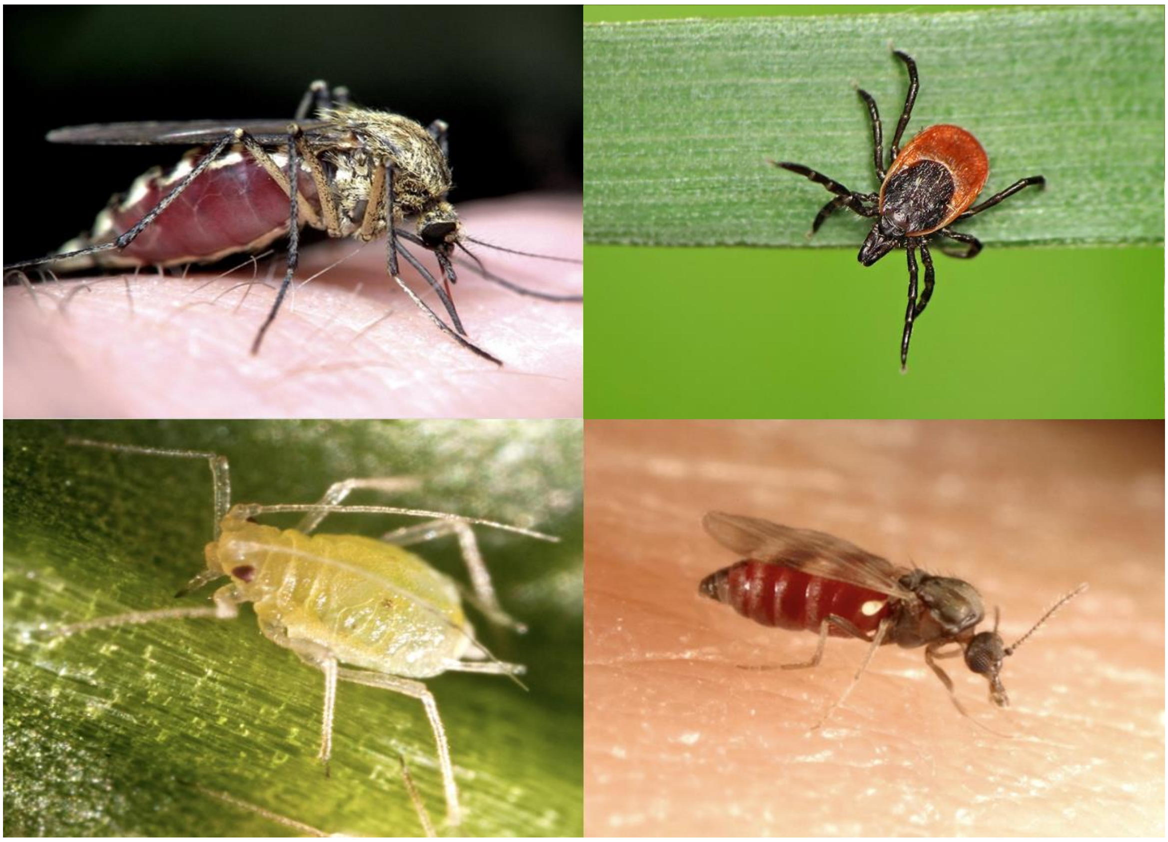
VECTOR-BORNE DISEASES IN THE UK: BIENNIAL CONFERENCE 2024



The Spine, Liverpool

Tuesday 3rd December - Wednesday 4th December 2024

THE PANDEMIC INSTITUTE

UNIVERSITY OF LIVERPOOL

Department for Environment Food & Rural Affairs

UKRI

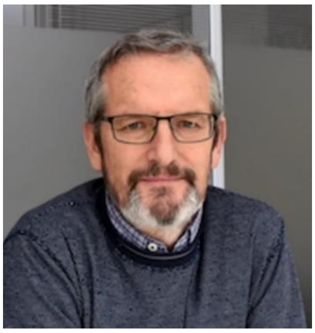
Biotechnology and Biological Sciences Research Council

NIHR | Health Protection Research Unit in Emerging and Zoonotic Infections at University of Liverpool

CONTENTS

WELCOME

A warm welcome to Liverpool for the 2024 biennial VBD conference. We hope you have a great time visiting the city and enjoy the packed programme over the coming days.



The threat to the UK from vector-borne diseases (VBDs) is increasing at astonishing pace. I started to undertake research in this field some thirty years ago when I joined the Pirbright Institute. In terms of vector-borne diseases people in the UK were, historically, affected by malaria, plague and typhus, and our livestock by several tick-borne diseases but not a lot else. My job at Pirbright was to consider threats to southern Europe and Africa. Roll forward to the present and these threats are either at our door or have entered the UK already. We have a mosquito-borne virus (Usutu) detected in London and further afield; exotic mosquito vectors have invaded the country; Lyme disease is rife and tick-borne encephalitis, transmitted by Ixodes ticks, was recently discovered. A newly emerged midge-borne disease of livestock (Schmallenberg) is now endemic, and an outbreak of bluetongue virus threatens. Looking to mainland Europe we see cases of West Nile, dengue, Chikungunya, CCHF, EHD, Oropouche, Xylella fastidiosa and other vector-borne diseases that could affect the UK's people, animals or plants at any time.

There are numerous drivers of this growing threat from VBDs, chief among them probably globalisation (travel and trade) and environmental (including climate) change. In my opinion the risk from VBDs is going to continue to increase and the UK research community, research funders, industry and policy makers need to come together to address the growing threats.

"The sixth meeting brings together members of the major UK academic research groups, government agencies, funders, and other stakeholders who share an interest in vectors or vector borne diseases of humans, animals or plants, and which are present in or threaten the UK"

It is, therefore, with great pleasure that I welcome you to the sixth UK VBD Conference. It will, I believe, be the largest ever gathering of people interested in vectors and VBDs of people, animals and plants in the UK. The series of meetings started in Liverpool in 2012; followed by meetings in 2014 (Liverpool), 2016 (Liverpool), 2018 (Norwich) and 2020 (online). There was no meeting in 2022, and, in 2024, it is wonderful to be able to relaunch the series in Liverpool, once again.

We are very grateful to our sponsors for supporting this year's meeting: BBSRC, Defra, The Pandemic Institute and the Health Protection Research Institute in Emerging and Zoonotic Infections.

This meeting is dedicated to the memory of Professor John Stephenson who led, and co-organised, all previous UK VBD meetings.

Matthew Baylis

On behalf of the organising committee, UK VBD 2024.

UK VBD Organising Committee

Professor Matthew Baylis, University of Liverpool

Matthew Baylis is the Executive Dean of the Institute of Infection, Veterinary and Ecological Sciences at the University of Liverpool. He works in the area of One Health, climate change impacts on health, and vector-borne diseases, focussing mainly on Africa and UK/Europe. While at the University of Bristol he spent 4 years based in Kenya studying tsetse flies, and then several years at the UK's Institute for Animal Health, studying midges as vectors of bluetongue and African horse sickness in North and southern Africa. In 2005 he moved to Liverpool and, in 2007, he established the Liverpool University Climate and Infectious Diseases of Animals group (LUCINDA) which undertakes research into viruses spread by midges (bluetongue, African horse sickness, Schmallenberg) and mosquitoes (West Nile, Japanese encephalitis, dengue, Zika), as well as plague, tick-borne diseases and liver fluke.

Dr Marcus Blagrove, University of Liverpool

Dr Marcus Blagrove was awarded his PhD from the University of Oxford in 2013 on using Wolbachia as a means to block dengue and chikungunya virus transmission in Aedes albopictus. Sinch then, he has worked for the University of Liverpool where his group works on the three-way interactions between environment, virus and mosquito; and the effect of these interactions on transmission. Blagrove's group has field, lab, and computational arms, with a view to taking a holistic approach to understanding and mitigating arboviruses.

Dr Sharon Zytynska, University of Liverpool

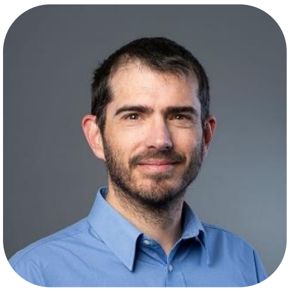
Dr. Sharon E. Zytynska is a Senior Lecturer at the University of Liverpool and BBSRC David Phillips Fellow. Her research explores ecological genetics and multitrophic interactions, focusing on plant-microbe-insect dynamics. Her work exploits soil and plant microbiomes to enhance insect pest control on crop plants, contributing to sustainable agriculture and vector-borne disease management.

UK VBD Organising Committee

Professor Heather Ferguson, University of Glasgow

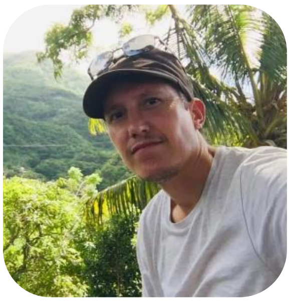
Heather Ferguson is a vector ecologist whose work encompasses study of the ecology, behaviour, surveillance and control of mosquitoes that transmit malaria and arboviruses. She is involved in the development of new tools for vector surveillance and control with partners from malaria endemic countries. Professor Ferguson has a long-term research and training partnership on malaria vector research with the Ifakara Health Institute in Tanzania, where she holds a position as a Visiting Scientist. Her recent work focusses on the impact of climate and other environmental change on mosquito vector-borne diseases. She co-leads a One Health research programme which is investigating the risk of zoonotic mosquito-borne disease emergence under current and future climate scenarios in Scotland. She is a former Co-Chair of the World Health Organization's Vector Control Advisory Group and current member of the Strategic Technical Advisory Group on Neglected Tropical Diseases.

Dr Chris Sanders, Pirbright Institute



Dr Christopher Sanders is a Research Fellow at The Pirbright Institute, UK. The Pirbright Institute is a leading centre of excellence in the research and surveillance of viral diseases of livestock and viruses that spread from animals to humans. Chris has more than 15 years' experience in studies of the interactions between insect vectors, livestock hosts and arboviruses, from field work to transmission studies in high containment. His research has focused on *Culicoides* biting midges and their role as vectors of bluetongue virus (BTV), the causative gent of bluetongue disease in ruminants. This includes investigating the dispersal behaviour of *Culicoides*, the impact of climate change on *Culicoides* populations, and the interactions between *Culicoides*, BTV and ruminants that facilitate transmission.

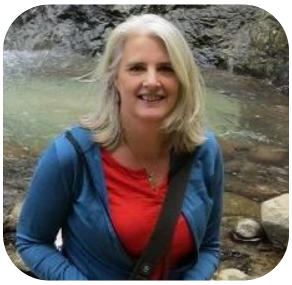
Dr Jolyon Medlock, UK Health Security Agency



Dr Jolyon Medlock is Head of Medical Entomology at the UK Health Security Agency at Porton Down. He has worked on vector-borne disease for >25 years and in UK Public Health since 2002. He has published ~200 scientific papers on VBD ecology, largely specific to UK tick and mosquito borne disease transmission systems and has worked extensively in Europe, Caribbean and Africa.

UK VBD Organising Committee

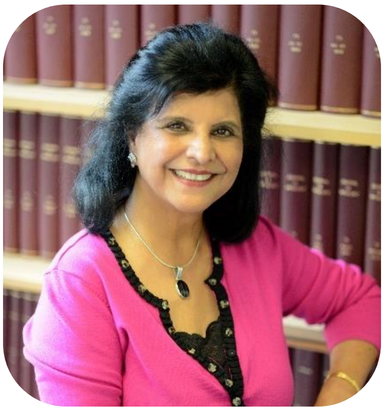
Professor Saskia Hogenhout, John Innes Centre



Professor Saskia Hogenhout is a Group Leader in the Department of Crop Genetics at the John Innes Centre and Honorary Professor at the School of Biological Sciences, University of East Anglia, Norwich, UK. Her research primarily delves into the intricate dynamics between plants and insects, particularly emphasizing the influence of microbes within these relationships. A significant focus of her work is the study of phytoplasmas—pathogens transmitted by insect vectors—which induce severe morphological changes in plants, such as witches' brooms and phyllody. Her team has made pioneering discoveries, revealing that these pathogens emit virulence proteins, or effectors, that specifically target and disrupt plant transcription factors crucial for developmental regulation. This interference promotes breakdown of these transcription factors, effectively short-circuiting plant pathways and circumventing the usual ubiquitination process, resulting in dramatic developmental defects. Furthermore, her research has highlighted that plants exhibiting symptoms of these diseases attract insect vectors more effectively, thereby facilitating the widespread dissemination of phytoplasmas. In addition, she has been instrumental in developing genomic tools and conducting functional analyses of effectors found in the saliva of various sap-feeding insects from the Hemiptera order, which are known carriers of plant pathogens. Her contributions span an array of fields including genomics, molecular genetics, entomology, plant pathology, virology, bacteriology, and recently, population biology and mechanistic modelling.

2024 Keynote Speakers

Professor Polly Roy
Professor of Virology, London School of Hygiene and Tropical Medicine



Polly Roy received her PhD in Molecular Virology from New York University/Columbia University Medical School, and continued to study RNA virology as a 3-year postdoc at the Waksman Institute, Rutgers University. She then moved to the University of Alabama, Birmingham USA, where she established her own laboratory and became a Full Professor, still working on different RNA viruses funded by multiple US grants. After this, she went to the University of Oxford, UK through a senior International Fogarty fellowship, where she gradually developed a second virology lab, whilst maintaining her research lab at UAB until 2005. In 2001, she moved to LSHTM, where she continues to lead a large group of researchers.

Roy's studies have contributed to many areas of virology, notably virus structure, assembly, RNA replication and vaccine development. Her pioneering work on co-expression of viral proteins to form immunogenic virus-like particles preceded their success as HPV vaccines. She has exploited innovative reverse genetics to construct synthetic complex viruses. Roy provides deep insight into cell and molecular virology as well as development of novel technology to generate safe vaccines and antivirals for human and animal viruses.

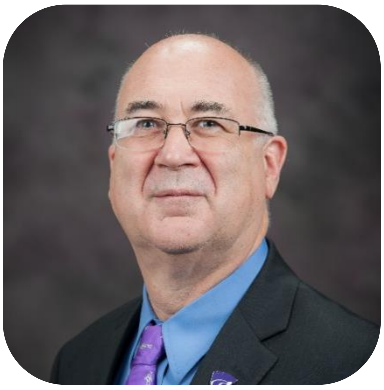
Her work has been recognised around the world and she has received many awards including: Officer of the Order of the British Empire (OBE) for services to Virus Research; Fellowship of the Academy of Medical Sciences; Indian Science Congress General President's Gold medal, awarded by the Prime Minister of India; and, Finalist of Biotechnology and Biological Sciences Research Council (BBSRC) 'Innovator of the Year' Award.

2024 Keynote Speakers

Dr Trisna Tungadi
Lecturer in Plant Health, Keele University, UK

Trisna obtained her PhD in plant virology from the University of Cambridge in 2014 working with Prof John Carr. Afterwards, she remained in the same group working as a postdoc for 5 years. In 2019, she moved to NIAB East Malling as a postdoc to work on spotted wing Drosophila, a major insect pest in the soft fruit industry. In October 2022, Trisna joined Keele University as a lecturer where she is building her first research group. Her main research focus is in plant-virus-vector interactions, specifically how vector biology influence virus transmission efficiency.

Stephen Higgs, Director, Biosecurity Research Institute (BRI)
Associate Vice President for Research, Kansas State University



Stephen Higgs is an infectious disease expert. He is responsible for the oversight, coordination and expansion of the BRI's multidisciplinary research and education programs for studies on diseases that impact the global food supply, including those affecting humans, livestock and plants.

Higgs holds the Virginia and Perry Peine Professor of Biosecurity and is a university distinguished professor in diagnostic medicine and pathobiology.

Higgs is an expert in vector biology, arthropod-borne infectious diseases, immune modulation, and vaccine evaluation, and has received funding through numerous competitive grants from Federal and private organizations to include the Bill & Melinda Gates Foundation.

Higgs has published more than 200 peer-reviewed papers, and 25 book chapters. He is a fellow of the American Society of Tropical Medicine and Hygiene (ASTMH) and a fellow of the Royal Entomological Society. He is editor-in-chief of the international journal Vector-Borne and Zoonotic Diseases, and an editorial board member of Health Security. In 2021, he was awarded the Harry Hoogstraal Medal for Outstanding Achievement in Medical Entomology by the American Committee of Medical Entomology of the American Society for Tropical Medicine and Hygiene. In 2022, Higgs was a co-recipient of the BIAL Award in Biomedicine in recognition of the most significant publication over 10-year period.

PRESENTER GUIDELINES

Talks

Oral presentations will take place on the 12th floor.

Presentations should be submitted to livvec@liverpool.ac.uk by Friday 29th November.

This should be your final version, however if a change is required to your presentation please speak to the IT technician in the conference room during the break before your session.

Suggested presentation timing:

- Full Talk: Total 15 minutes (10 minutes talk and 5 minutes questions)
- Flash Talk: Total 4 minutes (3 minutes talk and 1 minute questions)

Posters

All posters will be displayed across both days on floor 11.

Following registration, poster presenters should report directly to the poster area. There will be support provided to direct you to your assigned place. All posters have been arranged according to the relevant allocated session. Pre-cut Velcro tabs will be provided.

Posters can be displayed from 09:00 on 3rd December, and taken down at the end of the conference at 17:15 on 4th December.

All poster presenters should have been informed of their presentation time.

Sharing Content

It is encouraged to share updates from the conference on social media, however not all research is ready to be publicised. Please respect presenters wishes and do not share information if you see or are told not to on a slide or poster.

Follow us on X and BlueSky where we will be sharing content throughout the conference.

@UK_VBD @ukvbd.bsky.social

Feel free to share your own content using **#ukvbd2024**

PRIZES

Prizes (£50 voucher) will be awarded to the best talk, best flash talk and best poster from each of the five session themes:

1) VECTOR-HOST-PATHOGEN INTERACTION
2) EMERGING VECTOR-BORNE DISEASES
3) VECTOR AND DISEASE CONTROL
4) DIVERSITY AND GENOMICS
5) VECTOR ECOLOGY AND SURVEILLANCE

You can vote for your favourite via the following QR codes:

Day 1 Vote

Best Talks & Flash Talks

Day 1+2 Vote

Best Posters

Day 2 Vote

Best Talks & Flash Talks

DAY ONE: ORAL PRESENTATIONS
TUESDAY 3RD DECEMBER 2024

09:30 **Registration**

10:00 **Matthew Baylis**
Welcome and meeting arrangements

SESSION 1: Vector-host-pathogen interaction
Chair: Chris Sanders

10:15 **Mimi Cox, University of Glasgow**
Dissecting the interaction between the human malaria parasite Plasmodium falciparum and two highly diverse Anopheles mosquitoes in early infection.

10:30 **Sarah Reece, University of Edinburgh**
It's about time! How daily rhythms in mosquito biting time affect malaria transmission.

10:45 **Sara Rooney, Liverpool School of Tropical Medicine**
Exploring the interactions of Wolbachia & Usutu within British mosquito species.

11:00 **Maya Wardeh, University of Liverpool**
Debugging vectors: Active learning uncovers mosquito arbovirus competence blind spots.

FLASH TALKS

11:15 **Kevin Maringer, The Pirbright Institute**
Orthoflavivirus evasion of mosquito NF-κB-mediated innate immunity defines vector specificity and emergence potential.

Ian Cadby, Bristol Veterinary School (University of Bristol)
Structure-function analyses of secreted effector proteins at the Anaplasma phagocytophilum: eukaryotic host interface.

Maya Holding, UK Health Security Agency
Prevalence and predictors of tick-borne pathogens in deer communities.

Caroline Millins, University of Liverpool
A One Health approach to assessing tick-borne risk and impacts in UK upland habitats.

11:30am **Tea/Coffee Break and Poster Session**

SESSION 2: Emerging vector-borne diseases
Chair: Jolyon Medlock

12:15 **Kerry Louise Newbrook, The Pirbright Institute**

Clinical disease, infection and immune response kinetics and the potential for onwards Culicoides vector transmission of a newly emerged European strain of bluetongue.

12:30 **Jack Pilgrim, University of Liverpool**

Assessing the vector competence of UK mosquitoes for an endemic Usutu virus strain.

12:45 **William Thurston, Met Office UK**

Using atmospheric dispersion modelling in preparation for and response to airborne incursions of bluetongue to the UK.

13:00 **Arran Folly, Animal and Plant Health Agency**

Usutu virus, the United Kingdom's first, endemic, mosquito-borne viral zoonosis.

13:15

FLASH TALKS

Zoe Ward, University of Bristol

Climate drivers of uncertainty in Ixodes ricinus tick distribution models in Europe: a rapid review.

Gillian Armstrong, UK Health Security Agency

The UK Health Security Agency vector-borne disease matrix.

Benedict Fellows, University of Glasgow

Predicting dengue fever outbreaks globally: a phenotypically plastic model of Aedes Aegypti.

Emma Fairbanks, University of Warwick

Assessing the impact of host clustering and control strategies on African horse sickness virus transmission: A simulation-based analysis.

13:30 **Lunch Break**

SESSION 3: Vector and disease control
Chair: Heather Ferguson

14:30 **Saudamini Venkatesan, University of Liverpool**
Do woodland patch size and connectivity influence tick density, Borrelia burgdorferi prevalence and Lyme Disease hazard through impacts on hosts?

14:45 **James Bell, Keele University**
Presymptomatic virus detection in the field: Drones detect viral incidence and spread in plants before visible yellowing.

15:00 **Steven White, UK Centre for Ecology and Hydrology**
Phenotypic plasticity in vector traits drives trends in global disease incidence: Aedes albopictus and dengue.

15:15 **Adi Behar, Kimron Veterinary Institute**
Molecular basis of olfactory-driven behaviours of Culicoides imicola.

15:30
FLASH TALKS

Ross N. Cuthbert, Queen's University Belfast
Managing mosquito invasions: the cost of inaction.

Mara Rocchi, Moredun Research Institute
Addressing Tick Management & Control through collaboration.

Lawrence Bramham, Rothamsted Research
Pursuing aphid resistance and improved knowledge of UK barley yellow dwarf virus (BYDV) variation.

Richard Hassall, UK Centre for Ecology and Hydrology
Identifying hotspots and risk factors for tick-borne encephalitis virus emergence at its range margins to guide interventions.

15:45 **Tea/Coffee Break and Poster Session**

16:30 **The Defra-UKRI One Health VBD Hub Project** (led by Lauren Cator)

17:15
KEYNOTE SPEAKER

Professor Polly Roy, London School of Hygiene and Tropical Medicine
A closer look at Bluetongue virus, a complex nonenveloped arbovirus: from molecules to designer vaccines.

17:45 **Wrap Up Session**

19:00 **Conference Dinner**
The Lutyens Crypt, Liverpool Metropolitan Cathedral

DAY TWO: ORAL PRESENTATIONS
WEDNESDAY 4TH DECEMBER 2024

08:30 **Registration**

08:55 **Matthew Baylis**
Welcome and meeting arrangements

SESSION 4: Diversity and Genomics
Chair: Saskia Hogenhout

09:00 **Eugene Ryabov, The James Hutton Institute**
Unravelling the impacts of aphid vectoring and vertical transmission routes on the genetics and circulation of aphid-borne potato leafroll virus.

09:15 **George Seddon-Roberts, John Innes Centre**
A gene-expression atlas of the plant virus vector Myzus persicae reveals virulence factors produced in the salivary glands and foregut.

09:30 **Daniel Leybourne, University of Liverpool**
How does vector-virus diversity influence transmission efficiency in an important.

09:45

FLASH TALKS

Jing Jing Khoo, University of Liverpool
First genome assemblies for Wolbachia strain wPip from British Culex pipiens (Diptera: Culicidae)

Daniel Paul Carter, UK Health Security Agency
Metatranscriptomic sequencing of the Ixodes ricinus RNA virome in two tick-borne encephalitis endemic regions of the UK.

Alexander Sadykov, Exeter University
Predicting Mosquito Specialisation: An Eco-Evolutionary Olfactory Model.

Sean Brierley, University of Salford
Genomic Characterisation of Anaplasma phagocytophilum Strains from the United Kingdom and Optimisation of Metagenomic Enrichment Protocols.

Reuben James, John Innes Centre
Vitellogenin-Cas9 protein chimeras for targeted germline gene editing of aphids.

10:05

KEYNOTE SPEAKER

Dr Trisna Tungadi, Keele University
Manipulation of plant hosts and insect vectors by viruses.

10:35 **Tea/Coffee Break and Poster Session**

SESSION 5: Vector ecology and Surveillance
Chair: Marcus Blagrove

11:20 **Amirah Haziqah Binti Rashid, University of Liverpool**
Aedes aegypti in Warming World: Uncovering Sublethal Temperature Effects on Sterility for Accurate Risk Mapping.

11:35 **Sara Gandy, University of Glasgow**
Tick-borne disease hazard in urban green spaces and their surrounding rural environment.

11:50 **Dominic Brass, UK Centre for Ecology and Hydrology**
Exploring the effect of historic climate change on the population dynamics of Ixodes ricinus.

12:05 **Jolyon Medlock, UK Health Security Agency**
Spatial and temporal heterogeneity of Borrelia burgdorferi infection rates in Ixodes ricinus ticks in England and Wales, and how is environmental change likely to affect this?

12:20 **FLASH TALKS**

Joanna De Klerk, Lancaster University
Smart Sampling: An example of Adaptive Mosquito Surveillance in England and Wales.

Melanie Nicholls, The Pirbright Institute
Investigating opportunistic larval development sites of Culicoides biting midges in a zoo in the UK.

Mauro Pazmino Betancourth, University of Glasgow
Monitoring biological age in mosquitoes using infrared spectroscopy.

12:30 **Lunch Break**

SESSION 6: One Health approach to VBDs
Chair: Matthew Baylis

13:30 **Background to Programme, BBSRC/Defra**

13:40 UKRI/Defra Project Presentations

Heather Ferguson, University of Glasgow
"Ecology and viral transmission competence of potential mosquito vector species in Scotland" **Assessing the risk of mosquito vector-borne diseases in Scotland and their response to environmental change.**

Emma Widlake, Keele University
"Spatial distribution of UK Culex mosquitoes across England and Wales, a 2023 field survey" **Culex distribution, vector competence and threat of transmission of arboviruses to humans and animals in the UK.**

Katherine August, University of Greenwich | Holly Broadhurst, University of Salford
"Using retrotransposon blood meal analysis to understand the role of grey squirrel management on Lyme disease ecology in the UK" **One Health approach to tick-borne disease control through manipulation of reservoir host communities at landscape scale.**

Robert Calam Bruce, Animal and Plant Health Agency
"The utility of vector surveillance for elucidating arboviral emergence and persistence in temperate zones" **Vector-borne RADAR (real-time arbovirus detection and response).**

Ben Jones, Animal and Plant Health Agency
"TickTools: Using metagenomics approaches to unmask the organisms infecting Ixodes ticks in the United Kingdom" **TickTools: development of tools to monitor and control tick-borne diseases of humans and livestock.**

Mia White, UKHSA | Nina Billows, London School of Hygiene & Tropical Medicine
"The GenES-VBD network and high-quality reference genomes for three UK tick species" **Genomic epidemiology tools for the surveillance of vector-borne diseases network: applied to tick species, reservoirs and pathogens.**

David Omondi, Liverpool School of Tropical Medicine
"To investigate the use of Wolbachia for control of Culex mosquitoes" **Understanding, forecasting and mitigating zoonotic mosquito-borne viral disease in the UK.**

Bethan Purse, UK Centre for Ecology and Hydrology
"OPTICK – understanding and managing tick-borne disease threats in the UK's changing farmland environments" **OpTick: One health surveillance and management of tick-borne disease threats in a changing environment.**

15:00 **Tea/Coffee Break and Poster Session**

15:45 **UKRI/Defra Programme Panel Session**

16:30 KEYNOTE SPEAKER

Professor Stephen Higgs, Kansas State University

Forty years of mosquito research: Things we should know by now.

17:00 **Prizes and Wrap Up**

17:15 **Conference Close**

POSTER PRESENTATIONS
TUESDAY 3RD - WEDNESDAY 4TH DECEMBER 2024

Poster Session Themes

Session Theme	Presentation Day
1. Vector-host-pathogen interactions	Tuesday 3rd December 2024
2. Emerging vector-borne diseases	Tuesday 3rd December 2024
3. Vector and disease control	Tuesday 3rd December 2024
4. Diversity and Genomics	Wednesday 4th December 2024
5. Vector Ecology and surveillance	Wednesday 4th December 2024

Posters will be presented twice during the allocated day. Conference delegates will be split into two groups: morning viewing and afternoon viewing.

Your allocated viewing time will be displayed with a coloured dot on your name badge.

🟠 Tuesday 3rd December, 11:30-12:15 & Wednesday 4th December, 10:35-11:20

🟢 Tuesday 3rd December, 15:45-16:30 & Wednesday 4th December, 15:00-15:45

Poster Titles and Authors

POSTER NUMBER	TITLE, AUTHOR & AFFILIATION
1	*Stretching the wings further- susceptibility of Culex pipiens Linnaeus to bovine ephemeral fever virus infection under experimental conditions.* **Adi Behar, Kimron Veterinary Institute**
2	*The impact of host community composition on pathogen hazard in a tick-borne disease hotspot.* **Jonathan Yardley, University of Glasgow**
3	*Humidity matters: Refining vector-borne disease predictions in the face of climate-induced mosquito movements.* **Lorna Glenn, University of Liverpool**
4	*Investigating the sero-reactivity of indeterminate Lyme Disease cases against Borrelia miyamotoi.* **Daniel Carter, UK Health Security Agency**
5	*Elucidating the impact of nectar feeding on invasive mosquito species.* **Scott Tytheridge, Imperial College London**
6	*Determining the influence of water pollution on mosquito virome.* **Nicola J Fletcher, Liverpool School of Tropical Medicine**
7	*A single-sugar-fed modulates Aedes aegypti vectorial capacity.* **Christida Estu Wastika, Liverpool School of Tropical Medicine**
8	*Fall armyworm: Climate-related risks on major crops in China and Europe.* **Steffi Urhausen, Met Office, UK**

9	*Visualisation of bluetongue virus in the salivary apparatus of Culicoides biting midges highlights the accessory glands as a primary arboviral infection site.* **Marc Guimera Busquets, The Pirbright Institute**
10	*Dancing out of step: The adaptability of Anopheles stephensi rhythms and their impact on malaria development.* **Aidan O'Donnell, University of Edinburgh**
11	*Transmission pathways for the stem rust pathogen into Central and East Asia and the role of the alternate host, barberry.* **Catherine Bradshaw, Met Office, UK**
12	*Quantifying the effect of temperature on European Culex Pipiens longevity and reproduction in Italy.* **Yiran Wang, Imperial College London**
13	*Testing associations between West Nile Virus circulation in Culex mosquitoes and avian biodiversity in Emilia-Romagna, Italy.* **Yiran Wang, Imperial College London**
14	*The epidemic potential of Japanese encephalitis virus.* **Dana L. Vanlandingham, Kansas State University**
15	*Vector-Borne RADAR (Real-time Arbovirus Detection And Response).* **Arran Folly, Animal and Plant Health Agency**
16	*Estimating population exposure to tick-borne diseases in England, 2021-2022.* **Eilish Hart, UKHSA / University of Liverpool**
17	*Using correlative and mechanistic species distribution models to predict areas at risk of disease for the current and future environmental conditions: a case study of West Nile Virus in the United Kingdom.* **Amy Parkes-Withers, Animal and Plant Health Agency**
18	*Establishing a Laboratory Colony of Aedes vexans at London School of Hygiene & Tropical Medicine.* **Mariana Reis Wunderlich, London School of Hygiene and Tropical Medicine**
19	*STAR-IDAZ: a generic roadmap for "Vector Transmission Control".* **Goddeeris Bruno, KU Leuven**
20	*Olfaction in larval malaria mosquitoes Anopheles gambiae.* **Iman Jemal Muktar, Durham University**
21	*Testing the efficacy of vector-proof accommodation for UK livestock.* **Marion England The Pirbright Institute**
22	*Developing systematic guidelines for Mosquito Control in Built-Up Areas in Europe.* **Frederik Seelig, Frederik Seelig Consulting, Aarhus, Denmark; formerly: The Global Vector Hub, London School of Hygiene & Tropical Medicine**
23	*High quality reference genomes for three UK tick species.* **Susana Campino, London School of Hygiene and Tropical Medicine**
24	*Generating cell lines from UK arthropods – 25 years of challenges.* **Lesley Bell-Sakyi, University of Liverpool**
25	*The Tick Cell Biobank: tick and insect resources for UK vector-borne disease research.* **Catherine Hartley, University of Liverpool**
26	*Systematic discovery and high-throughput testing of novel cis-regulatory elements in insect vectors.* **Emily Chesters, Keele University**

27	*One Health DNA Barcoding in support for the identification of vectors of medical and veterinary importance in Ghana.* **Luis Miguel Hernandez Triana, Animal and Plant Health Agency**
28	*Complete Genome Sequencing of Siberian Tick-Borne Encephalitis Virus from preserved tick samples.* **Jake D'Addiego, UK Health Security Agency**
29	*Environmental risk factors for Anaplasma phagocytophilum in Scotland.* **Lucy Gilbert, University of Glasgow**
30	*Whole genome sequencing for surveillance and research of vector-borne diseases.* **Mirjam Schilling, Animal and Plant Health Agency**
31	*Optimized characterization of Culex pipiens biotypes from wild caught populations and hybrid laboratory-reared colonies.* **Estela Gonzalez Fernandez, Animal and Plant Health Agency**
32	*Babesia species diversity in Scottish Ixodes ricinus ticks and their zoonotic risk.* **Mara Rocchi, Moredun Research Institute**
33	*Exploring tick-borne pathogen communities in Mojave Desert Bighorn sheep and their ticks.* **Sophie Hawkes, University of Warwick**
34	*Leucocytozoon infection variation in black flies in west Scotland.* **Georgia Kirby, University of Glasgow**
35	*Surveillance and temporal population dynamics of Culex pipiens s.l. in Scotland.* **Georgia Kirby, University of Glasgow**
36	*Is Aedes detritus a migratory mosquito in the UK?* **Christopher Jones, Liverpool School of Tropical Medicine**
37	*Borrelia burgdorferi s.l. abundance and genetic diversity between urban greenspaces and surrounding hinterland across the UK.* **Grace Plahe, University of Salford**
38	*One Health approach to tick-borne disease control through manipulation of reservoir host communities at landscape scale.* **Steve Belmain, Natural Resources Institute, University of Greenwich**
39	*What kind of a threat is Bluetongue? Findings from a survey focused on Scottish farmers.* **Niamh Mahon, The James Hutton Institute**
40	*An update on the ecology, seasonality and distribution of Culex modestus in England.* **Alexander Vaux, UK Health Security Agency**
41	*The Ecology & Management of Aedes vexans in a British wetland.* **Alexander Vaux, UK Health Security Agency**
42	*RCG-GenES-VBD network: Genomic Epidemiology tools for the Surveillance of Vector Borne Disease, as applied to tick species, reservoirs, and pathogens.* **Mia White, UK Health Security Agency**
43	*An assessment of mosquito abundance and diversity across an urban-rural gradient in Scotland.* **Meshach Lee, University of Glasgow**
44	*Mosquitoes reared in distinct insectaries within an institution possess divergent microbiomes.* **Tara Joseph, Liverpool School of Tropical Medicine**

45	*UKHSA mosquito surveillance 2020 to 2024: First detection of Aedes aegypti eggs in the UK.* **Colin Johnston, UK Health Security Agency**
46	*Assessing the circulation of mosquito-borne pathogens and vector competence of Scottish mosquitoes.* **Jean-Philippe Parvy, MRC-University of Glasgow Centre for Virus Research**
47	*Mosquito Surveillance and Control in the UK Overseas Territories.* **Roz Taylor, UK Health Security Agency**
48	*Meta-analyses of Culex blood-meals indicates strong regional effect on feeding patterns.* **Jet Griep, University of Liverpool**
49	*Dermacentor reticulatus and Haemaphysalis punctata: two tick species of human and animal health importance in the UK.* **Sarah Biddlecombe, UK Health Security Agency**
50	*The distribution and abundance of Culicoides biting midges in England and Wales.* **Matthew Baylis, University of Liverpool**
51	*How does woodland creation affect Ixodes ricinus populations in Scotland?* **Benjamin Miller, University of Liverpool**
52	*Tick Surveillance Scheme: latest data and evidence for action at the local level.* **Kayleigh M Hansford, UK Health Security Agency**
53	*Monitoring biological age in mosquitoes using infrared spectroscopy.* **Mauro Pazmino Betancourth, University of Glasgow**
54	*A One Health approach to Tick-Borne Diseases in Changing Landscapes.* **Harry Marshall, Forest Research**
55	*Utility of the BG-Pro trap for understanding the ecology of the saltmarsh mosquito Aedes detritus.* **Nadja Wipf, Liverpool School of Tropical Medicine**
56	*Nationwide Mosquito Programme 2024.* **Anthony Abbott, UK Health Security Agency**
57	*Propensity to host seek and biting time of day are modulated by Anopheles gambiae nutritional status.* **Catherine Oke, University of Edinburgh**
58	*The Impact of Environmental Variation on Anopheles Mosquito Population Dynamics Across Heterogeneous Landscapes.* **Laura Anne Bissett, University of Glasgow**

EXHIBITIONS

Exhibitions will be held in Spaces 4 and 5 on floor 12.

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Royal Entomological Society
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Oral Presentation Abstracts

SESSION 1: VECTOR-HOST-PATHOGEN INTERACTION

Mimi Cox, University of Glasgow

Dissecting the interaction between the human malaria parasite Plasmodium falciparum and two highly diverse Anopheles mosquitoes in early infection.

*Mimi Cox*1, Duangkamon Loesbanluechai 1, Prince Ubiaru 1, Dorothy Armstrong 1, Antrea Pallikara 1, Lisa Ranford-Cartwright 1, Francesco Baldini 1, Virginia Howick 1. 1 Glasgow*

Insect vectors transmit a vast array of pathogens globally. Each pathogen operates in a highly adapted niche within specific species of vectors to leverage its transmission, which is influenced by the susceptibility of the host to different pathogens. Vectors respond to the pathogen presence through divergent innate immune responses which may drive susceptibility to pathogens and ultimately transmission. Although details of these responses are largely unknown. Using human malaria as a study system, we analysed gene expression responses of geographically distinct Anopheles species to Plasmodium falciparum, using bulk RNA sequencing. In An. albimanus (Panama from Central America) and An. gambiae (Kisumu from East Africa) we have identified a relatively limited, conserved pattern of genes likely involved in immune responses to parasite presence in both species, as well as some highly attractive differentially expressed targets for elucidating species differences in immunity. We are now working towards validation of key genes for their immune involvement using RNAi and infection phenotyping. This data will shape the understanding of responses to early P. falciparum infection in a species-specific and tissue resolved manner and how different pathogens can adapt to different vectors. This in turn will support the identification of potential transmission blocking processes in multiple Anopheles species. Additionally, as global warming raises the potential of the UK becoming a suitable environment for the invasion of vectors capable of transmitting malaria as well as other important vector borne diseases, understanding the molecular bases of different pathogen/vector interactions might be key to develop new species-specific interventions.

Sarah Reece, University of Edinburgh

It's about time! How daily rhythms in mosquito biting time affect malaria transmission.

Sarah Reece 1, Emily Robertshaw 1, Catherine Oke 1. 1University of Edinburgh,*

Life in a rhythmic world dictates the timing of activities for many organisms. This includes parasites, for whom the environments within their hosts and vectors change dramatically over 24 hours, and daily rhythms dictate the time-of-day that vectors bite hosts, allowing transmission to occur. The myriad daily rhythms of hosts and vectors offer time-of-day-dependent opportunities for parasites to exploit and presents dangers to evade. Yet, how parasites have evolved to cope with rhythms within their within-vector environment is a fundamental unanswered question. Changes in the time of day that mosquito vectors forage for blood from humans and other animals are widely reported but the consequences for the spread of the parasites/pathogens they transmit are unknown. Variation in vector biting rhythms is thought to be driven by evasion of insecticide treated bed nets and climate and habitat changes, but the role of individual variation in mosquito life history traits has been overlooked. My lab has revealed that the time-of-day mosquitoes forage for blood determines their susceptibility to malaria infection and the infectiousness of parasites, with biting at non-classical times of day substantially reducing the ability of parasites to complete their life cycle. Furthermore, biting time-of-day is associated with the nutritional reserves within individual mosquitoes, potentially exacerbating or ameliorating the impacts of rhythms on parasite fitness. Explaining the causes and consequences of shifts in biting-time-of day for parasite transmission requires integrating the roles of rhythms in all parties and how they interact with vector physiology. This challenge can be met by combining field, lab and theoretical approaches.

Sara Rooney, Liverpool School of Tropical Medicine

Exploring the interactions of Wolbachia & Usutu within British mosquito species.

Sara Rooney 1, Grant Hughes 1. 1 Liverpool School of Tropical Medicine*

Recently Usutu virus (USUV) has emerged across Europe, including the UK in 2020. This mosquito-borne flavivirus has caused mass die-off events in blackbirds and multiple instances of neurological symptoms in humans. Novel control methods are needed to manage this emerging threat. The use of Wolbachia pipientis for vector control is widely successful, being demonstrated to directly reduce prevalence and incidence of dengue virus in field trials of Aedes aegypti mosquitoes. Here, we investigate the interactions of USUV and Wolbachia. Interestingly, we observed that Wolbachia-induced blocking of USUV varied between viral strains. This is the first time varied Wolbachia blocking has been observed between strains of the same virus. We then studied the Wolbachia-USUV system in Culex pipiens molestus, one of the viruses' primary vector species, to explore the role natural Wolbachia infection plays on USUV infection and dissemination. For this study we compared viral growth in wild-type Culex pipiens molestus and a colony cured of their Wolbachia infection via antibiotic treatment. Collectively, these results provide new insights into Wolbachia-induced pathogen blocking and the potential mechanisms that underpin it. We discuss these findings and their potential to further our understanding of Wolbachia-pathogen blocking and the implications for developing Wolbachia -based controls for USUV in Europe.

Maya Wardeh, University of Liverpool

Debugging vectors: Active learning uncovers mosquito arbovirus competence blind spots.

Maya Wardeh 1, Marcus SC Blagrove 1. 1 University of Liverpool*

Mosquito-borne viruses are disproportionately prominent in emerging infectious diseases, and their climate-driven epidemiology means they are spreading to new areas at an ever-increasing rate, including now to the UK with West Nile and Usutu viruses. Following arboviral incursion into a new region, the risk of sustained local transmission is determined by whether competent vectors are present. While current research primarily focuses on established mosquito vectors, many local species have proven competent for arbovirus transmission. Notably, Zika, West Nile, chikungunya, and Usutu viruses have expanded their ranges, largely due to naïve native/local mosquito species. Assessing the risk of arboviral incursion to a region therefore requires two things: a comprehensive knowledge of all known component and refractory species for said arbovirus; and a framework for accurate computational prediction of unknown competence status. To this end we present: 1) The first exhaustive database of published mosquito competence experiments (~600 studies, >14,000 experiments, 264 mosquito populations, 659 viral strains); including outcomes and experimental variables recorded. 2) A machine-learning framework to predict mosquito vector-competence, trained on the above dataset. Uniquely, our framework is the first to integrate Active-Learning (AL) into the model training process. The AL component selects the most informative experiments and incorporates their outcomes into the training process, to maximise performance and produce reliable predictions, without need to incorporate all experimental data. Our framework demonstrates the applicability of AL as a robust method to estimate arbovirus transmission risk in new regions, and triage the resource-intensive laboratory experimentation required for any before-the-incursion testing regimen.

Flash Talks

Kevin Maringer, The Pirbright Institute

Orthoflavivirus evasion of mosquito NF-κB-mediated innate immunity defines vector specificity and emergence potential.

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Aedes aegypti is a highly human-associated mosquito capable of sustaining major epidemics, and evolving capacity for transmission by this vector is a prerequisite for mosquito-borne viruses to emerge as major human pathogens. Innate immunity is a known barrier to virus replication in mosquito vectors that influences vector tropism. We showed that double-stranded RNA and infection with model viruses activates NF-κB-mediated innate immune responses in A. aegypti-derived Aag2 cells and in vivo, and we now confirm that these responses are antiviral using novel CRISPR Cas9-mediated knockout cell lines. Interestingly, we identified a conserved ability of the A. aegypti-borne orthoflaviviruses dengue virus (DENV), yellow fever virus (YFV) and Zika virus (ZIKV) to inhibit NF-κB-mediated innate immunity via their nonstructural protein NS4A in cell culture and in vivo. By comparing NS4As from Culex spp. mosquito-borne, tick-borne and non-vector-borne orthoflaviviruses, we demonstrate that NS4A-mediated innate immune evasion correlates with transmission by A. aegypti. Using machine learning-informed approaches, we demonstrate that NS4A-like structural folds evolved uniquely in the vector-borne orthoflavivirus genus. Finally, we demonstrate that NS4A residues that are highly evolutionarily constrained in A. aegypti-borne orthoflaviviruses are essential for NF-κB-mediated innate immune antagonism in Aag2 cells. Our data indicate that NF-κB-mediated innate immunity exerts a strong evolutionary pressure on orthoflaviviruses and that evasion of NF-κB-mediated innate immunity may be a pre-requisite for transmission by A. aegypti. Our work informs our understanding of mosquito molecular barriers to arbovirus transmission and emergence, which could be exploited to develop refractory mosquitoes incapable of disease transmission.

Ian Cadby, Bristol Veterinary School (University of Bristol)

Structure-function analyses of secreted effector proteins at the Anaplasma phagocytophilum : eukaryotic host interface.

Ian Cadby 1, Hannah Burge 1, Mark Jepson 1, Lesley Sakyi, Jing Jing Khoo 2, Kelly Brayton 3, J. Stephen Dumler 4. 1. University of Bristol; 2 University of Liverpool; 3. Washington State University; 4. Uniformed Services University*

Tick-borne Anaplasma phagocytophilum (Ap) secretes effector proteins into host cells to subvert phagocyte activities and enable intracellular survival. Approximately 40 effector proteins are predicted to be delivered to host cells by the Ap type IV secretion system, most of which are proteins of unknown function and few of which have been subject of functional studies. Using structure-led and collaborative multi-disciplinary approaches, we have initiated investigation into the functions of Ap effectors to determine their roles in host manipulation. Here we present protein structure, biochemical, and infection data from our investigation of Ap effector functions and address a long-standing question in Ap biology, of how these bacteria manipulate the actin cytoskeleton. Remarkably, Ap effectors target actin both directly, and indirectly via selective targeting of multiple converging signalling pathways, hinting how Ap can disable key phagocyte microbicidal activities and favour Ap survival. These discoveries serve as a blue print for understanding the molecular basis for pathogenesis by Ap, demonstrate a novel mechanism for actin remodeling, and serve as proof of concept for our experimental approach to assigning function to these and other, cryptic, effector proteins.

Maya Holding, UKHSA

Prevalence and predictors of tick-borne pathogens in deer communities.

Maya Holding 1, Robert Kohl 2, Roger Hewson 1, Hein Sprong 2. 1 UK Health Security Agency; 2 National Institute for Public Health and the Environment (RIVM)*

It is expected that varying vertebrate communities affects presence, prevalence and diversity of ticks and their pathogens. How underlying mechanisms, such as amplification, dilution and spill-over, interact and generate the pathogen communities is understudied. We aimed to investigate this by determining the prevalence of vector-borne parasites, bacteria and viruses in different deer species with varying their community composition across the UK. Blood samples of ~2400 deer from six species were collected from across Great Britain in 2020 and 2021. These are being analysed and typed by PCR for presence of genetic material from Anaplasma phagocytophilum, Bartonella spp., Babesia spp., Borrelia burgdorferi sensu lato (s.l.), Borrelia miyamotoi, Coxiella burnetii, Francisella tularensis, Grotenhout virus, Hepatozoon spp., Midichloria mitochondri, Neoehrlichia mikurensis, Rickettsia spp., Rickettsiella spp., Spiroplasma ixodetis, Trypanosome spp., and Uukumeni-virus. Additionally, serology for tick-borne encephalitis virus. Our approach allows for detection of multiple Anaplasma ecotypes and Babesia species in singular samples. The possible associations of host factors, such as species, age, sex and condition, as well as environmental variables will be used as potential explanatory variables. So far, ~350 samples have been analysed, detecting DNA from A. phagocytophilum ecotype I and II, B. schoenbuchensis, Ba. divergens, Ba. venatorum, Ba. capreoli, Ba. odocoilei, F. tularensis, M. mitochondri, Rickettsia spp., Rickettsiella spp., and T. melophagium. Deer were frequently infected with two Babesia species, and occasionally with two Anaplasma ecotypes. Surprisingly, the RNA of two segments of the Grotenhout virus was found in 4 individuals. Analyses are ongoing and will be presented at the conference.

Caroline Millins, University of Liverpool

A One Health approach to assessing tick-borne risk and impacts in UK upland habitats.

*Laura Mackenzie 1, Mark Greener 2, Sarah Biddlecomb 2, Kayleigh Hansford 2, Festus Asaaga 3, Jennifer Duncan 1, Jonathan Rushton 1, Mara Rocchi 4, Nick Johnson 5, Jolyon Medlock 2, Caroline Millins*1. 1 University of Liverpool; 2 UK Health Security Agency; 3 UK Centre for Ecology and Hydrology; 4 Moredun Research Institute; 5 Animal and Plant Health Agency*

Risks from tick-borne diseases (TBD) to humans and livestock are increasing rapidly worldwide, including in temperate regions. In UK upland areas, TBDs rank highly among farmer priorities, can have severe impacts on livestock production and are an increasing public health threat. Policy driven changes to upland land management designed to deliver a range of environmental benefits may increase the suitability for ticks and tick-borne pathogen transmission. Therefore, it is vital to understand the management, environmental and ecological drivers of tick-borne disease risk and exposure of livestock to inform future policy and best practice recommendations to minimise animal and human disease burden. In this study, we firstly investigate the management, host and environmental drivers of tick hazard across different habitats on upland sheep farms in North Wales, secondly the drivers of sheep exposure/infection with key tick-borne pathogens Louping Ill virus, Anaplasma phagocytophilum, Babesia spp. and Borrelia burgdorferi s.l and thirdly impacts of these diseases on production. We predict that tick density and infection prevalence of tick-borne pathogens will be highest among ecotonal and scrub habitats (including areas of bracken, gorse etc.), due to their importance in off-host survival for ticks, and livestock shelter. Further, we predict that tick density and infection prevalence will increase with proximity to woodlands and continuous open grassland and moorland habitats due their importance for wildlife movement including deer. Our study will illustrate the possible effects of proposed agricultural policies in UK uplands and enable the design of effective management recommendations and intervention strategies.

SESSION 2: EMERGING VECTOR-BORNE DISEASES

Kerry Louise Newbrook, The Pirbright Institute

Clinical disease, infection and immune response kinetics and the potential for onwards Culicoides vector transmission of a newly emerged European strain of bluetongue.

Kerry Newbrook 1, Emmanuel Obishakin 1, Laura A Jones 1, Ryan Waters 1, Martin Ashby 1, Carrie Batten 1, Christopher Sanders 1. 1 The Pirbright Institute*

Bluetongue virus serotype 3 (BTV-3) was detected for the first time in cattle (and later sheep) in England in November 2023 following routine annual surveillance. This was the first detection of BTV in the UK since 2007. Bluetongue is a haemorrhagic disease of ruminants caused by infection with BTV and it's transmitted by Culicoides biting midges. Bluetongue is typically most severe in sheep, characterised by facial oedema, reddening of eyes/mucosal membranes and lameness, whilst cattle are often clinically mild/asymptomatic. A total of 126 cases (73 sites) across four counties (Norfolk, Kent, Suffolk, Surrey) have since been confirmed and there is now heightened risk of further BTV-3 incursions and/or outbreaks with increasing vector activity throughout 2024. Reports from the Netherlands suggest this newly emerging European BTV-3 strain is clinically severe in both sheep and cattle, however its potential clinical impact, infection dynamics and transmission potential for UK livestock are not yet known. The recently emerged BTV-3 strain was isolated from blood of a positive cow during the UK incursion and subsequently used to infect five UK sheep and four cattle in vivo using a highly representative arbovirus infection model. We assessed clinical disease, pathology, infection dynamics in blood/tissues, BTV antibody dynamics and the susceptibility of Culicoides vector species to infection and therefore transmission. Our study is the first to investigate the impact of this newly emerging BTV-3 strain in UK livestock in vivo and will provide vital insights to drive effective control measures and prevent spread of this arbovirus.

Jack Pilgrim, University of Liverpool

Assessing the vector competence of UK mosquitoes for an endemic Usutu virus strain.

Jack Pilgrim 1, Emma Widlake 1, Nicola Seechurn 1, Jolyon Medlock 2, Alexander Vaux 2, Nicholas Johnson 3, Jola Tanianis-Hughes 1, Matthew Baylis 1, Marcus Blagrove 1. 1. University of Liverpool; 2 UK Health Security Agency; 3 Animal and Plant Health Agency*

Usutu virus (USUV) is an emerging zoonotic virus transmitted primarily by Culex mosquitoes. Since its introduction into Europe from Africa during the late 20th century, it has caused substantial mortality within passerine populations of birds and can also sporadically cause disease in humans. USUV was first detected in the UK in 2020 and has become the country's first enzootic mosquito-borne virus on record, having been detected in birds and mosquitoes every subsequent year. Importantly, the vector competence of indigenous mosquitoes for the circulating UK (London) USUV strain at representative regional temperatures is still to be investigated. This work assesses the vector competence of 4 field-caught mosquito species, Culex pipiens molestus, Culex pipiens pipiens, Culiseta annulata and Ochlerotatus detritus using the London strain, with infection rates (IR) and transmission rates (TR) evaluated between 7 to 28 days post-infection. Infection and transmission were observed in all species aside from O. detritus. Cx. pip molestus demonstrated transmission potential at a temperature commonly observed in London subterranean structures where the species predominates, suggesting these populations should be monitored further for their role in transmission to humans. Furthermore, both Cx. pip pipiens and Cs. annulata from the North of England, where USUV is not currently detected, were shown to be viable vectors indicating spread of the virus to other UK regions is possible.

William Thurston, Met Office

Using atmospheric dispersion modelling in preparation for and response to airborne incursions of bluetongue to the UK.

William Thurston 1, Katie Coward 1, Sarah Millington 1. The Met Office, UK*

Bluetongue is a vector-borne disease of ruminants, caused by the bluetongue virus (BTV). Infection with BTV causes abortion, stillbirth, reduced milk production and can have a mortality rate greater than 50 % in sheep. BTV is transmitted between ruminants by various species of Culicoides biting midges, which can carry the disease hundreds of kilometres over the sea when blown on the wind. The Met Office atmospheric dispersion model, NAME, includes parametrisations to represent flight behaviours of Culicoides biting midges, and during the bluetongue season we perform twice-daily NAME simulations to estimate when Culicoides biting midges are likely to be blown from the near continent to the UK. These simulations routinely i) form part of a multi-agency fortnightly risk assessment of BTV airborne incursion convened by APHA; and ii) are aggregated over a season to select high-risk target counties in which to perform end-of-season surveillance required to maintain disease-free status. Here we describe our use of the NAME atmospheric dispersion model during the 2023 bluetongue season, firstly prior to the discovery of BTV-3 in the Netherlands, secondly how we modified our approach following the rapid spread of BTV-3 throughout the Netherlands, and thirdly our response to the subsequent detections of BTV-3 in southern and eastern UK. Although our main focus is on the preparation and response to recent UK BTV-3 incursions, we also touch upon how atmospheric dispersion modelling may be applied to a broad range of vector-borne diseases of animals, plants and humans.

Arran Folly, Animal and Plant Health Agency

Usutu virus, the United Kingdom's first, endemic, mosquito-borne viral zoonosis

Becki Lawson 1, Mirjam Schilling 2, Calam Bruce 2, Katharina Seilern-Moy,1, Andrew A. Cunningham 1, Ethan Wrigglesworth 1, Simon Spiro 1, Hugh J. Hanmer 4, Robert A. Robinson 3, Bathsheba Gardner 4, Anthony Abbott 4, Alex G.C. Vaux 4, Jolyon M. Medlock 4, Nick Johnson 2, Arran J. Folly 2 1.Zoological Society of London; 2. Animal and Plant Health Agency; 3 British Trust for Ornithology; 4 UK Health Security Agency*

UKRI/Defra One Health approach to vector borne diseases Research Consortium (RC) Grant. Usutu virus (USUV) Africa 3.2 lineage was detected in wild passerines in Greater London, during the late-summer of 2020. The initial investigation also identified USUV RNA in mosquito vectors from the index site, indicating a complete enzootic transmission cycle. However, at this point it was unclear whether the UK climate was suitable for the prolonged establishment of USUV. Molecular characterisation of repeat detections confirmed all UK sequences formed a monophyletic group. In addition, USUV neutralising antibodies were present in archived sera collected from captive birds since the USUV outbreak from ZSL London Zoo (the index site), highlighting that autochthonous transmission was occurring. Consequently, USUV is overwintering in the UK and should now be considered endemic in southeast England. While USUV is assessed as low risk to public health, it can have severe impacts on susceptible animal hosts, such as blackbird (Turdus merula), where infection can result in disease mediated population declines. Indeed, within the UK since the USUV outbreak, blackbird numbers in Greater London have declined by up to 39% and this trend may occur in other regions as USUV expands across the UK. Finally, enhanced surveillance in areas of southeast England deemed at high risk of viral incursion, has revealed new introductions of USUV to the UK. These represent the first known incursions of a mosquito-borne flavivirus since the 2020 USUV outbreak and highlight that the UK is susceptible to future incursions and outbreaks of mosquito-borne disease.

Flash Talks

Zoe Ward, University of Bristol

Climate drivers of uncertainty in Ixodes ricinus tick distribution models in Europe: a rapid review

Zoe Ward 1, Julia Colston 2, Rui Zhu 3, Peter Vickerman 1, Richard Wall 4, Dann Mitchell 3, Josephine Walker 1. 1 Bristol Medical School, University of Bristol 2. North Bristol NHS Trust 3. School of Geographical Sciences, University of Bristol 4. School of Biological Sciences, University of Bristol*

Ticks are blood-feeding vectors of zoonotic pathogens sensitive to temperature and humidity meaning their distributions and phenology are likely to shift under future climate change. Here, the uncertainty included in the climate projections used to assess the impact of climate on the future geographical distribution of Ixodes ricinus in Europe were evaluated. Methods A rapid review was conducted, searching Pubmed using ("model" or "distribution") and "ixodes" and "Europe" as search terms. At full text screening, studies which predict future Ixodes ricinus tick or tick-borne disease (TBD) distributions based on climate models were included. Information on location, model type and climate model projections (CMP) used in future projections were extracted. Results From 360 studies, 9 studies were identified which predicted tick or TBD distributions under future climate change scenarios. Five modelled Europe and 4 modelled specific countries, with 3 mechanistic and 6 statistical models. Uncertainty in climate projections were based on multiple global CMP in 5 studies, one CMP in one study and different average temperature changes in another study. Only one study explicitly discussed climate uncertainty in the results. In general, all the models projected small increases in the geographic range of suitability for ticks. Conclusions Given that uncertainty and extreme events are likely to be an important feature of future climate change scenarios, interdisciplinary approaches in which tick modellers work closely with climate scientists to project changes in tick distributions would allow for more nuanced inclusion and interpretation of uncertainty in climate projections.

Gillian Armstrong, UKHSA

The UK Health Security Agency vector-borne disease matrix.

G Armstrong 1, B Hack 1, Z Gibney 1, E Gallagher 1, R Pudney 1, P Veal 1, C Gordon 1, T Rampling 1, C Houlihan 1, C Warrell 1, J Medlock 1, D Mesher 1, K Russell 1, T Brooks 1, M Chand 1. 1 UK Health Security Agency*

Background The epidemiology of vector-borne diseases (VBDs) is changing in the UK and Europe. First locally acquired TBE and babesia cases have been reported in the UK, and autochthonous transmission of arboviruses in Southern Europe. The UK Health Security Agency (UKHSA) has developed a VBD matrix to inform monitoring activities and potential mitigations. Here, we describe the development of the matrix, and a VBD horizon scanning group established to monitor these VBDs. Methods Development of the matrix Initial VBDs of concern were identified through a literature search and epidemiological intelligence reports. Inclusion criteria were a human case in UK or Europe, or an outbreak/event of public health significance in last 10 years globally. Each VBD that met inclusion criteria was assigned a domestic transmission level based on UK surveillance data. Implementation of the matrix The UKHSA VBD horizon scanning group comprises technical specialists who meet monthly to monitor changes in epidemiology or other factors which may affect the risk from VBDs to the UK. The matrix is also used to systematically enhance capabilities for VBD diagnostics, surveillance, and control. Results A total of 40 VBDs met inclusion criteria (15 mosquito-borne, 12 tick-borne, 13 other). To date, the matrix has been used to inform responses to Usutu virus and cryptic malaria. Discussion To the best of our knowledge, this is the first time VBDs of concern have been systematically reviewed and categorised in a risk matrix to inform national response. The approach has been adopted within UKHSA for other infectious hazards.

Benedict Fellows, University of Glasgow

Predicting dengue fever outbreaks globally: a phenotypically plastic model of Aedes Aegypti.

Benedict Fellows 1. 1. University of Glasgow*

Dengue fever is the second most deadly vector-borne disease with an estimated 105 million infections in 2017 across 73 countries, with a 10-fold increase in the number of reported cases over the last two decades. Dengue virus (which causes dengue fever) is mainly spread by mosquitoes in the genus Aedes, with Aedes aegypti being the major urban vector due to its preference to feed on humans and bite during the day. To accurately predict the start date of dengue outbreaks, a full life-cycle model of Ae. aegypti that incorporates the environmentally-dependent development times, mortality rates and fecundity rates is needed. Ae. aegypti exhibits phenotypic plasticity, where its life-history traits in one stage can be affected by environmental conditions in past stages. Here, we use a fully tractable system of delay differential equations to model Ae. aegypti that allows for developmental and maternal plasticity between stages coupled with a compartmental SEIR model for dengue fever. We demonstrate how this approach can accurately predict the seasonality in abundance of each developmental stage of Ae. aegypti across the mosquito's global range, without the need for backfitting, and present preliminary results for the prediction of dengue fever outbreaks. Further, we discuss how this model can help to assess future risk of dengue fever, both on a local level predicting when seasonal outbreaks will occur and on a global level predicting the spread of Ae. aegypti (and therefore dengue fever) due to climate change.

Emma Fairbanks, University of Warwick

Assessing the impact of host clustering and control strategies on African horse sickness virus transmission: A simulation-based analysis

Emma L Fairbanks 1, Janet M Daly 2, Mike J Tildesley 1. 1. University of Warwick; 2. University of Nottingham*

African horse sickness virus (AHSV), spread by Culicoides midges, causes high morbidity in horses. Approval has been granted for direct horse movements from AHSV-endemic South Africa to the EU. Current AHSV vaccines cannot differentiate between infected and vaccinated animals (DIVA), risking a country's disease-free status and impacting the equine industry. While new vaccines are in development, governments may recommend stable netting to protect horses from Culicoides. We developed a model evaluating the impact of climate and vector control on AHSV transmissibility compared to other Culicoides-borne pathogens in Europe. This was integrated with a stochastic model for spatial transmission of AHSV between premises, previously parameterised using data from Morocco's 1989 outbreak. Using the UK as an example, we use estimates for the number of horses in 5km x 5km grids. In each simulation, equines in each grid are distributed into premises according to one of two distributions: lots of small premises or less but larger premises, dependent of data from Moroccan and UK premisies, respectively. Our model showed AHSV has a higher peak vectorial capacity than bluetongue virus (BTV), Schmallenberg virus (SBV), and epizootic hemorrhagic disease virus (EHDV). Simulations with more small premises resulted in few infected premises, while fewer larger premises sizes led to extensive outbreaks. Effective interventions depend on coverage; insecticide-treated stable netting significantly reduces transmission even at low coverage, whereas untreated netting has limited impact. The success of these strategies relies on horse owners' willingness to adopt and adhere to control measures and regulations.

SESSION 3: VECTOR AND DISEASE CONTROL

Saudamini Venkatesan, University of Liverpool

Do woodland patch size and connectivity influence tick density, Borrelia burgdorferi prevalence and Lyme Disease hazard through impacts on hosts?

Saudamini Venkatesan 1, Kayleigh Hansford 2, Sara Gandy 3, Mark Greener 2, Richard Hassall 4, Beth Purse 4, Roman Biek 3, Tom Morrison 3, Lucy Gilbert 3, Jolyon Medlock 2, Caroline Millins 1. 1 University of Liverpool; 2 UK Health Security Agency; 3 University of Glasgow; 4 UK Centre for Ecology & Hydrology*

Zoonotic tick-borne diseases are a rising concern in the UK, with Lyme disease incidence increasing over recent decades. Changing land-use through government policies to expand woodlands may affect human risk of exposure to tick-borne diseases by creating more suitable habitats for Ixodes ricinus ticks and impacting abundance and movement of key tick hosts. To understand how risks may change in the future, we tested the effect of landscape structure, specifically woodland patch size and connectivity, on I. ricinus density, Borrelia prevalence and Lyme disease hazard (density of infected nymphal ticks) from 60 woodland sites across two landscapes in the UK: i) Aberdeenshire, ii) Wiltshire/ New Forest referred to as Wessex. Additionally, we deployed trail cameras in the woodland patches, to assess the impact of habitat use of deer and livestock on Lyme disease hazard. We found patch connectivity had opposite effects on nymph densities in the two landscapes. In Aberdeenshire, more connected patches had higher nymph densities, whereas in Wessex, more connected patches had lower nymph densities. We further investigate and discuss if these contrasting effects are driven by the differing features within the two study areas, such as host habitat use and the land-use type between woodland patches. Our study highlights the potential impacts of large-scale woodland management policies, specifically those resulting in larger and more connected woodlands, on the distribution and density of I. ricinus and the Lyme disease pathogens.

Importantly, we show that these impacts can be context-dependent, possibly shaped by specific landscape characteristics.

James Bell, Keele University

Presymptomatic virus detection in the field: Drones detect viral incidence and spread in plants before visible yellowing.

James R. Bell 1,2, John Beale 3, Dion Garrett 1, Alistair J.D. Wright 4,5, Andrew Mead 1, Taro Takahashi 6,7, Toby Waine 3. 1 Rothamsted Research; 2 Keele University; 3 Cranfield University; 4 The University of Nottingham; 5 British Beet Research Organisation; 6 University of Bristol; 7 Agri-Food and Biosciences Institute*

Our recent BBSRC project titled 'Ecologically engineering a sustainable sugar beet landscape matrix informed by molecular tools, satellite imagery and bioeconomics', will be discussed, focussing on the use of drones and molecular tools to understand virus transmission and spread. In England, sugar beet is grown on 100,000 ha of arable land, meeting half of domestic sugar demand. Yields are threatened by virus yellows (VY) that comprise beet mild yellowing virus, beet chlorosis virus and beet yellows virus, all transmitted by the virus vector Myzus persicae, the peach-potato aphid, a global pest. We first show how virus spreads asymmetrically from a point source within a semi-field experiment. In this experiment, aphid counts and molecular diagnostics were taken every three days for six weeks to confirm colonisation and virus transmission by aphids. We then scaled the experiment to the field using a Micasense Altum multispectral sensor mounted on a small quad-copter drone. The imagery provided proof of concept that these devices can track disease progression before visible symptoms in the field using a range of vegetation indices. Uniquely, we show how multispectral data are correlated with ground sampling and diagnostic LAMP assays.

Steven White, UK Centre for Ecology & Hydrology

Phenotypic plasticity in vector traits drives trends inglobal disease incidence: Aedes albopictus and dengue

Steven White 1, Dominic Brass 1, Christina Cobbold 2, Bethan Purse 1, David Ewing 3, Amanda Callaghan 4. 1 UK Centre for Ecology and Hydrology ; 2 University of Glasgow; 3 Biomathematics and Statistics Scotland ; 4 University of Reading*

The incidence of vector-borne disease is on the rise globally, with burdens increasing in endemic countries and outbreaks occurring in new locations. Effective mitigation and intervention strategies require models that accurately predict both spatial and temporal changes in disease dynamics, but this remains challenging due to the complex and interactive relationships between environmental variation and the vector traits that govern the transmission of vector-borne diseases. Predictions of disease risk in the literature typically assume that vector traits vary instantaneously and independently of population density, and therefore fail to capture the delayed response of these same traits to past biotic and abiotic environments. We argue here that to produce accurate predictions of disease risk it is necessary to account for environmentally driven and delayed instances of phenotypic plasticity. To show this, we develop a novel stage and phenotypically structured model for the invasive mosquito vector, Aedes albopictus, and dengue, the second most prevalent human vector-borne disease worldwide. We find that environmental variation drives a dynamic phenotypic structure in the mosquito population, which accurately predicts global patterns of mosquito trait-abundance dynamics. In turn, this interacts with disease transmission to capture historic dengue outbreaks. By comparing the model to a suite of simpler models, we reveal that it is the delayed phenotypic structure that is critical for accurate prediction. Consequently, the incorporation of vector trait relationships into transmission models is critical to improvement of early warning systems that inform mitigation and control strategies.

Adi Behar, Kimron Veterinary Institute

Molecular basis of olfactory-driven behaviours of Culicoides imicola

*Yechial Shashar 1, Jonathan D. Bohbo t2 and Adi Behar*1. 1 Kimron Veterinary Institute; 2 The Hebrew University*

Culicoides imicola (Diptera: Ceratopogonidae) is a successful biting midge, infamous for its role as a biological vector for numerous pathogens of veterinary significance. Like in most insects, olfaction is likely to play a central role in the long-range attraction of Culicoides towards hosts and oviposition sites. However, studies of their sensory apparatus are scarce, and the vast majority of semiochemicals used by Culicoides are unknown. Our tanscriptome analysis shows that C. imicola exhibits many members of receptor gene families and provided for the first time evidence for molecular mechanisms mediating the detection of CO2, 1-octen-3-ol, Indoles, and lactic acid. Using behavioural experiments, we also establish the basic attractiveness to 1-octen-3-ol and lactic acid, two substances for which we identified corresponding olfactory receptors. Moreover, we investigated C. imicola's preference for oviposition sites. Our molecular analysis and comparison of bacterial populations residing in three different faecal sources indicated a unique bacterial population in equine faeces that may emit specific odorant cues. Our behavioural tests indicated that C. imicola prefers ovine and equine excrement over bovine. We created a bacterial library to examine the effect of different bacteria isolates on the oviposition preference of C. imicola. We have identified candidate bacterial species that emit mVOCs that may signal "suitable oviposition sites". This novel, basic information of the mechanisms governing C. imicola attraction to nutritional sources and oviposition sites may may find its way in several applications such as new monitoring and or biocontrol strategies aiming at the destabilization of these notorious veterinary pests.

Flash Talks

Ross N. Cuthbert, Queen's University Belfast

Managing mosquito invasions: the cost of inaction

Ross N. Cuthbert 1,¥, Danish A. Ahmed 2,¥, Emma J. Hudgins 3,4,¥, Melina Kourantidou 5,6, Christophe Diagne 7,8, Phillip J. Haubrock, 9, 10, 2, Brian Leung,k, Chunlong Liu,12, 13, Boris Leroy14, Sergei Petrovskii 15, Ayah Beidas 2, Franck Courchamp 8. 1 Queen's University Belfast; 2 Gulf University for Science and Technology; 3 University of Melbourne; 4 Carleton University; 5 Université de Bretagne Occidentale; 6 University of Southern Denmark; 7 Campus International de Baillarguet; 8 Université Paris-Saclay; 9 Senckenberg Research Institute and Natural History Museum Frankfurt; 10 University of South Bohemia in České Budějovice; 11McGill University; 12 University of China; 13 Chinese Academy of Sciences; 14 Université des Antilles; 15 University of Leicester; ¥ Equivalent contribution*

Ecological and socioeconomic impacts from biological invasions are rapidly escalating worldwide. Mosquito invasions are among the costliest globally, with Aedes aegypti and Ae. albopictus costing tens of billions in impacts in the least five decades, particularly to healthcare. While effective management underpins impact mitigation, such actions are often delayed, insufficient or entirely absent. Here, we provide such rationale by developing a conceptual model to quantify the cost of inaction, i.e., the additional expenditure due to delayed management, under varying time delays and management efficiencies. We apply the model to management and damage cost data from Aedes mosquitoes. Our model demonstrates that rapid management interventions following invasion drastically minimise costs. We also identify key points in time that differentiate among scenarios of timely, delayed and severely delayed management intervention. For Aedes spp., we estimate that the existing management delay of 55 years led to an additional total cost of approximately US$ 4.57 billion, compared to a scenario with management action only seven years prior (< 1% of the maximum cost). Moreover, we estimate that in the absence of management action, long-term losses would have accumulated to US$ 32.31 billion globally, or more than seven times the observed inaction cost. These results highlight the need for more timely management of invasive mosquito species—either pre-invasion, or as soon as possible after detection—by demonstrating how early investments rapidly reduce long-term economic impacts.

Mara Rocchi, Moredun Research Institute

Addressing Tick Management & Control through collaboration

Mara Rocchi 1, Andrew Kelloe 1, Simon Cousins 2, Beth Wells 1, Lucy Gilbert 3. 1 Moredun Research Institute; 2 Simon Cousins Media Ltd:; 3 University of Glasgow*

Tick burden in livestock is increasing and Tick-borne diseases (TBDs) outbreaks are expanding to new areas, posing threats to livestock and public health. Effective control requires a collaborative approach involving all stakeholders, fostering comprehension of conflicting matters and leading to the formation of a new cross-sectoral network. In response to this we have organised a Scottish Government-funded workshop to identify best practice and produce industry guidelines for ticks and TBDs control. The workshop aims to address the different challenges posed by ticks and TBDs. Factors such changes in wildlife distribution, agricultural practices, and human activities contribute to their spread. Traditional control methods, mainly relying on acaricides, have shown limitations and different priorities among farming communities, industry, public health bodies, government and conservationists have, until now, prevented the identification of opportunities towards common goals. The workshop, facilitated by experienced professionals, will be structured around interdisciplinary working groups focusing on key areas such as landscape management, disease diagnosis, acaricide use, public health and communication strategies. We will report on discussion and outputs. We aim to: foster network building by bringing together stakeholders and experts to form a collaborative network; produce practical guidelines by assessing available interventions and integrated management approaches; establish best practices; increase knowledge dissemination by providing publishable outputs; support and influence policy development; develop an action plan to draw a roadmap for implementing effective tick management strategies with defined roles and responsibilities. The workshop will be held on the 6th of September at the Moredun Research Institute, near Edinburgh.

Lawrence Bramham, Rothamsted Research

Pursuing aphid resistance and improved knowledge of UK barley yellow dwarf virus (BYDV) variation

Lawrence Bramham 1, Kim Hammond-Kosack 1. 1 Rothamsted Research*

Sap-sucking aphids detrimentally impact plants through direct feeding and the secretion of honeydew, promoting saprophytic fungi and reducing the photosynthetic ability of a colonised host. Combined with their ability to readily transmit devastative plant viruses, aphids represent a notable threat to important crops. Wheat cultivation is significantly impacted by aphids and associated viruses, most prominently barley yellow dwarf virus (BYDV). In terms of worldwide distribution and economic significance, BYDV is the most important viral disease affecting cereal crops. Genetic sources of resistance to aphids and/or or BYDV may provide a reliable, environmentally friendly, and economically attractive control solution. A notable genetic source of aphid resistance has been identified in the diploid species Triticum monococcum. Here, various genomic resources have been used to develop germplasm-specific KASP markers for tracking introgression of aphid resistance into a commercial wheat background, and QTL analyses using appropriate mapping populations. The presence and variation of BYDV strains across the UK has not been thoroughly explored. This is despite knowledge of UK BYDV strain diversity being crucial for robust disease monitoring, development of improved diagnostics, and the identification of resistance-breaking viral variants. Our work has explored UK BYDV strain diversity via BYDV coat protein sequencing and phylogenetic analyses using viruliferous aphid samples collected from suctions traps across the Rothamsted Insect Survey. Our results suggest the presence of previously unreported UK variants already predominant in other European countries. This has potentially significant ramifications for the UK and has assisted with development of refined assays.

Richard Hassall, UK Centre for Ecology & Hydrology

Identifying hotspots and risk factors for tick-borne encephalitis virus emergence at its range margins to guide interventions.

Richard M.J. Hassall 1, Maya Holding 2, Jolyon M. Medlock 2, Festus A. Asaaga 1, Sophie O. Vanwambeke 3, Roger Hewson 2, Bethan V. Purse 1. 1 UK Centre for Ecology & Hydrology; 2 UK Health Security Agency; 3 Université Catholique de Louvain*

Tick-borne encephalitis virus (TBEV) continues to expand its range westward in Europe, with reports of human cases increasing. In 2019, the virus was detected in the UK and since then five probable cases have been reported in humans. Many studies have outlined factors that may limit the distribution of TBEV in Europe but it's not clear which environmental and ecological factors are limiting TBEV foci at the edge of its range in Europe. Most existing studies focus on human cases that may provide a conservative estimate of the distribution of TBEV foci, particularly in a new area of emergence. In this study, part of the TickSolve project (https://ticksolve.ceh.ac.uk/), we used extensive UK Health Security Agency national surveillance data on exposure of deer species to tick-borne flaviviruses to develop spatial risk models for TBEV. We investigated the environmental and ecological factors that limit TBEV foci at its range edge, generated predictions of probability of TBEV occurrence or establishment across Great Britain and integrated predictions of recreational demand to understand where human exposure risk may be highest. TBEV was more likely to be present in sites with a greater percentage cover of coniferous woodland, occurrence of multiple deer species, higher winter temperatures and rates of spring warming. Using these models, overlaid with recreation intensity, we produced predictions of TBEV suitability in Great Britain that can be used by public health bodies to target further surveillance and provide decision makers with information on probable high-risk areas to guide awareness raising and vaccination policy.

Lauren Cator, Imperial College London

The Defra-UKRI One Health VBD Hub Project

Lauren Cator 1, Francis Windram 1, Sarah Kelly 1, Stanislav Modrák 1, Marion England 2, Will Pearse1, Steven White 3, Hannah Vineer 4, Christopher Sanders 2, Robert Jones 5, Samraat Pawar 1. 1 Imperial College London; 2 The Pirbright Institute; 3 UK Centre for Ecology & Hydrology; 4 University of Liverpool; 5 London School of Hygiene & Tropical Medicine*

UKRI/Defra One Health approach to vector borne diseases Research Consortium (RC) Grant. Responses to vector-borne diseases (VBDs) require a One Health approach that integrates data on pathogens, animals, and humans with environmental data. This is particularly true for the UK which is predicted to experience an increased threat from both endemic and invasive VBDs driven by changes in climate, land use, and biodiversity. The One Health VBD Hub project aims to enhance the links between data collection, analysis, and policy making to support responses to these threats. The Hub will provide infrastructure to enhance access and sharing of data on pathogens, vectors, and hosts, tools for linking these data to environmental data for forecasting applications, and visualisations and summaries to inform policy. Alongside these tools the project will deliver virtual and in person training and networking opportunities for the UK-VBD community. This project builds on existing investments in VBD repositories to deliver and maintain critical capacity and networks for the UK to respond to VBD threats. The Hub will form the basis for the UK research community to develop future surveillance, advanced analytics, modelling, and simulation to support evidence-based decision making. It is critical that the project is responsive to UK community needs. We will present the current progress on creating infrastructure and tools as well as solicit community feedback and suggestions for this resource.

KEYNOTE SPEAKER

Polly Roy, London School of Hygiene and Tropical Medicine

A closer look at Bluetongue virus, a complex nonenveloped arbovirus: from molecules to designer vaccines

Polly Roy 1. 1 London School of Hygiene & Tropical Medicine*

BTV is a structurally highly complex capsid of four consecutive protein layers and a genome of ten double-stranded RNA segments (S1-S10), which encode seven structural proteins (VP1-VP7) of the capsid and four or five non-structural proteins. Structural studies revealed that of the seven capsid proteins, VP2 and VP5 form the two outer layers and are responsible for virus entry into cells. Both proteins are attached to the inner capsid (core) formed by two additional layers of VP7 and VP3 protein which enclose a polymerase complex of three enzymatic proteins and the genomic RNA segments. To elucidate the different stages of BTV replication, we used a combination of *in situ* cryo-EM and cryo-ET structure together with a series of molecular and biochemical techniques, site-directed mutagenesis, reverse genetics-based virus recovery. My talk will highlight some examples of our recent studies which address: How the VP2 serotype-determining protein, impacts BTV antigenicity and virus virulence; How VP2 and VP5 coordinate virus entry and kick start the resident polymerase activity; and how the ssRNA genomic complement is selected for replication and subsequently packaged by pentameric VP6, the smallest structural protein of the capsid. The latter steps occur in a dynamic protein liquid-liquid phase separation boundary formed by virus protein NS2, which serves to exclude cellular factors and facilitate recruitment of all newly synthesised virus components into a virus assembly factory. Lastly, I will discuss how our detail molecular and structural information have allowed us to design and create new safe and efficient vaccines for BTV and the related AHSV.

SESSION 4: DIVERSITY AND GENOMICS

Eugene Ryabov, The James Hutton Institute

Unravelling the impacts of aphid vectoring and vertical transmission routes on the genetics and circulation of aphid-borne potato leafroll virus.

Eugene V. Ryabov 1, Graham Cowan 1, Lesley Torrance 1, Catherine Thomson 2, Christophe Lacomme 2. 1 The James Hutton Institute; 2 Science and Advice for Scottish Agriculture*

Potato leafroll virus (PLRV), a major pathogen of potato, occurs worldwide and shows high genetic diversity. PLRV is transmitted between susceptible plants by aphids in a persistent, circulative and non-replicative manner and may subsequently be transmitted vertically to the next vegetative generations via tubers. We used high-throughput sequencing to compare PLRV populations in the potato plants that were recently infected with PLRV by aphids and in plants where PLRV populations, wild-type or clone-derived, were vertically transmitted through several vegetative generations. This analysis allowed identification of potential genetic markers of adaptation of PLRV to the aphid-mediated and vertical transmission routes. Data on the impact of aphid and tuber transmission on PLRV circulation, genetics and pathogenicity is essential for modelling virus spread and for development of virus-control measures.

George Seddon-Roberts, John Innes Centre

A gene-expression atlas of the plant virus vector Myzus persicae reveals virulence factors produced in the salivary glands and foregut.

George Seddon-Roberts 1, Qun Liu 1, Sam T. Mugford 1, Saskia Hogenhout 1. 1 John Innes Centre*

The green peach aphid, Myzus persicae, is a polyphagous, phloem-feeding hemipteran insect from the family Aphididae. Capable of colonising over 400 plant species, and a vector of over 100 plant viruses, M. persicae is a hugely successful crop pest of huge agricultural significance. This success is in part due to its utilisation of salivary effector molecules, which are virulence factors deployed through the saliva during feeding, to modulate the immune response in otherwise resistant plant hosts. Recent findings from within and outside the group have provided evidence that effectors may not solely derive from salivary gland expressed genes, but other tissues in the aphid. Using an RNA-seq dataset examining the transcriptome of seven aphid organs, alongside mass spectrometry from aphid saliva, we discovered that most peptides found in aphid saliva corresponded to genes expressed in multiple tissues, with 55.4% (108 of 195) derived from transcripts expressed most highly in the salivary glands. However, a subset of the salivary peptides corresponded to transcripts with pronounced expression in the foregut, including transcripts in the Cathepsin B (CathB) gene family. Though other members of this family showed highest expression across various tissue, each CathB gene encoding a salivary peptide showed highest expression in the foregut. Our findings show that in addition to those originating in the salivary glands, some peptides in aphid saliva likely originate in the foregut. These peptides may be translocated into the saliva, and thereby into the host plant, via a similar pathway to foregut adherent viruses during aphid feeding.

Daniel Leybourne, The University of Liverpool

How does vector-virus diversity influence transmission efficiency in an important

Dr Daniel Leybourne 1,Elinor Baird 1, Dr Mark Whitehear 1, Dr Torsten Will 2. 1 University of Liverpool; 2 Julius Kühn-Institut*

Cereals are important global crops that contribute directly and indirectly to the production of food for human consumption. Cereals are attacked by a range of herbivorous insects, including several cereal aphid species that vector crop viruses. Barley yellow dwarf virus is the causal agent of yellow dwarf disease, one of the most devastating diseases affecting cereal crops. High levels of yellow dwarf disease infection can result in yield losses of c. 20%, rising to 80% if infection is high. The transmission efficiency of yellow dwarf virus can differ between vector populations. Intra-species diversity (genetic variation, endosymbionts) is a key determinant of aphid phenotype; however, the extent to which intra-species diversity contributes towards variation in virus transmission efficiency is unclear. Using multiple populations for two key aphid species that vector barley yellow dwarf virus, the grain aphid (Sitobion avenae) and the bird cherry-oat aphid (Rhopalosiphum padi), we have recently identified a link between intra-species diversity in vector populations and virus transmission efficiency; identifying 542 single nucleotide polymorphisms that potentially contribute towards variable transmission efficiency in R. padi. These results represent an important advancement in our understanding of the relationship between genetic diversity, vector–virus interactions, and virus transmission efficiency. In ongoing work, we are using our characterised vector populations and several virus variants to examine whether the vector-virus combination influences transmission efficiency.

Flash Talks

Jing Jing Khoo, University of Liverpool, Jing Jing Khoo

First genome assemblies for Wolbachia strain wPip from British Culex pipiens (Diptera: Culicidae)

Jing Jing Khoo 1, Alexandra Beliavskaia 1, Lesley Bell-Sakyi 1, Youseuf Suliman 1, Catherine Hartley 1, Alistair C. Darby 1, Benjamin L. Makepeace 1. 1 University of Liverpool*

The Culex pipiens species complex is a group of mosquitoes found globally and comprises four recognised species with distinct geographical and ecological distributions. Wolbachia pipientis is a bacterial endosymbiont first described in C. pipiens and is designated “wPip” in this host. It is known to induce bidirectional cytoplasmic incompatibility (CI), leading to complex patterns of crossing sterility in C. pipiens group mosquitoes. Although multiple variants of wPip with a considerable degree of diversity have been reported, contributing to the complexity of incompatible types, only a small number of genome assemblies of wPip from C. pipiens group mosquitoes are available currently. At the Tick Cell Biobank, two variants of wPip were isolated previously during generation of cell lines from UK C. pipiens group mosquitoes. One of the wPip variants was isolated from the CPL/LULS50 cell line, which contains cells from both C. pipiens

pipiens and C. pipiens molestus ecotypes. The other variant was isolated from the CPL/LULS56 cell line, which comprises cells only from the C. pipiens molestus ecotype. Using long- and short-read sequencing, we attempted to assemble the genomes of both wPip variants. Despite both assemblies displaying BUSCO scores of >99%, indicating recovery of near-complete protein-coding content, the genomes consisted of multiple contigs, with breakpoints corresponding to prophage regions. The plasmid of the Wolbachia endosymbiont of C. pipiens (pWCP) was also identified in both strains. Our study adds to the genomic resources available for research on wPip and demonstrates the utility of insect cell lines for the isolation, cultivation and characterisation of bacterial endosymbionts.

Daniel Paul Carter, UK Health Security Agency

Metatranscriptomic sequencing of the Ixodes ricinus RNA virome in two tick-borne encephalitis endemic regions of the UK

Daniel Carter 1,2, Maya Holding 1, Daniel Bailey 1, Jackie Duggan 1, Nicholas Evans 2, Steven Pullan 1. 1 UK Health Security Agency; 2 University of Liverpool*

Recent studies have found two different strains of tick-borne encephalitis (TBEv) in the UK which are similar to strains from two different regions of Europe (Holding, et.al. 2019 and 2020) suggesting that ticks and tick-borne viruses are being introduced to (or exported from) the UK through different routes such as migratory bird movements. A recently published study has also found the presence of Chimay rhabdoviruses in Ixodes ricinus ticks collected in England and Wales (Schilling, et.al. 2024). Despite the work of these recent studies, relatively little is known about the virome of Ixodes ricinus ticks found in the UK. Using RNA virus metatranscriptomic sequencing, a diverse range of RNA viruses which have not been previously detected in UK ticks have been identified including a novel peribunyavirus which is divergent from previously characterised strains. Two distinct clades of TBEv have also been identified using this approach suggesting different dynamics in the distribution and spread of TBEv in the UK. The array of different viruses identified and whole genomes constructed show the utility of methods such as metatranscriptomic sequencing coupled with de novo assembly for detecting novel viruses from complex samples such as questing ticks. By increasing the sample size and the geographic diversity of UK tick viromes, the prevalence and distribution of the viruses identified during this study including any additional novel viruses may provide a viromic fingerprint. This fingerprint can then be used to estimate the origin and movement of ticks between different regions of the UK and beyond.

Alexander Sadykov, Exeter University

Predicting Mosquito Specialisation: An Eco-Evolutionary Olfactory Model

Alexander Sadykov 1, Mario Recker1. 1 University of Exeter*

Mosquito host-seeking behaviour, a key determinant of vector-borne disease transmission, is shaped by a complex interplay of genetics, environment, and host choice. This diverse field of studies often relies on distinct methods like genetics, laboratory experiments, and field observations, generating valuable but frequently incompatible data. This fragmentation limits our ability to make consistent predictions about mosquito behaviour. Here, we introduce an eco-evolutionary model that integrates these diverse data streams. Our model incorporates genetic factors, gene-environment interactions, and environmental components such as host distribution, breeding site location, and seasonality. This unified framework allows us to investigate how environmental conditions might drive mosquitoes to specialise in specific hosts. This model has the potential to improve our understanding of mosquito olfactory behaviour and guide the development of targeted vector control strategies.

Sean Brierley, University of Salford

Genomic Characterisation of Anaplasma phagocytophilum Strains from the United Kingdom and Optimisation of Metagenomic Enrichment Protocols

Sean Brierley 1, Ian Goodhead 1, Lesley Sakyi 2, Ben Makepeace 2, Kevin Bown 3, Jing Jing Khoo 2, Alistair C. Darby 2, Alaa M. Al-Khafaji 1, Richard Birtles 1. 1 University of Salford; 2 University of Liverpool; 3 Liverpool John Moores University*

Objectives: To generate the first complete genome representations of Anaplasma phagocytophilum (Ap) isolated in the UK and develop optimised enrichment methodologies for high-resolution sequencing of Ap directly from infected host tissue. Methods: Seven Ap strains isolated from ruminants were sequenced using Illumina short-read and Oxford Nanopore long-read systems. Genomic analyses included phylogenetic reconstruction based on concatenated core gene alignments, pangenomic profiling, and average nucleotide identity. Enrichment strategies encompassing differential lysis (Molzym), CpG methylation depletion (NEB), biotinylated RNA bait capture (Agilent SureSelect), and adaptive sampling (ONT) were systematically evaluated on infected deer spleens. Alignment files were investigated to assess genome coverage and identify capture biases. An optimised approach was applied to a positive shrew carrying a genomically divergent ecotype III strain. Results: Phylogenomic analysis delineated UK Ap strains within the European Ecotype I cluster, while revealing potential subdivisions. The pangenome identified core and accessory genes, with ANI values suggesting species boundaries within Ap. Enrichment protocols combining Monarch HMW DNA extraction and NEB microbiome depletion yielded optimal pathogen representation. Gap analysis highlighted capture biases and the potential of the technology to capture complete Ap genomes, especially in the context of long read systems. An Ecotype III strain from a common shrew was partially captured with non-specific ecotype I baits identifying the limits of the capture technology. Linkage analysis of groEL genes supported existing ecotype classifications. Conclusions: This study generated the first complete Ap genomes from the UK, providing insights into genomic diversity and phylogenetic relationships. Optimised enrichment strategies were developed for high-resolution metagenomic sequencing, overcoming challenges posed by low bacterial loads and complex metagenomic samples. Whole genome analysis suggests the European ecotypes are representative of global Ap diversity, with ANI supporting the existence of four epidemiologically separate species within Ap. Continued genomic characterisation is crucial for understanding the drivers of host specificity, zoonotic potential, and epidemiological dynamics within this diverse tick-borne parasite.

Reuben James, John Innes Centre

Vitellogenin-Cas9 protein chimeras for targeted germline gene editing of aphids

Reuben James 1, Amber S. K. Hall 1, Sam T. Mugford 1, Wendy Harwood 1, Marcus Guest 2, Grant L. Hughes 3, Saskia A. Hogenhout 1. 1 John Innes Centre; 2 Syngenta, Jealott's Hill; 3 Liverpool School of Tropical Medicine*

Aphids (order Hemiptera) cause substantial crop damage worldwide. Some aphids are specialists, whilst others, like the green peach aphid Myzus persicae, have a wide host range, heavily affecting crop yields. In addition to direct feeding damage, aphids are proficient vectors of plant viruses, compounding agricultural losses. Investigating aphids via gene editing approaches may lead to novel avenues for understanding aphid biology, which could inform innovative pest management strategies. While gene editing of aphids by egg injection is possible, the process is challenging and time consuming. Hence, we explore aphid gene editing via receptor-mediated ovary transduction of cargo (ReMOT control). This involves injecting female insects with gene editing cargo that directly targets aphid early embryos. The cargo should include chimeric proteins consisting of Cas9 fused to peptide chaperones derived from vitellogenins (Vgs) or other yolk precursor proteins. This approach has successfully enabled gene editing in mosquitoes and black-legged ticks, making it a promising method to obtain gene-edited clonal lineages of aphids. We investigate aphid Vgs. Analysis using Alphafold indicates similarities in the VgR binding domains compared with other hemipterans. We have purified chimeras of mCherry fused to a range of peptides obtained from Vgs of aphids and other insects. Microscopy analyses suggest that upon injection, some of these chimeras migrate to early embryos, supporting the hypothesis that the Vg peptides mediate uptake into the developing embryo and showing their potential for efficient cargo delivery to the aphid germline. We have begun experiments to knock out M. persicae genes via ReMOT control.

KEYNOTE SPEAKER

Trisna Tungadi, Keele University

Manipulation of plant hosts and insect vectors by viruses

Trisna Tungadi 1. 1 Keele University*

Plant viruses cause significant yield loss in crop production. Most plant viruses are transmitted (vectored) by insects that feed on the plants such as aphids. Plant viruses can alter how plant 'taste' and 'smell' to their insect vector, which can influence vector migration and virus spread. Previous work will be summarised where we assessed aphid fitness on virus-infected plants and identified virus factors responsible. We utilised two model plants, *Arabidopsis thaliana* and *Nicotiana tabacum* to elucidate how Cucumber mosaic virus (CMV) infection affect the fitness of its aphid vector, the green peach aphid, *Myzus persicae*, and how this may promote onward transmission of the virus. CMV has a wide host range and able to infect around 1,000 plant species including economically important crop plants. We then translated principle findings from the lab to the field in Kenya using common beans, *Phaseolus vulgaris*. Lastly, I will highlight current work whereby we are investigating factors that determine aphid's efficiency as virus vector.

SESSION 5: VECTOR ECOLOGY AND SURVEILLANCE

Amirah Haziqah Binti Rashid, University of Liverpool

Aedes aegypti in Warming World: Uncovering Sublethal Temperature Effects on Sterility for Accurate Risk Mapping

Amirah Haziqah Binti Rashid 1, Soeren Metelmann 2,1, Kenneth Sherlock 1, Ewa Chrostek 3, Matthew Baylis 1, Marcus Blagrove1. 1 University of Liverpool; 2 UK Health Security Agency; 3 Jagiellonian University*

Dynamic shifts in the climate are impacting species distribution through changes in mortality rates, larval rearing sites, growth and reproduction, with an increased likelihood of more pronounced changes in the coming decades. Current risk maps focus on predicting species distribution by correlating environmental temperature with lethal and optimal temperature limits. However, a Drosophila melanogaster study underscores the significance of sublethal temperature effects on the lethal fertility limit in the fruit fly, which provides a more accurate prediction of global distributions. Since the thermal sterility limit is still unknown in mosquitoes, our study aims to demonstrate the effects of sublethal temperature in Aedes aegypti and Culex pipiens. In Ae. aegypti, we observed that adult male mosquitoes are significantly more sensitive to high and low temperatures as compared to females. At 38 °C, both sexes exhibit a high survival rate but are sterile (with fewer than 50% hatching). Conversely, males display sterility effects at cold temperatures (2 °C), while females exhibit greater tolerance. These temperature effects are further supported by comparing the dissections of normal reproductive organs and those of heat-exposed adults. Considering the resilience of Aedes eggs to desiccation, we investigated potential differences between constant and fluctuating temperatures to provide a more realistic diurnal temperature range (DTR) data than the current constant temperature focus. All of these results will be incorporated in a climate model with lethal sterility limit added, to produce a more accurate and biologically aware risk map. Ultimately, this will better inform mitigation policy, preparedness and surveillance efforts.

Sara Gandy, University of Glasgow

Tick-borne disease hazard in urban green spaces and their surrounding rural environment

S.G. Gandy 1, J.L .Hall 1, G. Plahe 2, R. J. Birtles 2, L. Gilbert 1. 1 The University of Glasgow; 2 The University of Salford*

Urban greenspaces provide ecosystem services such as climate change mitigation and recreation. However, ticks and tick-borne diseases have been reported in urban greenspace across Europe, which could present the disservice of a public health hazard. Most studies investigate only urban centres where ticks are present, so the extent of the issue across large regions is unknown. The objective of this study was to take a nationwide approach to characterize tick and Lyme disease hazard in 16 towns and three cities across the United Kingdom. For each town, we surveyed questing Ixodes ricinus ticks and Borrelia burgdorferi s.l. in five urban greenspaces and five sites in the surrounding rural environment. For each of the three cities, we also surveyed five suburban sites. Surveys were conducted between 2021 and 2023. We found ticks in 37.5% (6/16) towns and 75% (12/16) hinterlands, with fewest ticks across the central parts of England. The probability of ticks and Lyme disease hazard in urban greenspaces were significantly lower than in the surrounding countryside. Tick presence and Lyme disease hazard were positively correlated with the density of ticks and the percentage of woodland cover in the rural environment and negatively associated with the percentage of urban cover. These results highlight that recreating in urban greenspaces poses a lower hazard of ticks and Lyme disease than in rural woodlands and demonstrates tick presence and Lyme disease hazard in urban greenspaces are influenced by the hinterland context within which the town lies.

Dominic Brass, The UK Centre for Ecology & Hydrology

Exploring the effect of historic climate change on the population dynamics of Ixodes ricinus

Dominic P Brass 1, Steven M White 1, Bethan V Purse 1. 1 UK Centre for Ecology and Hydrology*

The burdens and impacts of tick-borne diseases are increasing across Europe in response to multiple interacting drivers, including changes in climate, land use, and host distributions. The distribution and intensity of transmission is highly dependent on seasonal tick population dynamics, and in turn tick demographic rates are sensitive to climate variability and the activity of host populations. By modelling how abiotic and biotic environmental variability influences tick population dynamics, we can better understand the changing patterns of tick-borne disease. To this end, we develop a novel environmentally driven stage-structured system of delay-differential equations to predict the population dynamics of the tick Ixodes ricinus. We extensively validate the model against field data from 77 tick populations in 20 European countries and find that 51% of the variation observed in the population dynamics of questing nymphs can be attributed to the effect of climatic variation on tick life-history. We predict that over the last 40 years there has been a concurrent increase in both the abundance of ticks and the length of time over which ticks are active across most of Europe. This suggests that the underlying suitability of the European climate for Ixodes ricinus has increased independently of concurrent changes in host-communities and land-use.

Jolyon Medlock, UKHSA

Spatial and temporal heterogeneity of Borrelia burgdorferi infection rates in Ixodes ricinus ticks in England and Wales, and how is environmental change likely to affect this?

Jolyon M Medlock 1, Kayleigh M Hansford 1. 1UK Health Security Agency*

Ixodes ricinus ticks are widely distributed across the UK, but recent surveillance of the ticks for a range of pathogens shows varying infection rates for both Borrelia burgdorferi and Anaplasma phagocytophilum. To understand the spatial and temporal heterogeneity of Borrelia infection rates in Ixodes ricinus we conducted field studies at three spatial scales. Ticks were collected and tested for Borrelia at 35 National Parks and Landscapes across England and Wales over 10 years (2013-2023). At one of these locations, ticks were sampled and tested at 37 rural locations across five years in Wiltshire (2013-2017). Furthermore at one of these sites, ticks were sampled at 18 separate parts of the same wood (2018-2022). This enabled a national borrelia infection rate of 4-6% to be determined for England and Wales, varying from 7-8% in southern England, to very low (~0%) in parts of Wales. The regional study highlighted that infection prevalence can vary depending upon habitat type and can vary three times in magnitude over a five year period, with a dominance for Borrelia garinii. Drivers for change in Borrelia infection rates was subsequently investigated through field studies on the role of deer on the Isle of Wight (2019-2021), the role of large ungulate grazers in the New Forest (2021-2024) and the impact of rewilding at the Knepp estate in Sussex (2022-2024). A summary of these relationships are discussed.

Flash Talks

Joanna De Klerk, Lancaster Ecology and Epidemiology Group, Lancaster University

Smart Sampling: An example of Adaptive Mosquito Surveillance in England and Wales

Joanna De Klerk 1, Luigi Sedda 1. 1 Lancaster University*

Mosquitoes, often regarded as mere nuisances, play a pivotal role in transmitting deadly diseases, making their surveillance an essential component of public health initiatives. This talk examines the intricate world of mosquito surveillance, exploring its advantages and cautionary considerations in the context of vector and disease monitoring, control, and elimination. We will discuss common practices employed in mosquito surveillance and novel methods for their optimisation. We present an adaptive spatial sampling design developed and applied for mosquito surveillance in England and Wales during the summers of 2023 and 2024. The first phase of our design involved using a 'stratified and proportional grid with close-pairs sampling design' to maximize spatial coverage, representativeness of land use, and account for spatial dependence in mosquito counts. In the second phase, we employed a spatial adaptive sampling design focusing on maximising Culex collections while minimizing Culex distribution uncertainty. We will critically examine both the strengths and limitations of the proposed adaptive sampling and provide guidance for future mosquito surveillance interventions.

Melanie Nicholls, The Pirbright Institute

Investigating opportunistic larval development sites of Culicoides biting midges in a zoo in the UK.

Melanie Nicholls 1, Paul Pearce-Kelly 2, Marion England 1. 1 The Pirbright Institute; 2 London Zoological Society*

Culicoides midges are responsible for the spread of bluetongue virus (BTV), Schmallenberg virus (SBV) and African Horse Sickness virus (AHSV). Of the 50 species of Culicoides found in the UK, six are thought to be vectors of BTV and SBV in northern Europe. Previous studies have found up to 20 different species of Culicoides biting midges are present at London Zoo and Whipsnade Zoo. These species included the six putative vectors of BTV and SBV, and these were found to be biting a range of exotic animal hosts. The breeding habitat preferences of these species within the zoo environment are currently unknown, so a follow-on study was carried out over two summers at Whipsnade zoo to investigate the habitat preferences of Culicoides within a zoo environment. Given that they are feeding on exotic animals, it was hypothesized that they are also utilising the faecal matter of these exotic animals as a larval habitat. To test this theory, emergence traps were set up over the dung of four different exotic species and the traps were run for four months during Culicoides breeding season. The results of the trapping showed that five species of Culicoides midge were breeding in the dung of all four exotic animal species investigated in this study, and all of these midges were putative vectors of BTV. This demonstrates that some Culicoides species are opportunistic in their choice of breeding habitat as well as their host preference, and further highlights the importance of considering preventative and mitigating measures to protect zoo animals against the risk of BTV.

Mauro Pazmino Betancourth, University of Glasgow

Monitoring biological age in mosquitoes using infrared spectroscopy

Mauro Pazmiño-Betancourth 1, Jacqueline N Mgaya 2, Doreen J. Siria 1,2, Mario Gonzales-Jimenez 3, Maggy T. Sikulu 4, Fredros O. Okumu 1,2, Francesco Baldini 1,2. 1 University of Glasgow; 2 Ifakara Health Institute; 3 University of Glasgow; 4 University of Queensland*

The age of vector populations is the most important factor that determines vectorial capacity, hence disease transmission. However, there are no effective methods to measure age in mosquitoes. Infrared spectroscopy (IRS) has shown promising results as all-in-one solution to determine the age of vectors. However, models trained with laboratory mosquitoes require re-calibration to generalize and predict the age of wild samples. This caused by the different ageing rates between laboratory and field collected, which are exposed to different environmental conditions. Here, we characterized how temperature affects ageing rates in mosquitoes and how these changes are reflected in IRS spectra to produce ML models that can predict the biological age of mosquitoes and generalize across different ecological settings. The effect that temperature has on biological age was tested using two different average temperatures: 24 and 27 ºC and with two different ranges: ±3ºC and ±6ºC using environmental chambers. The survival of Anopheles coluzzii and An. gambiae was monitored for approximately 30 days across different replicates, in the presence and absence of a sublethal exposure to deltamethrin insecticide. Mid infrared spectra of mosquitoes at different time points were obtained and their life expectancy was analysed to determine their biological age. Mosquito survival varied depending on temperature, insecticide exposure and species. Accuracy for predicting biological age was higher compared to chronological age in both species, suggesting that IRS signal is directly associated with mosquito ageing rates. Ongoing analysis will validate these models in mosquitoes reared in semi field settings and collected from the field.

SESSION 6: ONE HEALTH APPROACH TO VBD's

Heather Ferguson, University of Glasgow

Ecology and viral transmission competence of potential mosquito vector species in Scotland

Heather Ferguson 1. 1 University of Glasgow*

UKRI/Defra One Health approach to vector borne diseases Research Consortium (RC) Grant. Ticks are an important vector of numerous pathogens, and populations in the UK have been expanding causing infections in humans and livestock. A number of studies have investigated the virome of European ticks. In many cases these studies are unearthing previously unknown viruses, some of which may be linked to human and animal diseases. However, there have been few studies looking at the complete repertoire of biomes including bacteria, viruses and eukaryotes in ticks. To investigate the complete microbiome, or "infectome", of Ixodes ricinus ticks, total nucleic acids (RNA & DNA) were extracted from adult I. ricinus collected from England and Wales and fully sequenced (Illumina). The results reveal the presence of multiple viruses within the Bunyavirales and Mononegavirales orders, which share similarities to the viromes found in ticks from Europe and North America. The majority of the infectome was composed of common tick endosymbiont species such as Candidatus midichloria mitochondrii and Rickettsia spp., with three species of Borrelia also detected from two locations. Collectively, this research has highlighted the core infectome of I. ricinus and detected known and potential pathogens circulating in ticks in the United Kingdom.

Emma Widlake, Keele/Liverpool University

Spatial distribution of UK Culex mosquitoes across England and Wales, a 2023 field survey.

Emma Widlake 1, Jack Pilgrim 1, Jolanta Tanianis-Hughes 1, Ken Sherlock 1, Marcus Blagrove 1, Matthew Baylis 1, Roksana Wilson 2, Alexander Vaux 2, Jolyon Medlock 2, Luigi Sedda 3. 1 University of Liverpool; 2 UK Health Security Agency; 3 Lancaster University*

UKRI/Defra One Health approach to vector borne diseases Research Consortium (RC) Grant. West Nile virus (WNV) is a medically important arbovirus that has spread throughout Europe over the past few decades. With WNV currently circulating in neighbouring countries, and the establishment of Usutu virus in the UK since its detection in 2020, it is imperative we understand the areas most at risk of a WNV outbreak. Culex pipiens pipiens (Cx p. pipiens) and Cx. torrentium are common vectors for medically important arboviruses, with potent ability to act as reservoir vectors due to their ornithophilic nature, whilst Cx p. molestus and their hybrids with Cx p. pipiens are important bridge vectors for arboviruses due to their tendency to readily bite humans. Despite Cx. torrentium having the highest transmission potential for WNV, its distribution throughout the UK remained relatively understudied. We present a comprehensive field survey of the distribution of each of these mosquito species across 200 sites in England and Wales during peak Culex season in the summer of 2023. Using the BG-PRO sentinel trap we collected a total of 2156 Culex mosquitoes. Species ID was confirmed using microsatellite targeted PCR, giving a total of 1479 Cx p. pipiens, 5 Cx p. molestus, 22 hybrids of Cx p. pipiens/molestus and 37 Cx. torrentium. Showing clear regional differences, this study has confirmed the presence of the important bridge vector Cx p. molestus in both new and expected areas. Our study provides a comprehensive map of the four Culex species, providing a large dataset for modelling the risk of transmission of medically important arboviruses.

Katherine August and Holly A. Broadhurst, Universities of Greenwich & Salford

Using retrotransposon blood meal analysis to understand the role of grey squirrel management on Lyme disease ecology in the UK

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UKRI/Defra One Health approach to vector borne diseases Research Consortium (RC) Grant Tickborne diseases like Lyme disease (Borrelia burgdorferi), transmitted by Ixodes ricinus, pose an escalating threat to public health in the UK. Identifying tick hosts is vital for elucidating their involvement in disease transmission and formulating effective control strategies. However, the relative importance of vertebrate species as reservoir hosts remains uncertain. This is particularly relevant for the non-native grey squirrels Sciurus carolinensis as its populations might expand following the UK increase in tree planting A retrotransposon blood meal analysis (Rt-BMA) has been developed for identifying tick hosts in the United States, but it has never been applied in the UK. Using isolated woodlands across Cumbria, UK, we assessed grey squirrel and tick densities before and after each culling treatment: no culling, full cull and simulated fertility treatment achieved by culling juveniles only. Although fertility control is yet to be tested for significantly reducing significantly grey squirrel numbers, juvenile squirrels are more mobile, and they may contribute disproportionately to disease spread. We extracted DNA from the ticks' blood meals, performed Rt-BMA analysis for grey squirrels, voles, shrews, sheep and deer, and tested for the presence of Lyme disease. We aim to establish comprehensive baseline data on the importance of hosts for ticks and to provide valuable insights into the prevalence of Lyme disease in tick populations. Additionally, our results will provide evidence on the effectiveness of different grey squirrel control methods for reducing squirrel and tick abundances. These findings are vital for informing targeted interventions to mitigate tick-borne disease risks.

Robert Calam Bruce, Animal and Plant Health Agency

The utility of vector surveillance for elucidating arboviral emergence and persistence in temperate zones

Robert C. Bruce 3, Becki Lawson 1, Andrew A. Cunningham 1, Robert A. Robertson 2, Alex G.C. Vaux 4, Jolyon M. Medlock 4, Bathsheba Gardner 4, Anthony Abbott 4, Arran J. Folly 3. 1 Zoological Society of London; 2 British Trust for Ornithology; 3 Animal and Plant Health Agency; 4 UK Health Security Agency*

Emerging vector-borne pathogens present a growing biosecurity threat to countries across Europe. For example, Usutu virus (USUV, family: Flaviviridae), a mosquito-borne zoonotic virus, was detected in wild birds in the UK for the first time during 2020. Primarily, flavivirus surveillance efforts within the UK have concentrated on avian hosts, through post-mortem examination of found dead wild birds. In contrast, even though mosquito vectors are essential for transmission cycles and exist in relatively high densities, vector surveillance was typically deployed reactively, limiting our knowledge of complete enzootic cycles in the UK. Through the Vector-Borne RADAR project (www.vb-radar.com) we have enhanced vector surveillance in the UK to elucidate areas that might be at heightened risk of vector-borne disease. Extensive trapping of mosquitoes across southern England between April and October, inclusive, 2023, culminated in the collection over 17,000 individuals across 15 species. Through rt-PCR and sequencing methodologies, we successfully identified USUV RNA in samples from several species, predominantly ornithophagic Cx. pipiens (s.l.) but also bridge vectors such as Culex modestus and Aedes cantans. In addition, we detected transovarial transmission of USUV in Cx. pipiens (s.l.) populations in Greater London . Furthermore, phylogenetic analysis of viral genomes highlighted that vector surveillance, presumably due in part to its relatively high throughput, can identify incursions of new viral strains before detections in wild hosts occur. Consequently, our results show that vector surveillance enhances our ability to identify areas which might be at higher risk of flavivirus incursion or outbreaks and therefore warrant targeted mosquito control measures.

Ben Paul Jones, Animal and Plant Health Agency

TickTools: Using metagenomics approaches to unmask the organisms infecting Ixodes ticks in the United Kingdom.

Ben P. Jones 1, Nicholas Johnson 1,2. 1 Animal and Plant Health Agency; 2 University of Surrey*

UKRI/Defra One Health approach to vector borne diseases Research Consortium (RC) Grant. Ticks are an important vector of numerous pathogens, and populations in the UK have been expanding causing infections in humans and livestock. A number of studies have investigated the virome of European ticks. In many cases these studies are unearthing previously unknown viruses, some of which may be linked to human and animal diseases. However, there have been few studies looking at the complete repertoire of biomes including bacteria, viruses and eukaryotes in ticks. To investigate the complete microbiome, or "infectome", of Ixodes ricinus ticks, total nucleic acids (RNA & DNA) were extracted from adult I. ricinus collected from England and Wales and fully sequenced (Illumina). The results reveal the presence of multiple viruses within the Bunyavirales and Mononegavirales orders, which share similarities to the viromes found in ticks from Europe and North America. The majority of the infectome was composed of common tick endosymbiont species such as Candidatus midichloria mitochondrii and Rickettsia spp., with three species of Borrelia also detected from two locations. Collectively, this research has highlighted the core infectome of I. ricinus and detected known and potential pathogens circulating in ticks in the United Kingdom.

Mia White Nina Bellows, London School of Hygiene and Tropical Medicine

The GenES-VBD network and high-quality reference genomes for three UK tick species

Matthew Higgins 1, Nina Billows 1, Mirella de Jesus 1, Emma Collins 1, Joseph Thorpe 1, Jody Phelan 1, Mojca Kristan 1, Taane G. Clark 1, Susana Campino 1, Mia L. White* 2, Amy Nettlemill 2, Hassan Hartman 2, Emma L. Wise 2, Steven T. Pullan 2, Kayleigh M. Hansford 2, Faye V. Brown 2, Helen Collins 2, Jolyon M. Medlock 2. 1 London School of Hygiene & Tropical Medicine; 2 UK Health Security Agency*

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David Omondi, Liverpool School of Tropical Medicine

To investigate the use of Wolbachia for control of Culex mosquitoes

David Omondi 1. 1 Liverpool School of Tropical Medicine*

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Bethan Purse, UK Centre for Ecology & Hydrology

OPTICK – understanding and managing tick-borne disease threats in the UK's changing farmland environments"

Bethan Purse 1. 1 UK Centre for Ecology & Hydrology*

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KEYNOTE SPEAKER

Stephen Higgs, Kansas State University

Forty years of mosquito research: things we should know by now

Stephen Higg 1. 1 Kansas State University*

During over 40 years of research on mosquitoes, with a goal to better understand virus-vector-vertebrate host relationships, many different techniques and approaches have been used. At the London School of Hygiene and Tropical Medicine, artificial blood meals and intrathoracic inoculation were used to infect mosquitoes, with titrations on cell cultures and immunofluorescence microscopy used to evaluate progress of infections. Research on rodent models and work with monoclonal antibodies including over 50 different viruses. From the Institute of Virology and Environmental Microbiology in Oxford, I was sent to Colorado State University (CSU) to learn microinjection to genetically engineer mosquitoes. Subsequently, research at CSU was the first to use viral expression systems in mosquitoes to express or knock-out heterologous and homologous genes. This work included work with scorpion toxin and the first expression of green fluorescent protein in mosquitoes, that ultimately became the marker of choice for genetic engineering. Work on the effects of mosquito saliva on viral infections and immune responses to these, began at CSU. At the University of Texas Medical Branch (UTMB), infectious clones were developed and used to study the genetic determinants of infections with wild type and vaccine viruses in mosquitoes. This included the proof that a single mutation in chikungunya virus significantly increased infection of *Aedes albopictus* mosquitoes that were involved in the global spread of the virus. Working on West Nile virus, a novel method of transmission by mosquitoes was identified. The presentation will discuss the research but importantly put this in the context of critical gaps in our understanding that remain as challenges for current and future researchers.

Poster Presentation Abstracts

1. Adi Behar, Kimron Veterinary institute

Stretching the wings further- susceptibility of Culex pipiens Linnaeus to bovine ephemeral fever virus infection under experimental conditions

Alexi Chizov-Ginzburg 1, Yehuda Stram 1, Asael Rot 1, Lilach Taub-Umansky 1, Omer Izhaki 1, Adi Behar* 1. 1 Kimron Veterinary Institute

Bovine Ephemeral Fever (BEF) poses a significant threat to cattle in various climatic zones, characterized by a short duration of illness often referred to as "three-day sickness." Despite its brief nature, BEF can lead to substantial economic losses, including decreased milk production and fertility, as well as occasional fatalities. While the virus is suspected to be transmitted by hematophagous insects, the identity of a competent vector remains elusive. In this study, we investigated the potential role of Culex pipiens as a vector for BEFV. Using nested-qPCR, we monitored BEFV abundance in Cx. pipiens over a 14-day period post-infection and examined the presence of the virus in eggs laid by infected females and subsequent developmental stages of F1 mosquitoes. Our findings suggest that Cx. pipiens mosquitoes may indeed serve as vectors for BEFV, with evidence of potential vertical transmission from infected female parents to their offspring. Interestingly, our results align with recent research indicating similar replication durations of BEFV in Culicoides sonorensis, raising questions about vector competence and the influence of co-evolutionary factors. While both Cx. pipiens and C. sonorensis have shown low competence as vectors, likely due to limited co-evolution with the virus, the possibility of an "ephemeral" nature of BEFV warrants further investigation. The unexpected discovery of vertical transmission in Cx. pipiens highlights a potential mechanism for the persistence of BEFV within vector populations, despite short viremia periods in hosts and vectors alike. These findings provide valuable insights into the dynamics of BEFV-vector interaction and transmission and underscore the need for continued research in this area.

2. Jonathan Yardley, University of Glasgow

The impact of host community composition on pathogen hazard in a tick-borne disease hotspot

Jonathan Yardley* 1, Mafalda Viana 1, Caroline Millins 2, Lucy Gilbert 1, Roman Biek 1. 1 University of Glasgow; 2 University of Liverpool

Lyme Disease (LD), caused by the Borrelia burgdorferi sensu lato (Bbsl) bacterial complex, is the most prevalent vector-borne zoonosis in Europe. Both the pathogen and tick vector rely on hosts for completion of their life cycle. This PhD aimed to quantify the density of infected vectors in the environment as well as the related tick reproduction and Bbsl reservoir hosts contributing to LD hazard. Small islands with simple host species communities can be ideal natural study systems to investigate this. The Uist islands of the Outer Hebrides are a hotspot for LD with approximately 600 cases per 100,000 population, 100-fold higher than the Scottish average, despite their lack of woodland more usually associated with LD hotspots. Neighbouring islands Barra and Harris have different host communities to the Uists (i.e. no deer, voles or hedgehogs) and LD case numbers here follow national averages. Ticks were collected and quantified from both hosts and the environment, and tick and host Bbsl prevalence was analysed across the Uists and neighbouring islands, allowing determination of Bbsl/vector hosts which may contribute to the increased LD risk of the Uists.

3. Lorna Glenn, University of Liverpool

Humidity matters: Refining vector-borne disease predictions in the face of climate-induced mosquito movements

Lorna Glenn* 1, Steven White 2, Liam Dougherty 1, Jane Hill 3, Matthew Baylis, 1Marcus Blagrove 1. 1 University of Liverpool; 2 UK Centre for Ecology and Hydrology; 3 University of York

As a result of climate change affecting global temperature and humidity patterns, the geographic range of mosquitoes has shifted towards more temperate areas. A recent, high-consequence example includes the ongoing spread of Aedes albopictus throughout Europe, as far north as the UK, resulting in multiple autochthonous outbreaks of dengue and chikungunya viruses in the species new range. Current mathematical models predicting vector distribution focus primarily on temperature, but their predictive power falls short due to their omittance of relative humidity (RH). Changes in RH can exacerbate or buffer the negative effects of high temperatures on mosquito fitness and pathogen transmission. Although RH has a fundamental relationship with temperature, there is limited knowledge of this relationship on vector biology. Field studies have shown increased RH can positively affect desiccation tolerance, egg production and development, survival and activity but negatively affect biting rate. We aim to study the effects of RH on Ae. albopictus and develop a distribution model incorporating both temperature and RH. Using binary saturated aqueous salt solutions, we will create a matrix of RH (10-90%) and temperature (10-40°C) to investigate whether these factors interact additively or synergistically by measuring the biting rate, longevity, and fecundity of Ae. albopictus. Results will be used to parameterize an R0 model to aid in the informing of the spatial and temporal emergence and persistence of these vectors, thereby identifying at-risk areas where potential mitigation action by policy makers and public health officials may need to be implemented.

4. Daniel Carter, UK Health Security Agency

Investigating the sero-reactivity of indeterminate Lyme Disease cases against Borrelia miyamotoi

Daniel Carter* 1,2, Steven Pullan 1, Nicholas Evans 2, Daniel Bailey 1, Jackie Duggan 1. 1 UK Health Security Agency; 2 University of Liverpool

Lyme disease serology is complex and there are challenges with sensitivity and specificity due to factors such as low spirochaetaemia during infection and infection being localised to the site of tick-bite all which lead to a dampened antibody response. This may lead to a higher number of false negatives or indeterminate results where a patient may have been exposed to Borrelia but has not developed the expected antibody reaction. An indeterminate diagnosis may lead to concerns from patients and clinicians about the accuracy and quality of existing tests and diagnoses especially where patients continue to experience symptoms. Uncertainty caused by negative or inconclusive testing can also impact on a patient's quality of life. This study found that patients with an indeterminate Lyme diagnosis are more likely to have been exposed to B. miyamotoi than those with confirmed or negative Lyme diagnoses. This study also provides the first evidence of antibodies raised against B. miyamotoi in symptomatic patients seeking treatment for Lyme Borreliosis in the United Kingdom. The development and optimisation of a B. miyamotoi serological assay allows for further work to understand the level of exposure and disease burden of B. miyamotoi in the United Kingdom as well as providing a resource for detecting other relapsing fever species in groups such as returning travellers.

5. Scott Tytheridge, Imperial College London

Elucidating the impact of nectar feeding on invasive mosquito species

Scott Tytheridge* 1,2, Arran J. Folly 2, Lauren J. Cator 1. 1 Imperial College London; 2 Animal and Plant Health Agency

Invasive mosquito species are a significant global animal and public health threat. Transmission of mosquito-borne pathogens occurs during blood feeding and the behavioural and physiological effects of blood meals on mosquito fitness and pathogen transmission have been an area of intense research. There are relatively limited data, however, on broader mosquito nutritional ecology. Nectar is an important energy source in both male and female mosquitoes and contributes to plethora of functions including swarming, host-seeking, and egg development. Interestingly, in pollinating insects, consumption of sugar and phytochemicals (plant compounds which may have bioactive properties) can impact foraging behaviour and mediate parasitic infections. Consequently, sugar feeding and nutritional quality in mosquitoes may have unexplored impacts on vectorial capacity. Therefore, understanding how the availability of nutritional plant resources will shape risk of establishment and potential disease transmission are critical for formulating responses to invasive mosquitoes. We measured the effects of sucrose concentration on the survival and fecundity of female Aedes albopictus (Montpellier strain), a competent vector for several zoonotic arboviruses with a relatively high risk of incursion into the UK. Our results indicate that nutrition-based impacts on life history traits may affect the predicted lifetime reproductive success of this important invasive species. The future aims of the project are to determine the effect of plant sugar sources on fitness of other mosquito species, and their susceptibility to viral infections.

6. Nicola J Fletcher, Liverpool School of Tropical Medicine

Determining the influence of water pollution on mosquito virome

Nicola Fletcher* 1, Dr Jennifer Lord 1. 1 Liverpool School of Tropical Medicine

Every time a female mosquito lands in a water source to lay her eggs, those progenies are exposed to any contaminants in the water for a significant portion of their life cycle. Sewage is pumped directly into water, wastewater from factories and mines and contaminants leaching from roads and cropland contaminate water with metals, nitrates and calcium, among others. A small number of papers have linked the presence of some pollutants in larval water to infection or dissemination rates of viruses in mosquitoes. Notably, nutrient-enriched wastewater resulting from human activities containing increased nitrogen and carbon decreases Zika virus dissemination. Meanwhile, sewage outflow sites were correlated with increased West Nile virus infections. Vector competence of viruses is known to vary spatially, even within one species of mosquitoes, due to genetic and environmental influences. I want to investigate further how much and in what way pollution contributes to this, as Water quality and contaminants from anthropogenic pollution vary spatially depending on the surrounding area. My PhD is focused on determining the influence of water pollution on the mosquito virome, and I have designed two experiments to explore this. The first one will look at the virome of wild mosquitoes in three different habitats alongside water analysis data. The second will focus on the effect of field water from different habitats on a single virus to track and compare prevalence in a lab-reared mosquito strain.

7. Christida Estu Wastika, Liverpool School of Tropical Medicine

A single-sugar-fed modulates Aedes aegypti vectorial capacity

Christida Estu Wasrika* 1, Tara S. Joseph 1, Samiksha Venkatesan 1, Grant L. Hughes 1. 1 Liverpool School of Tropical Medicine

Urban mosquitoes in Orthoflavivirus endemic areas, which are likely to hatch in clean water and containers inside a house, such as a bathroom tub or water collection container, consume diverse sugars. However, the impact of these sugar variations on vectorial capacity has yet to be studied. We aim to investigate the vectorial capacity of lab-reared Aedes aegypti strain Liverpool (LVP) and Galveston (GALV) mosquitoes fed on three different sugars against Orthoflavivirus ziakense (Zika virus; ZIKV). The adult mosquitoes were fed 10% sucrose, 10% glucose, or 10% fructose for ten days. Then, ZIKV-infected blood was given for 1 hour, followed by ten days of incubation before virus detection in the body and legs by plaque assay to determine the virus infection (body samples) and dissemination (legs sample). As a result, LVP fed with sucrose, glucose, and fructose exhibited higher infection and dissemination rates compared to GALV. Moreover, Fructose and glucose enhance ZIKV infection in LVP and GALV, respectively, while sucrose suppressed ZIKV dissemination in GALV but not in LVP. Our results indicate the vectorial capacity of susceptible vectors is modulated by the mosquito strain and their dietary sugars.

8. Steffi Urhausen, Met Office, UK

Fall armyworm: Climate-related risks on major crops in China and Europe

Steffi Urhausen* 1, Catherine D. Bradshaw 1,2, Jemma Davie 1, Dominic Eyre 3, Deborah Hemming 1, Hongmei Li 4, Bryony Taylor 5, Feng Zhang 4. 1 Met Office, UK; 2 University fo Exeter; 3 Department for Environment, Food & Rural Affairs; 4 CABI, China; 5 CABI, UK

The Fall Armyworm (FAW), Spodoptera frugiperda, is an invasive plant pest originating from the Americas which has spread rapidly across many countries of the globe since 2016, particularly in Africa and Asia. Although the larvae are polyphagous, they prefer maize or rice and can cause substantial crop loss. FAW moths are highly migratory, and they can utilise high-altitude winds to migrate hundreds of kilometres in one night. FAW require warm temperatures (above 7°C) to overwinter in an area, thus they prefer tropical or subtropical climates. We present results that assess the suitability of climate conditions in China (Yangtze River basin area) to estimate the suitability of seasonal temperatures for FAW survival. We also present results from a novel 'migration potential' metric combining suitable wind direction for migration towards maize crop areas in China with temperature suitability for FAW survival in these areas. We then apply the methods and knowledge used to assess FAW risks to maize crops in China to investigate the potential for climate conditions to be suitable for FAW to establish in Europe (from its current breeding areas in northern Africa) or become a transient seasonal pest migrating from outside Europe. In 2023, the European and Mediterranean Plant Protection Organization (EPPO) has reported the presence of FAW in Greece and Romania and, the European Commission has published a regulation to prevent the introduction, establishment and spread within the EU (2023/1134). Our results indicate that temperatures are currently suitable for FAW survival and breeding across areas of southern Europe and given favourable wind directions it would be possible for seasonal migrations of FAW across most of Europe, posing significant risks to maize and other crops.

9. Marc Guimera Busquets, The Pirbright Institute

Visualisation of bluetongue virus in the salivary apparatus of Culicoides biting midges highlights the accessory glands as a primary arboviral infection site

Marc Guimerà Busquets* 1, Faye V. Brown 1, Simon T. Carpenter 1, 2, Karin E. Darpel 1,3, 4, Christopher J. Sanders 1. 1 The Pirbright Institute; 2 University of Cambridge; 3 Institute of Virology and Immunology (Mittelhäusern); 4 University of Bern

Arthropods transmit a wide range of pathogens of importance for the global health of humans, animals, and plants. One of these arthropod vectors, Culicoides biting midges (Diptera: Ceratopogonidae), are the biological vector of several human and animal pathogens, including economically important livestock viruses like bluetongue virus (BTV). Like other arboviruses, Culicoides-borne viruses must reach and replicate in the salivary apparatus, to be transmitted to susceptible hosts through the saliva during subsequent blood feeding. Despite the importance of the salivary gland apparatus for pathogen transmission, these structures have received little attention, perhaps due to the small size and fragility of Culicoides. Here, we developed techniques to visualize the infection of salivary glands and other soft tissues with BTV, in some of the smallest known arbovirus vectors, using three-dimensional immunofluorescence confocal microscopy. We showed BTV infection of specific structures of the salivary gland apparatus of female Culicoides following oral virus uptake, and related visualisation of viral infection in the salivary apparatus to high viral RNA copies in the body. Furthermore, we demonstrated for the first time, that the accessory glands are a primary site for BTV replication within the salivary apparatus, revealing a novel site of virus-vector interactions, and a novel role of the accessory glands of Culicoides in arbovirus amplification and transmission. Our approach is applicable to a wide range of arbovirus vector groups, and provides a powerful tool to investigate arbovirus infection and dissemination, particularly where there are practical challenges in the visualization of small and delicate tissues of arthropods.

10. Aidan O'Donnell, Unviersity of Edinburgh

Dancing out of step: The adaptability of Anopheles stephensi rhythms and their impact on malaria development

Aidan O'Donnell* 1, Sarah Reece 1. 1 University of Edinburgh

The role of biological rhythms in infections is gaining traction because explaining the regulatory mechanisms and fitness consequences of rhythms exhibited by parasites, vectors and hosts offer new avenues for infection control. In mice, malaria parasites exhibit asexual development that is synchronized with host feeding time and the development of transmission stages are also synchronized with the biting time of the mosquito vector. Disruption of parasites synchrony in the mammalian host leads to fewer growth & transmission stages, greatly reducing transmission potential. Yet, while mammalian host rhythms significantly impact parasite fitness, the role of mosquito rhythms in parasite development during transmission remains uncertain. Moreover, field observations reveal the adaptability of mosquitoes' daily rhythms, such as adjusting their feeding times in response to interventions like bed nets and thriving amidst urban environments flooded with artificial light at night. However, the potential fitness repercussions for mosquitoes with altered rhythms remain unexplored. Here we disrupted the rhythms of An. stephensi by subjecting mosquitoes to photoschedule durations (i.e hours of day plus night) that are longer or shorter than 24 hours and investigate the consequences for both mosquito life history traits such as egg lay, survival, nutrition and the timing of flight activity. Second, we explore the impacts of these conditions for malaria development within mosquitoes including the likelihood of infection, the duration of development, and overall parasite density. By unraveling the intricate interplay between biological rhythms, parasite development, and vector behavior, our study offers insights into the complex landscape of infectious disease transmission.

11. Catherine Bradshaw, Met Office

Transmission pathways for the stem rust pathogen into Central and East Asia and the role of the alternate host, barberry

Catherine D. Bradshaw* 1,2, Deborah L. Hemming 1,3, Tamás Mona 4, William Thurston 5, Marion K. Seier 6, David Hodson 7, Christopher A. Gilligan 4, Jacob W. Smith 4, Dominic Eyre 8, Tai-Guo Liu 9, Bryony Taylor 6, Jemma Davie 1, Steffi Urhausen 1, Thomas Crocker 1, Sarah Millington 5, Matthew Hort 5, Feng Zhang 10, 11, Hongmei Li 10. 1 Met Office Hadley Centre; 2 University of Exeter; 3 University of Birmingham; 4 University of Cambridge; 5 Met Office; 6 CABI Europe-UK; 7 International Maize and Wheat Improvement Center (CIMMYT); 8 Plant Health Risk and Horizon Scanning Team, Defra; 9 Chinese Academy of Agricultural Sciences (CAAS); 10 CABI Beijing Representative Office; 11 Chinese Academy of Agricultural Sciences

Atmospheric spore transport is a major transboundary vector of plant disease. After decades of stem rust control caused by Puccinia graminis f.sp. tritici (Pgt), race TTKSK/Ug99 of Pgt identified in Uganda in 1998 reignited concerns about epidemics worldwide – including in the UK - because ~90% of world wheat cultivars had no resistance to the new race. Since detection, Ug99 variants have now been identified in 14 countries in Africa, South Asia and the Middle East. Many past control programs relied on resistant cultivars in combination with eradication of barberry (Berberis spp.), the alternate host required for the stem rust pathogen, but in East Asia, barberry is native and widespread. Using an integrated modelling framework applicable to all wind-dispersed vector-borne carriers globally, we combine estimates of fungal spore deposition from an atmospheric dispersion model, environmental suitability for spore germination, and crop calendar information to investigate potential transmission pathways for stem rust outbreaks to reach East Asia. We incorporate a new generic barberry species representation into the lifecycle and find viable transmission pathways and that an initial infection in the Middle East could persist in East Asia for up to three years because of the alternate host. Our results indicate the need for further assessment of barberry species distributions, infection characteristics and appropriate methods for targeted surveillance and mitigation strategies should stem rust incidence increase. This study would help apply the developed modelling framework and assess the risks to the UK as barberry is still widely distributed.

12. Yiran Wang, Imperial College London

Quantifying the effect of temperature on European Culex Pipiens longevity and reproduction in Italy

Yiran Wang* 1, Daniele Arnoldi 2, Giovanni Marini 2, Ilaria Dorigatti 1 1 Imperial College London; 2. Fondazione Edmund Mach

Background Culex Pipiens is the primary vector of West Nile Virus (WNV), an arboviral zoonosis that can cause fatal West Nile Neuroinvasive Disease (WNND). In recent years, there has been a rapid increase in the number of human WNND cases reported in Europe, particularly in Italy, which raises a significant public health concern. Several computational studies suggest that global warming can facilitate WNV transmission in the European Mediterranean region through different mechanisms. However, how temperature affects the life and gonotrophic cycles of European Culex Pipiens remains to be investigated. Method This study aims to quantify how temperature affects the life and gonotrophic cycle of European Culex Pipiens through laboratory experiments. We have collected larvae of Culex Pipiens from San Michele all'Adige, Italy, and reared under laboratory conditions. Female adults have been provided with blood meals and monitored for oviposition behaviour at different test temperatures. We will use the empirical data obtained from this experiment to characterize the thermal dependency of entomological traits such as longevity, the length of gonotrophic cycle, and the number of eggs produced per cycle for the European Culex Pipiens mosquito. Significance This study will fill current knowledge gaps on the effect of temperature on the life and gonotrophic cycles of European Culex Pipiens. Such findings will inform downstream epidemiological modelling studies investigating WNV transmission in Europe under the current and changing climate.

13. Yiran Wang, Imperial College London

Testing associations between West Nile Virus circulation in Culex mosquitoes and avian biodiversity in Emilia-Romagna, Italy

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Background: West Nile Virus (WNV) is a zoonotic arbovirus that is maintained in a transmission circle between Culex mosquitoes and birds, and occasionally spills over into the human host. Previous studies have shown inconsistent effects of avian biodiversity on WNV circulation, with dilution effects (negative correlations) observed in some parts of the world and amplification effects (positive correlations) observed in others. In Europe, this relationship remains largely unexplored including in regions with high WNV circulation, such as Emilia-Romagna in Italy. Method: We explored the statistical association between WNV circulation from mosquito surveillance data collected in Emilia-Romagna (Italy) from 2013 to 2023 and observed avian biodiversity data collected in the region during the study period as part of the Farmland Bird Index project. Regression models were employed to test the association between multiple measures of WNV circulation and avian biodiversity, including species richness and diversity indexes, in combination with climate and environmental data. Results: We observe a significant negative association between WNV circulation in mosquitoes and avian biodiversity in Emilia-Romagna, Italy, providing the first evidence of the dilution effect of WNV in Europe. Significance: This study unveils the local effects of avian biodiversity on WNV transmission in Emilia-Romagna, which can inform surveillance programmes as well as policies integrating biodiversity protection into public health planning.

14. Dana L. Vanlandingham, Kansas State University

The epidemic potential of Japanese encephalitis virus

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Japanese encephalitis virus (JEV) is a mosquito-borne arbovirus belonging to the family Flaviviriade. Reflecting its complex transmission cycle involving multiple species, Japanese encephalitis is regarded as a "ONE Health" disease. Transmission of JEV in endemic regions is maintained in a cycle between Culex tritaeniorhynchus and amplifying hosts such as avian and swine species, with potentially fatal infections in dead-end hosts including humans and equines. Over two billion people live in the endemic area, with an estimated 20,000 deaths occurring despite the widespread use of highly efficacious vaccines. In addition to the endemic vector Cx. tritaeniorhynchus, other Culex species mosquitoes such as Cx. quinquefasciatus and Cx. pipiens have also been demonstrated to be capable of transmitting JEV. Similar to West Nile virus (WNV), another member of the JEV serocomplex, JEV has an exceptionally wide host range and susceptible vector species. If introduced into non-endemic areas, it would likely be nearly impossible for disease eradication following the establishment of an enzootic transmission cycle between asymptomatic amplification hosts and competent vectors. Here we discuss the potential for the introduction and establishment of JEV into regions where competent mosquito vectors and susceptible vertebrate hosts occur, including the United Kingdom.

15. Arran Folly, Animal and Plant Health Agency

Vector-Borne RADAR (Real-time Arbovirus Detection And Response)

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UKRI/Defra One Health approach to vector borne diseases Research Consortium (RC) Grant. Understanding the emergence and transmission of zoonotic flaviviruses, such as Usutu virus (USUV) and West Nile virus (WNV) is paramount for safeguarding animal and human health. The United Kingdom (UK) was considered free of mosquito-borne viral zoonotic diseases until USUV was detected in Greater London in both avian hosts and mosquito vectors in 2020. Subsequent USUV detections across the southeast of England since the initial outbreak, indicate that the virus is persisting and is now likely endemic in this region. Moreover, presence of the virus has been implicated as a driver of blackbird (Turdus merula), a host highly susceptible to USUV infection, population decline in Greater London. Although the related flavivirus WNV, which may have a greater impact on animal and public health, has not yet been detected in the UK, its occurrence in neighbouring countries in continental Europe, highlights the need to remain vigilant for its potential incursion. The Vector-Borne RADAR (Real-time Arbovirus Detection And Response) project (www.vb-radar.com) was established in 2023 to enhance mosquito-borne flavivirus surveillance in the UK. The primary focus of the project is to investigate, through enhanced surveillance, the emergence and transmission pathways for flavivirus incursion in wild birds and mosquito vectors. The project will combine data from avian disease surveillance and population monitoring to facilitate the development of an early warning system to identify flaviviral disease outbreaks in wild birds. The VB-RADAR team comprises governmental animal and public health organisations, in collaboration with conservation NGOs, exemplifying a One Health approach to protect UK biosecurity.

16. Eilish Hart, UKHSA / University of Liverpool

Estimating population exposure to tick-borne diseases in England, 2021-2022

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Antibodies specific for the causative agents of tick-borne diseases can persist in the blood for several years after initial infection, allowing determination of seroprevalence as an estimate of cumulative past population exposure. Plasma samples (n=10,000) from NHS Blood and Transplant blood donors (2021-22) were tested to estimate the seroprevalence in the English adult population of IgG antibodies against the causative agent of Lyme disease, Borrelia burgdorferi sensu lato (Bbsl). This used a standard two-tiered testing (sTTT) strategy with a sensitive B. burgdorferi VlsE/pepC10 IgG/IgM ELISA (Zeus Scientific) followed by a specific Borrelia ViraChip IgG immunoblot array (Viramed Biotech AG) for any samples with positive or indeterminate reactivity in the ELISA. A subset of these samples (n=2,500) was tested to estimate population exposure to tick-borne encephalitis virus (TBEV) using an anti-TBE IgG ELISA (Euroimmun), and Anaplasma phagocytophilum using the Micro-blot Array (MBA) Borrelia IgG assay (Testline), followed by an immunofluorescence assay (A. phagocytophilum IFA, IgG, Focus Diagnostics) for any samples with positive or borderline reactivity in the MBA. sTTT gives a seroprevalence estimate of 0.49% (95% CI 0.36 – 0.65) for B. burgdorferi s.l. seroprevalence in England (2021 - 2022), lower than an earlier seroprevalence estimate for Scotland (2010 - 2011) of 4.2%. Of the 2,500 samples tested for IgG antibodies to TBEV, 38 [1.52% (95% CI 1.08 – 2.08)] were seroreactive, and for A. phagocytophilum, 23 [0.92% (95% CI 0.58 – 1.38)] were positive after confirmatory IFA. Work is ongoing to run the TBEV seroreactive samples through secondary assays to exclude cross-reactive results.

17. Amy Parkes-Withers, Animal and Plant Health Agency

Using correlative and mechanistic species distribution models to predict areas at risk of disease for the current and future environmental conditions: a case study of West Nile Virus in the United Kingdom.

Parkes-Withers, A. J* 1) Croft, S. 1, Budgey, R. 1, Warren, D. 1, Johnson, N. 1. 1 Animal and Plant Health Agency

Vector-borne diseases have a significant impact on animal and human health globally, and climate change is predicted to lead to shifts in areas at risk. Understanding this changing risk can inform surveillance and control measures to minimise the impacts. Here, we propose a novel approach for determining disease risk using correlative species distribution modelling of vectors that are further validated by mechanistic models, and then combining these with correlative species distribution models of disease hosts. West Nile Virus (WNV) is used as a case study as the virus is not currently present in the United Kingdom (UK) but the risk of an incursion is high. WNV is a mosquito-borne flavivirus with a natural transmission cycle between mosquitos and birds, with Culex mosquitos, specifically Cx. pipiens and Cx. modestus, likely to be key vectors. It can spread into non-reservoir hosts (e.g., equids, humans) via mosquito bites leading to illness and mortality in severe cases. Species distributions of the two vector species and representative avian hosts (corvid and non-corvid Passeriformes) were produced individually for current and future environmental conditions, then combined to produce UK WNV risk maps. These highlighted areas at greater risk due to higher habitat suitability for both hosts and vectors, and predicts how risk may change by 2100 under a best- and worst-case climate scenario. Generally, WNV risk in the future would increase in south-eastern UK and decrease further north. Overall, this study presents how combining correlative and mechanistic species distribution modelling could predict areas at risk of novel diseases.

18. Mariana Reis Wunderlich, London School of Hygiene and Tropical Medicine

Establishing a Laboratory Colony of Aedes vexans at London School of Hygiene & Tropical Medicine (LSHTM)

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Introduction: Aedes vexans, until recently only reported in small numbers in the UK, poses a significant public health threat as a vector of arboviruses such as Zika, Tahyna, Rift Valley Fever and West Nile Virus. Its impact remains understudied despite its increasing numbers. Objective: This study aims to establish a sustainable laboratory colony of Aedes vexans at LSHTM to enhance research on arbovirus transmission and assist the UK Health Security Agency in developing a surveillance strategy for Tahyna virus. Methods: Eggs from the Aedes vexans Green River strain were sourced from the Federal Institute for Animal Health, in Germany. The LSHTM colony is maintained in controlled conditions (24-26°C, 60-85% relative humidity, 16:8 light/dark photocycle). Females lay eggs on damp sterile moss. Once submerged in water, this stimulates hatching of larvae, which feed on koi fish food pellets. Adults receive a 10% glucose solution and regular blood meals to support egg production. Eggs can be stored at 10°C for up to six months. Results: The establishment of the colony is progressing, with efforts focusing on achieving stable reproduction and consistent developmental cycles across generations, to support virus - host research work. Conclusion: The successful establishment of a laboratory colony of Aedes vexans in the UK represents a significant advancement for arbovirus research and surveillance, providing essential insights into the species' role in disease transmission and aiding in the development of a monitoring strategy for Tahyna virus.

19. Bruno Goddeeris, KU Leuven

STAR-IDAZ: a generic roadmap for "Vector Transmission Control"

Bruno M. Goddeeris* 1, Isabel Kinney Ferreira de Miranda Santos 2, Cynthia Baldwin 3, Madeline Newman 4. 1 KU Leuven; 2 University of São Paulo; 3 University of Massachusetts Amherst; 4 Department for Environment, Food and Rural Affairs

The Strategic Alliance for Research on the Major Infectious Diseases of Animals and Zoonoses (STAR-IDAZ) International Research Consortium (IRC) is a global initiative to coordinate global animal health research at international level to accelerate delivery of new and improved animal health strategies and disease control tools. To achieve these goals, the IRC partners agree to coordinate their research programmes to address identified research needs relating to the various topics and to share results. Research gaps identified by the Working Groups are organized into research roadmaps, which map out the key research questions needing to be addressed, working from a target product profile back to basic science. The roadmaps are based on steps or "Leads" which each consider the Research Question ("What is the problem needing to be solved?"), Challenges ("What are the scientific and technological challenges/knowledge gaps needing to be addressed"), Solution Routes ("What approaches could/should be taken?"), Dependencies (What needs to be done first) and State of the Art (Existing knowledge including success and failures) (Entrican et al. 2020). One of STAR-IDAZ priority topics is "Vector Transmission Control" (VTC), in addition to several vector-borne diseases. The generic roadmap for VTC can then be used in conjunction with STAR-IDAZ roadmaps specific to vector-transmitted diseases. A roadmap for VTC has been constructed and aligned on three routes, i.e. vector biology, vector host and vector biotope, with their respective building blocks, leading from the arthropod vector itself towards its control. Each building block of this routes has been complemented by state-of-the-art information on the relevant Leads to address the necessary research gaps for identification and design of relevant projects. Entrican et al., 2020. Transbound. Emerg. Dis. 68: 1513-1520.

20. Iman Jemal Muktar, Durham University

Olfaction in larval malaria mosquitoes Anopheles gambiae

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Anopheles gambiae mosquitoes is the primary vector for malaria in sub-Saharan Africa, causing numerous fatalities. Although current strategies focus on adult mosquitoes, increasing insecticide resistance and rising malaria cases necessitate innovative interventions. Targeting mosquito larvae offers a promising approach to reducing adult mosquito populations. Like adults, mosquito larvae use their olfactory senses to find food and evade predators. Therefore, manipulating larval olfaction could effectively disrupt their development. The olfactory system of mosquito larvae includes a sensory cone in their antennae, containing olfactory sensory neurons (ORNs). These ORNs express 12 distinct olfactory receptors (ORs), which combine with an odorant receptor co-receptor (ORCO) to form ORx/ORCO complexes. These complexes respond to a range of host-derived odors with either narrow or broad tuning. This simpler olfactory model allows researchers to study how ORCO-positive cells respond to various soluble compounds predicted to bind to these olfactory receptors. Previous research, including unpublished work from our laboratory, has demonstrated the behavioural significance of certain soluble compounds for larvae. This project's primary goal is to understand the neuronal mechanisms behind olfactory attraction and repellence in mosquito larvae. Using calcium imaging, I will characterize the in vivo responses of ORCO neurons to behaviourally relevant compounds and identify specific OR-ligand pairings. A newly developed transgenic line (Orco-QF2, QUAS-GCamp6s) will be used to visualize ORCO neuron responses in larval antennae directly. By elucidating the cellular and molecular basis of odorant perception in Anopheles gambiae larvae, this research could lead to novel, olfaction-based methods for larval control.

21. Melanie Nicholls, The Pirbright Institute

Testing the efficacy of vector-proof accommodation for UK livestock.

Marion England 1, Melanie Nicholls* 1, Simon King, 1, Jake Scales 1, Paul Pearce-Kelly 2. 1 The Pirbright Institute; 2 Zoological Society of London

Bluetongue virus serotype 3 (BTV-3, a Culicoides-borne virus) emerged for the first time in the Netherlands in September 2023 and spread very rapidly across most of the country, causing 3.9% loss within the sheep population. The virus subsequently spread to Belgium and Germany, reaching the United Kingdom (UK) in November 2023. Overwintering and re-emergence of BTV-3 in the Netherlands is considered to be very likely during 2024. The UK had been officially BTV-free since 2011, but there is a high risk of repeated incursion to the UK this year, where indeed the virus may have also overwintered. A vaccine has been approved under emergency licence for use in the Netherlands, but there is currently no approved vaccine for use in the UK. As such, control measures to protect livestock are limited to movement restrictions. Vector control is challenging, due to the extremely high abundance of Culicoides at livestock holdings, and the inability of insecticide/repellents to prevent BTV transmission in the field. Previous studies have shown that insecticide treated mesh to prevent entry of Culicoides into livestock accommodation has failed to prevent all vectors from accessing stables. In this study, we explore the use of a range of vector-proof options across four stable set ups, housing pygmy goats. We will present results of Culicoides collections across these four set ups. The findings generated will help to provide advice for livestock keepers on how to protect their animals from BTV in the absence of a BTV vaccine in the UK.

22. Frederik Seelig, Frederik Seelig Consulting, Aarhus, Denmark; formerly: The Global Vector Hub, London School of Hygiene & Tropical Medicine

Developing systematic guidelines for Mosquito Control in Built-Up Areas in Europe

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There is a growing risk of mosquito-borne diseases (MBDs) worldwide, including in the European region. To address this problem, a dedicated group of experts from the European Mosquito Control Association (EMCA), with support from WHO/TDR, set out to establish clear guidelines and recommendations for effective surveillance and control measures against mosquitoes of public health concern. In the absence of systematic clinical studies assessing the impact of vector control interventions on the epidemiology of human MBDs, it was agreed to use entomological endpoints as proxy for the biting activity of mosquitoes (and thus the risk of disease transmission) instead. A scientific review revealed a very heterogeneous landscape of various entomological endpoints supported by generally poor evidence as suggested by the GRADE system, which is meant to evaluate the quality of evidence and strength of recommendations. This reduces the strength of our recommendations for or against certain mosquito control measures. However, some interventions might be recommended in specific settings, such as larviciding, or chemical control of adult mosquitoes under specific conditions (outbreak of disease, high infestation with adult mosquitoes). There is an urgent need to evaluate the efficacy of mosquito control interventions in a systematic fashion that would also include epidemiological endpoints. We further recommend standardizing the data collection process for future field studies by providing technical guidance to build a database related to vector control.

23. Susana Campino, London School of Hygiene and Tropical Medicine

High quality reference genomes for three UK tick species

Ticks are hematophagous ectoparasites that feed on the blood of mammals, birds, and sometimes reptiles and amphibians. In the UK , there are >20 indigenous species of ticks, but among these Ixodes ricinus, Dermacentor reticulatus and Haemaphysalis punctata are the main disease vectors, each with its own ecological niche. I. ricinus is of most concern to human and animal health, with a wide distribution throughout the UK. It is a vector for B. burgdorferi s.l., A. phagocytophilium, Babesia spp., louping-ill virus and TBEV. H. punctata is involved in the transmission of Babesia spp. and T. luwenshuni in livestock, and D. reticulatus is an important vector of Babesia canis which causes serious disease in dogs. The knowledge of tick's biology and development of anti-tick measures have been hindered by the lack of a high-quality genome. This is particularly because ticks possess large genomes (e.g., I. scapularis, ~ 2 Gbp) with a high repetitive content (>50% of genome). Therefore, only 12 tick species reference genomes have been published, but only one for the dominant species in the UK (I. ricinus, from The Netherlands). The lack of reference genomes for UK tick species is a roadblock to molecular surveillance. As part of the GenES-VBD network project (UKHSA/LSHTM), we generated and annotated genomes for I. ricinus, Dermacentor reticulatus and Haemaphysalis punctata ticks collected in the UK, using long-sequenced reads from Oxford Nanopore tecnnology (ONT). Here we present the analysis of each tick genome and comparison between these species and other available worldwide reference genomes.

24. Lesley Bell-Sakyi, University of Liverpool

Generating cell lines from UK arthropods – 25 years of challenges

Lesley Bell-Sakyi* 1. 1 University of Liverpool

Continuous cell lines derived from arthropods are important tools for research into many aspects of vector-borne diseases of medical, veterinary and agricultural importance. However, most in vitro studies are carried out using a limited panel of arthropod cell lines which may not be geographically, or even biologically, compatible with the disease agent of interest. These mis-matches are particularly prevalent in studies on UK pathogens transmitted by blood-feeding vectors, which have historically utilised a small number of cell lines derived from tropical mosquitoes, African and North American ticks and North American midges. Here I summarise 25 years of attempts, both successful and unsuccessful, to generate continuous cell lines from "harmful" and "beneficial" arthropods of UK origin. These include the mosquito Culex pipiens, the biting midge Culicoides nubeculosus, the ticks Ixodes ricinus and Dermacentor reticulatus, the poultry mite Dermanyssus gallinae, the honey bee Apis mellifera and, most recently, the ladybird Adalia bipunctata.

25. Catherine Hartley, University of Liverpool

The Tick Cell Biobank: tick and insect resources for UK vector-borne disease research

Catherine Hartley* 1, Jing Jing Khoo 1, Youseuf Suliman 1, Alistair Darby 1, Benjamin Makepeace 1, Lesley Bell-Sakyi 1. 1 University of Liverpool

Arthropod cell lines have played important roles in research on vector-borne diseases of medical, veterinary and agricultural importance for over 75 years. The need for new cell lines continues today as novel pathogens emerge and vectors invade new areas because of climate change and globalisation. The Tick Cell Biobank (TCB) at the University of Liverpool, the world's only dedicated culture collection for cell lines derived from ticks and other arthropods (mosquitoes, midges, sand flies, tsetse flies, fruit flies, triatomine bugs, honey bees), specialises in generation of cell lines from neglected and challenging vector species. As well as housing and distributing a growing collection of tick and insect cell lines, and training in their maintenance, to scientists across the UK and worldwide, the TCB is currently working to generate new cell lines from various arthropod species of UK relevance, including ticks, honey bees and ladybirds. All cell lines are screened for contaminating bacteria, and studies are carried out to characterise selected cell lines genotypically and/or phenotypically. The TCB also houses a small collection of intracellular, arthropod-borne bacteria including multiple UK strains of Anaplasma phagocytophilum, causative agent of tick-borne fever in sheep. The TCB welcomes collaborations with scientists seeking to use arthropod cell lines in their research. Cell lines are distributed subject to Material Transfer Agreements; for further information, contact tickcellbiobankenquiries@liverpool.ac.uk.

26. Emily Chesters, Keele University

Systematic discovery and high-throughput testing of novel cis-regulatory elements in insect vectors

Emily Chesters* 1, Roberto Galizi 1. Keele University

Novel discovery of tissue-specific genetic regulatory elements in the germline of the human malaria vector is vital for the development of effective genetic control strategies such as gene drives. Currently, we have very limited knowledge of cis-regulatory elements in the germline, of which only a few are suitable for strategies such as gene drive. Discovery of novel elements has thus far proven difficult due to experimental and computational methods requiring prior knowledge of cis- and trans-acting regulatory elements, which we do not have in large across insects. Additionally, functionally characterising putative regulatory elements in living insects is time-consuming and requires creation of individual transgenic lines. Here we propose a computational method to identify tissue-specific cis-regulatory elements in Anopheles gambiae, which could be used to infer regulatory elements across other insect vectors and pests. We also propose a novel barcoded reporter assay which can be used for the multiplexed testing of cis-regulatory elements in insects without the need for transgenic line creation. This work provides a novel strategy for the systematic discovery and testing of genetic cis-regulatory elements in the malaria mosquito and other vectors, thus widening the bottleneck currently faced in the development of genetic control strategies.

27. Luis Miguel Hernandez Triana, Animal and Plant Health Agency

One Health DNA Barcoding in support for the identification of vectors of medical and veterinary importance in Ghana

Luis M. Hernández-Triana 1, Paula Soskin 1. 1 Animal and Plant Health Agency

Arthropod vectors are of great public health and veterinary concern due to their debilitating effects to humans and livestock. The rapid change in the distribution of local vector species and growing number of invasive species has increased the risk of VBD introduction into new areas. Therefore, the Animal and Plant Agency is working with national and international organizations to develop the capabilities of affected areas to detect and act on disease incursions caused by arthropod-borne diseases before they impact local communities. In this study, specimens of target vector groups identified through both traditional morphological methods and DNA Barcoding region by amplifying the COI (659 bp) gene. All specimen metadata, traces and sequences were uploaded into The Barcoding of Life Database (BOLD). Phylogenetic analysis using Neighbour Joining (NL) and Maximum Likelihood (ML) were employed to visualise specimen grouping and determine phylogenetic relationships. All processes from tissue sampling, specimens' preservation, metadata submission and molecular analysis were transferred to our colleagues in Ghana via a One Health DNA Barcoding workshop in Accra. Specimens of Hyalomma, Sergentomyia and Simulium showed deep splits in the phylogenetic trees, indicating the presence of cryptic diversity. Specimens in the Simulium damnosum complex separated in discrete groups confirming its status as a species complex. The application of DNA barcoding provided useful molecular support for the morphological identification of species. It was implemented in Ghana through training, skills transfer, and resources, which strengthened their surveillance capabilities.

28. Jake D'Addiego, UKHSA

Complete Genome Sequencing of Siberian Tick-Borne Encephalitis Virus from preserved tick samples.

Jake D'Addiego* 1, Mollie Curran-French 1, Jack Smith 1, Asankadyr T Junushov 2, Olga N Gavrilova 3, Barry Atkinson 1, John Hay 4, Roger Hewson 1. 1 UK Health Security Agency; 2 National Academy of Sciences of the Kyrgyz Republic; 3 Ministry of Healthcare of the Kyrgyz Republic; 4 State University of New York

Recent advances in whole genome sequencing technologies have significantly enhanced our understanding of Tick-Borne Encephalitis Virus (TBEV). We developed a targeted tiling multiplex PCR method for Siberian TBEV and recovered 100% of a genome from a tick sample collected in Kyrgyzstan. This new sequencing approach marks a substantial improvement over previous studies that were only able to analyse partial sequence of the virus. The ability to analyse the full genome provides deeper insights into the virus's genetic diversity and migration patterns. Tick born virus studies in Kyrgyzstan have played important role in elucidating the ecological dynamics and host interactions of Siberian TBEV, particularly highlighting its adaptability and the complex ecological niches it occupies. By pinpointing the virus's presence in different tick species, notably Ixodes persulcatus, and assessing its interaction with local fauna like Apodemus pallipes mice, this work has shed light on how Siberian TBEV maintains its transmission cycle across diverse environmental conditions, even at higher altitudes than previously observed. These foundational findings have been central in emphasising the adaptability of TBEV to various ecological zones and host species, enhancing our comprehension of its potential to spread to new areas. The integration of advanced genomic tools with detailed ecological studies underscores the necessity for ongoing research to monitor and control the spread of the TBEV complex in Kyrgyzstan and beyond, providing a more informed basis for predicting potential outbreaks and implementing targeted public health interventions.

29. Lucy Gilbert, University of Glasgow

Environmental risk factors for Anaplasma phagocytophilum in Scotland

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Anaplasma phagocytophylum (AP) includes several ecotypes that vary in their pathogenicity and transmission hosts. The environmental drivers of AP have received less ecological research attention than some other tick-borne pathogens such as Borrelia. Here we test the hypothesis that higher densities of transmission hosts are associated with higher prevalence and hazard of AP, while hosts that do not transmit AP can dilute pathogen prevalence. We conducted surveys of questing Ixodes ricinus ticks at ~150 sites throughout Scotland and PCRd the ticks for Anaplasma phagocytophylum (AP). We measured environmental variables including host abundance indices. We found that most areas of Scotland have no or very low AP prevalences in the I. ricinus population. The highest prevalence sites were in the north of Scotland. Of the AP-positive samples, 86% were ecotype I, while 14% were ecotype II. AP (I+II) prevalence and hazard were higher with higher deer abundance indices, which was expected as ecotypes I and II are associated with roe and red deer. Rodents and birds are not thought to transmit ecotypes I and II and, as predicted, birds showed a strong negative relationship with AP. We found a clear negative relationship between AP (I+II) prevalence and Borrelia prevalence in questing I. ricinus nymphs. To conclude, deer are key AP (I+II) risk factors while birds are dilution hosts. This could be one of the mechanisms for the negative Borrelia-AP relationship, but further research is needed to tease apart the interactions between these two highly complex pathogen groups.

30. Mirjam Schilling, Animal and Plant Health Agency

Whole genome sequencing for surveillance and research of vector-borne diseases

Mirjam Schilling* 1, Yogesh Kumar Gupta 1.1 Animal and Plant Health Agency

Global climate changes have increased the risk of emerging vector-borne diseases in temperate countries. To mitigate this threat, early detection of newly arriving pathogens in the United Kingdom (UK) and a deeper understanding of their persistence mechanisms are crucial for preventing transmission to susceptible humans, animals or plants. Next-generation sequencing (NGS) technology provides a robust platform to detect and analyse genetic material of pathogens, identifying existing or emerging diseases in an unbiased manner and complementing targeted molecular techniques. The Genomics for Animal and Plant Disease Consortium (GAP-DC2) aims to develop both pathogen-agnostic and targeted approaches for detecting emerging and advanced biological hazards and threats in animal and plant health landscape. By exploiting pathogen genomes and biomes, the consortium aims to link genotype to phenotype to inform early detection and mitigation strategies. This project brings together leading organisations for pathogen detection and genomics in terrestrial and aquatic animals (Animal and Plant Health Agency, Royal Veterinary College, Centre for Environment, Fisheries and Aquaculture Science, The Pirbright Institute) and plants (Fera Science, Forest Research) in the UK. Through our cooperative metagenomics approaches, we can fill knowledge gaps and contribute to the reduction of spillover events from wild animals and vector species.

31. Estela Gonzalez Fernandez, Animal and Plant Health Agency

Optimized characterization of Culex pipiens biotypes from wild caught populations and hybrid laboratory-reared colonies

Estela Gonzalez* 1, Nicholas Johnson 1,2, Karen L Mansfield 1. 1 Animal and Plant Health Agency; 2 University of Surrey

Culex pipiens, known as the common house mosquito, is found throughout Europe, and is a known vector of pathogens such as West Nile Virus and Usutu virus. In both Europe and the United Kingdom, two forms coexist: C. pipiens pipiens and C. pipiens molestus. Despite being morphologically indistinguishable, they exhibit distinct ecological preferences and behaviours. C. pipiens pipiens is predominantly ornithophilic, while C. pipiens molestus has adapted to urban environments and often takes a bloodmeal from mammals, including humans. Characterizing Culex populations is important to elucidate their ecology and implement the correct control measures. To this end, we have optimized a molecular methodology to differentiate C. pipiens populations into the two biotypes. Briefly, live mosquitoes were immobilised using ice, and one leg from each mosquito was removed and transferred to an individual microtube containing nuclease free-water. The live mosquitoes were individually transferred to separate tubes. The leg samples were homogenized, and the DNA extracted by heating for 5 minutes in a microwave (800W). Extracted DNA was assessed using a multiplex real-time PCR targeting a fragment of the CQ11 gene, where separate probes enabled differentiation between the two biotypes. The results are obtained in two hours, enabling the mosquitoes to be sorted appropriately into different cages for further maintenance or procedures. This method has been successfully employed for the characterization of wild caught mosquitoes, for colonisation, and also for the isolation of a C. pipiens molestus colony from an original mixed/hybrid laboratory colony.

32. Mara Rocchi, Moredun Research Institute

Babesia species diversity in Scottish Ixodes ricinus ticks and their zoonotic risk

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Objective: The prevalence of tick-borne diseases (TBD) has increased globally in recent years, likely due to climate warming, which enhances tick survival over winter and alters their distribution. Ixodes ricinus is the most prevalent tick vector for TBD in Europe and the UK and transmits Babesia species, a genus of intracellular protozoan parasites affecting numerous host species worldwide. In the UK, Babesia divergens and Babesia venatorum are among the most common species. Both can affect cattle, causing babesiosis, and can also affect immunocompromised individuals. This preliminary study aimed to investigate the genetic diversity of Babesia spp. found in I. ricinus ticks from Scotland. Methods: A total of 562 ticks were collected from various habitats and locations in Scotland using blanket dragging. Conventional PCR and

Sanger sequencing were utilized to detect and identify Babesia-positive 18S ribosomal RNA sequences. To assist in species identification, a BLAST search of the sequences was conducted using the NCBI database, and phylogenetic analysis was performed to further explore the relationships among the individual sequences. Results and conclusions: Babesia was detected in 83 out of the 562 samples, indicating a prevalence of 14.7%. Sequence analysis of these 83 positive samples identified four Babesia species, with B. divergens being the most common. Phylogenetic analysis revealed significant genetic diversity among B. divergens-positive samples, which formed multiple clades. When compared to sequences from continental Europe, the Scottish isolates showed high sequence similarity within Babesia species, regardless of the country of origin, suggesting a comparable risk of zoonotic transmission.

33. Sophie Hawkes, University of Warwick

Exploring tick-borne pathogen communities in Mojave Desert Bighorn sheep and their ticks.

Sophie Hawkes* 1. 1 University of Warwick

Tick-borne pathogens, including Anaplasma, Ehrlichia, Babesia, and Theileria, may impact the health of wild mammals. In desert bighorn sheep (Ovis canadensis nelsoni), studies have mainly focused on serological or molecular methods to detect genus- level identification, but it is unclear how many and/or which species are present. To determine the diversity of tick-borne pathogens in bighorns and desert bighorn ticks (Dermacentor hunteri), we performed genomic-based diagnostics focusing on Anaplasma, Ehrlichia, Babesia, and Theileria. We then characterised pathogen-specific genetic variation and epidemiology. PCRs revealed Anaplasma in 75.7% of ticks and 67.1% of bighorn; Babesia species in 88.6% of ticks and none in bighorn; and no Theileria or Ehrlichia in either host. Pathogen-specific PCRs and Sanger sequencing identified A. ovis in 67.1% of bighorns and 7.9% coinfected with both A. ovis and A. marginale, while 72.9% and 18.6% of ticks were infected and coinfected, respectively, with only 2.9% of ticks singly infected with A. marginale. Surprisingly, we detected B. vogeli only in D. hunteri, a Babesia species typically found in canines. A. marginale was only present in ranges which overlap with livestock allotments, suggesting livestock spill-over as A. marginale has not been previously documented in bighorns. Our results provide new evidence on the tick-borne pathogens in this system, offering a finer-scale characterisation of Anaplasma and Babesia species.

34. Georgia Kirby, University of Glasgow

Leucocytozoon infection variation in black flies in west Scotland

Georgia Kirby* 1, Francesco Baldini 1,Heather Ferguson 1. 1 University of Glasgow

Black flies in the genus Simulium are the principal vectors of Leucocytozoon, a haemosporidian parasite that can cause a malaria-like disease in birds. Despite high prevalence of Leucocytozoon in Scottish passerine populations, relatively little is known about the disease ecology, including the possible role of the endosymbiont Wolbachia in Leucocytozoon transmission. Here, we studied Leucocytozoon infections in field populations of ornithophilic Simulium black flies to better understand ecological drivers of infection prevalence and transmission. Sampling was conducted over five consecutive years at a site in west Scotland where passerine monitoring is ongoing. Adult female black flies were trapped using carbon dioxide-baited CDC light traps. Leucocytozoon and Wolbachia were detected and quantified in black flies using quantitative PCR. Three hundred and ninety-nine adult black flies were analysed individually during the study. The predominant taxa captured were Simulium cryophilum, S. vernum and S. aureum. Mean Leucocytozoon infection prevalence in vectors during the study period was 48.1% ± 4.9%. Prevalence was positively associated with rainfall in the week preceding sampling and ambient temperature four weeks prior to sampling. Leucocytozoon density varied between vector species and was highest in S. vernum. An interaction between Wolbachia presence and Leucocytozoon infection was not found. A trend was observed indicating that Leucocytozoon prevalence in vectors may be associated with host phenology, with earlier bird breeding linked to lower infection prevalence in vectors. These findings offer new insights into avian malaria vector ecology and transmission dynamics in temperate areas.

35. Georgia Kirby, University of Glasgow

Surveillance and temporal population dynamics of Culex pipiens s.l. in Scotland

Georgia Kirby* 1, Meshach Lee 1, Susanne Krabbendam 1, Luca Nelli 1, Jolyon Medlock 2, Alexander Vaux 2, Steven White 3, Dominic Brass 3, Jean-Philippe Parvy 4, Emilie Pondeville 4, Heather M. Ferguson 1. 1 University of Glasgow; 2 UK Health Security Agency; 3 UK Centre for Ecology and Hydrology; 4 University of Glasgow

The risk of emergence of mosquito-borne disease is dependent on vector species distributions and ecology. In Britain, the distribution and population dynamics of the native vector species Culex pipiens s.l. are likely determinants of the future establishment of West Nile Virus and other zoonotic diseases. The objective of the "Mosquito Scotland" project is to assess the risk of mosquito-borne disease establishment in Scotland, where previously there has been no formal mosquito surveillance. Our recent work has confirmed that Cx. pipiens s.l. is widespread throughout mainland Scotland. Here, we aimed to characterise the ecology and seasonality of Scottish populations of Cx. pipiens s.l. through targeted surveillance. Sampling was conducted between April and October 2024 at three sites along a latitudinal gradient. Buckets filled with hay infusion were placed at each site to attract ovipositing females. Immature stages were monitored and quantified 2-3 times per week throughout the season. Adults were collected up to twice per week using Biogents BG Pro traps baited with carbon dioxide and a BG Lure. Traps were run for 48-hour intervals. In addition to the field surveillance, an online citizen science tool was developed to facilitate public reporting of mosquitoes in Scotland. This initiative had a secondary objective of detecting populations of Cx. pipiens molestus via reports of nuisance biting in urban residential areas. The collected data will be used to inform disease risk maps and build the framework for an epidemiological model of zoonotic virus establishment in Scotland.

36. Christopher Jones, Liverpool School of Tropical Medicine

Is Aedes detritus a migratory mosquito in the UK?

Christopher M. Jones* 1, Nadja C. Wipf 1, Jason W. Chapman, Peter T. Enevoldson 2. 1 Liverpool School of Tropical Medicine; 2 University of Exeter

The inter-tidal saltwater pools of the Dee Estuary adjacent to the Wirral Peninsula support high abundances of the salt marsh mosquito, Aedes detritus. Seasonal adult peaks coincide with the Spring Tides that flood the high marsh with the intermittent flooding of saline water causing eggs to hatch. Past surveys and anecdotal evidence suggest that adult females of Ae. detritus are caught much further inland and away from the Dee Estuary salt marsh habitat than expected, with the prevailing south-westerly winds offering possible atmospheric transport. Based on the salt marsh ecology of other Aedes mosquitoes in the United States, we hypothesise that Ae. detritus is potentially a migratory species in the UK, with at least some individuals exhibiting migratory behaviour upon adult emergence. We present preliminary data and future experimental methods to test this hypothesis. The potential of a wetland mosquito vector to use atmospheric transport as a means of maximising the chances of a blood meal has implications for modelling and understanding the risk of invasive mosquito-borne diseases in the UK.

37. Grace Plahe, University of Salford

Borrelia burgdorferi s.l. abundance and genetic diversity between urban greenspaces and surrounding hinterland across the UK

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Over 200,000 cases of Lyme disease, caused by Borrelia burgdorferi sensu lato, occur in Europe each year. B. burgdorferi s.l. is maintained in a range of wildlife reservoir hosts between which it is transmitted by Ixodes ricinus. As reservoir hosts and vectors are more abundant in woodland, it's widely perceived that Lyme disease is acquired in rural rather than urban settings. However, the presence of urban tick populations has been reported across Europe, occupying greenspaces that are favoured by urban planners and the public alike for the ecosystem services and well-being benefits. Given footfall of urban greenspaces dwarves that of remoter, rural settings, the likelihood of human-tick encounter may be greater in urban settings even if tick abundance is lower. Thus, it's timely to consider the urban ecology of B. burgdorferi s.l. We hypothesize tick populations in urban greenspaces are maintained through connectivity with surrounding hinterland. Questing ticks were collected from urban and rural greenspaces in 16 towns across the UK in 2022 and 2023, and molecular methods were used to determine the presence of B. burgdorferi s.l. in ticks and genospecies identity. Ticks and B. burgdorferi s.l. were found to be more abundant in the hinterland than urban greenspaces, but we observed a correlation between the density of ticks collected at urban and hinterland sites suggesting that the two populations are indeed linked. We also encountered B. bavariensis in the UK and as this genospecies is considered highly pathogenic, its presence in the UK is of public health concern.

38. Steve Belmain, Natural Resources Institute, University of Greenwich

One Health approach to tick-borne disease control through manipulation of reservoir host communities at landscape scale

Steven R. Belmain* 1, Katherine August 1, Richard J. Birtles 2, Daniel P. Bray 1, Holly A. Broadhurst 2, Simon Croft 3, Harry Marshall 4, Giovanna Massei 5. 1 University of Greenwich; 2 University of Salford; 3 Animal and Plant Health Agency; 4 Forest Research, Northern Research Station; 5 University of York,

The grey squirrel (Sciurus carolinensis) is an invasive species in the UK, with detrimental impacts on the conservation of the native red squirrel and bark stripping damage to trees costing the UK Â£37 million per year. Greys are also important amplifying and reservoir hosts for ticks (Ixodes ricinus) and Lyme disease (Borrelia burgdorferi). As deer are considered incompetent hosts for Borrelia and the highest densities of I. ricinus are found in woodland, removal of grey squirrels could result in a reduction in Lyme disease environmental hazard. However, the relative importance of greys as reservoir hosts compared to that of other wildlife species remains inconclusive. The impact of removal of greys on Lyme disease will depend on their relative contribution to pathogen transmission and impact on host community competence after removal, including changes in other reservoir host species densities. This project will take an integrated approach to understand the wider impacts of changing landscapes on environmental and public health producing evidence on how tick-borne disease risk could be minimised. We aim to summarise the importance of grey squirrels in the ecologies of I. ricinus and B. burgdorferi; explore the impact of grey squirrel management through culling vs. fertility control on tick abundance and Lyme disease; adapt grey squirrel management models to incorporate Lyme disease dynamics; understand existing knowledge, attitudes and behaviours of different stakeholder groups across the UK with respect to Lyme disease and grey squirrels; and develop new tools for tick monitoring, surveillance and control.

39. Niamh Mahon, The James Hutton Institute

What kind of a threat is Bluetongue? Findings from a survey focused on Scottish farmers

N. Mahon*, C. Kyle*, C. Hardy*, O. Shortall* * - James Hutton Institute

Here we present findings from an online survey into cattle and sheep keepers’ perceptions of the threat of a Bluetongue virus (BTV) incursion into the UK, the type of risk this poses, and the actions these individuals are taking to mitigate this risk. BTV is a notifiable, midge-borne, viral disease that affects ruminant species. Until recently the UK was free of BTV serotype 3 (BTV-3). However, cases of BTV-3 were first confirmed in southern England in 2023. At the time of writing, BTV is not believed to be routinely circulating in midges in the UK, however this may change soon. An online survey (recruiting participants during summer 2024), focused on Scotland, explores animal keepers’ awareness of the signs and symptoms of BTV, potential areas of risk on farms for midge breeding, and the use of protective measures against midges. The survey also seeks to investigate keepers’ degree of concern about the risk of BTV to themselves and the wider industry, support for a range of BTV control measures, and potential uptake of a vaccine, if this became available in the UK. Understanding livestock keepers’ perceptions of BTV, and potential risk it may pose to their animals will help inform policy makers and other relevant bodies in decision making when dealing with the disease. Following on from the online survey a series on qualitative interviews will produce more in-depth reflections from keepers of farm animals on this emerging threat.

40. Alexander Vaux, UKHSA

An update on the ecology, seasonality and distribution of Culex modestus in England

Alexander G.C. Vaux* 1,2, A.J Abbott 1,3, C. Johnston1, F. Hawkes 3, R.J. Hopkins 3, B Cull 1, G. Gibson 3, R.A. Cheke 3, A. Callaghan 2 and J.M. Medlock 1.UK Health Security Agency; 2 University of Reading; 3 University of Greenwich

Culex modestus is considered a primary vector of West Nile virus (WNV) in Europe. Prior to 2010, it was considered that without the presence of abundant bridge vectors together with migratory birds and particularly an absence of Culex modestus there was a low risk of WNV in the UK as the incidence of human biting by Culex mosquitoes was limited and only occurred in foci where Cx. pipiens molestus was problematic1,2. Detection of a population of Cx. modestus in wetlands of the Thames estuary in 2010 meant that populations of potentially suitable bridge vectors for WNV, with the ability to bite humans, were now present. Furthermore, their foci in wetland habitats coincided with areas of wetlands where potentially infected migratory birds spend the summer months and hence these areas were the most likely for future circulation of WNV to humans following importation of the virus by migratory birds. Here we provide an update on the distribution of Cx. modestus in the UK, reporting on extensive surveys conducted in England between 2016 and 2022, including specific targeted surveillance for Cx. modestus. For completeness we bring together previously published records on the species’ distribution. We also presents extensive new adult and larval data from sites where it is known to occur, and using larvae abundance data, aim to characterise the preferred aquatic habitat of Cx. modestus in England.

41. Alexander Vaux, UKHSA

The Ecology & Management of Aedes vexans in a British wetland

Alexander G.C. Vaux*1,2, Colin J. Johnston 1, Amanda Callaghan 2, Jolyon Medlock 1. 1 UK Health Security Agency; 2 University of Reading

Aedes vexans is a rare mosquito in the UK, known to occur at a small number of locations in low numbers. In 2018, we responded to an enquiry from Bassetlaw DC regarding extreme nuisance biting, and by running an adult mosquito trap (Mosquito Magnet), identified Aedes vexans as the dominant species. This study aims to develop ecological understanding of Aedes vexans, a species rarely recorded in the UK, and vector of Rift Valley fever and Tahyna viruses1. Understanding the habitat requirements of vector species is necessary to inform risk assessment of pathogens of human health concern, identify potential distribution of the species, and inform a targeted control strategy in the event of a mosquito borne disease (MBDs). Habitats were mapped across the wetland, and weekly immature surveys were conducted, and in addition water depth and temperature, and vegetation data were collected at each sampling site. Aedes vexans was the most common mosquito recorded. Other species typically described as summer floodwater species were also recorded and often co-located with Ae. vexans: Ae. cinereus, Ae. flavescens, Ae. sticticus. Species present was strongly related to the length of time the water was present, with Ae. vexans present 1-3 weeks after rewetting, whilst Cx. pipiens and An. maculipennis were not found until 5 weeks after flooding.

42. Mia White, UKHSA

RCG-GenES-VBD network: Genomic Epidemiology tools for the Surveillance of Vector Borne Disease, as applied to tick species, reservoirs, and pathogens

Mia L. White* 1, Amy Nettlemill 1, Hassan Hartman 1, Emma L. Wise 1, Steven T. Pullan 1, Kayleigh M. Hansford 1, Faye V. Brown 1, Jolyon M. Medlock 1, Emma Collinsv2, Mojca Kristan 2, Taane Clark 2, Susana Campino 2. 1 UK Health Security Agency; 2 London School of Hygiene and Tropical Medicine

In the UK, tick surveillance is routinely performed by morphological identification, followed by targeted qPCR assays to detect individual pathogens. Although these methods give reliable data on pathogen prevalence and presence in tick populations, both the number of targets that can be tested as well as what is targeted using this approach is limited. We have previously developed a multiplexed amplicon sequencing assay, using Nanopore, to identify tick species, characterise the bacterial microbiome present, and determine the source of the latest bloodmeal. These targets have been validated in multiplex on ticks of varied species, at different stages of feeding and from a wide range of both mammalian and bird hosts. During the GenES-VBD network project (UKHSA/LSHTM), the assay will be developed further, to include species specific targets for both detection and typing of pathogens relevant to human health, belonging to the genera Borrelia, Bartonella, Coxiella, Rickettsia, Ehrlichia, Francisella, Anaplasma, as well as Babesia. To identify viral pathogens a parallel RNA metagenomic workflow will be incorporated (based on the clinical workflow operating with UKHSA). Phylogenetically informative targets identified from the GenES-VBD tick genome sequencing workstream will also be incorporated into the final assay. Data on the validation of these targets in multiplex, will be presented at this meeting.

43. Meshach Lee, University of Glasgow

An assessment of mosquito abundance and diversity across an urban-rural gradient in Scotland.

Meshach Lee* 1, Georgia Kirby 1, Rebecca E. Brown 1, Emilie Pondeville 3, Jolyon Medlock 2, Alexander Vaux 2, Jean-Philippe Parvy 3, Francesco Baldini 1, Heather M. Ferguson1.1 University of Glasgow; 2 UK Health Security Agency; 3 MRC Centre for Virus Research

Introduction As vector-borne diseases (VBDs) increasingly affect northern Europe, monitoring temperate mosquito populations becomes crucial for assessing disease risk. In Scotland, where mosquitoes are understudied, understanding the risk of mosquito-borne VBDs to humans and wildlife and in different ecozones (urban vs. rural) is vital. Here, for the first time, we assessed how mosquito density and species composition vary across an urban-rural gradient in Scotland. Methods A longitudinal study was conducted across four sites along an urban-rural gradient from Glasgow to Loch Lomond in 2023 (July-Sept) and 2024 (May-Sept), including two urban sites (Kelvingrove Park- KG) and Kilmardinny Loch -KM) and two rural sites (Mugdock -MG) and SCENE-SC). Adults were trapped for four days twice monthly using BG-pro traps baited with CO2 and a BG-lure. Results Across 96 trap nights in 2023, 119 mosquitoes were collected. Mosquitoes were collected at all sites, most found at urban locations (KM= 48, KG = 41). Species diversity was highest at urban sites, with five and four caught at KM and KG and 3 and 1 at MG and SC. Culex pipiens sl was the most abundant mosquito, followed by Culiseta morsitans, Culiseta annulate and Anopheles plumbeus. Discussion Mosquitoes were present at all sites along an urban-rural gradient around

Glasgow, with numbers and species diversity highest in urban areas. Culex pipiens sl, a potential vector of West Nile Virus, was common in urban sites, suggesting a potential risk of zoonotic transmission if this pathogen is established in Scotland.

44. Tara Joseph, Liverpool School of Tropical Medicine

Mosquitoes reared in distinct insectaries within an institution possess divergent microbiomes.

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The microbiome affects many facets of mosquito biology and differences in microbial composition can affect the outcomes of laboratory studies. To determine how the biotic and abiotic conditions in an insectary affect the composition of the mosquito microbiome we reared mosquitoes from a single cohort of eggs in each of three different insectaries within one institution. Using three replicate trays per insectary, we assessed and compared microbiome composition as mosquitoes developed. We also characterised the microbiome of the mosquitoes' food sources, measured environmental conditions over time in each climate-controlled insectary, and recorded mosquito development. While mosquito development was similar between all three insectaries, we saw differences in microbiome diversity between mosquito larvae in each insectary. Furthermore, we found that bacterial input via food sources, potentially followed by the selective pressures of different temperatures did affect the microbiome composition. At both adult and larval stages, specific members of the mosquito microbiome were associated with particular insectaries. These results highlight the necessity of considering the variability and effects of different microbiome composition even in experiments carried out in a laboratory environment.

45. Colin Johnston, UKHSA

UKHSA mosquito surveillance 2020 to 2024: First detection of Aedes aegypti eggs in the UK

C.J. Johnston* 1, A.G.C. Vaux 1, H. Hardy 1, C. Strode 1, A. Murchie 1, A. J. Abbott 1, F.V. Brown 1, S. Biddlecombe 1, S. Gandy 1, N. Jones 1, J.M. Medlock 1. 1 UK Health Security Agency

Multiple countries in Europe have established populations of Aedes albopictus, causing severe nuisance biting and vector-borne disease outbreaks. Due to the risk of these mosquitoes entering the UK, the UK Health Security Agency (UKHSA) has been conducting invasive mosquito surveillance since 2010. This update covers the surveillance from 2020 to 2024, aimed at coordinating national efforts, detecting incursions of Aedes albopictus, and determining if populations have become established. The surveillance involves local environmental health teams, port health officers, the Royal Air Force, and Animal and Plant Health Agency staff. Surveillance was conducted at 24 sites in 2020 and 2021, 42 sites in 2022, 58 sites in 2023, and 116 sites in 2024. Sites are chosen based on a risk-based approach, focusing on ports of entry and main highway routes, including airports, seaports, international train stations, service stations, and lorry parks. At each site, at least five ovitraps with water and polystyrene blocks were collected every two weeks from June to October. Water samples were sent to UKHSA for checking for eggs and larvae. Additionally, 20 sites were monitored by MEZE in London and along the south coast between July and October, using the same method to assess whether unknown populations of Aedes albopictus had become established. No populations or incursions were detected between 2020 and 2022. In 2023, two suspected Aedes eggs were found in blocks from an import warehouse near Heathrow Airport. One egg was identified as Aedes aegypti by Edge Hill University. Further traps were placed around the warehouse, but no additional Aedes aegypti mosquitoes or eggs were found. This project supplements UKHSA's other mosquito surveillance activities, including a citizen science mosquito recording scheme and a local authority questionnaire.

46. Jean-Philippe Parvy, MRC-University of Glasgow Centre for Virus Research

Assessing the circulation of mosquito-borne pathogens and vector competence of Scottish mosquitoes

Jean-Philippe Parvy 1, Georgia Kirby 1, Heloise Planté 1, Buthaina Preston 1, David Kerrigan 1, Richard Orton 1, Davide Dominoni 1, Heather Ferguson 1, Emilie Pondeville* 1. 1 University of Glasgow

In recent decades, invasive mosquito species have spread across Europe, leading to an increase in mosquito-borne diseases. This spread is linked to increased travel, international trade, and climate changes, which create favourable conditions for new mosquito species and their diseases. While the United Kingdom (UK) has been less affected due to its geography and climate, extensive travel and climate variations still pose a risk for vector-borne diseases (VBDs) to emerge. Birds are key reservoirs for many emerging zoonotic VBDs in Europe, like West Nile Virus (WNV) and Usutu Virus (USUV), potentially carrying these diseases into the UK along migratory routes. Since 2009, mosquito surveillance in England and

Wales has identified various vector species. However, there is limited data for Scotland, despite the presence of favourable wetland habitats for both potential vector species and avian reservoirs. The primary objective of the Mosquito Scotland project is to evaluate the risk of mosquito-borne disease emergence in Scotland in the light of climatic change by addressing surveillance gaps. We will present findings regarding the establishment and characterization of a Culex pipiens pipiens colony from field collected mosquitoes. Additionally, we will present vector competence assays showing that this Scottish Cx. pipiens population is competent to transmit Usutu and Sindbis arboviruses, and that this is influenced by temperature. We will also discuss initial pathogen RNAseq screening data in mosquito vectors and avian reservoir populations in Scotland.

47. Roz Taylor, UKHSA

Mosquito Surveillance and Control in the UK Overseas Territories

Roz Taylor* 1, Alexander Vaux 1, Jolyon Medlock 1. 1 UK Health Security Agency

The Medical Entomology and Zoonoses Ecology (MEZE) Team at the UK Health Security Agency provides technical support to the UK Overseas Territories (UKOTs) on vector surveillance and control of mosquito vectors. Most of these locations are islands in the Caribbean that are home to mosquitoes such as Aedes aegypti and Culex quinquefasciatus. Several islands experience sporadic outbreaks of dengue and are at high risk of importation of other arboviruses. MEZE also works with vector surveillance and control teams in Gibraltar. MEZE supports local vector control teams in several aspects of their response, including training in trap-based surveillance and species identification, data analysis and geospatial mapping, and developing island-specific novel interventions for mosquito management. Recently, MEZE has recently produced a set of e-Learning modules on mosquito vector ecologies, surveillance and control to help strengthen and align the knowledge of staff across local teams. MEZE is also supporting the development of native mosquito surveillance in the UKOTs, in order to assess PH risk of other pathogens including malaria.

48. Jet Griep, University of Liverpool

Meta-analyses of Culex blood-meals indicates strong regional effect on feeding patterns

Jet S. Griep* 1, Eve Grant 1, Jack Pilgrim 1, Olena Riabinina 2, Matthew Baylis 1, Maya Wardeh 1, Marcus Blagrove 1. 1 University of Liverpool; 2 Durham University

Understanding host utilization by mosquito vectors is essential to assess the risk of vector-borne diseases. Many studies have investigated the feeding patterns of Culex mosquitoes by molecular analysis of blood-meals from field collected mosquitoes. However, these individual small-scale studies only provide a limited understanding of the complex host-vector interactions when considered in isolation. Here, we analyse the Culex blood-feeding data from 90 publications over the last 15 years to give a global insight into the feeding patterns of Culex mosquitoes, with particular reference to vectors of currently emerging Culex-borne viruses such as West Nile and Usutu. Data on 26,857 blood-meals from 71 different Culex species were extracted from published literature. The percentage of blood-meals on amphibian, avian, human, non-human mammalian, and reptilian hosts was determined for each Culex species. Our analysis showed that feeding patterns were not significantly explained by mosquito species-level phylogeny, indicating that external factors play an important role in determining mosquito feeding patterns. For Cx. quinquefasciatus, Cx. pipiens complex, and Cx.tritaeniorhynchus, feeding patterns were compared across the world's seven biogeographical realms. Culex tritaeniorhynchus, Cx. pipiens complex and Cx. quinquefasciatus all had significantly varied feeding patterns between realms. These results demonstrate that feeding patterns of Culex mosquitoes vary between species but can also vary between geographically distinct populations of the same species, indicating that regional or population-level adaptations are major drivers of host utilization. Ultimately, these findings support the surveillance of vector-borne diseases by specifying which host groups are most likely to be at risk.

49. Sarah Biddlecombe, UKHSA

Dermacentor reticulatus and Haemaphysalis punctata: two tick species of human and animal health importance in the UK

Sarah Biddlecombe* 1, Kayleigh M Hansford 1, Jolyon M Medlock 1, Nicholas Johnson 2, Paul Phipps . 21UK Health Security Agency; 2 Animal and Plant Health Agency

Vector-borne disease risk is intrinsically linked to the distribution of tick vector species. To assess risk and anticipate disease emergence, an understanding of vector distribution, host associations and seasonality are needed. The UK Heath Security Agency and Animal and Plant Health Agency have been conducting surveys for target tick species for several years. Whilst most surveys focus on the UKs most widespread vector species Ixodes ricinus, two other species are also important from both a human and animal disease perspective. Dermacentor reticulatus is established in several coastal grazed grassland or dune habitats in the UK and has been linked to cases of canine babesiosis and feeding on cattle. Tick-borne disease transmission from this species to humans has not yet been identified in the UK, but evidence suggests that human biting occurs. Haemaphysalis punctata is another species of tick associated with grazed grassland habitats and infestation of sheep, and more recently expanded it distribution in southern England. Disease in livestock in these locations has been reported and increasing numbers of records of human tick bites have been recorded. Tick surveys conducted in 2024 have monitored the distribution of these key tick species. This poster summarises the latest distribution data available and highlights the need for tailored tick awareness information and/or management practices.

50. Matthew Baylis, University of Liverpool

The distribution and abundance of Culicoides biting midges in England and Wales

Matthew Baylis* 1, Cyril Caminade1, Peter Diggle 2, Rebecca Hoyle 1, Andrew Morse 1, Barry Rowlingson 2, Ken Sherlock 1, Joanne Turner 1, Georgette Kluiters 1. 1University of Liverpool; 2 University of Lancaster

Culicoides biting midges are vectors of numerous viral diseases of livestock. Bluetongue serotype 8 affected UK ruminants in 2007 and serotype 3 was detected in the UK in 2023. Schmallenberg is endemic in UK ruminants with high levels of disease reported in 2024. Epizootic Haemorrhagic Disease was recently reported in France. Given the threat to UK livestock, it is important to better understand the distribution and abundance of Culicoides. To date there have been small-scale but no structured surveys. We undertook snapshot surveys of Culicoides midges in England and Wales. OVI-based light traps were set at 144 farms for 2 rounds of three nights within June-August 2013. The largest nightly catches in each round were sorted and counted. We report on the catches of the three most important vector species. Catches were larger in round 1 (June-July, total Culicoides caught 523K) than 2 (July-August, 242K). Catches were dominated by C. obsoletus group (75-85% of all Culicoides), which were present at all sites. The largest nightly catches of C. obsoletus group were in northern England (Crewe, >70K, Stoke, >40K). C. pulicaris and C. punctatus comprised 2.4 to 4.5% of Culicoides caught with the highest catches also in northern England, with largest catches from 650 to 9000. There were significant associations between catches of the 3 species, between the 2 rounds, and with the density of livestock and certain climate variables. In conclusion, Culicoides are hugely abundant vectors associated with, and able to transmit viruses to, livestock throughout England and Wales.

51. Benjamin Miller, University of Liverpool

How does woodland creation affect Ixodes ricinus populations in Scotland?

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Emerging tick-borne zoonoses such as Lyme borreliosis (LB) are an increasing threat to the health of people, causing thousands of infections in Europe annually. The primary vector of LB is Ixodes ricinus, which thrives in woodlands. Policy-driven woodland creation to benefit biodiversity and mitigate climate change could result in increased risks from tick-borne zoonoses. Currently, little is known about how tick-borne disease risks will be affected by the increase in size, complexity and connectivity of planted woodlands. Additionally, how host species utilise these habitats remains poorly understood. We predicted that increasing woodland creation would increase connectivity and promote utilisation by species such as deer which are important for I. ricinus reproduction. Furthermore, as newly planted woodlands mature they could favour small mammal populations, which are the transmission hosts for LB. To investigate this, 60 broadleaf woodlands in Scotland were sampled over two consecutive summers in 2023 and 2024. Woodlands were selected along gradients of patch size, connectivity and woodland age, and visited to measure I. ricinus density, ground vegetation, temperature and humidity. Ticks were found in 32 out of 60 woodlands. Proximity to other broadleaf woodland increased the likelihood of ticks being present,

indicating the effect of woodland connectivity. Where ticks were found, higher relative humidity had a negative effect on their density. The results from this study will be used to inform woodland managers and users about the risk from tick-borne pathogens and how these risks could change over time as a consequence of woodland planting.

52. Kayleigh M Hansford, UKHSA

Tick Surveillance Scheme: latest data and evidence for action at the local level

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Long-established vector surveillance programmes can provide powerful datasets for the detection and assessment of new or changing vector-borne disease (VBD) risk. They can also provide baseline data for monitoring possible impacts of drivers of VBD such as climate, host, or habitat changes, which are particularly relevant for tick-borne disease. Crucially, they can also provide evidence for action at local levels to ensure response capabilities are sufficient. The UK Heath Security Agency have been running a national Tick Surveillance Scheme (TSS) since 2005, collecting data and mapping UK tick species. The Scheme is supported by a wide range of recorders who submit data, including members of the public, animal, and public health experts, as well as wildlife charities and entomologists. With over 12,000 records of both native and non-native tick species, this paper provides an update on the latest TSS data generated over the years 2021-2023. Summaries of tick species found, seasonal activity and host associations are presented, for both UK acquired and overseas acquired ticks on humans and animals. Trends over time in Ixodes ricinus records are explored and a new metric is developed to assist with local action in response to tick-bite exposure. Distribution maps highlighting recent records of I. ricinus are also included, to identify new areas potentially at risk from this key vector species.

53. Mauro Pazmino Betancourth, University of Glasgow

Monitoring biological age in mosquitoes using infrared spectroscopy

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The age of vector populations is the most important factor that determines vectorial capacity, hence disease transmission. However, there are no effective methods to measure age in mosquitoes. Infrared spectroscopy (IRS) has shown promising results as all-in-one solution to determine the age of vectors. However, models trained with laboratory mosquitoes require re-calibration to generalize and predict the age of wild samples. This caused by the different ageing rates between laboratory and field collected, which are exposed to different environmental conditions. Here, we characterized how temperature affects ageing rates in mosquitoes and how these changes are reflected in IRS spectra to produce ML models that can predict the biological age of mosquitoes and generalize across different ecological settings. The effect that temperature has on biological age was tested using two different average temperatures: 24 and 27 °C and with two different ranges: ±3°C and ±6°C using environmental chambers. The survival of Anopheles coluzzii and An. gambiae was monitored for approximately 30 days across different replicates, in the presence and absence of a sublethal exposure to deltamethrin insecticide. Mid infrared spectra of mosquitoes at different time points were obtained and their life expectancy was analysed to determine their biological age. Mosquito survival varied depending on temperature, insecticide exposure and species. Accuracy for predicting biological age was higher compared to chronological age in both species, suggesting that IRS signal is directly associated with mosquito ageing rates. Ongoing analysis will validate these models in mosquitoes reared in semi field settings and collected from the field.

54. Harry Marshall, Forest Research

A One Health approach to Tick-Borne Diseases in Changing Landscapes

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Lyme disease is the most common tick-borne diseases (TBDs) in the Northern Hemisphere. The combination of tree cover expansion, alongside increasing populations of ticks and their hosts, and recreational use of green spaces, may lead to increased risk of TBD transmission to humans. One Health (OH) is a concept which acknowledges that the health of humans, animals, and ecosystems are interlinked. Given the dynamics involved in the transmission of tick-borne diseases, using an OH lens to explore the socio-ecological dimensions of TBDs enables a holistic view of disease interactions and potential mitigation measures. Awareness and perceived risk of zoonotic diseases determine attitudes and actions towards their management. Despite cases of TBDs increasing, there has been minimal research on the awareness and risk perception of key stakeholders. This research addresses this gap using an OH framework to engage with users and managers of woodland about their awareness, risk perception, and management approaches to TBDs. Additionally, we explore whether the risk of TBDs influences their behaviour and use of the land, and how ever-growing forested landscapes could change this in the near future. We focus on three locations in the UK with ongoing woodland creation, high Lyme Disease prevalence, and high levels of recreational use. Key stakeholders include medical professionals, recreational users of woodland, and woodland managers. We will present the outcomes of exploratory interviews with key stakeholders, providing a timely snapshot of awareness and risk perception of TBDs. Our research helps develop practical approaches for managing TBD risk in changing landscapes.

55. Nadja Wipf, Liverpool School of Tropical Medicine (LSTM)

Utility of the BG-Pro trap for understanding the ecology of the saltmarsh mosquito Aedes detritus

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The saltmarsh mosquito, Aedes detritus, is a significant biting nuisance in the Neston area next to the Dee Estuary, UK. This ongoing study is evaluating the efficacy of BG-Pro traps in capturing host-seeking Ae. detritus to improve our understanding of their ecology and dispersal patterns. Initial experiments are being conducted within the Liverpool School of Tropical Medicine's mosquito flight laboratory. The aim is to identify the most efficacious combination of odour attractants for host-seeking Ae. detritus. In a series of 48-hour trapping sessions, we will simultaneously set BG-Pro traps, each with a different combination of attractants. In each session, 150 female Ae. detritus will be released, and the traps will be rotated to ensure that each attractant combination is tested at each position. The most efficacious combination identified in these indoor experiments will be used in subsequent field trials. Our fieldwork will focus on investigating the abundance and diversity of mosquito vectors within different land uses on Wirral and the dispersal patterns of Ae. detritus from breeding sites in the salt marshes of Neston/Parkgate. BG-Pro traps equipped with the optimal combination of attractants will be placed along transects extending 8 km (5 miles) inland from the salt marsh with traps stratified within one of three habitat types (suburban, woodland, agriculture). This research will provide valuable insights into the ecology of Ae. detritus, informing vector control strategies in UK coastal regions and enhancing our understanding of its potential to spread emerging mosquito-borne diseases.

56. Anthony Abbott, UKHSA

Nationwide Mosquito Programme 2024

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The Nationwide Mosquito Programme has been run since 2010, at over 70 Wetlands across the UK. The project aims to better understand the seasonality and distribution of native mosquitoes and detect new and novel mosquito species. Native mosquito populations can pose a public health risk, with some UK species known to be competent bridge vectors for Usutu virus, which has recently been detected in mosquito and bird populations in the UK, and West Nile Virus, Notably Culex modestus. In addition, some native mosquitoes, such as Aedes vexans and Aedes caspius are prolific human biters, leading to nuisance biting complaints where they occur. This poster provides an update on the 2024 Nationwide Mosquito Programme. During this year, mosquito traps were run by volunteers at over 45 sites across England and Wales. The traps were run from June to October, on a fortnightly basis. The 2024 campaign focused primarily on wetland habitats, reflecting the diverse ecological niches these environments offer for mosquito populations. A small number of nature reserves in urban areas were also included, this allows us to study the seasonal and distribution of mosquito species in areas where they are most often interacting with the human population, and therefore most likely to pose a public health risk. By better understanding the seasonality and distribution of native mosquitoes, we can better advice local authorities and wetlands where nuisance biting does occur, and be better prepared for emerging mosquito borne disease.

57. Catherine Oke, University of Edinburgh

Propensity to host seek and biting time of day are modulated by Anopheles gambiae nutritional status

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Vector-borne disease transmission follows daily rhythms, with parasites/pathogens being taken up from an infected host when vectors forage for blood meals, and passed to a new host during sequential, rhythmic, blood-feeding events. Vector control tools exploit rhythmic vector behaviour to reduce transmission, with bed nets interrupting the nocturnal biting behaviour of *Anopheles* mosquitoes. Unfortunately, residual transmission still occurs, in part driven by mosquitoes shifting their biting to times-of-day when people are unprotected by bed nets. However, the extent to which mosquito temporal biology can shift is poorly understood. For mosquitoes, the availability of blood and sugar meals determine their lifespan and reproductive output, so we tested whether nutritional resources influence the time-of-day that host seeking behaviour occurs. We varied the amount of blood and sucrose that female *Anopheles gambiae s.l.* received and used baited traps in a semi-field system to quantify the time-of-day they seek a human host. We find that feeding treatments influenced both the likelihood and time-of-day that host seeking occurs. Specifically, low-resourced mosquitoes were 2-fold more likely to host seek than mosquitoes provided with high levels of sucrose and 3-fold more likely than those receiving high sucrose and an additional blood meal. Moreover, low-resourced mosquitoes were 2-fold more likely to host seek at an earlier time-of-day than well-resourced mosquitoes, which were predominantly host seeking in the second half of the night time. Overall, our results indicate that mosquito nutritional condition is an underappreciated contributor to residual malaria transmission by driving plasticity in biting time-of-day.

58. Laura Anne Bissett, University of Glasgow

The Impact of Environmental Variation on Anopheles Mosquito Population Dynamics Across Heterogeneous Landscapes

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Vector control aimed at Anopheles gambiae mosquitoes is critical to protect human populations against malaria. The importance of understanding An. gambiae population dynamics is therefore becoming increasingly recognised for improving control. Modelling has been crucial for this, however the way changes in environmental conditions impact these dynamics has been difficult to incorporate. Environmental factors such as temperature and rainfall have a large impact on the life history of Anopheles gambiae mosquitoes not only by influencing their developmental and survival rates, but also by contributing to breeding site availability. Currently, the majority of Anopheles population dynamics modelling that account for environmental impacts either focus on temperature effects, largely omitting rainfall, or assume both are constant through life stages. Here, we present a model for Anopheles gambiae population dynamics, based on delay-differential equations that account for through-stage fluctuations in both temperature and rainfall. The model is parameterised using laboratory derived data and validated against long-term surveillance data from 40 villages in the Cascade region of Burkina Faso. We found that the inclusion of rainfall and allowing for variation in responses by different life stages improves characterisation of An. gambiae population dynamics. Subsequently, we interrogate the model to determine the key environmental drivers causing the variation amongst geographically close villages. This framework could also be extended to explore the impacts of a targeted intervention approach or land use characteristics on the population dynamics of Anopheles mosquitoes.

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