Francisella tularensis* und Dirofilarien isoliert, und in Laborversuchen wurde die Vektorkompetenz für weitere Viren nachgewiesen.
Allgemein existieren zur Biologie, Ökologie und Vektorrolle von *Ae*. *vexans* noch zahlreiche Wissenslücken, Unklarheiten und Widersprüche, die weitere Untersuchungen der Spezies erfordern. Möglicherweise sind diese darin begründet, dass *Ae*. *vexans* keine einheitliche Art ist, sondern ein Artenkomplex darstellt. In diesem Kontext gibt es Hinweise darauf, dass auch die europäische Mückenvariante genetisch nicht homogen ist.

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Medical importance of ants

Pospischil, R.

Ants (Hymenoptera, Formicidae) are one of the most successful insect families in the world due to their eusocial lifestyle and effective defense strategies. In nature, ants are of great ecological importance. In the last decades more than 200 species were displaced

from their natural habitats mainly by international trade. Mainly species with low demands on their habitat and invasive potential became a medical problem in their new habitats especially in urban areas. Due to their eusocial associations, in which the survival of the entire colony and the clear allocation of tasks among the workers are crucial, even small numbers of ants can establish large colonies within a short time that extend over large territories after settling in a new habitat. Their effective defense strategies in conjunction with the large number of individuals are further prerequisites for their success.

The Ponerinae are an anciant subfamily whose members are mainly found in warmer regions. The workers have a sting that is used for defense and, in some species, also for killing small arthropods. The colonies are mostly subterranean and have less than 200 individuals. In Europe *Hyoponera punctatissima* lives in greenhouses in the soil and is occasionally carried with potted plants into other buildings, where residents may be stung. *Dinoponera* species have a body length of 30 mm and are among the largest ants in the world. They live in the rainforests of Latin America and possess a paralyzing neurotoxic peptide which belongs to the neurotoxins. It paralyzes insects and is considered extremely painful for humans.

Many species oft the Formicinae, like the genera, *Lasius*, *Formica*, and *Camponotus* can cause skin injuries through bites and skin irritation especially in the wound areas by spraying secretions from their abdominal glands including formic acid. The workers of *Lasius fuliginosus* produce additionally a sweet smell which can be detected near the nests by humans and consists of dendrolasin and undecane in their mandibular glands. These compounds are released, when the nest is disturbed or threatened. The two substances serve to put the entire nest on alert and also have a deterrent effect on other insects species with special regard of ants.

The Dolichoderinae do not have a stinger and the workers defend their area aggressively when disturbed with the help of their mandibles and the toxic secretions released simultaneously from the acidoporus at the rear end of the gaster. The species of the *Tapinoma magnum* complex produce ketones and dialdehydes, which are highly toxic to practically all other ant species. The dialdehydes prevent the toxic ketones from evaporating, so that their effectiveness is maintained for a longer time.

Many members of the Myrmicinae have a functional sting and produce protein-containing poisons, which vary greatly depending on the genus. The stings can cause severe and long-lasting skin reactions in sensitive people.

The venom of fire ants (*Solenopsis* spp.) consists of piperidine-containing alkaloids. The sting causes a burning pain and the formation of necrotic pustules. The symptoms can last for several days to weeks. *Pogonomyrmex* species produce hyaluronidases and phospholipases, which are responsible for the toxic skin reactions to stings.

The bulldog- and jumper-ants of the subfamily Myrmecinae have a proteinaceous venom which consists of eight components. Due to the very small amounts of toxins synthesized in the glands and the small size of the individuals very little is known about the venoms of ants until today.

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The implications of field survey design for insect species distribution modelling

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Species distribution models are extensively applied in insect research, playing a vital role in conserving insect biodiversity, protecting endangered insect species, and identifying high-risk areas for vector-borne diseases. A key component of these models is occurrence data, which documents the presence or absence of insect species. By integrating occurrence data with environmental variables, species distribution models delineate the ecological niche of a species. They then identify sites that fall within the defined niche boundaries. Based on the degree of fit, these models generate suitability maps, highlighting areas where an insect species can potentially establish itself under specific environmental conditions.

However, insect occurrence data is often biased. For example, urban areas, easily accessible locations, or regions with similar environmental conditions may reflect only a subset of a species' broader ecological niche, where detection is easy. Opportunistic citizen science approaches, such as insect sampling in projects like "iNaturalist", "naturgucker" or systematically focused initiatives like mosquito sampling in the "Mückenatlas", further exacerbate these biases by gathering data at unsystematic times and locations across extensive geographic areas. Ignoring these biases may profoundly affect modelling results. While alternative methods to account for such biases have been developed, algorithmic bias

correction can introduce uncertainty regarding the reliability of the results.
This presentation will show how the design of insect field surveys influences subsequent modelling outcomes. Ideal structures of an occurrence dataset from a modelling perspective will be highlighted, and strategies to enhance data reliability for insect distribution modelling without introducing new uncertainties will be proposed. Additionally, the critical importance of absence data compared to presence data in insect research will be explained. Finally, the relationship between field survey practices and the limitations of distribution modelling will be discussed, aiming to foster interdisciplinary efforts in understanding insect habitat ecology.

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Identification of bacterial isolates and the mutualistic symbiont of *Triatoma infestans*, vector of Chagas disease– A review

Schaub, G.

There are around 150 triatomine species in Latin America, many of which are naturally infected with the protozoan *Trypanosoma cruzi*, the causative agent of Chagas disease. The flagellate develops in the intestinal tract together with the microbiota, including mutualistic symbionts. These are only known for one triatomine species, *Rhodnius prolixus*. Therefore, we focused on another important vector, *Triatoma infestans*, using samples from the field. Based on colony morphology and Gram staining, we separated 16 different isolates and identified them using classical methods and molecular analysis. In addition to eight different *Bacillus* spp., *Moraxella nonliquefaciens*, *Micrococcus varians*, and *Candida* sp. we classified five Actino-mycetales isolates: *Streptomyces* sp., *Cellulomonas* sp., *Rhodococcus* sp., and two *Rhodococcus triatomae*. After separate infections of sterile nymphs of the third instar of *T. infestans* with these isolates, only the two *R. triatomae* isolates permanently colonized the intestinal tract. The symbiont of *R. prolixus*, *Rhodococcus rhodnii*, did not establish in *T. infestans*. Other Actinomycetales that are weakly pathogenic to mammals, *Nocardia farcinica*, *N. asteroides* and *Rhodococcus equi*, colonized the intestinal tract of *T. infestans*. When comparing the effects of infection, the nymphs infected with non-Actinomycetales and *N. asteroides* did not develop into adults. All other Actinomycetales, including the non-establishing *R. rhodnii*, allowed develop-ment to the adult stage, but reproduction rates differed greatly. *R. rhodnii* was sufficient for the production of some eggs, but 80% of these were sterile. *Nocardia farcinica*, *R. equi*, and *Rhodococcus* sp. were partly symbiotic, resulting in more eggs, but about 40% were sterile. Groups infected with the two *R. triatomae* isolates produced the highest number of eggs, of which only about 20% were sterile. Since the two known symbionts of triatomines are species of the genus *Rhodococcus*, the compounds that support the normal development of the nymphs should be identified.

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Stechmücken-übertragene Krankheitserreger in Stechmücken (Diptera: Culicidae) in europäischen Zoos und Tierparks

Telli, N.; Werner, D. & Kampen, H.

Faktoren wie Klimawandel, Globalisierung und veränderte Lebensräume haben zur Ausbreitung von einheimischen und invasiven Stechmückenarten sowie von ihnen übertragener Pathogene in Europa geführt. Unter diesen stellen Viren, Protozoen und Filarien ein erhebliches Risiko für Mensch und/oder Tier dar.
Zoos und Tierparks bieten eine Vielzahl heimischer und nicht-heimischer Wirbeltierarten als potenzielle Blutwirte sowie geeigneter Brutstätten für Stechmücken. Aufgrund ihrer vielfältigen Ökosysteme spielen sie eine bedeutende Rolle für die Übertragung von Stechmücken-assoziierten Krankheitserregern. Untersuchungen auf verschiedenen Erdteilen verdeutlichen die Funktion von Zoos und Tierparks als Sentinelstandorte für das Auftreten von vektorbasierten Krankheiten. Durch den Einsatz verschiedener Fangmethoden konnten in Zoos zahlreiche potenzielle medizinisch und veterinärmedizinisch relevante Krankheitserreger in Stechmücken identifiziert werden. In Europa sind solche Untersuchungen noch spärlich. In Deutschland konnten in Zoos und Tierparks allerdings bereits diverse Pathogene wie Viren (z.B. Sindbis-, West-Nil- und Usutu-Viren), Hämosporidien (*Haemoproteus* spec., *Leucocytozoon* spec. und *Plasmodium* spec.) und Filarien (*Dirofilaria repens*, *Setaria tundra*) in gefangenen Stechmücken nachgewiesen werden. Ähnliche Studien existieren aus einigen Zoos anderer europäischer Länder: in Mückenweibchen des *Culex pipiens*-Komplexes wurden z. B. im Zoo Barcelona diverse Hämosporidien (*Plas-*

modium sp., *Haemoproteus* sp.) und im Zoo London das Usutu-Virus detektiert.
Vor dem Hintergrund eines Überblicks über die in Europa nachgewiesenen Pathogene in Stechmückenfängen aus Zoos und Tierparks werden vorläufige eigene Ergebnisse zum Pathogen-Screening von Stechmücken, die in deutschen Zoos gefangen wurden, präsentiert. Die Bedeutung der gefundenen Krankheitserreger für Mensch und Tier sowie die Vektorkompetenzen der infizierten Stechmückenarten werden diskutiert. Die Datenlage regt zur Intensivierung der Überwachung von Zoos sowie weiteren Vektorkompetenzstudien mit europäischen Stechmückenarten an.

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Deutschlandweites Monitoring von Gnitzen (Diptera: Ceratopogonidae) auf landwirtschaftlichen Betrieben, April–Oktober 2021

Voigt, A.; Kampen, H. & Werner, D.

Gnitzen der Gattung *Culicoides* (Diptera: Ceratopogonidae) sind Vektoren von Arboviren mit besonderer veterinärmedizinischer Bedeutung. Hämatophage weibliche Gnitzen der *obsoletus*-Gruppe und des *pulicaris*-Komplex gelten als Hauptüberträger des Blauzungenvirus und des Schmallenberg-Virus, die Erreger der Blauzungenkrankheit und der Schmallenberg-Krankheit. Infiziert werden können Rinder, Schafe, Ziegen, Wildwiederkäuer und Neuweltkameliden. Die Blauzungenkrankheit ist eine, meist akut verlaufende, anzeigepflichtige Tierseuche, deren Überwachung und Eindämmung in der EU-Verordnung 2020/689 geregelt sind.
Von April bis Oktober 2021 wurden bundesweit auf 17 ausgewählten landwirtschaftlichen Betrieben mittels BG Sentinel-UV-Licht-Fallen phototaktisch positiv reagierende *Culicoides* Weibchen angelockt und gefangen. Die Probennahmen wurden von Landwirten vor Ort durchgeführt, die einmal pro Woche für 24 Stunden die Fallen in Betrieb nahmen. Die Weiterverarbeitung der Gnitzen erfolgte im Labor mit der morphologischen Bestimmung in die Untergattungen *Avaritia* und *Culicoides*, in andere *Culicoides* und andere Ceratopogonidae. Die Untergattung *Avaritia* umfasst die Arten der *obsoletus*-Gruppe, die Untergattung *Culicoides* umfasst die Arten des *pulicaris*-Komplex.
Im Untersuchungsjahr 2021 konnten insgesamt ca. 620.000 Gnitzen gefangen werden, davon stellten die Individuen der Untergattung *Avaritia* den Hauptanteil mit ca. 87%. Die Untergattung *Culicoides* machte ca. 6% der Fänge aus, andere *Culicoides* und andere Ceratopogonidae kamen jeweils auf ca. 3%. Im gesamten Untersuchungszeitraum von KW 13 bis KW 43 konnten Gnitzen gefangen werden, wobei ab KW 22 eine wöchentliche Zunahme der Fangzahlen bis zum Maximum in KW 29 mit über 70.000 Individuen zu verzeichnen war. Hervorzuheben ist ein Fallenstandort in einem Rinderstall in Baden-Württemberg, der mit ca. 358.000 gefangenen Gnitzen (*Avaritia* 97%, *Culicoides* 1%, andere *Culicoides* 0,5%, andere Ceratopogonidae 1,5%) den Großteil der Fänge in der Untersuchungsperiode ausmachte.
Ziel des Monitorings war es, die äußerst limitierte Datenlage zum räumlichen und zeitlichen Auftreten der potenziellen Vektoren, deutschlandweit zu verbessern und dadurch die aktuelle und zukünftige Gefährdungssituation in Deutschland durch Gnitzen-übertragene Viren besser beurteilen zu können.

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Cellular and functional characterisation of a reproductive immune organ in female bedbugs (*Cimex lectularius*)

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Reproductive immunity (RI) investigates interactions of microbes, gametes and host immune system on a molecular and cellular level. It is mostly restricted to the medical and veterinary field focussing on fertility and sexually transmitted diseases. The common bedbug *Cimex lectularius* L., 1758 is an excellent model for RI that allows researching the molecular and cellular foundation of gamete-immune cell interactions without the influence of adaptive immune factors.
Bedbug reproduction involves traumatic insemination (TI), where the ejaculate is injected directly into the female body with a needle shaped intromittent organ. This comprises two main peculiarities: i) sexually transmitted microbes are directly introduced into the body cavity, and ii) sperm are transmitted without involvement of the female reproductive tract and come into direct contact with the haemocoelic immune cells, posing the danger of being recognised as harmful intruders. Both factors are detrimental for the female health and reproductive success. A female counter-adaptation to TI is the mesospermalege (MSL), an immune organ with short term sperm storage function, which localises at the site of TI. It is filled with single amoeboid cells

and serves as immunological checkpoint that clears the ejaculate from cointroduced microbes. This process demands a high degree of specialization that allows the MSL cells to recognize and remove microbes while sperm are spared.
We analysed the cellular and anatomical composition of the MSL, developed an in vitro system using MSL cells to study phagocytosis and other immune mechanisms, and developed a flow cytometry protocol for high throughput analyses. Using this novel platform for the study of innate reproductive immunity, we analysed the functional and cellular composition of the MSL and the influence of male factors on female immunity. Here, we present the cellular subpopulations of the MSL, functional differences between these populations and the first results targeting the question whether male derived factors influence the female cellular immune response. We propose the MSL as a promising model system for both in vitro and in vivo analyses of mating related immune mechanisms that helps to unravel the cellular and molecular basis of RI.

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Effects of larvae density and temperature on the development of *Aedes aegypti* (Diptera: Culicidae)

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The container-breeding yellow fever mosquito, *Aedes aegypti*, is the primary vector for dengue and Zika virus, posing a significant risk in tropical and subtropical regions. Understanding its breeding ecology is crucial for predicting vector capacity of mosquito populations. Moreover, the environmental conditions during larval development can lead to carry over effects, influencing fitness parameters of the emerging adults, such as longevity. This study aims to investigate the effects of temperature and larval density on larval development time and emergence rates, as well as the sex ratio and wing size of the emerging adults.
Among the factors influencing larval development, density-dependent resource limitation and temperature play important roles. To quantify density and temperature impacts, laboratory experiments in mesocosms were performed. First instar larvae of *Ae*. *aegypti* were reared in plastic food storage containers filled with 0.4 L of tap water in controlled climate chambers. The densities consisted of 10, 100, and 1.000 specimens per container. The experiments were carried out at two temperature profiles with daily fluctuations: 19–24°C (Ø=21,5°C) and 22–27°C (Ø=24,5°C) with the temperature peaking daily at noon. Each treatment combination was replicated four times. Replicates received a single dose of food at the start of the experiment. The initial feeding dose was 0.5 g of commercial fish food, with a reduced dose of 0.25 g for a follow up trial. Data on emergence rates, development time and gender distribution were collected. In addition, mosquito wings of the emerged adults were removed, and photographed to measure wing length, which is considered an indicator for adult fitness parameter. The collected data was analysed through univariate statistical analysis and structural equation modelling.
Emergence rates depend on the initial density. In the initial trial, an emergence rate of 95% was observed for the 10 larvae density in both temperature treatments. The emergence rate in the 100 larvae density was 84.5% in the high temperature treatment and 90% in the low temperature treatment. In the high-density treatment, larvae emergence rates were 15.4% and 16.8% respectively. A shorter development time between males and females was observed over all treatments and replicates. The mean development time of larvae exposed to the high temperature treatment was 11.6 days for males and 12.5 days for females. For the low temperature treatment, mean development time were 14.6 days and 16.1 days, respectively. Generally, larvae exposed to the higher temperature treatment developed approximately three days faster. The results indicate a change in sex ratio with increasing larvae density. In the high density with 1.000 larvae, the mean ratio of emerged males to females was approximately 2:1, compared to 1:1 in the 100 larvae and 10 larvae densities. Wing morphometrics will be used to analyse the effects of temperature and larval density on the wing shape and size. This study demonstrates that temperature and larval density strongly influence the population development of *Ae*. *aegypti*, providing critical insights to accurately predict its vector capacity.

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Sektion Morphologie, Systematik, Evolution / Section Morphology, Systematic, Evolution

Talks

sorted by category and main authors

Keynote

Spider mating systems: finding, choosing and securing mating partners

Uhl, G.

Spiders constitute the most significant group of natural predators of insects. It is estimated that 400–800 million tons of insects are consumed by spiders globally each year–a quantity surpassing that consumed by birds. Despite the fact that spiders are not generally perceived as charismatic organisms, comprehensive knowledge of their biology is essential for understanding ecological interactions. This presentation will examine the predominantly solitary lifestyle of spiders, with particular emphasis on their mate-finding strategies, mating rituals, mate selection processes, and reproductive peculiarities. Additionally, we will explore the sophisticated adaptations that enable females to maintain control over reproduction post-mating, as well as the mechanisms employed by males to ensure paternity. The focus will primarily be on European spider species, with the aim of elucidating the fascinating characteristics of these insectivorous arachnids that inhabit our immediate environment.

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Morphological Features and Genetic Differentiation of *Lymantria dispar* Populations in Kazakhstan: Evolutionary Aspects of Asian and European Race Introgression

Dairbekova, Z.; Dulat, B.; Makhambetov, A.; Sagitov, A. & Gritsenko, D.

The spongy moth (*Lymantria dispar*) is a significant forest pest, causing severe ecological and economic damage due to its highly polyphagous nature and capacity to devastate vast forested areas. Previous studies based on morphological and molecular analyses identified the presence of the Asian subspecies (*L. dispar asiatica*) or the European subspecies (*L. dispar dispar*) with Asian introgression in Kazakhstan. This study investigates the genetic diversity and distribution of *L. dispar* subspecies in Kazakhstan, a region situated at the intersection of European and Asian populations, using molecular methods.
Subspecies identification was conducted using real-time PCR with probes containing single nucleotide polymorphisms in the 5' region of the mitochondrial cytochrome c oxidase I gene and the nuclear marker „FS1," enabling detection of Asian introgression (Stewart et al. 2016). Genetic diversity was assessed through polymorphic DNA analysis with randomly amplified polymorphic DNA (RAPD) markers. Five markers namely AB1-4, AB2-2, AB6-15, AB9-3, and UBC278 revealed high levels of polymorphism among the analyzed samples. Population structure was examined using STRUCTURE 2.3.4 software and phylogenetic trees based on Nei's genetic distances.
Molecular analysis was performed on 85 *L. dispar* samples from nine populations collected from various host trees across southern Kazakhstan in 2023. Mitochondrial and nuclear markers identified *L. dispar dispar* with prominent Asian introgression in most samples, indicating extensive hybridization between European and Asian subspecies. Among the 85 samples, 83 showed markers of Asian introgression, while two samples were exclusively of the European subspecies. No samples of the pure Asian subspecies (*L. dispar asiatica*) were identified.
The genetic structure of spongy moth populations revealed substantial diversity. The RAPD markers produced between 17 fragments (AB2-2) and 26 fragments (UBC278). STRUCTURE analysis, with Evanno method optimization, indicated optimal cluster numbers of K=2, K=4, and K=9. At K=2 and K=4, three main genetic groups were identified with varying levels of diversity. Two groups, comprising samples from Ketpentau, Sumbe, Almaty, Butakovka, Pavlodar, and Sharbakty, exhibited high genetic homogeneity. In contrast, the third group, encompassing samples from Kazachka, Zhelezinka, and Yertis, displayed high genetic diversity. At K=9, populations were further divided into four groups. Two groups, including samples from Almaty, Butakovka, Pavlodar, Kazachka, and Sharbakty, were genetically homogeneous. Samples from Ketpentau and Sumbe exhibited high heterogeneity, while the fourth group displayed significant heterogeneity, reflecting intensive hybridization. Phylogenetic analysis using Nei's genetic distances corroborated these findings, showing close relationsh*ips* between populations from Ketpentau and Sumbe, as well as between Almaty, Butakovka, and Pavlodar.
The detection of Asian introgression, particularly in flight-capable females, underscores

the potential for rapid and widespread dispersal, complicating pest management efforts. This study offers critical insights into the genetic dynamics of *L*. *dispar* in Central Asia, emphasizing the necessity of integrated pest management strategies. The observed genetic diversity and hybridization patterns warrant further research using advanced genomic tools to monitor population dynamics and mitigate the ecological and economic risks posed by this invasive species.

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Reference:

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New insights into the taxonomy of the wasp-mimicking mantispid genus *Euclimacia* from Southeast Asia (Neuroptera: Mantispidae)

Ehlers, S.

Euclimacia is a remarkable genus of Mantispidae with 33 described species. Despite its striking body coloration and sometimes remarkable size, the genus is poorly studied. The majority of species is described based on a single or very few specimens. Historically, coloration has been employed as the most important diagnostic character, but intraspecific variation is almost unexplored. Even more, it cannot be excluded that the color pattern of species in *Euclimacia* is polymorphic based on available mimicry models. In this presentation, I will provide an overview of *Euclimacia*, highlighting the challenges associated with studying this genus. I will present recent findings and contribute to a deeper understanding of its diversity and taxonomy.

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Der Levitator: Multiperspektivische Bildgebung und 3D Modellierung von Insekten mittels Ultraschallwellen

Klug, N.; Kramer, M.; Mazrek, F.; Wührl, L.; Shirali, H.; Meier, R. & Pylatiuk. C.

Die Identifizierung bekannter Insektenarten und Entdeckung neuer Arten stellt eine komplexe Herausforderung dar, da sie häufig die Betrachtung der Insekten aus verschiedenen Perspektiven erfordert. Die automatisierte 3D Rekonstruktion kann den Prozess erleichtern und die Arbeitsbelastung der Taxonom:innen verringern, indem sie umfassendere Informationen für die Identifizierung und Beschreibung der Arten bereitstellen. Traditionelle Methoden der 3D Modellierung erfordern häufig die Fixierung der Insekten mit Nadeln, um sie vor der Kamera zu positionieren, was jedoch das Exemplar beschädigen kann.
Am Karlsruher Institut für Technologie, in Zusammenarbeit mit dem Naturkundemuseum Berlin, wird eine innovative Methode entwickelt, die diese Einschränkungen überwindet. Durch den Einsatz von akustischer Levitation können kleine und leichte Insekten in der Luft schwebend und ohne Pin positioniert werden. Entweder können die Ultraschallsender so gesteuert werden, dass sie die Insekten mittles Druckwellen in der Luft halten und um die eigene Achse drehen, damit eine stationäre Kamera Bilder aufnehmen kann, oder eine Kamera kann um das stationär schwebende Insekt geführt werden.
Die aufgenommenen Bilder werden anschließend mit Hilfe von Photogrammetrie oder maschinellem Lernen zu fotorealistischen 3D-Modellen verarbeitet. Diese Modelle ermöglichen es Entomolog:innen, die Insekten aus jeder gewünschten Perspektive zu betrachten und unterstützen die taxonomische Klassifizierung. Sie bieten zudem die Möglichkeit zur kollaborativen Forschung, indem digitale Modelle anstelle physischer Exemplare geteilt werden. Die 3D-Modelle tragen auch dazu bei, Messungen zur Bestimmung von Biomasse und Körpergrößenänderungen durch den globalen Klimawandel zu erleichtern.

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When opposites attract–Extinct *Glaesacarus rhombeus* interacting with the bradytelic *Polyxenus* aff. *P. lagurus*

Le Cadre, J.; Melzer, R.R.; Hammel, J.U. & Arce, S.I.

The discovery of morphologically stable groups/lineages and the conceptual development of ”Living Fossils“ led to new debate and understandings on how “Evolution” is at work. To this date this concept is still debated and is we do not have yet the full grasp. Evolution is not only directed toward strong changes at normal rate (“horotely”), nor high rates (“tachytely”), but sometimes lineages adapt at a slower rate (“bradytely”). These groups adapting at slower rates, which seem to undergo a certain stasis can be considered “champions at survival”, overcoming evolutionary challenges without experiencing major changes over long-period of time.

The group of bark-dwelling millipedes (Diplopoda, Penicillata), present for at least 130 million years is likely one of these bradytelic group: most fossils can be identified to extant groups. In this research we have uncovered a new well-preserved female specimen of *Polyxenus* in Baltic amber (40 mya), that is surprisingly undistinguishable from the extant species *Polyxenus lagurus*, one of the most widespread millipedes in Europe. The persistence of their habitat, i.e., living along tree-bark, stable behaviors, and possibly reproduction (i.e., telythokous parthenogenesis) likely explain this long-term persistence.
Within that amber piece this specimen was not alone, but was accompanied with two specimens of *Glaesacarus rhombeus*, a species of mites (Acari). *Glaesacarus rhombeus* ecology is thought to be linked with a life on tree and tree resin, resulting in their omnipresence in Baltic amber and Rovno amber >15% of occurrences). However, surprisingly, they are now completely extinct and yet their ecology is still unknown: hyphae-feeders, algae-feeders, saprophagous, or all at once.
All specimens are exceptionally well-preserved but these two groups are not only syninclusions. Indeed, what is more signals of specimens interacting with each other ("Frozen behavior") can also be found in the syninclusion, or at least the mites did. Although no direct interaction is visible (i.e., mites attached), one of the mites is entangled in the defensive setae of the millipede and their location on the ventral side of the millipede is intriguing. Three possible stories of this common encapsulation can be concluded from the characteristics of the syninclusion: 1) Post-mortem interaction; 2) Interaction while alive; 3) Shared microhabitat.

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Exploring molecular data from pinned beetles: Chances and challenges

Lukic, D.; Gerstmeier, R.; Petersen, M. & Eberle, J.

Molecular data is essential to many biological disciplines, including systematics, taxonomy, population genetics, and conservation, among others. However, obtaining such data often presents significant challenges, such as finding specimens, obtaining collection permits, the political situation in the countries, and the time and financial costs associated with travel. One example is the bee-beetles (Cleridae: *Trichodes*), a well-known genus to most entomologists and well-represented in collections. It has a wide distribution across the Palearctic, North America and Africa, comprising 94 species. While some of them are abundant, others are rarely found and therefore, their evolutionary history is poorly understood. These circumstances make *Trichodes* an ideal model system to explore alternative sources of molecular data. In the drawers of natural history museums and private collections dry preserved material is a rich source even for rare species from all over the world. These collections represent a valuable yet underutilized resource for obtaining molecular data. To unlock this potential a better understanding of both the quality and quantity of historic DNA, as well as the most effective methods for extracting high-quality DNA isolates from these specimens is required. In this study, we analysed three methods of DNA extraction from dry-preserved material and examined how dry preservation impacts DNA quality. Our findings revealed a large variability in DNA concentration between samples. Fragment length data indicated an initial rapid decline in fragment size, followed by a much slower rate of degradation. On average, the fragment sizes were 78 base pairs (bp), which is shorter than those observed in butterflies. Future research is needed to investigate the reasons behind these differences in fragment lengths across taxa.

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Analysis of the odorant receptor gene repertoire in newly generated genome from the darkling beetle species *Carchares macer*

Palitzsch, K.; Korsching, S. & Wiehe, T.

Within our sub-project of the interdisciplinary CRC1211 'Earth evolution at the dry limit', we investigate the evolution of organisms under extreme climate conditions over short periods of time. We are interested in understanding the impact of extreme aridity on evolutionary dynamics and adaptation. Within the group of insects, beetles (Coleoptera), especially darkling beetles (Tenebrionidae), are particularly successful in colonizing desert habitats. To investigate such adaptation processes, genes involved in environmental interactions are useful models. Chemosensory recognition of molecules is essential for complex interaction with the environment. The localization of food sources, the identification of toxins, the communication with conspecifics, spatial orientation or the identification and localization of predators are main functions of chemosensory perception. In insects, there are three main chemo-receptor types: odorant receptors

(ORs), gustatory receptors (GRs) and ionotropic receptors (IRs), each encoded by distinct multigene families. The family of ORs fulfills a key function for the sensory perception of volatile molecules and is subject to rapid evolution by diversification, gain and loss. This gene family is therefore particularly well suited as a model for the investigation of evolutionary dynamics in the context of adaptation. Previous authors have shown that while GRs and IRs occur within the entire group of arthropods, ORs are insect-specific, and their number varies widely between species. Expansions of the OR gene family have been observed in *Tribolium castaneum*, which belongs to the darkling beetles (Tenebrionidae). This raises whether OR expansions also occur in other Tenebrionidae and whether there are differences in the OR gene repertoires that could be correlated with lifestyle and environmental conditions. To address this question, we have annotated and characterized the OR gene repertoire in our de novo generated reference genomes of the Namib Desert native Tenebrionidae *Carchares macer* and *Brinckia debilis*. Here I will present the latest results of our research.

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Unraveling Host-Specific Genetic Divergence in *Cacopsylla melanoneura* (Hemiptera, Psylloidea, Psyllidae)

Ragionieri, L.; Corretto, E.; Serbina, L.; Stauffer, C. & Schuler, H.

Apple proliferation (AP) is a severe disease in European apple cultivation, caused by the bacterial pathogen '*Candidatus* Phytoplasma mali'. The insect vectors of '*Ca*. P. mali' are the apple psyllids *Cacopsylla melanoneura* and *C*. *picta*. The former species is associated with both apple and hawthorn, and in regions where *C*. *picta* is absent, it acts as the sole vector for the spread of '*Ca*. P. mali' in apple orchards. Laboratory experiments suggest that populations developing on apple are ecologically different from those on hawthorn. The goal of our study is to identify the genetic basis of the different reproductive host preferences in *C*. *melanoneura* and to define evolutionary significant units. To achieve this, we first generated a reference nuclear genome of *C*. *melanoneura* using a combination of long- and short-read technologies. Based on our newly generated genome, we investigated the genetic variants associated with host preferences in sympatric wild populations collected from apple and hawthorn plants across Europe (Austria, Italy, Germany, the Czech Republic, Romania, and Serbia). Mitochondrial data suggest that *C*. *melanoneura* represents a species complex with at least two cryptic lineages, while nuclear SNPs support the presence of two genetically distinct groups of individuals with different host preferences across Europe. These findings will also be useful for monitoring the spread of '*Ca*. P. mali' vectors in Europe and for gaining insights into the genetic basis of reproductive host preferences in *C*. *melanoneura*.

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Recurrent genomic dynamics linked to parallel evolution of secondary phytophagy in Hymenoptera

Reinisch, R.; Steidle, J.L.M.; Remmel, A.; Lammers, M. & Sann, M.

The phytophagous lifestyle is a key innovation in insects and has evolved in only one third of all insect orders. The evolution of phytophagy likely involves fundamental behavioural and morphological changes accompanied by chemosensory and metabolic adaptations. To date, the genomic basis and genetic innovations related to evolutionary dietary shifts are poorly understood. Here we focus on two monophyletic groups within the Hymenoptera, Aculeata and Chalcidoidea, that secondarily developed larval phytophagy independently several times. To shed light on evolutionary processes that shaped the diversity of nutritional adaptations in Hymenoptera we address the following main research questions: (1) Is parallel evolution at the phenotypic level reflected by parallel genome evolution? And (2) did similar genomic innovations appear when independent lineages realized convergent dietary transitions? Here I want to introduce the current state of the project and give insights into newly sequenced genomes of representative phytophagous aculeates. These genomes will be the basis of further analyses that will be of interest to scientists in the fields of functional genomics, systematic biology and protein function analysis of insects.

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Citrus in Rescue: Revision of the genus *Diaphorina* (Hemiptera: Psylloidea: Psyllidae) using morphological and molecular techniques

Serbina, L.; Van Dam, A.; Mauda, E.V.; Maseko, Z. & Burckhardt, D.

The psyllid genus *Diaphorina* comprises over 80 described species and at least as many undescribed ones in the Old World. Its most

prominent member, *Diaphorina citri*, is the vector of the bacteria '*Candidatus* Liberibacter', which cause the economically devastating Huanglongbing (HLB or Citrus Greening disease). This species likely originated in China or India and is now widespread in tropical and subtropical Asia, the Americas, and parts of Africa, including Benin, Kenya, Nigeria, and Tanzania. However, it has not yet been detected in South Africa, where it is continuously monitored. Unlike most psyllid genera, which are typically restricted to a single host family or order, *Diaphorina* develops on plants from over 18 families across several unrelated orders. Despite this wide host range, the genus is morphologically homogeneous, making species identification challenging, especially when multiple species co-occur. Based on new field collections and museum material, 20 new *Diaphorina* species from South Africa are described using both molecular (e.g. DNA barcoding) and morphological data, with at least as many remaining to be described. This project also aims to develop modern tools to facilitate rapid species discovery and to design new methods for automated identification, employing machine learning techniques for geometric morphometrics.

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Insights into the Paleodiversity of Paleogene Hymenoptera (Insecta) and their interactions with flowers

Wedmann, S.; Bouchal, J.M.; Boudet, L.; Engel, M.S.; Geier, C.; Grímsson, F.; Poschmann, M.J.; Schindler, T. & Wappler, T.

Insects are extraordinarily species-rich and critical plant-insect interactions have evolved to benefit both lineages, especially via pollination biology. Our project explores the evolution of insect-flower interactions by investigating the paleoecology of select groups of hymenopteran insects (e.g., bees and diverse wasps). The paleobiodiversity of fossil Hymenoptera is explored in close comparison to extant taxa. From analysis of in-situ pollen grains preserved on or in the bodies of these insects, conclusions will be drawn on the ecological roles of different hymenopteran lineages. Insights into foraging behavior, feeding behavior, and pollination biology will contribute to our understanding of the evolution of flower-insect interactions from the globally warm Eocene, through the gradual cooling of the Oligocene, and ultimately to our current environments and climates. The research focuses on the Eocene Fossillagerstätte Messel (Germany) and on the Oligocene Fossillagerstätte Enspel (Germany). Both fossil sites have yielded numerous excellent preserved hymenopterans, and well-preserved in-situ pollen grains can be extracted from those fossils. Innovative methods are employed to identify the fossil pollen grains, aiming to classify them with extant plant families and genera. These insights will enrich the fossil record of the studied groups and widen our knowledge of paleoecology.

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Sektion Künstliche Intelligenz in der Entomologie / Section Artificial Intelligence in Entomology

Talks

sorted by category and main authors

Keynote

Globally standardised species monitoring with insect camera traps and deep learning models

Høye, T.T.

With computer vision and deep learning, insect camera traps have become important tools to improve our understanding of insect responses to environmental change. Through computer eyes, it is potentially possible to effectively, continuously, and non-invasively observe insects throughout diurnal and seasonal cycles and deep learning models can provide estimates of their abundance, biomass, and diversity. I will unpack and visualize the rich and multidimensional data that novel camera-enabled monitoring systems are capable of generating automatically and in a globally standardized manner. Through results from national and continental scale pilot programs deploying insect camera traps, I will provide a glimpse into the insights that can be derived from the trap images and what the future of automated insect monitoring might look like. I will also highlight outstanding challenges and future research avenues to facilitate the broad scale implementation of insect camera traps for day active and nocturnal insects.

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An efficient artificial intelligence technique for identification of individual pests and beneficial insects: A case study of Colorado potato beetles and ladybirds

Aminu, R.; Cook, S.M.; Ljungberg, D.; Hensel, O. & Nasirahmadi, A.

Sustainable agricultural practices aim to protect agricultural produce against insect pest damage while preserving biodiversity and the environment. However, insecticide applications are currently not targeted against individuals but are applied as blanket treatments across all parts of the field. This implies that a significant portion of the applied insecticide does not reach its intended target; instead, it pollutes the environment. A key approach to mitigating these effects is targeted insecticide application, which targets pests without harming the beneficial organisms and the entire ecosystem. To accomplish this, optical detection methods are required. This study explores digital imaging and artificial intelligence (AI) to develop a method for accurately detecting and discriminating between insect pests and beneficial non-targets in agricultural fields. We collected a diverse plant-insect dataset, consisting of insect pests (Colorado potato beetle, *Leptinotarsa decemlineata*) and the beneficial ladybird (*Coccinella septempunctata*) on potato plants. Using image segmentation, we identified the region of interest (ROI) in the images before extracting multiple statistic-based features representing shape, colour and texture from ROIs. We evaluated and compared four feature selection and machine learning techniques. Results showed that mutual information combined with a random forest classifier achieved the highest accuracy of 91.88% and fewer computational parameters (7.22 x107) compared to other methods. This work offers an alternative approach toward automatic insect pest identification, which facilitates the development of new pest control measures such as on-the-spot spray and mechanically targeted insect removal methods that are more environmentally friendly than the broadscale application of synthetic chemicals.

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Comparison of Machine Learning Features Predicting Flight Activity of Rapeseed Insect Pests

Fontaine, J.; Steinhaus, L.; Briem, F.; Schieler, M.; Winkler, A.; Schmitt, J. & Kleinhenz, B.

The EntoProg project develops decision support systems for several important insect pests of winter oilseed rape (*Brassica napus* L.) in Germany. Oilseed rape cultivation is threatened by various insect pests, which are difficult to control due to insecticide resistance, and restricted authorization of insecticide active ingredients or number of applications. First pest occurrence prediction can be used to improve the planning of control strategies with decision support systems. Nevertheless, currently available underlying predictive models have limited performances and scope. This is likely due to an incomplete representation of the complex insect biology and related external factors. Given the current state of knowledge, feature engineering offers a simple method to find relevant predictive features and thus to better understand the differences between pests. In this project, the

following 5 rapeseed pests have been monitored in spring or autumn since 2022 with yellow water traps: cabbage stem weevil (*Ceutorhynchus pallidactylus*), rape stem weevil (*C. napi*), pollen beetle (*Brassicogethes aeneus*), rape flea beetle (*Psylliodes chrysocephala*), and rape winter stem weevil (*C. picitarsis*). Additional data for hundreds of locations in 10 federal states of Germany produced by federal crop protection services from 2020 to 2024 were also used for modelling. First occurrence predictions by various machine learning algorithms (e.g. random forest or neural network) used data features representing time, location, weather conditions and plant variety. The data was enriched by a set of features measuring various differences in time. Robust and accurate models could be built for each pest (area under ROC curves greater than 0.90 and balanced accuracy from 0.88 to 0.96). Current and past weather conditions, together with time-related features potentially representing seasonal information were particularly important but differently used by the models for different pests. Innovative feature engineering can extend commonly used predictive variables to better represent biotic and abiotic factors important to the first occurrence prediction of rapeseed insect pests.

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Next Generation Biodiversity Assessment– Accelerating Arthropod Identification through AI

Meyer, P.; Scharnhorst, V.; Lechner M.; Haslinger H. & Meimberg, H.

Traditional methods of insect identification are fundamental to biodiversity research but quickly reach practical limits given the high diversity and abundance of species. New approaches such as metabarcoding also exhibit considerable weaknesses in terms of accuracy and verifiability of the results they produce. Our AI-based method aims to overcome these limitations to provide an efficient, reliable, and scalable solution for biodiversity assessments.

In this procedure, collected insects are first separated into different size fractions using a specially developed sorting machine, thereby optimizing them for subsequent photographic capture. A photo installation then generates high-resolution composite images in which individuals of each size class are depicted collectively. These images are analyzed by a visual detection AI within a dedicated software environment to accurately isolate individual insects and store them as separate image files. A hierarchical AI model architecture subsequently assigns each object systematically to the appropriate taxon in the taxonomic tree. This enables highly reliable identifications, with the taxonomic resolution dependent on the availability of models for each rank. While most classifications currently occur at the family level, ongoing improvements to the model structure are increasingly bringing genus- and species-level identifications within reach.

The initial results of this method are promising, demonstrating a considerable increase in both the efficiency and scope of biodiversity analyses. A pilot project further confirms the practical suitability of the approach, highlighting its potential to sustainably address existing challenges in insect monitoring.

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Using artificial intelligence to identify mosquito species based on wing images

Sauer, F.; Nolte, K. & Lühken, R.

Mosquitoes are the most important arthropod vectors of pathogens, e.g. malaria parasites or dengue virus. Global change processes such as climate change are driving the spread of mosquito species and their pathogens into previously less affected regions, such as Europe. Consequently, surveillance and monitoring programs are conducted to assess mosquito-associated health risks. Thereby, accurate species identification is essential since the medical significance varies greatly among different mosquito species. The identification usually relies on taxonomic keys based on morphological characters or molecular assays, but these methods require specialized entomological experience of the observers and well-equipped laboratories. Herein, we would like to present our research, conducted over the past few years, on the development of a cost-effective and accessible AI tool for identifying mosquito species based on wing images.

In a preliminary study, we trained convolutional neural networks (CNN) using systematically taken wing and body images of four morphologically similar *Aedes* species. The results demonstrated superior performance in wing-based compared to body-based classification. The nearly two-dimensional structure of mosquito wings is likely advantageous for CNN-based classification as it eliminates the

need for images of different body postures or perspectives and thus simplifies the standardization during the imaging process. Motivated by this, we built up a comprehensive database, which currently contains 18,104 wing images representing 72 mosquito taxa. The dataset involves images collected with three different devices: two professional stereomicroscopes and a smartphone equipped with a macro-lens. An image pre-processing pipeline was developed to eliminate undesired features associated with the different devices (e.g., background or colour variations), which could significantly improve the CNN performance. Using this approach, the trained CNN models consistently achieved an accuracy exceeding 95% in distinguishing 21 mosquito taxa and an additional "other" class, summarizing all mosquito taxa with fewer than 80 specimens available. A web-hosted application is available to provide access to the system for a wide range of users (https://balrog.bnitm.de). This prototype is currently still password-protected but can be accessed upon request by interested users. The results highlight the potential of AI to facilitate insect identification. Our system offers a valuable tool for mosquito surveillance and research, and suggest its applicability to the identification of other Dipteran insects.

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AI-driven advances in Species Identification and Biomass Analysis

Shirali, H.; Wührl, L.; Klug, N.; Meier, R. & Pylatiuk, C.

Artificial Intelligence (AI) is reshaping our understanding of the natural world, bringing transformative changes to entomology and biodiversity studies. The emergence of user-friendly AI-driven applications, recognizable in daily life through tools that identify various species from images or sounds, marks a new era in entomological research. These advancements facilitate citizen scientists' and professionals' research by simplifying species identification. However, the potential of AI extends far beyond the familiar terrains of the global North, where it has predominantly been utilized due to earlier access to advanced technologies.
In this presentation, we delve into how AI, synergized with innovative and cost-effective technologies like DIY microscopes, is breaking barriers in biodiversity research, especially in resource-limited settings. This novel approach empowers researchers to assess species diversity, abundance, and biomass efficiently, offering faster and more cost-effective ways to understand ecological patterns and change. We have advanced these efforts by applying AI to image-based biomass estimation of invertebrates. We developed methods to estimate insect biomass from single images using machine learning and image processing techniques, enabling accurate and scalable ecological assessments. Our discussion also includes a specific focus on the application of these AI techniques for analyzing bulk samples from pan-traps and Malaise traps, highlighting their utility in classifying the most common species encountered in these traps.
Furthermore, we are collaborating with colleagues from the Center for Integrative Biodiversity Discovery at the Natural History Museum Berlin to address biological problems with AI methods and engineering tools. Our collective efforts aim to bridge gaps in biodiversity research and pave the way for innovative solutions to pressing ecological questions.
Overall, our discussion aims to illuminate AI's broad capabilities in entomology, underscoring its role as a pivotal tool in global biodiversity conservation and study.

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Insect Detect 2.0: Automated plant-pollinator interaction monitoring with an AI-enabled camera trap

Sittinger, M.; Stefan, V.; Zhong, Y.; Knight, T. & Herz, A.

Monitoring of plant-pollinator interaction changes over space and time can give insights into potential drivers of declining insect abundance/diversity and quantify their effects on the essential ecosystem service of pollination. However, many of the traditional monitoring methods are time-consuming and expensive. For this reason, they are often deployed with a low number of replicates, which restricts the potential for analysis and interpretation. Automated monitoring methods require significantly less human effort and can therefore acquire data autonomously at a potentially much higher spatiotemporal resolution. In the project MonViA (National Monitoring of Biodiversity in Agricultural Landscapes), we developed and tested the Insect Detect DIY camera trap in 2023, which is based on low-cost off-the-shelf hardware components and open-source software. The first version uses an artificial flower platform as standardized attractant and background for reliable insect detection and tracking in real time with custom trained deep-learning models. A second version of the camera trap was developed in the

project SEPPI (Standardized European monitoring of plant-pollinator interactions). The modified hardware, software and models are adapted to monitor plant-pollinator interactions on real flowers, a much more challenging background for AI-based detection due to a high variety, complexity and moving vegetation. For the initial field test in 2024, we deployed a total of 58 camera traps in eight European countries at sites along differing environmental gradients. Each sampling event also included traditional monitoring methods, such as transect walks, sweep netting and pan traps. One of the goals in the SEPPI project is to investigate if it is possible to capture similar spatial trends in several response variables (e.g. pollinator diversity and composition, visitation rate) with both approaches, which would allow for a first validation of our proposed automated method for large-scale field deployment. With millions of captured images, including a broad range of flowering plant species and their visitors, we plan to curate an annotated dataset that will be used to train a general detector for flower visitors in Europe. The cropped insect images will be used to train custom classification models that are able to identify insects to differing taxonomic levels, ranging from order to species level.

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ATR-FTIR spectroscopy and machine learning for species and age identification of insect traces in forensic case work

Thümmel, L. & Amendt, J.

Fourier Transform Infrared (FTIR) spectroscopy is a fast and cost-effective method to (bio-) chemically characterize all sorts of materials and can be used to answer a variety of entomological research questions. It is based on the absorption of electromagnetic energy by the functional groups of molecules in the sample; the resulting spectra can therefore be seen as the chemical fingerprint of that sample. If the spectrometer is equipped with an Attenuated Total Reflection (ATR) unit, a diverse range of samples can be measured, as they only need to be a few square millimeters in size. However, spectroscopic data sets are high-dimensional. Therefore, supervised machine learning algorithms are required to analyze the data adequately. While models based on classification algorithms such as Random Forests or Support Vector Machines can be used to identify the insect species, regression algorithms like Support Vector Regression and eXtreme Gradient Boosting are used to determine the age of given insect material. Due to the versatile nature of ATR-FTIR spectroscopy, it has received increasing attention in the entomological field in recent years, and we will present our current application of ATR-FTIR combined with machine learning in the context of forensic entomology.
Blow flies are usually the first colonizers of dead bodies and by successfully determining the species and age of collected insect specimen at the scene, a minimum time since death can be estimated. As long as only immature stages are present on the body, the age of the oldest specimen is determined by using reference developmental data on larval growth or the time required to reach the next developmental stage. However, determining the age of a fly pupa is difficult because morphological changes are not visible from outside the puparium. This is regrettable, since this period can account for about 50% of the complete development. We used ATR-FTIR spectroscopy to improve the age estimation of the pupal stage in the blow fly *Calliphora vicina*, as well as to identify the species of (fragmented) empty puparia that are left at the crime scene after hatching of the adult flies. In addition, we tested the assumption that the spectra can be used to estimate the weathering time of these traces, which would greatly improve long-term estimates of times since death.

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Sektion Freie Themen / Section Free Topics

Talks

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Energy Allocation to Reproduction in Parasitoid Wasps: Insights from Modeling and Reproductive Biology

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In reproductive biology, species can be categorized into two groups based on their reproductive strategy: proovigenic and synovigenic species. Proovigenic species complete the egg maturation process by the time the adult emerges, while synovigenic species continue oocyte maturation during the adult stage. The ovigenic index (i.e., the fraction of mature eggs at adult emergence compared to the potential life time fecundity) is used to classify species into one of these groups. However, while the timing of energy allocation for egg maturation is clearly defined for proovigenic species, it is not as straightforward for synovigenic species. There are several substrategies in synovigenic species, e.g. ensuring a degree of flexibility in the adaptation to environmental conditions, which may explain the broad range of ovigenic indices observed, compared to the fixed value for proovigenic species.
In recent years, it has become increasingly common to model energy allocation to different physiological processes in species using DEB-TKTD models (Dynamic Energy Budget Theory-based models complemented with toxicokinetic and toxicodynamic modules). These models allow the simulation of life history alterations as a function of constant or variable conditions, such as pesticide exposure and environmental factors like temperature. However, to consider variable environmental conditions or to extrapolate from lab experiments to field conditions, it is crucial first to accurately capture the normal physiological behavior of a species under unstressed control conditions, as explained by the DEB component of the model.
The DEB model simulates the life history of an organism based on clearly defined rules for energy uptake from food and its allocation to key physiological processes, such as growth, maturation, and reproduction. Species-specific physiological rates are represented through different parameterizations, and different life cycles (e.g., those of holometabolous insects with a pupal stage) are modeled using variant model types (such as hex, hax, and hep models). For holometabolous insects, the current standard assumption is that energy is invested in reproduction only during the larval phase (using a reproduction buffer), with no further energy allocation to this buffer once the organism reaches the adult stage. One source of uncertainty in this approach is that the number of matured eggs may not necessarily reflect the actual energy invested in the reproductive buffer for egg production.
This presentation aims to address the differences in assumptions between disciplines, harmonize understanding, and discuss a case study on the development of a DEB model for the parasitoid wasp species *Aphidius rhopalosiphi*.

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Green Nanoparticles: Termiticidal effects of silver nanoparticles mediated neem plant parts on termite (*Nasutitermes kemneri* Dudley)

Olaniran, O.A.; Alao, F.O.; Lateef, A. & Adebayo. T.A.

Use of green nanoparticles plays a significant role as substitutes to synthetic insecticides in the control of insect infestations. Therefore, this experiment was conduct to study the effects of biosynthesized silver nanoparticles (AgNPs) using neem plant parts on termites. Biosynthesized AgNPs neem leaf(NL-AgNPs), neem seed(NS-AgNPs), neem bark(NB-AgNPs), mixture of neem seed+leaf(NSL-AgNPs), neem seed+bark(NSB-AgNPs), neem leaf+bark(NLB+AgNPs) and neem seed+ bark+leaf(NSBL-AgNPs) were evaluated and compared with synthetic insecticide(dichlorvos) and control. The studied insect was exposed to these treatments through contact and fumigant method. The biosynthesized AgNPs (N-AgNPs) displayed dark brown colour with maxima absorbance ranging from 215 to 216 nm. FTIR peaks at 3441, 2928, 1654, 1419, 1087 and 871 cm-1 for NL-AgNPs while 3417, 1635, 1508, 1404, 1080 and 875 cm-1 for NS-AgNPs meanwhile 3452, 1635, 1508, 1404, 1080 and 821 cm-1 for NB-AgNPs. These are the indication of the presence of alcohols and phenols in the biofabrication of AgNPs used as nano-insecticides. Biosynthesized AgNPs exhibited insecticidal effects on the Nasutitermes kemneri workers with nano neem seed, neem bark, and all other nano-insecticide mixtures had highest insecticidal efficacy (83–97%) when applied through fumigant after 24 h whereas 20–47% efficacy was observed when applied through contact. The effectiveness of the nano-insecticides increased as the hours

of exposure increased. These observations suggested that nano-insecticides killed termites faster through fumigant than contact and the biosynthesized AgNPs used as nano-insecticides had delayed effect on the target insect compared to dichlorvos. Therefore, nano-insecticides from neem plant parts can be incorporated into pest management programme of termites.

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Flower-derived environmental DNA reveals community diversity, species abundances and ecological interactions in bee pollinators

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Flower-derived eDNA holds great promise as a rapid and non-invasive tool for monitoring pollinators and their plant-associations. However, pollinators often only briefly interact with a plant and leave little eDNA, making them particularly challenging to detect. In addition, taxonomic biases in eDNA deposition and PCR amplification prevent quantitative analysis of pollinator diversity. These limitations have so far precluded the widespread use of eDNA in pollinator monitoring. Comparing flower-derived eDNA with conventional monitoring in flower strips and apple orchards, we here explore the utility of eDNA to detect community diversity, species abundances and ecological specificity of plant-associated arthropods. We show that read abundances are a bad predictor of true abundances at the community level. Instead, the occupancy of individual species in replicated flower eDNA samples provides reliable quantitative estimates of pollinator biodiversity and detects their ecological specificity very well. Also, we find that pollinator eDNA can be collected non-invasively, by washing off from flowers in the field. Our work highlights eDNA analysis as a powerful tool for the rapid future monitoring of plant-arthropod interactions and plant-pollinator networks.

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Unlocking historical plant archives to reveal long-term arthropod-plant interactions and biodiversity changes

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Community changes and interactions play an important role in biodiversity research. Long-term sampling is particularly important for detecting changes in arthropod communities. For example, studying the temporal plant-arthropod interactions can provide insights for understanding the consequences of global change in relation to their role in the establishment of terrestrial food webs. Due to a lack of standardized temporal monitoring data the specificity and longevity of interactions and changes in arthropod communities are poorly understood. Here we attempt to provide new insights into both questions using two different archived plant collections. One of these collections are herbaria. Due to the mass of historical plant records from all over the world, these are not only valuable for studying the population genetics of the plants themselves but can also provide insights into understanding the structure of plant-associated communities. We used DNA metabarcoding to analyse the arthropod communities from archived herbarium specimens of different ages and origins. The herbarium specimens yield arthropod DNA across various ecological guilds and trophic levels over multiple decades. Furthermore, specialists could be detected on their known host plants. In an experiment, we demonstrate that the typical dry storage of plants does not alter the recovered arthropod diversity and community composition. By analysing a time series of leaf samples from a forest monitoring project, we have characterized changes in arthropod biodiversity over nearly two decades. Despite major fluctuations, our results show that arthropod richness remains stable over time in the studied forest sites. Our study demonstrates the untapped potential of herbaria and plant archives to gain better insights into plant-arthropod interactions and further possibilities of monitoring spatiotemporal changes in arthropod communities.

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The lepidopteran model *Manduca sexta* forms embryonic haemocytes in a transient site of haematopoiesis

von Bredow, Y.M.; von Bredow, C.-R. & Trenczek, T.E.

Haemocytes are circulating or sessile cells in the haemolymph of insects. They are key components of the immune response, but also main players in developmental processes such as tissue remodelling and ECM deposition and degradation. We asked the question when and where these important cells are formed in the *Manduca sexta* embryo. With a tool box of species-specific haemocyte type markers we were able to resolve this question. Earlier studies were mostly confirmed: Haemocytes appear very early in embryogenesis, and the larval haematopoietic organs form during embryogenesis. Additionally, we were able to identify the spatial and temporal appearance of embryonic oenocytoids, which form in the head region at early katatrepsis. The larval haematopoietic organs form earlier in embryonic development than expected. We present a completely novel find, the formation of a paired abdominal cluster of haematopoiesis, the haemocyte clusters in abdominal segment 7 (A7-HCCs). They form at early katatrepsis, interestingly the same time point the earliest oenocytoids appear in the head, and release embryonic plasmatocytes during embryogenesis. These embryonic haemocyte clusters completely disappear before the larva hatches and are therefore a transient site of embryonic haematopoiesis. That is in stark contrast to the larval haematopoietic organs, which exhibit larval antigenic characteristics in the late embryo, and persist to the larval stages.

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Bernstein Workshop / Amber Workshop

Talks

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Keynote

Unearthing Cretaceous amber in Spain

Pérez-de la Fuente, R.

Amber, fossilised plant resin, opens unique windows into the past. Small organisms or parts of them are preserved in amber for millions of years with exceptional detail and, often, in a near life-like fashion, providing invaluable evolutionary, ecological, and behavioural data. A multidisciplinary, international team jointly led since 2014 by the University of Barcelona and the Geological and Mining Institute of Spain-Spanish National Research Council (IGME-CSIC) has been excavating and studying the Cretaceous amber from Spain and its palaeobiological content for more than 25 years. After recovering more than 200 kg of amber and discovering more than 4,000 inclusions, almost 200 species belonging to more than 15 insect orders and other terrestrial arthropods have been described. Two of the most successful lines of palaeoentomological research focus on plant-insect relationships, such as pollination, and arthropod-vertebrate interactions. Spanish amber has already become a noteworthy source of data on terrestrial ecosystems and the entomofauna that inhabited them from the Early Cretaceous, a time of profound biotic change on land, but it has the potential to keep providing exciting discoveries for many years to come.

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Exploring parasitic behaviour in Baltic amber: the case of a long-legged fly and its enigmatic companion

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A syninclusion consists of two or more organisms preserved together in a piece of amber. When there are signals of interactions between these organisms in the amber piece, it can be referred to as “frozen behaviour”. Since animals entrapped in the tree resin try to escape it, the behaviour into which they were engaged before fossilisation can be difficult to interpret. Hence, cases of clear frozen behaviour are rare. However, they are extremely relevant, since they can be used to reconstruct past interactions between organisms and their ecological roles. Most reported cases of frozen behaviour in amber are linked to parasitism sensu lato, from phoretic behaviour to parasitism sensu stricto, in which feeding is involved. Among these, ectoparasitic mites are one of the most commonly reported parasites in amber. The most compelling cases of parasitic frozen behaviour are the ones in which parasites are fossilised while still attached to their host, since there is no doubt of the interaction between these specimens. However, in such cases, the host often obscures key characteristics needed to identify the parasites.
Here we report a syninclusion in Eocene Baltic amber, in which an unidentified representative of Euarthropoda is attached to a long-legged fly (Dolichopodidae). To assess the morphology of the attached specimen, light microscopy as well as synchrotron-radiation based x-ray computed micro-tomography (SRµCT scan) were applied.
Based on the close contact with the fly and the place of attachment of the unidentified euarthropodan, it seems to be a parasitic relationship. The setae placement, striated cuticle and apparent leg shape of the unidentified euarthropodan are compatible with parasitic mite larvae (Acari) of the group Parasitengona, an ingroup of Trombidiformes. In particular, SRµCT scanning further confirms that the specimen bears three pairs of legs and reveals that the positions of the basipods (coxae) of the first and second pair of legs are close to each other, which is characteristic of the larvae of velvet mites (Trombidioidea). In fact, long-legged flies have been frequently reported as hosts of parasitengonan larvae, both in fossil and extant fauna.
However, the apparent segmentation of the posterior part of the body is not typical of velvet mites. Moreover, this resembles the larvae of certain holometabolan insects, e.g. beetle larvae. An expanded and horizontally striated idiosoma (trunk region in mites) is found in other ingroups of Trombidiformes, in which gravid females develop an extreme physogastry. Nevertheless, contrary to the reported specimen, these are four-legged adult mites. Although the identity of the specimen attached to the long-legged fly in this syninclusion remains a mystery, we here show how SRµCT scan are useful to reveal morphological details of parasites obscured by their hosts.

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Aquatic and semiaquatic bugs in Myanmar amber including insights into their behavior

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Insects have evolved extraordinary adaptations in morphology and behavior to inhabit water and the water surface. Nevertheless, the exploration of the origin and early evolution of ephemeral behaviors in insects is greatly hampered by the scarcity of fossilized evidence. Here, we present two cases from the Upper Cretaceous Kachin amber of northern Myanmar, highlighting the mating behavior of water striders (Gerromorpha, Gerrioidea) and the feeding behavior of water boatmen (Nepomorpha, Corixoidea) during the late Mesozoic. 1) The fossil record of a group of water striders Burmogerris rarus in copulation was discovered preserved in a piece of amber, showing smaller males riding on the backs of females. Morphological studies revealed the conspicuous dimorphism associated with sexual conflict: the male is equipped with a specialized protibial comb as a grasping apparatus, likely representing an adaptation to overcome female resistance during struggles. This discovery reveals a mating system dominated by males and sheds light on the potential sexual conflicts of water striders in the Cretaceous. 2) We discovered unusual nepomorphan insects in Kachin amber, exhibiting general characteristics similar to water boatmen but possessing a segmented labium, shortened and flattened tarsi (distinctly shorter than the tibiae), and well-developed, hooked claws. The phylogenetic analyses recovered the position of the new fossils as the sister lineage to Corixoidea. The new fossils exhibit several tarsal adaptations, including a curved internal margin, a serrated inner edge, and basal macrosetae. These features are known to enhance grasp strength and prey fixation supporting the interpretation of a raptorial mechanism. Given the body length of the new fossils at approximately 2.5 mm, its likely prey may have included small arthropods such as insect larvae and crustaceans from groups like Cladocera, Copepoda, and Ostracoda, as well as other small animals.

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Recognising ecological substitutions by the use of quantitative morphology

Haug, C.

Convergent evolution describes the phenomenon of two not closely related lineages of organisms that evolved similar appearing morphologies and coupled to these similar ecological functions. Setting this phenomenon in a timely frame can lead to the recognition of cases in which ecological functions have been performed by a certain group of animals at one point in history, yet after their extinction these been performed by another group that convergently had evolved a similar appearing morphology. Such a case represents an ecological substitution. The details may vary; it is possible that the second group of organisms is the direct cause for the extinction of the first one, or alternatively, the second one is not the direct cause but simply could fill an unoccupied ecological role after a mass extinction. There are few well established cases throughout Earth's history in which such events could be recognised. I present here additional cases from the group of Pterygota. Similarity between different animals, fossil and extant, has been recognised using quantitative morphology. With this framework we can also recognise cases that are not easily detectable by the naked eye. Any structure that interacts with food items is ideal for such an approach as the mechanics of handling dictates the shape of such a structure. Not closely related animals dealing with the same food items are therefore exposed to similar selective pressures, potentially leading to similar resulting morphologies. While this is not easily demonstratable for any two lineages of organisms, within Pterygota the structure of mouthparts and legs is highly conserved in their basic build, yet very flexible in their overall shape. These structures are therefore ideal for identifying cases of convergent evolution within this quantitative frame. Combined with an excellent fossil record, especially due to preservation in amber, I will present cases in which some groups had morphologies in the past that are no longer present in the modern fauna in this very group, but had evolved later in another not closely related group of Pterygota. I will discuss in how far these cases can indeed represent ecological substitutions and in how far this aspect matters for the ongoing biodiversity crisis.

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The Art of Remains: Reconstructing Fossil Organisms in a Creative Way

Haug, G.; Haug, C. & Haug, J.T.

A major part of the scientific process within different fields is the reconstruction of complex systems based on partial or incomplete information. Often this information is incomplete due to methods of research (quantum mechanics), distance between the scientist and the studied subject (astronomy, deep sea research), or being lost to time (cosmology, historical geology, palaeontology). Depending on the scientific field, these reconstructions can be displayed in a lot of different ways. Within the field of palaeontology, a for most people very approachable type of this display is palaeoart. Palaeoart is the creative process of reconstructing prehistoric organisms or even ecosystems in an artistic, interpretive fashion. Palaeoart is used in both the visualisation of less well preserved fossils, as well as in the communication of scientific discoveries to the broader public (science communication). The challenge with a lot of palaeoart is the implementation of widespread assumptions without data to back it up (for example colour and skin texture). This thin line of better visualisation for communication and too far-fetched interpretation leading to false information is the most delicate part when creating palaeoart.
In recent years we have been creating several pieces of palaeoart to better visualize and summarize our data about different holometabolan larvae. The palaeoart in such cases is to a certain extent less speculative than those of fossils from the group Vertebrata, because of the common preservation of the fossils of interest in amber. Amber provides some very good, almost life-like preservation, preserving pigments, the reconstruction of behaviour, or in rare cases even predator-prey interactions. Combining these pieces of information with the data of closer related modern relatives allows to create both visually appealing and fact-based, but still creative reconstructions.
The pieces of palaeoart, which are showcased here, depict different reconstructed behaviours from lacewing and beetle larvae preserved in amber. First we document the specimen in the amber under a light microscope to analyse them, as well as getting a good reference for the morphology of the specimen. After analysing the specimen, we look for similar morphologies within the modern fauna and draw conclusions on the behaviour of the fossil animal. The last step is trying to create a plausible reconstruction of the specimen and its behaviour with pencil, pens, and alcohol-based colour markers on 250 g/m^2 paper. Palaeoart is an important communication tool, yet only a detailed stepwise work process will minimize unfounded assumptions and ultimately mistakes in this tool.

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Quantitative morphological analysis of the fossil record of Neuropterida demonstrates that we loose more than just numbers of species in extinctions

Haug, J.T.

The ongoing biodiversity crisis demands that we improve our understanding of extinctions. The extent of extinctions is often expressed as the loss of numbers of species, the current loss in addition has been also expressed in the loss of biomass. Yet, the grave danger is the loss of ecological functions. Expressing loss of ecological function in a quantitative way is therefore key to improve our understanding of extinction processes. Counting species and measuring biomass are ultimately only proxies for this central aspect. Yet, when studying past extinction events in the fossil record, both common measures make a comparison with processes in the modern fauna challenging, as estimating biomass in fossils is highly biased, and the number of recognised species is usually significantly lower than in the modern fauna. I will present examples of lacewings and their closer relatives in which we used quantitative morphology as a proxy for ecological function, by doing so recognising losses that could not be detected quantitatively by other methods. Neuropterida, the group of lacewings and their closest relatives, is a prime example for studying extinctions, as everybody seems to agree that this group had its highest diversity in the Mesozoic, but declined afterwards, but recognising this loss quantitatively with common methods has so far failed. We concentrated on larvae of this group. As in other holometabolans, the larvae represent the life phase of growth in which the animals have numerous interactions with other components of the food web, consuming massive amounts of prey animals or being eating by larger animals. Diversity assessments often neglect larvae and are centred among adults, yet especially when focussing on ecological functions and their loss, larvae need to be considered, as their ecological functions are fundamentally different from those of their corresponding adults. Luckily, amber deposits of different ages have provided us an astonishing wealth of exquisitely preserved fossil neuropteridan larvae. Explored quantitative aspects focus on structures directly coupled to the ecological interac-

tions of the neuropteridan larvae, such as the mouthparts, and functionally tightly interconnected to them the shape of the head capsule, but also for example the eyes. With this approach we can demonstrate significant losses of distinct hunting and feeding strategies in various lineages of Neuropterida, yet we can also demonstrate that in some lineage diversification events occurred after the Mesozoic. Although these could partially compensate losses in other lineages, the overall loss is still strongly recognisable. While modern-day neuropteridan larvae represent fascinating and often alienating superlatives as effective predators with examples such as the economically important aphidlions and the widely famous antlions, we can demonstrate that there have been even more extreme morphologies and ecologies in the past of now extinct larvae. Neuropterida hence offers us an example to improve our understanding of how losses of diversity manifestate and should teach us a lesson what the modern biodiversity crisis may lead to.

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Neuropteran insect larvae in amber– Reconstructing lifestyles and behaviour

Hörnig, M.K.; Haug, J.T. & Haug, C.

Insects today are extremely species-rich and diverse in their morphology, but also in their lifestyle and strategies, e.g. in terms of feeding habits, defense and reproduction. This extreme range of strategies does not only exist between different insect groups, but also within a species the lifestyle can change dramatically during ontogeny, especially in holometabolan insects. Many studies focus on the adults, but the larvae are of great ecological importance, as the life span of larvae can be much longer than that of adults and not every individual reaches the adult stage, resulting in a higher number of immature individuals. For this reason, it is of great importance to study insect nymphs and larvae to understand their role in a (palaeo-)ecosystem.
Neuroptera (lacewings) is a group of holometabolan insects in which we can observe an extreme change in lifestyle from the larval stages to the adult. The adults are usually of rather gracile morphology and can differ in their feeding behavior within herbivorous and carnivorous groups. However, the larvae of (nearly) all extant groups are exclusively predators or parasites. Most prominent are their massive, sucking and piercing stylets with which they inject venom and feed on the liquefied tissue of their prey. Neuropteran larvae can pursue various predatory and defensive strategies, such as building funnels (as in the most famous antlions) or decorating behavior (camouflage).
Holometabolan larvae, including those of neuropterans, were thought to be rare in amber, but studies in recent years have shown that this may not be the case for all groups. Especially in Cretaceous amber, the number of specimens has increased dramatically in recent years and now comprises several hundred specimens. To better understand the evolution of the neuropteran groups and their strategies in deep time, we have studied numerous fossil specimens, mainly in amber. Clues to their lifestyle can be obtained by studying morphology in comparison to living forms, syninclusions and cases of “frozen behavior”. We give a brief overview of the current state of fossil record in the context of reconstructing behavioural aspects of neuropterans from the Cretaceous onwards.

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A Cretaceous like larva in Eocene amber– Eocene differs from modern entomofauna

Linhart, S.; Haug, J.T.; Baranov, V. & Haug, C.

The Eocene and its fauna has become an important time to study. The global warming and the changing environment during that time period can support our understanding of the challenges we face today. Up to now the fauna of the Eocene period has been considered as close to the modern time and especially different to the Cretaceous period. Here we report a larva of the neuropteran (lacewings) group Chrysopidae (green lacewings), also known as aphidlions, preserved in Rovno amber (Ukraine) from the Eocene period. Aphidlions have specialised mouthparts, stylets, constituted by the mandible and a part of the maxilla that form a suction channel. This structure is common for all neuropteran larvae. Aphidlions can be recognized by stylets without teeth, trumpet-shaped empodia (adhesive structures) on the legs and labial palps with three elements each. The specimen that we report here has a similar morphology to aphidlions known only from the Cretaceous period, but not for other Eocene or modern ones. The specimen has long stylets, more than twice as long as the head capsule, and long processes arising from the back of the larva with numerous setae. This traits and trait combination was so far known only from aphidlion specimens of the Cretaceous period.

This is an example of a Cretaceous morphology surviving into the Cenozoic. The specimen also combines traits that are especially known for the modern morphology of aphidlions. The traits of a specimen can indicate the ecological function it fulfilled. The specimen of this study indicates that the ecological functions that were fulfilled by the long stylets and processes during the Cretaceous could still be fulfilled during the Eocene and were then lost or substituted in the modern time. As previous studies already indicated on a quantitative level, the results of this study indicate on a qualitative level that the Eocene was a more intermediate fauna between the Cretaceous and modern one and not a modern-day fauna as often assumed.

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Calyptratae flies in fossil resin: Examining preservation frequency

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Mesembrinellidae and Muscidae are relatively young families now abundant in forests, with their most recent Calyptratae ancestor dating back to the Cretaceous period, around 64 million years ago. Fossil assemblages offer diverse insights into ancient environments but are often incomplete and biased. The type and abundance of organisms preserved in resin depend on numerous taphonomic and ecological factors. Actuo-taphonomic studies are crucial for understanding these gaps, helping us to interpret past events and reconstruct ancient ecosystems and relationsh*ips* between organisms. In this study, we present two rare flies preserved in amber and copal from Hymenaea resin. We also study modern specimens collected in Defaunation resin and yellow sticky traps from two different forests. The first specimen, a Mesembrinellidae, is preserved in a piece of Mexican amber from Simojovel, Chiapas (Mexico), dated to 23 million years ago (Aquitanian age, Miocene). The second specimen, a Muscidae, is preserved in Holocene copal from Tanzania, dated from about 772 AD according to ^{14}C analysis. Calyptratae are ecologically diverse, with many species associated with decaying animal matter. Our actuo-taphonomic studies found few specimens in the sticky traps around Hymenaea trees. However, they were abundant in Cormorant National Park, where the presence of dead birds created an ideal environment for these flies. We hypothesize that the presence of Calyptratae in resin may be due to the proximity of decaying animal matter near resin sources.

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Untangling the ‘Entangling’ Fossil Record of Larvae of Dermestidae

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Representatives of Dermestidae are ubiquitous scavengers of animal- and plant-derived organic matter. Some of these beetles exhibit specialized feeding behaviors, burrowing into bones, skins, and meats, thereby playing a critical role in the decomposition of organic material. This ecological function has led to their vernacular names skin, hide, leather, or larder beetles. However, their feeding activity on stored products, books, and museum specimens has also rendered them significant pests. Both adults and larvae are typically characterized by a hairy habitus, with adults bearing short fine setae on their bodies, whereas larvae bear long, specialized defensive hairs. Two morphologically distinct types of these setae have been recognized: spicisetae, with barbed pedicels, and hastisetae, distinguished by arrowhead-shaped „heads“. The hastisetae can be actively erected to enhance defensive coverage and readily break at the pedicel upon contact, entangling potential predators, sometimes with lethal consequences.
Despite their ecological significance and widespread distribution, the fossil record of larvae of Dermestidae remains understudied. Previous reports of fossilized larvae have been sporadic. Our study significantly expands this record, documenting 36 new specimens preserved in amber. These fossils originate from deposits spanning three geological periods and seven distinct localities, including the Miocene (German Lausitz, Dominican Republic, and New Zealand Hyde and Roxburgh amber deposits), the Eocene (Baltic coast amber deposits), and the Cretaceous (Canadian Grassy Lake and Myanmar Kachin amber deposits).
Additionally, we analyzed the morphometry and morphology of specialized larval setae, particularly hastisetae, across extant and fossil specimens. We documented interspecific variation in the morphology of hastisetae, such as differences in length and „head“ shape, and explored their implications for defensive strategies. Furthermore, we examined the

relationship between the presence or absence of hastisetae and larval lifestyle, including potential defensive mechanisms during pupation. Finally, we discussed the evolutionary trajectory of these defensive structures, and whether changes in the length of setae were possibly connected with shifts in substrate preference over geological time.

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Workshop: Praktische Entomologie, Museumsentomologie / Workshop: Practical Entomology, Museum Entomology

Talks

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Klebstoffe in entomologischen Sammlungen

Händel, J.

Klebstoffe spielen in entomologischen Sammlungen eine wichtige Rolle. Dabei hängt die Art des verwendeten Klebers von der Zielsetzung und den jeweiligen Anforderungen ab. Hier soll analysiert werden, welche Stoffe in der Vergangenheit zur Anwendung kamen und welche unter Berücksichtigung kuratorischer Gesichtspunkte gegenwärtig empfohlen werden können.

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Schutz der Exponate im Museum aus der Sicht eines Entomologen

Pospischil, R.

Viele Insektenarten nutzen trockene organische Materialien als Nahrung. In der Natur ist dies eine wichtige ökologische Funktion, um Nährstoffe in den ökologischen Kreisläufen wiederzuverwerten. Sollen diese Materialien jedoch in Museen für die Nachwelt erhalten bleiben, ist dieser Abbau durch Insekten unerwünscht. Der Schutz gelagerter Güter vor der Zerstörung durch Insekten ist daher für Museen eine ständige Herausforderung.
Eine besondere Bedeutung hat auch der Versand von Kulturgütern zwischen Museen und wissenschaftlichen Instituten über die Grenzen der Kontinente. In Museen spielt vor allem die Einschleppung von Arten eine Rolle, die sich in trockenen, organischen Materialien tierischer oder pflanzlicher Herkunft entwickeln. In Mitteleuropa haben vor allem Familien der Käfer (Coleoptera), Schmetterlinge (Lepidoptera) und Fischchen (Zygentoma) eine große Bedeutung als museale Schädlinge. Die Bausubstanz des Gebäudes muss ebenfalls beachtet werden. Vor allem bei Gebäuden in denen viel Holz verbaut wurde, ist mit holzzerstörenden Käfern zu rechnen.
Da sich die neu eingeschleppten bzw. eingewanderten Arten in ihrer Lebensweise zum Teil grundlegend von den bodenständigen Arten unterscheiden, sind die Kenntnis der Arten sowie die Beachtung ihrer Lebensweise wichtige Voraussetzungen für eine frühzeitige Erkennung des Befalls und die Bekämpfung. Detaillierte Beschreibungen der wirtschaftlich wichtigen Arten finden sich zum Teil in deren Ursprungsländern. Um eine effektive Kontrolle dieser „exotischen“ Schädlinge zu erreichen, ist ein Erfahrungsaustausch betroffener Museen untereinander wünschenswert.
Um die Einschleppung dieser Spezies in das Innere von Museen zu vermeiden, dürfen Paletten, Wellpappekartons sowie Füllmaterial nicht in das Museum gelangen. Exponate sollten bei der Ankunft inspiziert werden. Eine optimale Lösung bieten Quarantäneräume, in denen neu eingetroffene Objekte über 2 bis 4 Wochen gelagert und in regelmäßigen Abständen kontrolliert werden können. Das Monitoring kann unter anderem mit Hilfe von Klebe-, Pheromon- oder Lichtfallen erfolgen. Diese Methoden können zwar das Vorhandensein bestimmter Arthropoden aufzeigen, der genaue Befallsort wird in der Regel erst durch genaue Sichtkontrollen erkennbar. Bei sehr kleinen Arten sowie versteckt lebenden Larven eignet sich ein Exhaustor, mit dem man Insekten sowie deren Häute und Kotpartikel auch aus Ritzen und kleinen Ausschlupflöchern aufnehmen kann, ohne die Exponate zu gefährden. Danach ist eine korrekte Bestimmung der Schädlingsart notwendig, um eine effektive Bekämpfung einzuleiten.

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