



Ento24

10 – 12 September

University of Liverpool

Abstract Book

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Tuesday 10 September

- **Pests and natural enemies**

Lecture Theatre 1 (LT1)

Session Chair: Chris Ranger

10:45 – Md Munir Mostafiz, Teagasc

Life-history traits of English grain aphid, *Sitobion avenae* (Fabricius) on winter barley

The English grain aphid, Sitobion avenae (Fabricius), is one of the most damaging cereal aphids in Western Europe, feeding on all cereals, including barley, wheat, and oats. Sitobion avenae is a major carrier of barley yellow dwarf virus (BYDV), a globally significant plant virus that can result in yield reductions of up to 80%. Studying the biology of S. avenae in different crops is crucial for developing efficient control strategies. We used the age-stage, two-sex life table theory to examine the life history parameters (such as lifespan) of S. avenae on winter barley. The findings indicated that S. avenae effectively completed its whole life cycle on winter barley, with a pre-adult survival rate of 80%. The pre-adult duration and mean longevity were 7.79 days and 22.17 days, respectively. However, the mean fecundity of reproductive females (Fr) and the net reproductive rate (R0) of the population were 20.42 offspring/♀ and 15.82 offspring/individual, respectively. Furthermore, the finite rate of increase (λ) and mean generation time (T) were 1.2217 d⁻¹ and 13.78 d, respectively. These findings might be valuable for predicting the population dynamics of S. avenae, understanding its potential impact and in developing the next generation of decision support tools.

Other authors: Stephen Byrne (Teagasc), Louise McNamara (Teagasc)

11:00 – Charlotte Howard, University of Reading (Online Talk)

Powerful Flowers

Flower strips boost biodiversity in agricultural landscapes, encouraging natural pest control. We measured the effect of sown flower margins on the percentage of fruit damaged by an economically significant crop pest, rosy apple aphid (Dysaphis plantaginea), in conventional UK orchards over two years. To explore the extent of spillover into the orchard we also compared effects at distances into the orchards and in different orchard habitats.

The presence of flower margins significantly reduced the incidence of rosy apple aphid on trees compared to control orchards, and consequently, reduced apple damage. Spill-over of these effects from flower margins reached 50 m into the orchards during a year of severe infestation. There was increased diversity of predators and parasites in flower margins. Results show that, for rosy apple aphid fruit damage alone, flower strips can be a positive financial investment depending on the location and the level of pest infestation. This study is the first to detect a reduction in the percentage of trees with fruit damage by pests at harvest in orchards with a flower margin compared to control orchards. Our results support the potential for flower margins to deliver measurable rosy apple aphid control benefits.

Other authors: Michelle T Fountain (NIAB), Claire Brittain (Syngenta), Paul J. Burgess (Cranfield University) & Michael P. D. Garratt (University of Reading)

11:15 – Lami Jinatu Wamdeu, University of Ghana**Influence of cropping system in the management of Fall army-worm, *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae) and natural enemies' conservation in Kpong, Ghana.**

Prior to the incidence of fall armyworm, Spodoptera frugiperda, in Ghana, farmers have not used insecticides in maize cultivation, therefore with the invasion, there was increased production cost and risks of negative impact of insecticides on biodiversity and environment. Crop diversification is known to provide breeding space for natural enemies of pests and hinder the development of pest. This study ascertains the efficacy of legumes-maize intercrops in the management of fall armyworm infestations and damage, as well as conservation of natural enemies. Treatments comprised cowpea, groundnut, and soybean, intercropped with maize and compared against sole maize. The experiment was laid in a randomized complete block design with four replications. Data was collected on the number of damaged maize plants, FAW larvae and egg masses on maize and abundance of natural enemies. The results showed that average number of larvae recorded on maize plants was significantly lower in maize-legume plots than in sole maize in both growing seasons investigated with a notable increase during the minor season. Parallel results were noticed regarding the average number of damaged maize plants. Arthropod predators were recorded in all plots viz ants, earwigs, ladybird beetles, spiders, Blattidae and Reduviidae with varied abundances among treatment

Other authors: Agboyi Koku Lakpo (Centre for Agriculture and Bioscience International - CABI), Babatoundé Ferdinand Rodolphe Layodé (ARPPIS), Okyere Stanley Osafo (ARPPIS), Gyabeng Clinton (ARPPIS) and Fening Ken Okwae (ARPPIS & University of Ghana)

11:30 – Amanuel Tamiru, International Centre of Insect Physiology and Ecology (icipe)**Unravelling mechanisms of Push-Push farming for managing fall armworm (*Spodoptera frugiperda*) pest**

Fall armyworm, Spodoptera frugiperda, is a serious invasive pest in Africa but “Push-Pull” companion cropping can substantially reduce infestation. Our study elucidates the underpinning chemical ecology mechanisms. Headspace volatiles were collected from companion plants (Desmodium intortum, Desmodium uncinatum and Brachiaria Mulato II) and used in bioassays and electrophysiological recordings with S. frugiperda and parasitoid wasps. Insect populations, plant damage and herbivore parasitism were assessed under field conditions. Coupled GC-electroantennogram (GC-EAG) recordings showed robust responses to certain aromatic and terpenoid volatile compounds. In wind tunnel bioassays, maize volatiles mixed with Desmodium volatiles were less attractive to moths than maize alone. In oviposition bioassays, S. frugiperda laid fewer eggs on maize when Desmodium volatiles were present. In an olfactometer bioassay, parasitoid wasps were attracted to the scent of both Desmodium spp. (intercrop) and the Brachiaria border crop. Our data provide evidence of the mechanisms underpinning the reduced S. frugiperda infestation in the Push-Pull companion cropping system i.e. volatiles from companion crops repel S. frugiperda while attracting its parasitoid natural enemies. These findings explain why Push-Pull field plots had fewer S. frugiperda larvae and lower crop damage than monocropped maize.

11:45 – Will Paine, University of Oxford**Parasitoids Drive Associations Between Aphid Biotype and Protective Symbiont**

Alongside their obligate symbiont, Buchnera aphidicola, Pea aphids (Acyrtosiphon pisum) can harbour a diverse range of facultative, symbiotic bacteria. The most well-studied is Hamiltonella defensa which provides the host with protection against parasitoid wasps. H. defensa lineages show a strong association with the host's biotype and may only protect against specific wasp species. H. defensa strains found in aphids from Medicago sativum most often defend against Aphidius ervi, and strains found on Lotus pedunculatus defend against Aphelinus abdominalis. Here, we build on lab studies and use a field experiment to ask whether it is the attraction of parasitoid species to a specific plant that is driving these associations. We exposed aphid lineages without their protective symbionts to wild parasitoid populations,

either on their native host or a universal host plant (*Vicia faba*) and compared the rates of parasitism. If parasitoids are driving the associations between aphid biotypes and protective symbionts we would expect rates of parasitism for each parasitoid species to differ across the two host plants. This could help to explain the diversity of symbionts seen across host plants.

Other authors: Ailsa McLean (University of Oxford)

12:00 – Megan Parker, University of Liverpool

Reducing aphids on barley by exploiting beneficial species interactions with rhizobacteria and natural enemies

Aphids reduce agricultural yield and quality by extracting plant nutrients and vectoring diseases. Pesticides, although effective, can damage ecosystems and pest populations are evolving resistance. There is increasing evidence for using soil microbiome manipulation as a pest control strategy. We inoculate barley with beneficial rhizobacteria to reduce aphids by inducing plant defences and recruiting natural enemies such as parasitoid wasps in the field. We present results from full season outdoor pot and glasshouse experiments using rhizobacteria inoculation across different barley varieties to explore aphid and natural enemy colonisation. We saw earlier arrival and more parasitoid wasps on rhizobacteria inoculated barley compared to the control treatment. Aphid suppression was variable between barley varieties and across time, with some inoculated plants even attracting more aphids in the outdoor pot experiment. We investigated this further through controlled aphid choice experiments and chemical analysis of barley leaves. Ongoing work explores effects of rhizobacteria inoculation on plant volatiles in relation to parasitoid behaviour as well as aphid susceptibility to parasitism. Overall, we aim to provide practical solutions for agriculture and food security.

Other authors: Sharon Zytynska (University of Liverpool)

12:15 – Maximilian Schughart, Teagasc

Identifying the impact of insecticide resistant grain aphids (*Sitobion avenae*) on barley yellow dwarf virus epidemiology in Ireland

*Since 2013, resistance to pyrethroids in the English grain aphid (*Sitobion avenae*) has spread throughout Europe, including Ireland. *S. avenae* that survive spray applications can cause damage to crops by feeding on the grain and by transmitting barley yellow dwarf viruses (BYDV). The 2018 EU-ban on neonicotinoids leaves pyrethroid applications as the remaining control option, and it has been hypothesized that BYDV pressure will increase because of the favourable selection of pyrethroid resistant *S. avenae* after spray applications. Given the enormous potential agricultural impact, a three-year in-field and suction tower network survey was conducted. Surprisingly, the results showed a decrease in the incidence of insecticide resistant *S. avenae* and no link between aphid resistance and high BYDV levels was found. Additionally, virus transmission experiments showed that the resistant *S. avenae* clone is not a better BYDV transmitter than other susceptible *S. avenae* clones. However, virus-aphid behavioural manipulation experiments revealed that BYDV-carrying aphids show an increased movement activity and that different BYDV species manipulate aphid behaviour in different ways. The results highlight the complex tripartite interactions between aphids, viruses, and crops, all of which affect BYDV epidemiology. This should be considered when developing the next generation of decision support tools.*

Other authors: Emmanuel Jacquot (INRAE), Stephen Byrne (Teagasc), Louise McNamara (Teagasc)

12:15 – Hayden Tempest, Harper Adams University & NIAB

***Forficula auricularia* as a natural enemy of woolly apple aphid in commercial apple orchards**

The woolly apple aphid (Eriosoma lanigerum, Hausmann) (WAA) is an economically important pest of commercial apple trees (Malus domestica, Bork). When feeding on woody tissue such as the branches, trunk, and roots of the tree, WAA induces galls which disrupt nutrient transport systems in the tree and can act as sites for pathogenic infection, particularly canker (Neonectria ditissima). The common European earwig (Forficula auricularia, L.) is a polyphagous and omnivorous insect which occurs naturally in commercial apple orchards. Studies investigating the ability of this species to control WAA haven given mixed results in the past. We studied populations of F. auricularia and WAA in a variety of commercial apple orchards in Kent, England, to see if there was evidence that higher numbers of F. auricularia was associated with lower numbers of WAA. We also looked for any features of orchards which were strongly correlated with the presence/abundance of either species. To supplement these surveys, over 800 individual F. auricularia were tested for the presence of WAA DNA. We found evidence that F. auricularia negatively impacts WAA, but only under certain management conditions.

- Taxonomy and diversity

Location: Lecture Theatre 3 (LT3)

Session Chair: Shaun Winterton

10:45 – Beulah Garner, Natural History Museum (London)

Concatenating historical specimens with phylogenetics: accelerating biodiversity discovery by high throughput imaging and sequencing.

Insect specimens held in museum collections are increasingly our only resource for assessing the state of biodiversity backwards to pre-industrial times. Many species, especially from the diverse tropics may not be discovered ever again, and if they are, their recognition requires access to digital resources and more complete levels of species description. To understand the utility of these collections for phylogenetic study, we piloted semi-automated specimen imaging and associated label transcription for a collection of ~29,000 pinned ground beetles (Carabidae: Lebiinae) in the Coleoptera collections of the Natural History Museum, London, resulting in research-ready digitised records of 40% of known species of Lebiinae. This enabled us to investigate the chronology of species acquisition and description. Our knowledge of historically described species provide a baseline dataset with which to monitor current diversity and distributions through global mechanical collecting methods. High throughput DNA barcoding and metagenomics for lineages that remain phylogenetically unknown and incomplete, paired with lineages no longer collected in the wild, form the basis for populating the global Coleoptera phylogenetic tree. This methodology seeks to address the taxonomic deficit by linking historic taxonomy with phylogenetic diversity into an overarching species discovery, ultimately shedding light on global change and species loss.

Other authors: Alfried P. Vogler (Natural History Museum, London & Imperial College London)

11:00 – Kirstin Williams, KwaZulu-Natal Museum (Online Talk)

The state of the genus *Hybomitra Enderlein* (Diptera: Tabanidae) in the Afrotropics including the discovery of a new species from South Africa

The taxonomy of horse flies in the Afrotropics has been neglected in recent times. The genus Hybomitra Enderlein is considered to be Holarctic but 15 species are recorded from the Afrotropics. A collecting trip in South Africa led to the discovery of a new species in the Hybomitra genus, Hybomitra phalaros. Phylogenetic analysis using both mitochondrial and nuclear regions supports a paraphyletic Hybomitra, comprising biogeographically distinct clades. Taxonomic revision of the Afrotropical Hybomitra is complex

due to unavailable type specimens and lack of available material. The whereabouts of these type specimens are discussed and the type localities are mapped and discussed in relation to barcode voucher specimens from the region.

Other authors: Louwtjie Snyman (Royal Alberta Museum)

11:15 – Bikash Sahoo, National Institute of Science Education and Research (NISER) (Online Talk)
Dual Taxonomy Dilemma: Unraveling taxonomic challenges in army ant genus *Aenictus* Shuckard 1840 (Hymenoptera, Formicidae)

*Dual taxonomy arises when a single species is delineated into two distinct taxa based on the disparate morphological characteristics of its castes, especially workers and reproductives. This phenomenon is exemplified in certain ant species, within the *Aenictus* genus, where males exhibit markedly different morphological traits compared to workers. Historically, males collected independently during night in light traps were often designated as separate species, perpetuating a dual taxonomy approach. While this practice has diminished, its remnants still persist in literature. Addressing this issue necessitates comprehensive sampling methodologies to obtain all castes from a single colony. However, in species like army ants, male specimens are scarce within colonies and are available only during reproductive period. DNA analysis offers a viable solution, yet limited availability of male specimens, scattered across multiple museums, poses challenges. Thus, thorough sample collection during reproductive periods is imperative to ensure simultaneous capture of all castes for accurate taxonomic delineation.*

Other authors: Aniruddha Datta -Roy (National Institute of Science Education and Research)

11:30 – James Buxton, Agriculture Victoria (Online Talk)
Towards a standardised approach to Australian ant species delimitation

In Australia, ants are influential components of terrestrial systems that boast exceptionally high endemic diversity. Exotic species have the potential to pose a devastating threat to ecosystems, with timely distinction between exotic species and their native counterparts essential to reduce the risk of establishment. However, native species delimitation is a source of some controversy. Several studies strongly suggest the presence of overlooked cryptic diversity, even ‘megadiversity,’ in certain species groups that conflict with traditional taxonomic treatments, including those that adopt an integrated approach.

Perhaps in consequence, there has been relatively little major revisionary work on native ant genera in the last decade, despite a pressing need for species-level understanding, leaving some of the most diverse and widely distributed genera unmonographed as the debate continues. Whilst emerging molecular approaches may provide the ultimate resolution, continued neglect in the immediate future could result in a failure to account for undescribed species in threatened environments and substantial delays when identifying Australian species introduced overseas.

Here we briefly explore the variety and limitations of past approaches before presenting research that has taken steps towards improving the practical standardisation of species delimitation.

Other authors: Isabel Valenzuela (Agriculture Victoria), Francesco Martoni (Agriculture Victoria), Mark Blacket (Agriculture Victoria)

11:45 – Luis Moliner Cachazo, King's College London & Natural History Museum (London)
Characterising aquatic macroinvertebrate diversity in the Okavango Delta (Botswana) using taxonomical and molecular techniques

In the Okavango Delta wetland, in northern Botswana, plant and animal communities switch from terrestrial to aquatic species when the floodplains and connected waterbodies are inundated by the annual flood pulse. Aquatic macroinvertebrates provide many direct and indirect benefits to local people in the region, however, the knowledge about their distribution across the Delta and community composition at species level is scarce, in addition, the chironomids have never been studied. By using taxonomic and molecular techniques (eDNA), we aimed to improve our understanding on distribution and composition. The collection of 50 macroinvertebrate bulk samples, 33 UV-trap samples and 3 adult chironomid samples taken in 24 locations during recession and peak phase, across 4 major areas of the Delta, in 4 different types of waterbodies, resulted in 258 morphospecies of macroinvertebrates and 73 morphospecies of chironomids, of which at least 87 are new records in the country, including two very rare species of Bryozoa. eDNA analysis resulted in additional 56 taxa not found with traditional taxonomy. These results led us to conclude that biodiversity in the Delta is considerably higher than previously thought and eDNA can be a useful complementary tool for characterising biodiversity in tropical wetlands.

Other authors: Kaelo Makati (Okavango Research Institute), Ineelo Mosie (Okavango Research Institute), Michael Chadwick (King's College London), Ben Price (NHM) & Jane Catford (King's College London)

12:00 – Alison Karley, The James Hutton Institute

Has the diversity of flying aphids changed over the past 70 years? An analysis of Scottish suction trap data.

Much has been written about insect declines in response to anthropogenic drivers. Aphids are a widespread and often abundant component of insect communities; due to their biology and life cycle, they provide an excellent indicator of changing environmental conditions. The UK suction trap network has been operating for several decades and is used to monitor aphid flights and virus risk to agricultural crops. It provides a long-term dataset for examining temporal trends in aphid diversity and abundance and their relation to environmental conditions.

Using the Scottish suction trap data, we are analysing temporal trends in aphid abundance, composition and diversity. Initial analyses have highlighted shifts in aphid taxonomic composition during certain decades and changes in within-year seasonal composition. We have applied time-varying autocorrelation methods to understand how species vary in abundance from one year to the next, which has revealed three types of patterns – increasing, decreasing and stable trends along with changes in autocorrelation over time.

We will present these analyses alongside current work to examine whether aphid taxonomic composition varies with land use and meteorological conditions. This could highlight taxa acting as indicators of change, aiding predictions about biodiversity impacts of future climate or land use scenarios.

Other authors: John Addy, Katharine Preedy (Biomathematics and Statistics Scotland), Alon Zuta, Susan Verrall, Gaynor Malloch (James Hutton Institute) & Fiona Hight (Science and Advice for Scottish Agriculture)

12:15 – Stuart E. Reynolds, University of Bath

Marine insects: exclusion of hexapods from the sea by limited reproductive capacity

A new database of marine hexapods shows that colonisation of the sea by insects and their relatives is extremely rare but has occurred many times during their evolution. Species from only four hexapod orders

occur in marine environments to any extent: Diptera, Hemiptera, Coleoptera and Psocodea. Most of these insects do not live so much in the sea as on its surface. Why are there so few insects in the sea? Hexapods and Crustacea are both members of the clade Pancrustacea, but while the former are almost entirely excluded from the sea, most of the latter lead marine lives. It is argued that this is because winged adult dispersal limits the reproductive output of insects. Only where insects can colonise their specialised niches in a directed way can they successfully colonise the sea. Randomly directed dispersal as a larva, as in crustaceans, enables the reproductive adult to go on moulting, potentially producing many more offspring than can be produced by an adult insect, which can never moult again and must produce all of its offspring in a single stage.

12:30 – Dominic Phillips, Natural History Museum (London)
Darwin Tree of Life: An Insecta Perspective

The Darwin Tree of Life Project (DToL) is an ambitious undertaking, aiming to sequence the full genomes of all ~77,000 eukaryotic organisms found within the British Isles. DToL brings together a host of British research organisations and special interest groups to collect species and generate comprehensive data sets that is revolutionising our understanding of the biodiversity and evolutionary history of the United Kingdom. This undertaking involves the collecting, sampling and sequencing of a wide range of organisms. Insects make up around 31% of these species, consisting of some 24,000 species over 29 orders.

DToL is not only providing a wealth of information on the genetic diversity of life in the UK but contributing data towards research conducted on the evolutionary relationships of different species. Though the scope of the project is enormous, it is already making rapid progress thanks to the continuing advancements made in DNA sequencing technology and analysis.

This talk will provide a brief overview of the Darwin Tree of Life Project, the current numbers for insect species collected and showcase a few case studies highlighting some of the recent outputs and impressive discoveries made by the project thus far.

Other authors: Inez Januszczak (NHM) & Chris Fletcher (NHM)

- Host-microbiome interactions

Location: Lecture Theatre 1 (LT1)

Session Chair: Sharon Zytynska

14:45 – Ailsa McLean, University of Oxford

Realistic climate warming scenarios produce little change in symbiont-mediated resistance of aphids against parasitoids

Many insects carry symbiotic bacteria that are not required for successful growth and reproduction, but persist by conferring biological advantages on their host. However, these benefits are often conditional upon the environment. For example, several different bacterial species have been shown to protect aphids against diverse Hymenopteran parasitoids, although in some cases the protection has been observed to fail under severe heat stress. A warming climate might therefore reduce aphid defence against parasitoids in future, but experiments using realistic current and future climate scenarios are lacking. We tested the ability of protective symbionts to maintain their defensive capabilities against parasitoid wasps when pea aphids are experiencing mild heat stress (representative of warmer than average summer conditions) and severe heat stress (representative of recent UK heatwave conditions). We found no evidence of reduced protection under conditions representing warmer summers and aphids also continued to benefit from symbiont-mediated protection under heatwave conditions. Our results suggest that realistic warming

scenarios for current and near-future conditions are unlikely to lead to breakdown of parasitoid resistance in the aphid populations we investigated.

Other authors: Mukta Mala (University of Oxford)

15:00 – Laura Martinez-Chavez, Harper Adams University

Is there a link between protective endosymbionts, genotypes and parasitoids of the potato aphid (*Macrosiphum euphorbiae*) on strawberry crops?

*The potato aphid (*Macrosiphum euphorbiae*) is an economically important pest of strawberry crops for which the management relies on biological control. The description of resistance to a parasitic wasp in some populations of *M. euphorbiae* could indicate reduced effectiveness of its biological control. Resistance of aphids to parasitoids has been linked to aphid genotype and endosymbiotic infections, but most of the research on this topic have been done under laboratory conditions, which oversimplifies the complexity of the factors involved in the interaction. Here, we aim to test under field conditions whether the endosymbiont communities or genotypes of *M. euphorbiae* have a protective effect on their hosts and whether they are linked to parasitoid communities. We monitored four polytunnels in a strawberry farm over one cropping season and we collected data that will help us understand if facultative symbiotic associations or aphid genotypes respond to parasitoid pressure of varying intensity and will provide an insight into the relationships between symbiotic communities, genotypes, and parasitoid communities in terms of diversity. Together, this information will inform on the likely effect of endosymbionts and genotypes on the effectiveness of biological control programmes based on parasitic wasps for control of *M. euphorbiae* in strawberry crops.*

Other authors: Alison J. Karley (The James Hutton Institute), Francis Wamombe (NIAB East Malling), Joe Roberts (Harper Adams University) & Tom W. Pope (Harper Adams University)

15:15 – Hongbo Sun, University of Exeter

Effect of the microbiome on pathogen susceptibility across host species

*Microbiome-mediated protective effects on pathogen infection are common in nature. Numerous studies have revealed the importance of the host microbiome in infection, but few have focused on multiple host studies. Here, we have used four *Drosophilidae* species, with intact or manipulated microbiomes, with three pathogens. We cleared the *Drosophila* microbiome by treating newly emerged flies with antibiotic food. We then created microbe-recolonised flies, in which the sterile flies were associated with either *Providencia* and one *Acetobacter*. Flies were then challenged with three pathogens. We sought to explain whether the host microbiome can protect the host from infection across species and whether any protective effect is general or specific across species. We found that the host microbiome exhibits host-specific effects, and the microbiome can improve the probability of survival in certain infections, but such a protective effect is not general across species.*

15:30 – Christopher Ranger, USDA-Agricultural Research Service

Stress-Induced Tree Metabolites Influence Ambrosia Beetle-Fungus-Host Interactions

*Wood-boring ambrosia beetles tunnel into host trees to excavate galleries for growing their nutritional fungal mutualists and rearing offspring. Some invasive species within the Tribe Xyleborini preferentially select trees weakened by abiotic or biotic stressors. Ethanol is a stress-induced semiochemical that ambrosia beetles use to locate vulnerable hosts. Acetic acid is also induced in response to stress. Our overall objective was to assess the influence of ethanol and acetic acid on the colonization success of ambrosia beetles. Stem sections (i.e., bolts) of deciduous trees were infused with dilute ethanol and acetic acid or water solutions. Individual ambrosia beetles (*Xylosandrus germanus* and *Anisandrus maiche*) were then confined*

to the bolts under no-choice conditions. Sawdust ejected during tunneling was quantified. X-ray tomography was used to generate three-dimensional images of the galleries from which the gallery volume was calculated. Ambrosia beetle tunneling, gallery excavation, and offspring production dramatically increased in the presence of ethanol and acetic acid. Quantitative PCR confirmed higher amounts of fungal mutualists grew in the presence of ethanol and acetic acid. These results improve our understanding of how stress-induced host tree metabolites influence the colonization of invasive ambrosia beetles, along with optimizing a rearing protocol using bolts.

Other authors: Jessica Raubenolt (The Ohio State University), Juan Carlos Cambronero (University of Padova), Vipa Phuntumart (Bowling Green State University), Davide Rassati (University of Padova), Peter Biedermann (University of Freiburg) & Michael Reding (USDA-ARS)

15:45 – Ida Cecilie Jensen, Aarhus University

Fungus Fighters: Associated Microbes of Wood Ants (*Formica polyctena*) and Weaver Ants (*Oecophylla smaragdina*) Inhibit Plant Pathogens

Recently, ants have shown inhibitory effects against plant diseases, and this effect might at least partially be caused by antimicrobial compounds produced by ant-associated microorganisms. Here, we compare the microbiomes of wood ants (*Formica polyctena*) and weaver ants (*Oecophylla longinoda*) and test their effect against economically important plant pathogens.

In an apple orchard, wood ants were found to reduce the plant pathogenic fungus, apple scab (*Venturia inaequalis*), by 61 and 34% on apples and leaves, respectively.

Laboratory tests showed that wood ants and weaver ants leave microbial footprints when walking. The inhibitory effect of these microbes was tested against the plant pathogenic fungi *Botrytis cinerea*, *Fusarium graminearum*, and *Monilinia fructigena*. Of 23 wood ant isolates 11 inhibited all three pathogens, and several were closely related to known biocontrol species. Isolates from the weaver ants are currently being tested and results will be presented at the conference.

16S rRNA sequencing revealed that the bacterial communities differ significantly between ants and their nests, while similarities were found between the two species, including antimicrobial taxa like *Pseudonocardia* and *Nocardia*.

These findings suggest that ants' inhibitory effects on plant pathogens are partially due to their associated microbes and highlight their potential in biocontrol.

Other authors: Anders Lander Mogensen (Aarhus University), Seven Nazipi Bushi (Aarhus University), Kemo Badji (Directorate of Plant protection, Senegal), Andreas Schramm (Aarhus University) & Joachim Offenberg (Aarhus University)

16:00 – Jacqueline Wahura, International Centre of Insect Physiology and Ecology (ICIPE) & University of Cape Town (Online Talk)

An Influential Insider: Microsporidia MB Influences the Host Gut Microbiota Profile

Mosquito associated microbiomes play an important role in the insect's overall fitness. However, diverse factors including infection with insect endosymbionts can influence these microbial communities. Here, we evaluated the influence of Microsporidia MB (MB) - an endosymbiont of *Anopheles arabiensis* that impairs *Plasmodium falciparum* transmission - on the midgut bacterial communities in infected mosquitoes. The aim of this work was to determine whether the gut microbiota in infected mosquitoes shifts importantly in a manner to explain the endosymbiont's *Plasmodium* transmission blocking phenotype. By sequencing the V3-V4 16S rRNA region, *Serratia*, *Elizabethkingia* and *Pseudomonas* were the most abundant genera with

relative abundances of 48.07%, 14.2% and 6.2% respectively. While the three were generally highly abundant, *Serratia* and *Pseudomonas* were significantly higher in MB negative mosquitoes, while *Elizabethkingia* was significantly higher in MB positive mosquitoes. *Serratia* and *Pseudomonas* activate mosquito immune systems against *Plasmodium*. Their significantly low abundances in MB infected mosquitoes indicates that MB transmission blocking does not occur in synergy with other microbes. Conversely, *Elizabethkingia* distinctively enhances mosquito development and its higher abundance in MB infected mosquitoes could be intensifying MB's enhanced effect on mosquito development. These results will be foundational in developing an MB field dissemination strategy.

Other authors: Cynthia King'ori (icipe), Lydia Siele (icipe), Anne Wairimu (icipe), Fidel Gabriel Otieno (icipe), Nicola Mulder (University of Cape Town), Daniel Masiga (icipe) & Jeremy Herren (icipe)

16:15 – Tara Joseph, Liverpool School of Tropical Medicine

Mosquitoes reared in distinct insectaries within an institution possess divergent microbiomes

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.

Other authors: Laura E. Brettell (University of Salford), Ananya F. Hoque (Roslin Institute), Vishaal Dhokiya (Liverpool School of Tropical Medicine), Emily Hornett (Liverpool School of Tropical Medicine), Grant L. Hughes (Liverpool School of Tropical Medicine) & Eva Heinz (Liverpool School of Tropical Medicine)

- Evolution, plasticity and phenotypic adaptation

Location: Lecture Theatre 3 (LT3)

Session Chair: Sheena Cotter

14:45 – Sheena Cotter, University of Lincoln

Lifelong effects of the larval environment on adult traits

*The juvenile environment is vital for adult fitness in many species, but especially holometabolous insects, with most of the resources for growth gathered as larvae and adult size determined at pupation. We asked how the quality of adult burying beetles, *Nicrophorus vespilloides*, was affected by the juvenile environment, and whether the impact of a poor environment could be rescued by the adult diet. Burying beetles provide elaborate care for their offspring, preparing a vertebrate carcass as an edible nest, keeping it clean and feeding begging larvae directly. We manipulated the environment so that larvae received no care (parents removed upon hatching) or full care. Upon adult emergence, beetles were maintained on diets varying in their protein: fat content and their nutrient intake was measured. We also assessed reproduction, survival and investment in immunity. Our results demonstrate that beetles who were reared without parents produced fewer, smaller larvae, had reduced immunity and a shorter lifespan. Moreover, this reduction in adult quality could not be ameliorated by nutritional compensation,*

with low and high care adults consuming a similar ratio of protein to fat, but no-care larvae eating less food overall. The juvenile environment is therefore vital in determining adult fitness.

Other authors: Ekhlas Al Shareefi (Babylon University)

15:00 – Uroš Savković, University of Belgrade

Long-term laboratory evolution experiment: Host shift changes the life-history strategies and the levels of phenotypic plasticity in seed beetle (*Acanthoscelides obtectus*)

*Many phytophagous insects are able to exploit a novel food source in their diets. This process, known as the host shift, includes insects' ability to recognise, utilise and ultimately persist on a new plant host. During the host shift process, insects are faced with many challenges and new conditions can change insects' behaviour, physiology, life-history strategies and population dynamics. Adaptive phenotypic plasticity could help populations to receive signals from the new environment and constitute a functional phenotype. Using a long-term laboratory evolution experiment in seed beetles (*Acanthoscelides obtectus*) we have tested how different plant hosts (common beans, chickpeas and mung beans) change life-history strategies over many generations. Furthermore, we have established iso-female lines and conducted a reciprocal transplant experiment in order to test the level of plasticity in life-history traits. We have demonstrated that populations of seed beetles adapted to different hosts not only show changes in life-history traits, but also demonstrate clear differences in the levels of phenotypic plasticity for those traits. This research is discussed in the context of how plant hosts affect populations' ability to influence long-term (evolutionary) modes of populations' change and allow survival and ecological competence of organisms in new conditions.*

Other authors: Uroš Savković (University of Belgrade), Sanja Budečević (University of Belgrade), Snežana Pešić (University of Kragujevac), Dragana Predojević (University of Kragujevac), Filip Vukajlović (University of Kragujevac), Lea Vlajnić (University of Belgrade), Mirko Đorđević (University of Belgrade), Biljana Stojković (University of Belgrade)

15:15 – Kumari Riya Pati, University of Edinburgh

The Plasticity of Ageing for Competitive ability in 'Burying beetles' *Nicrophorus vespilloides*

The environment plays a critical role in an individual's lifespan and ageing through diverse processes. As ageing is environmentally plastic, the environmental context needs to be considered when measuring it. Furthermore, some studies have suggested that environments with higher levels of stress should hasten the ageing process. However, the actual relationship between environmental stress and ageing affecting the individual's life history traits are still not well understood.

In life-history traits, investment in competitive behaviour is important part of reproductive investment (limited by availability of reproductive resources) which can lead to trade-offs in investment, e.g. between reproduction and survival, or between different environment. Life-history theory: as individuals age increases, their residual reproductive value decreases and they should increase investment in contest behaviour. Also, the evolutionary theory of aging predicts that contest behaviour should decrease as the age increase. Among these conflicting predictions, therefore, this is important and interesting to observe the age effects on contest. If Ageing is environmentally Plastic, we are expecting to get the variation in Contest pattern between two contrasted environments such as captive (or laboratory) versus in wild.

Other authors: Jacob Moorad (University of Edinburgh) & Per Smiseth (University of Edinburgh)

15:30 – Erin Foley, University of Leicester

Establishing a tractable epigenetic clock in the parasitic jewel wasp *Nasonia vitripennis*

*A large body of ageing research is based on simple model invertebrate organisms. However, these current models lack detectable DNA methylation which renders them impractical to study epigenetic alterations, one of the nine hypothesised hallmarks of ageing. *Nasonia vitripennis*, an emerging model organism possesses a fully functional DNA methylation system, which makes it an ideal candidate to measure the effects of a number of ageing interventions on both lifespan and epigenetic ageing.*

*Epigenetic clocks are an emergent property of the DNA methylation status of a number of genes, the epigenome, which is calculated using supervised machine learning methods. We propose that *Nasonia* may be key in answering the question of whether short-term decreases in epigenetic clock scores correlate with changes in lifespan.*

*We predict that two main areas where our establishment of an epigenetic clock in *Nasonia* will be useful; firstly, to investigate the underpinning biology of epigenetic clocks and secondly, how influenced epigenetic clocks are by ageing interventions. As an example, we propose larval diapause as a model for early life experience effects on ageing. Early life effects are a predictor of lifespan, and diapause can increase adult lifespan in insect species, an example of senescence plasticity.*

Other authors: Eamonn Mallon (University of Leicester), Flaviano Giorgini (University of Leicester), Hollie Marshall (University of Leicester)

15:45 – Christophe Patterson, Durham University

Multivariate trait evolution of a seasonal polyphenism at the continental scale

*Many species exhibit seasonal polyphenism where two or more phenotypes arise with the changing environmental conditions across the year. In many polyphenic species developmental constraints limit the divergence between alternative morphs. For seasonally polyphenic species, selection acting on the phenotype present in one season may constrain the phenotypes present in another season. Smoky rubyspot damselflies (*Hetaerina titia*), exhibit a striking seasonal polyphenism in wing melanisation, but the degree of polyphenism varies between regions. We quantified the wing phenotypes in >5,600 smoky rubyspots through field research and via a participatory science initiative. Combined with a population-level phylogeny we use multivariate models of trait evolution, to test whether the peak and off-peak phenotypes have co-evolved and whether there is geographic variation in the tempo of evolution. We find no significant evidence of co-evolution between seasonal phenotypes. We do find evidence that the seasonal polyphenism is evolving under different selective regimes across geographic regions, suggesting either melanisation has different trade-offs in different regions or there has been developmental release in certain lineages. To our knowledge, our study presents the first empirical research into the evolution of polyphenism with sufficient data to model the seasonal variation in polyphenism across the entire range of a species.*

Other authors: Jonathan Drury (Durham University)

16:00 – Joseph Rees, University of Lincoln

Hands off or helicopter parenting? The role of parenting in shaping aposematic signals of *Nicrophorus vespilloides*

*The burying beetle, *Nicrophorus vespilloides*, is a carrion species that exhibits remarkable aposematism and biparental care. The parents prepare a carcass in preparation for their larvae, preventing decay of the carcass and helping larvae feed in the initial days post-hatching. While research has previously focussed on the size and aposematism of the primary stripe on the elytra, there has been limited research into the*

shape of the signal. The larvae were exposed to varying levels of parental care: 3 treatments of low care (0 hours, 8 hours, and 24 hours) and the control treatment. The shape of both the parents' and offspring's stripe was then analysed using geometric morphometrics to determine whether parental care can affect this aposematic component. The analyses exhibited significant differences between low care and the controls, showing that parental care mechanisms can affect the stripe. This means that the stripe shape is phenotypically plastic, dependant on environment as well as genetics.

Other authors: Sheena Cotter, University of Lincoln; Carita Lindstedt, University of Helsinki; Marcello Ruta, University of Lincoln

16:15 – Benjamin Jarrett, Bangor University

The evolution of plasticity in response to host plants in *Narnia femorata* (Hemiptera: Coreidae)

*Developmental plasticity is the ability to produce different phenotypes as a function of an environment in which an organism develops. In many cases, developmental plasticity is adaptive, increasing the fitness of an individual in a certain environment, but our understanding of how adaptive plasticity can evolve and how quickly it can do so is limited. Here, we use experimental evolution of a leaf-footed bug (*Narnia femorata*) to ask how morphological plasticity evolves on different host plant species (*Opuntia* spp.). We evolved populations on one of two *Opuntia* species, with a third treatment experiencing alternating host plants. We found that plasticity did not evolve after three generations of experimental evolution, but we found that evolutionary history affected morphology when individuals were reared on a completely novel *Opuntia* species. Our work highlights that rapid evolution that appears neutral with respect to contemporary environments, can have a large influence in novel environments.*

Other authors: Kaili Sherman, University of Florida; Merrick Graham, University of Florida; James Boothroyd, University of Florida; Christine Miller, University of Florida

- **Biocontrol**

Location: Lecture Theatre 1 (LT1)

Session Chair: Alison Karley

17:00 – Toby Bruce, Keele University

Bioactive volatiles from push-pull companion crops repel fall armyworm and attract its parasitoids

*Fall armyworm, *Spodoptera frugiperda*, is a serious invasive pest in Africa but "Push-Pull" companion cropping can substantially reduce infestation. Here we investigated how it works. We hypothesized that companion crop volatiles repel herbivores (push) while attracting natural enemies (pull). Headspace volatiles were collected from companion plants (*Desmodium intortum*, *Desmodium uncinatum*, *Brachiaria Mulato II*) and used in bioassays and electrophysiological recordings with *S. frugiperda* and parasitoid wasps. Insect populations, plant damage and herbivore parasitism were assessed in field plots. Coupled GC-electroantennogram (GC-EAG) recordings showed insect responses to certain aromatic and terpenoid volatile compounds. In wind tunnel bioassays, maize volatiles mixed with *Desmodium* volatiles were less attractive to moths than maize alone. In oviposition bioassays, *S. frugiperda* laid significantly fewer eggs on maize when *Desmodium* volatiles were present. Conversely, in an olfactometer bioassay, parasitoid wasps were attracted to the scent of both *Desmodium* spp. (intercrop) and the *Brachiaria* border crop. Our data provide evidence of the mechanisms underpinning reduced *S. frugiperda* infestation in the Push-Pull companion cropping system, i.e., volatiles from companion crops repel *S. frugiperda* while attracting its parasitoid natural enemies. These findings explain why Push-Pull field plots had fewer *S. frugiperda* larvae and lower crop damage than monocropped maize.*

Other authors: Islam S. Sobhy, Keele University; Amanuel Tamiru, Xavier Chiriboga Morales, Dickens

Nyagol, Duncan Cheruiyot, Frank Chidawanyika, Sevgan Subramanian, Charles A. O. Midega, and Zeyaur R. Khan, International Centre of Insect Physiology and Ecology (icipe)

17:15 – Julia Morgan, Royal Horticultural Society

Natural enemies and cultural control of aphids on runner bean, *Phaseolus coccineus*, for home gardeners

Aphids are an extremely common enquiry to the RHS (Royal Horticultural Society) Gardening Advice and were particularly prevalent in 2023. Currently, RHS advice on aphid management emphasises biodiversity-friendly measures including encouraging natural enemies and hand removal. These cultural control measures are more practical for home gardeners than commercial growers, but there is limited scientific research demonstrating their effectiveness. To begin to tackle this knowledge gap, a summer student project was developed, funded by the Royal Society of Biology as part of their Plant Health Undergraduate Studentship programme.

The chosen study system is runner beans, grown in a diverse edible garden setting at RHS Garden Wisley. A designed replicated trial was used to test four aphid management techniques:

- *Tolerate (no action/ negative control)*
- *Hand removal of aphids*
- *Pruning affected shoots*
- *Encourage natural enemies: earwig shelter*

The beans were monitored throughout the growing season to record aphid identity and density, natural enemy identity and density, and growth and productivity of the beans under these different treatments. The results of this project can feed into RHS Gardening Advice, including web pages that are accessible to all. This will enable gardeners to make informed decisions when investing time and effort in managing aphid populations.

Other authors: Hayley Jones (Royal Horticultural Society), Yana Konoplin (Royal Horticultural Society)

17:30 – Wan Nurainie Wan Ismail, University of Edinburgh & Universiti Malaysia Sarawak (UNIMAS)

Parasitoid nectar provision hypothesis: Does floral nectar improve biological control by parasitoids?

*The nectar provision hypothesis suggests that introducing nectar-bearing plants in agroecosystems enhances parasitoid efficacy and improves biological control. This is typically achieved by intercropping the main crop with companion plants that provide nectar for parasitoids. Intercropping cereals with faba beans (*Vicia faba*) introduces nectar sources into otherwise sugar-devoid systems. However, the nectar provision hypothesis has rarely been evaluated at the field scale in such intercropped systems. This paper presents findings from our recent controlled experiment assessing the ability of nectar-bearing flower species to sustain the parasitoid *Aphidius ervi* in the absence of aphids, specifically targeting the control of the cereal aphid *Sitobion avenae*. Overall, the study demonstrates increased wasp longevity and mummification ability in the presence of nectar-bearing plant species.*

Other authors: Gail Jackson, University of Edinburgh; Alf Gathorne-Hardy, University of Edinburgh; Barbara Smith, Coventry University; Henry Creissen, SRUC and Pietro (Pete) Iannetta, James Hutton Institute

17:45 – Christopher Williams, Liverpool John Moores University

Forest Applications of Entomopathogenic Nematodes

The application of entomopathogenic nematodes (EPNs) to the control of insect pests of trees in the broadest sense is reviewed. First considered are pests of trees outside of woodlands and forests, typically

in urban environments. Next, pests of deciduous forests and their control is dealt with before moving on to pests of coniferous forests. It should be noted that out of the 99 serious pests of forestry identified by Day and Leather (1997) only 16 (16.2%) have had any research on applications of EPNs for their control. These examples and others are presented in this talk as well as more broadly addressing the challenges faced in controlling these pests. Finally, a case study of the control of the most serious pest of forestry in Europe, *Hylobius abietis* is presented, which takes account of life cycle, current control methods, factors affecting efficacy of EPNs, environmental safety of EPNs and interaction with other biological control agents.

18:00 – Sonja Steinke, Forest Research

Nematodes and predators: Biocontrol strategies against insect forest pests in Scotland

The large pine weevil (Hylobius abietis) is a pest of young trees, and particularly a problem for restocked commercial conifer forests. A variety of solutions are available for control of the weevil; however, the British timber industry is widely dependent on the use of insecticides. We discuss research on and options for non-chemical alternatives to protect young trees from damage by H. abietis in UK forestry.

Another extremely successful invasive pest of spruce is the great spruce bark beetle (Dendroctonus micans), which left uncontrolled can cause considerable economic damage. To control D. micans and slow down its spread, Forest Research is running a breed and release programme for Rhizophagus grandis, a predatory beetle that exclusively preys on the juvenile stages of D. micans. Experiences from the biocontrol program and the current distribution and recent spread of D. micans in Scotland will be discussed.

18:15 – Jordan Cuff, Newcastle University

Networking nutrients: integrating nutrients into networks to investigate the drivers of biocontrol and the structure of entomological interactions

The ecological interactions of insects and other invertebrates are crucial for ecosystem services like biocontrol and pollination, and they form the fundamental building blocks of functional ecosystems. Nutrients are a crucial driver of ecological interactions but remain poorly integrated into ecological network analyses despite the immense potential for understanding the structuring of interactions gained through the consilience of nutritional and network ecology. Concepts like nutrient-specific foraging have the potential to explain the mechanisms structuring complex ecological systems, and nutrients may help to guide predictions of dynamic processes, such as interaction rewiring and extinction cascades.

In this talk, I will present the concept of nutritional networks and demonstrate this approach with an empirical spider-prey network. I will show how networks can be constructed with nutritional data and how this can illuminate the way in which nutrients structure ecological networks in natural systems and drive processes like biocontrol. I will also highlight pertinent ecological topics which could be advanced in a nutritional network context, including nutritional niche differentiation, functional responses, ecological invasions and ecosystem robustness. By integrating nutritional data and ecological networks, we envisage significant advances to our understanding of ecological processes from individual to ecosystem scales.

Other authors: Darren M. Evans, Newcastle University; Ian P. Vaughan, Cardiff University; Shawn M. Wilder, Oklahoma State University; Maximilian P.T.G. Tercel, Cardiff University; Fredric M. Windsor, Cardiff University

- Behavioural and sensory ecology

Location: Lecture Theatre 3 (LT3)

Session Chair: Toby Bruce

17:00 – Aphrodite Kantsa, ETH Zurich (Online Talk)

What do insects see and smell in flowers and leaves?

Biocommunication is a major decision-making tool for living organisms. Plants have evolved diverse strategies to communicate with mutualists and antagonists, primarily reflected on floral forms, textures, scents, and colours. But how do these strategies work in real-life community settings, where different species must co-exist while exchanging millions of bits of information with animals? In a natural community of flowering plants, we monitored in detail the pollination and herbivory networks, we analysed floral stimuli, leaf functional traits, as well as the primary and secondary metabolomes of leaves, petals, and nectar of all the study species, in order to decipher the interconnection between insect visitation, flower advertisement, and the nutritional value of the different plant parts for antagonists or mutualists. Our work reveals what pollinators and herbivores can "smell" and "see" in flowers, and provides novel insights in interactions ecology.

17:15 – Abra Ash, Cranfield University & UK Centre for Ecology and Hydrology

Designing Artificial Flowers for Automated Pollinator Monitoring

Artificial flowers have been used in insect research since the late 1800s with much of the research centred around studying insect behaviour. With the recent rise in automated insect monitoring that use machine learning, there has been a demand for more effective and standardised attractants under the camera. This project looks to design these attractants as 3D printed artificial flowers with multimodal attraction cues that can last long term under a remote automated insect monitoring camera trap. In the summer of 2024, 3D printed artificial flowers with different combinations of attraction cues such as colour, scent, ultraviolet, and nectar guides will be placed in a field site in Krka National Park, Croatia. The goal will be to see which combination of attraction cues attracts the largest diversity and abundance of insects and provides the most effective population count under the insect camera trap. Furthermore, the experiment will compare volunteer counted data of the same artificial flower systems to the camera traps showing the benefits and disadvantages of each. The outcome will show which combinations of attraction cues are the most effective at attracting insects for automated insect monitoring.

Other authors: Tom August, UKCEH; Stephen Hallett, Cranfield University; Claire Carvell, UKCEH; Leon Williams, Cranfield University

17:30 – Ritabrata Chowdhury, University of Cambridge

"Game of thorns": Counter-adaptions of Heliconiini caterpillars to Passiflora leaves with sharp trichomes

*Plants protect themselves against herbivory with a variety of chemical and physical defences, whereas some insects have evolved counter-adaptations to feed on these plants. However, the mechanisms underlying insect counter-adaptations to physical plant defences are largely unexplored. We investigated the role of hooked trichomes in *Passiflora adenopoda* as a physical defence against heliconiini caterpillars and how certain caterpillars can cope with them. We found that hooked trichomes arrest the movement of *Heliconius melpomene* and *Heliconius erato* caterpillars by piercing their soft cuticle and causing wounds near the prolegs in large caterpillars and on the main body in small caterpillars. However, *Heliconius charithonia* and *Dryas iulia* caterpillars could easily deal with the hooked trichomes due to thicker and more puncture-resistant cuticle. Interestingly, only *H. charithonia* caterpillars were able to feed and survive on *P. adenopoda* with hooked trichomes. Moreover, we discovered that the hooked trichomes could kill non-*

resistant *Heliconiini* caterpillars post-ingestion by internally piercing their gut, but that this never happened for *H. charithonia*, suggesting the presence of counter-adaptations in the gut of *H. charithonia*. This is one of the first studies characterising the mechanisms underlying insect counter-adaptations to physical plant defences, whilst also describing a co-evolutionary arms-race between the two.

Other authors: Erika C.P. de Castro, Chris Jiggins, Walter Federle (Department of Zoology, University of Cambridge)

17:45 – Sofia Dartnell, University of Cambridge

The role of olfaction in cuckoo bumblebee host-finding behavior: choice experiments on the accuracy and drivers of invasion

Cuckoo bumblebee queens are unable to rear their own workers and must successfully locate and invade a colony of their host bumblebee species to achieve reproductive success. The sense of smell plays a large role in the lives of social insects, who use it to differentiate sisters and strangers within the colony setting. It has also been suspected that cuckoos use scent when locating a host colony. To understand the role of scent in this host-parasite system, we conducted a series of choice experiments with wild-caught cuckoo bumblebees *Bombus vestalis* and lab-reared colonies of their host *Bombus terrestris*. Female cuckoo bumblebees were introduced to a flight arena containing four identical opaque boxes, each of which featured holes to release volatiles from a colony placed within. When only one box contained a host colony, the cuckoos were significantly able to locate their hosts among the four boxes. When *B. terrestris* brood, workers, and the queen were placed in separate opaque boxes, the cuckoos did not make a clear choice among them, but still avoided the empty control box. This is an initial step in understanding host detection in cuckoo bumblebees.

Other authors: Hamish Symington, Department of Plant Sciences, University of Cambridge; Lynn V. Dicks, Department of Zoology, University of Cambridge

18:00 – Mandela Fernandez-Grandon, Natural Resources Institute

Developing proboscis extension reflex assays for hoverflies to explore learning and memory

Hoverflies can play an important role in agriculture, providing pest regulation in their larval stages, and pollination services as adults.

Proboscis extension reflex has been used for decades to study bee learning and memory. Here we work on this applying this technique to hoverflies using the commercially available European migrant hoverfly, *Eupeodes corollae*. We identify compounds to which they are responsive. We go on to explore their potential for learning through classical conditioning, and the implications of pathogens which may hinder learning or caffeine which may enhance memory.

18:15 – Maria-Rosa Paiva, NOVA University of Lisbon (Online Talk)

New tools to meet industry needs: decoding *Coroebus undatus* (Coleoptera; Buprestidae) chemical ecology

The endemic Western Mediterranean *Quercus suber* L. grows under agro-silvopastoral systems, considered protected biodiversity hotspots. Cork oaks produce a bark layer that regenerates nine years after removal. Cork is a versatile sustainable material used since 3000 BC, present applications ranging from building construction to composite innovative materials for aero-spatial vehicles. Portugal produces ~ 50% of the world cork, yielding ~ €1.2B. Yet, the flathead cork borer can attack up to 40% of trees in a stand, causing losses of €9M/year. A collaborative research project with Amorim cork industry aims at decoding *C. undatus* chemical ecology and developing control methods based on semiochemicals. Virgin adults were caught in the field and their sexual behaviour and mating requirements studied, leading to infer that a

short-range pheromone is emitted by females. Volatiles emitted by both sexes and by host trees were analysed using Gas-chromatography-electroantennographic detection combined with Flame-Ionization-Detector (GC-EAD/FID); for volatile identification Gas-Chromatography Time-of-Flight Mass Spectrometry (GC-TOFMS) and Linear Retention Indices (LRI) were used. Behavioural tests showed adult responses to a wide range of semiochemicals that can be used in baits for *C. undatus* IPM programmes. Funding: Portuguese Foundation Science & Technology (FCT) grants UIDP/04085/2020, LA/P/0121/2020 UIDB/50006/2020 and LA/P/0008/2020, partner Amorim Florestal, SA.

Other authors: Sofia Branco, CENSE, NOVA School of Science and Technology, NOVA University of Lisbon, PT // Marco Gomes da Silva, LAQV, REQUIMTE, NOVA School of Science and Technology, NOVA University of Lisbon, PT // José P. Fernandes, Amorim Florestal SA, Longomel, 7400-402 Ponte de Sor, PT // Stefan Schütz, Department of Forest Zoology and Forest Conservation, Buesgen-Institute, Göttingen University, 37077 Göttingen, DE // Eduardo Mateus, CENSE, NOVA School of Science and Technology, NOVA University of Lisbon

Wednesday 11 September

- Conservation and diversity

Location: Lecture Theatre 1 (LT1)

Session Chair: Jane Hill

11:00 – Helen Barber-James, Ulster Museum, National Museums Northern Ireland

Diversity of Ephemeroptera, Plecoptera and Trichoptera species in Ireland, filling in the gaps

Ephemeroptera, Plecoptera and Trichoptera are widely recognised as important indicators of ecological health of freshwater ecosystems. Sound baseline species occurrence data is foundational and all-Ireland studies are currently building up stronger baseline data. Recent studies in the Ballinderry River catchment produced 14 species of Ephemeroptera, including Ephemera notata, endangered in the Irish Ephemeroptera IUCN Red List, and Rhithrogena germanica (IUCN vulnerable). Eleven species of stonefly included Nemurella pictetii and Leuctra nigra, both on the Northern Ireland Priority Species 2023. We have numerous first records for Rathlin Island, such as the caddis Diplectronea felix and Oecetis furva, both with few Irish records. The karst landscape of the Burren has very few surface streams or bodies of standing water, and numerous groundwater-fed lakes and turloughs. Fourteen species of Ephemeroptera were collected recently, including Kageronia fuscogrisea (near-threatened) and others of interest but needing adult material for confirmation. Seven species of Plecoptera have been recorded. Forty-six Trichoptera species included two new records for the Burren, and one possible new record for Ireland. Further ground truthing is needed for some species. To date, red listing has not been done for Irish Trichoptera, and this work contributes to the data needed for that.

Other authors: Hugh B. Feeley, Environmental Protection Agency, McCumiskey House, Richview, Clonskeagh Road, Dublin 14, D14 YR62, Ireland.

11:10 – James Bell, Keele University

Drivers and Repercussions of UK Insect Declines (DRUID): Artificial Neural Networks predict species distributions for a wide range of insect taxa.

We show how an artificial neural network (ANN), given some novel specific developments, can capture the relationship between species response traits and environmental drivers to predict the probability of occurrence and therefore individual species distributions. Using our ANN architecture, we present community-wide occupancy predictions at the species level for 1335 species across three decades in Great Britain. We combine independent models of nine insect groups (butterflies, macromoths, odonates,

carabids, orthoptera, bees, ladybirds, wasps and hoverflies) to take a high-level look at the key environmental drivers of insect occupancy, and to highlight the trait mediations underlying the resulting trends. We consider morphological (wing indices, body size etc), physiological (voltinism) and ecological (number of host plants and type etc) traits as well as proportions of different landcover types (urban, broadleaf woodland etc), weather (temperature, rain, wind etc) and environmental (altitude, slopes, aspect etc) covariates.

Across this wide taxonomic range, we identify common trends and drivers correlated with distributional shifts. Specifically, this approach highlights a well-known causes of biodiversity loss, notably urban sprawl, and also shows the key role of voltinism in mediating the effects of increasing temperatures on insect life cycles.

Other authors: Yoann Bourhis, Rothamsted Research, Rothamsted, UK, Chris Shortall, Rothamsted Research, Rothamsted, UK, Bill Kunin, School of Biology, University of Leeds, UK, Alice Milne, Rothamsted Research, Rothamsted, UK & the UK Citizen Scientists Community. .

11:30 – Dylan Carbone, UK Centre for Ecology and Hydrology

The role of Local Expertise in Enhancing Biodiversity Monitoring in Data-Sparse Regions

Biodiversity monitoring is evolving with the adoption of digital methods that capture large quantities of images and audio over an extensive monitoring period. Such methods often rely on species classification algorithms to derive occurrence data. However, in regions where data available for the training of algorithms is limited, their performance can be compromised. At the UK Centre for Ecology & Hydrology (UKCEH), we are developing the Automated Monitoring of Insects (AMI) system. The system pairs traditional moth monitoring techniques with species classifier algorithms and can identify thousands of moths nightly over months of deployment. AMI systems have been deployed in Panama, Costa Rica, and Thailand, where training data limited. To illustrate the challenges of AI classification in data-sparse regions, we compare the results of AMI system surveys with historical data, using metrics including the number of species classified by the algorithm versus the number of species recorded in the region. We describe how we are establishing networks of local taxonomists to validate classification algorithm predictions and show how the process of validation and re-training has improved performance. This study underscores the importance of local knowledge of wildlife in meeting the potential of AI-assisted classification methods in biodiversity monitoring.

Other authors: Tom August, UK Centre for Ecology and Hydrology; Jonas Beuchert, UK Centre for Ecology and Hydrology; Katriona Goldmann, TURING; Alba Gomez-Segura, UK Centre for Ecology and Hydrology; Jenna Louise Lawson, UK Centre for Ecology and Hydrology; Abhi Mandela Ravivarman, UK Centre for Ecology and Hydrology; Grace Skinner, UK Centre for Ecology and Hydrology; Aoife Cecilie Tetsche Sweeney, UK Centre for Ecology & Hydrology; Simon Teagle, UK Centre for Ecology and Hydrology; David Roy, UK Centre for Ecology and Hydrology; Easy RIDER (Real-time identification for ecological research and monitoring) group, UK Centre for Ecology & Hydrology, Smithsonian Tropical Research Institute, Insectarium de Montréal, Department of Ecoscience, Naturalis Biodiversity Center, Canadian National Collection of Insects, Arachnids, and Nematodes.

11:45 – Lindsey Barnes, University of Cambridge

Here be dragons: Mapping global dragonfly and damselfly exposure to major threats

Trends in insect biodiversity declines have been well studied, but the severity and relative impacts of underlying drivers are less certain, especially on a global scale. In 2021, the IUCN Red List of Threatened Species published the first comprehensive global assessment of an insect order, the Odonata. A relatively small but well-studied order, dragonflies and damselflies are affected by both aquatic and terrestrial-based threats, making them an effective case study for examining the distribution and severity of insect

threats. Using data from the IUCN Red List and the Global Insect Threat-Response Synthesis (GLiTRS) project, this study maps species richness and threat intensity to investigate the global distribution of six major threats to Odonata. We analysed the spatial intensity of these threats to identify geographic hotspots of threat exposure, determining locations where at-risk species and high threat intensity coincide. Our results highlight the variation of these hotspots across threats, showing recurring areas of high threat exposure in East Africa and knowledge gaps in species richness in the Western Hemisphere. As far as we know, this work is the first examination of insect threat exposure on a global scale, and demonstrates the utility of comprehensive Red List assessments for invertebrate taxa.

Other authors: Andrew Bladon, Charlie Outhwaite, Lynn Dicks

12:00 – Norashikin Fauzi, Universiti Malaysia Kelantan (Online Talk)

Bioindicators of Water Quality Under Threat: Assessing Microplastics Presence and Correlation with Functional Feeding Groups in Immature Aquatic Insects of EPT.

Microplastics (MPs) contamination has been identified in aquatic ecosystems worldwide. However, there remains a notable research gap concerning MP accumulation in living organisms, with limited investigation focused on immature aquatic insects in Malaysia. These insects play crucial roles as bioindicators of good water quality and primary contributors to the aquatic food chain, notably supporting fish populations. The study targeted immature aquatic insects, namely Ephemeroptera (mayflies), Plecoptera (stoneflies) and Trichoptera (caddisflies). In total, 16 types of microplastics were detected in these EPT taxa. The most common microplastic identified was poly (2,2,2-trifluoroethyl vinyl ether), followed by polyethylene glycol 200 dibenzoate. The study also identified a positive correlation between the functional feeding groups of immature aquatic insects and the abundance of microplastics. Collector-gatherer organisms, characterized by their predominant consumption of available food sources within the ecosystem, demonstrated an increased propensity for the accumulation of MPs. The ingestion and accumulation of MPs by immature aquatic insects may have detrimental impacts on their life histories, survival rates, growth rates and emergence patterns. Moreover, the presence of microplastics in these insect taxa could facilitate the transfer of microplastics to other aquatic organisms, potentially affecting higher trophic levels in the food chain and posing risks to overall ecosystem health.

Other authors: Nuramirah Mat Zain and Noor Syuhadah Subki

12:15 – Jamie Weir, University of Edinburgh

Does timing matter for caterpillars? - revisiting the paradigm of phenological mismatch

*The effects of climate change on seasonal timing ('phenology') can vary among species. Climate change therefore has the potential to disrupt the synchronised timings of species which interact temporally. Understanding the significance and pervasiveness of so-called 'phenological mismatch' has become a major topic in the ecological literature. The spring-time caterpillar fauna of temperate woodlands—particularly the winter moth *Operophtera brumata*—has become a model system for investigating the effects of mismatch among trophic levels. Conventional wisdom assumes that caterpillars hatching asynchronously with spring bud-burst on their host-plants will have low fitness, and that climate change is driving increasing mismatch between the two. Because of their significance in woodland food-webs as herbivores and prey, this could have serious, ecosystem-wide negative impacts. I will argue, however, that while synchrony is important, its severity may have been overstated. For example, a broad, flexible diet and the ability to withstand starvation could buffer caterpillar mismatch, and high phenotypic variation among offspring enables evolutionary bet-hedging in uncertain conditions. Furthermore, many of the buffering mechanisms we find in these caterpillars have analogues in other taxa such that populations may be more resilient to some of the effects of climate change than has previously been supposed.*

12:30 – Jeremy Thomas, University of Oxford

Successful restoration of the Endangered Large blue butterfly (*Phengaris/Maculinea arion*) to the Cotswolds following selection for advanced phenology in Somerset

All initial attempts to restore Phengaris arion direct from Sweden to restored sites in its former stronghold of the Cotswolds failed, owing to the adults emerging too late to oviposit on the flower-buds of its initial larval food, Wild Thyme. All eggs were laid on a few late-flowering plants growing in the coolest spots, the only parts of restorations where the main larval resource, Myrmica sabuleti ant colonies, were absent or too weak to support this brood parasite. In contrast, under the warmer climate of Somerset, the initial overlap of adults with suitable Thyme was ~50%, resulting in high survival and strong selection for early-emerging individuals. Thus after 10 generations, the peak of emergence had shifted about 12 days earlier, enabling all Thyme plants and most Myrmica sabuleti nests to be exploited. When this early-emerging phenotype was later translocated to the Cotswolds, adult emergence coincided closely with Thyme flower-bud production there and exactly matched emergence dates of the extinct UK race. Consequently, numbers in the Cotswolds already exceed the globally important populations of Somerset, and include one of the two largest known populations of this Endangered Species in Europe.

Other authors: David Simcox, Royal Entomological Society. Sarah Meredith, Royal Entomological Society

12:45 – Helen Taylor, Royal Zoological Society of Scotland

The forgotten masses: challenges and opportunities in invertebrate conservation translocations

Invertebrates are in crisis, and we need innovative solutions to assist those working on invertebrate conservation translocations. Unfortunately, our review of the IUCN Global Conservation Translocation Perspectives (GCTP) series shows that, of the 421 case studies recorded between 2008 and 2021, only 8% feature invertebrates. While the majority of translocation efforts (63%) focused on insects, two orders, Orthoptera and Lepidoptera, accounted for more than half of all invertebrate translocation case studies, leaving the vast majority of insects neglected by translocation science and practice.

The Royal Zoological Society of Scotland conservation department currently runs invertebrate breeding for translocation programmes for two insect, one snail, and one annelid species. Over the past five years, we have gathered experience and data on these species, and invertebrate conservation translocations in general. Here, we demonstrate that the major issues facing invertebrate translocation programmes are: a lack of life history data; a lack of veterinary expertise in invertebrate disease; the often short and multistage lives of many invertebrate species; the challenges of post-release monitoring and forming exit strategies for many invertebrate taxa; and the lack of funding for invertebrate work. We highlight potential methodological innovations to improve outcomes for some of our most crucial ecosystem players.

Other authors: Carl Allott, RZSS; Adam Button RZSS; Georgina Lindsay, RZSS; Helen Senn, RZSS

- **Genetics and genomics**

Location: Lecture Theatre 3 (LT3)

Session Chair: Cecilia Tamborindeguy

11:00 – Zhijian (Jake) Tu, Virginia Tech

Stably heritable sex conversions in an arboviral vector aedes aegypti: New insights and applications

Maleness is determined by the presence of a dominant male-determining locus (M locus) embedded in a homomorphic male-determining chromosome in the yellow fever mosquito Aedes aegypti. The M locus (~1.3 Mbp) contains the male-determining factor Nix, a myo-sex gene that encodes a myosin heavy chain

protein required for male flight. We previously showed conversion of genetic females to fertile but flightless males through ectopic expression of a *Nix*-transgene. Here, we report the establishments of multiple lines in which the *Nix* and *myo-sex* transgenes together were sufficient to convert genetic females into fertile and flying males that sustained a population that is completely devoid of the *M* locus. The *mm* males are competitive in the laboratory. Further genetic crosses indicate that the *m* locus is largely dispensable in males. We also established synthetic homomorphic sex chromosomes that provide the foundation for investigating the evolution of sex chromosomes and for genetic applications to control mosquito-borne infectious diseases.

Other authors: Azadeh Aryan, James Biedler, Yumin Qi, Chujia Chen, Melanie Hempel, Jiangtao Liang, Ben Potters, Austin Compton, Atashi Sharma, Karthikeyan Chandrasegaran, Clement Vinauger, Department of Biochemistry, Genetics Bioinformatics and Computational Biology Program, and the Fralin Life Sciences Institute, Virginia Tech, Blacksburg, VA 24061, USA

11:15 – Jay Goldberg, John Innes Centre

Towards understanding the genetic basis of polyphagy in the green peach aphid (*Myzus persicae*)

The green peach aphid, capable of feeding on hundreds of distantly related plant species, is one of the most generalist insect herbivores known and a significant global crop pest; however, the genetic basis of its remarkably generalized lifestyle remains unclear. Herein, we report a large transcriptomics study of aphids feeding on different host plants over time. We found over 500 significantly differentially expressed genes. Most of these genes were annotated as having various enzymatic functions, pointing towards metabolic plasticity as a significant driver of polyphagy in the green peach aphid (*Myzus persicae*).

Other authors: Matteo Gravino, Sam T Mugford, Saskia Hogenhout - Department of Crop Genetics, John Innes Centre, Norwich, UK

11:30 – Antonella Bacigalupo, University of Glasgow (Online Talk)

Whole genomes for Reduviidae (Hemiptera: Heteroptera): Comparative genomics between predatory and hematophagous vector species

Hemiptera is a speciose Order with >160 Families. The subfamily Triatominae (Reduviidae) is relevant as vectors of *Trypanosoma cruzi*, which causes Chagas disease. Only four reduviid whole genomes are available. We gathered samples from triatomine species across Latin America and an African predatory reduviid; extracted the DNA and performed long-read (ONT) and short-read (Illumina) sequencing, assembly and annotation, both homology and evidence-based. Orthogroups, ortholog genes and species tree were obtained using OrthoFinder.

We produced a whole genome assembly for the predatory reduviid *Platymeris biguttatus* (909 Mbp), and produced eight new triatomine whole genome assemblies, for *Belminus herreri* (1.1 Gbp), *Mepraia spinolai* (977.1 Mbp), *Panstrongylus geniculatus* (1.2 Gbp), *Psammolestes arthuri* (542.9 Mbp), *Rhodnius brethesi* (550.7 Mb), *Rhodnius ecuadoriensis* (583.8 Mbp), *Rhodnius prolixus* (583.9 Mbp) and *Triatoma infestans* (1.1 Gbp). All of them present high gene completeness in their assemblies and annotated proteins (BUSCOs >90%).

Harpactorini remains in a basal position within Reduviidae, followed by Reduviinae and Triatominae. We compared hematophagous triatomines with predatory reduviids, focusing on genes related to prey detection and digestion. The high number of shared orthologs with predatory reduviids might explain the facultative hemolymph feeding shown by several triatomine species.

This work was supported by: Wellcome [204820/Z/16/Z]; Lister/Bellahouston Fellowship; MR/Y001338/1; Agencia Nacional de Investigación y Desarrollo (ANID): Programa Becas-Doctorado Becas Chile 2019_72200391, FONDECYT_1221045, ANILLO-PIC2-ATE230025, MILENIO-ICN2021_044.

Other authors: Carolina Hernández & Juan David Ramírez, Universidad del Rosario, Colombia; Sebastián Pita Universidad de la República, Uruguay; Clara Gyhrs, University of Glasgow, UK; Bachar Cheaib, Universitätsklinikum Heidelberg, Germany; Anita G. Villacís, Pontificia Universidad Católica del Ecuador, Ecuador; Mario J. Grijalva, Ohio University, United States; Kirstyn Bruncker, University of Glasgow, UK; Carezza Botto-Mahan & Macarena A. Varas, Universidad de Chile, Chile; Miguel L. Allende, Universidad de Chile, Chile; Pedro E. Cattán, Universidad de Chile, Chile; Kathryn R. Elmer & Martin S. Llewellyn, University of Glasgow, UK

11:45 – Laura Campbell, Durham University
Genome evolution of plant farming ants

*Agriculture has been central to the rise of the human-dominated world, consequently it is of great interest to us when we observe other species engaging in farming-like behaviours. Such behaviour has evolved repeatedly as seen in many species including bacteria, snails, damselfish and sloths. While ants are most famous for farming fungi, they are also prolific plant-farmers having evolved this so-called “ant-garden” behaviour at least 15 times. How the origin of farming impacts ant genome evolution is unclear. Here, I use the genus *Philidris* (Dolichoderinae), which displays a spectrum of dependence – from facultative and generalist farmers to obligate and specialised – to trace the impact of farming on insect genomes. Using whole genome sequencing, I provide a strongly supported phylogeny based on over 2000 nuclear genes. Using this framework, I show that facultative agriculture has switched back and forth, while obligate agriculture evolved only once and was never lost. My work highlights various genomic drivers associated with the evolution of farming, using comparative techniques, such as gene family expansion and contraction analysis, tests for strength of selection and comparison of genome sizes.*

12:00 – Zedi Gao, University of Hertfordshire
Comparative Genomic and Functional Analysis of Olfactory Receptor Genes in *Psylliodes* Species to Determine Host Plant Choice

*Our research undertakes a comparative genomic analysis of olfactory receptor genes in *Psylliodes dulcamarae* and *Psylliodes chrysocephala* (cabbage stem flea beetle), the latter being an important pest affecting the Brassicaceae family, with particular detriment to oilseed rape (*Brassica napus* L.), an important source of vegetable oil and biofuel. Focusing on *P. dulcamarae*, a species closely related to *P. chrysocephala* but with distinct host preferences within the Solanaceae family, the research explores the genomic factors influencing host plant selection from an olfactory perspective. Through the *de novo* assembly of a high-quality genome for *P. dulcamarae* (1.08Gb size, 4.4Mb N50, 99.4% BUSCO score), this stage of the project establishes the foundation for exploring the evolutionary implications of olfactory receptor genes. A *k*-mer based genome survey demonstrated its efficacy for ensuring sample quality in genome sequencing of single individual small insects. By comparing the olfactory receptor gene repertoire between the two species, the study seeks to reveal olfactory gene candidates that could influence host specificity. These findings lay the groundwork for our next-stage study to validate the functional roles of key olfactory genes using Gas Chromatography-Olfactometry (GC-O) and behaviour assays.*

Other authors: Henrik Stotz, University of Hertfordshire; Benjamin Richard, Isara; Michael Schmuker, University of Hertfordshire

12:15 – Julien Devilliers, University of Leicester**Molecular evolution of vision: combining single-cell, bulk RNA-seq and microscopy to unravel the visual system in mosquitoes**

*Vision plays a key role in mosquitoes' innate preferences, including host choice. Opsins, photosensitive proteins express in the retina, show an intense diversification in mosquitoes with 10 copies on average compared to 4 in other insects. If opsin proteins are involved in other processes, the implication of these copies in mosquitoes' vision remains unclear. Here we combined bulk RNA-sequencing of the eye of 3 mosquito species (*Aedes aegypti*, *Anopheles gambiae* and *Toxorhynchites brevipalpis*) and single-cell transcriptomics of the whole head (*Anopheles gambiae* and *Aedes aegypti*) to understand (1) which copies are used in vision, (2) a potential sexual dimorphism in the visual process, and (3) what other cell types in the head are opsin genes expressed. Finally, using microscopy we targeted opsin genes expressed in the adult to observe the spatial pattern of expression of these genes across the retina in males and females of *Anopheles gambiae*. Our results suggest a strong interaction between vision and smell in mosquitoes. Opsin proteins involved in host choice are expressed in the eye but also in specific neurons, suggesting a new role for these proteins. We identify specific patterns of expression of opsin genes with strong variations among species.*

12:30 – Aschalew Lemma Demie, Wageningen University and Research**Insights into the genetic diversity and insecticide resistance of the Fall Armyworm (*Spodoptera frugiperda*) in Ethiopia**

*The fall armyworm (FAW), *Spodoptera frugiperda*, is a migratory and polyphagous noctuid moth native to the Americas and has become a significant invasive pest, severely affecting maize and other crops worldwide. However, the FAW's genetic diversity and insecticide resistance in Ethiopia remain understudied.*

To fill this knowledge gap, we analyzed 250 FAW larvae from Ethiopia using Cytochrome oxidase subunit I (COI) and Triosephosphate isomerase (Tpi) genetic markers. Additionally, 30 samples underwent whole-genome resequencing (WGS), and insecticide bioassays were conducted for five insecticides.

While a mixture of the rice (R) and corn (C) strains was found, our WGS analysis revealed low genetic diversity and neutral evolution in the Ethiopian FAW population. This suggests a recent introduction and rapid migration of the FAW into Ethiopia. Amino acid substitutions associated with organophosphate resistance were observed in the acetylcholinesterase-1 gene. Insecticide bioassays indicated low sensitivity to Lambda-cyhalothrin, while Indoxacarb emerged as the most effective among the tested chemicals.

Our findings support a common origin for the FAW invading Ethiopia and other Eastern regions, highlighting the potential risk of resistance alleles for other insecticide classes. Identifying prevalent resistance alleles and potential origins enables tailored pest management strategies for this invasive species in Ethiopia.

Other authors: 1. Bart A. Pannebakker, Wageningen University and Research (WUR), Laboratory of Genetics, Wageningen, the Netherlands; 2. Bas J. Zwaan, Wageningen University and Research (WUR), Laboratory of Genetics, Wageningen, the Netherlands; 3. Joost van den Heuvel, Wageningen University and Research (WUR), Laboratory of Genetics, Wageningen, the Netherlands; 4. Kasahun Tesfaye, Bio and Emerging Technology Institute (BETin), Addis Ababa, Ethiopia

12:45 – Matteo Gravino, John Innes Centre**Aphid effector interacts with AMSH deubiquitinases to suppress pattern-triggered immunity**

*Mp10, a chemosensory protein (CSP) from the potato-peach aphid *Myzus persicae*, is delivered to the plant cytoplasm during aphid feeding where it suppresses the plant Pattern Recognition Receptors (PRR)-*

triggered immunity (PTI), thus acting as local anaesthetic. CSPs are implicated in diverse processes in arthropods, yet the precise role of Mp10 in modulating plant signalling pathways remains incompletely understood. In this study, we have delved deeper into elucidating the signalling components involved in Mp10 activity in plants. We discovered that Mp10 interacts with plant AMSH deubiquitinases in yeast and in planta interaction assays. Interestingly, the interactions of Mp10 with AMSHs in plants are predominantly membrane-associated. Since AMSHs play essential roles in the trafficking and stabilization of plasma membrane proteins, we investigated effects of Mp10 on membrane-associated receptor kinases (RKs). Our results demonstrate that in the presence of plant AMSH2, Mp10 precipitates membrane-associated RKs. Furthermore, Mp10 destabilizes and induces the relocation of cell surface RKs to internal cell membranes, thus explaining the Mp10-mediated PTI suppression phenotype. This 'anaesthetic' ability of Mp10 and interactions with plant AMSHs are shared among orthologues of divergent hemipteran insects, suggesting its evolution over 250 million years ago, before the divergence of sap-feeding hemipteran herbivores.

Other authors: Sam T Mugford, John Innes Centre; Nathan Kreuter, John Innes Centre; Abbas Maqbool, John Innes Centre; Yeshveer Singh, John Innes Centre; Joshua Joyce, John Innes Centre; James Canham, John Innes Centre; Claire Drurey, John Innes Centre; Christine Wilson, John Innes Centre; Thomas C Mathers, John Innes Centre; Saskia A Hogenhout, John Innes Centre

- Vectors and pathogen transmission

Location: Lecture Theatre 1 (LT1)

Session Chair: Jake Tu

16:00 – Cecilia Tamborindeguy, Texas A&M University

Transmission of 'Candidatus Liberibacter solanacearum' by the potato psyllid *Bactericera cockerelli*

The potato psyllid, *Bactericera cockerelli*, is an insect pest native to the United States - Mexico border where it transmits haplotypes A and B of the bacterial pathogen 'Candidatus *Liberibacter solanacearum*' to solanaceous plants. We have previously shown differences in pathogenicity between these haplotypes, with haplotype B being more aggressive. To better understand the molecular events leading to the transmission of these two bacterial haplotypes, we used multi-pronged approaches involving transmission assays, analyses of the psyllid gut transcriptome in response to pathogen acquisition, and microscopy among others. The analyses were performed to compare the response of adult and nymph psyllids to each haplotype. Our results revealed differences in the responses induced in nymphs and adults as well as by each of the haplotypes. These findings can shed light on the epidemiology of the diseases associated with these pathogens and the potential for invasion into other regions.

Other authors: Junepyo Oh, Texas A&M University; Xioatian Tang, Texas A&M University; Brenda Leal, Texas A&M University; Tafim Hrithik, Texas A&M University

16:15 – Daniel Leybourne, The University of Liverpool

Genetic diversity in aphid populations drives successful transmission of barley yellow dwarf virus

The transmission efficiency of aphid-vectored plant viruses can differ between aphid 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. Here, we used multiple populations of two key aphid species that vector barley yellow dwarf virus, the grain aphid (*Sitobion avenae*) and the bird cherry-oat aphid (*Rhopalosiphum padi*) and examine how diversity in vector populations influences transmission efficiency of barley yellow dwarf virus PAV. We used Illumina sequencing to characterize genetic and endosymbiont variation in aphid populations and carried out BYDV-PAV transmission assays to identify links between intra-species diversity and virus transmission

efficiency. We observed limited variation in the transmission efficiency of *S. avenae*. However, for *R. padi*, we observed a range of transmission efficiencies and show that BYDV transmission efficiency is influenced by genetic diversity within the vector, identifying 542 single nucleotide polymorphisms that potentially contribute towards variable transmission efficiency. These results represent an important advancement in our understanding of the relationship between genetic diversity, vector–virus interactions, and virus transmission efficiency.

Other authors: Dr Mark Whitehead (The University of Liverpool); Dr Torsten Will (Julius Kühn-Institut)

16:30 – Enakshi Ghosh, Colorado State University (Online Talk)

Towards a 'disease-smart' assisted migration strategy for insects: leveraging immune priming to enhance population fitness and pathogen resistance

Insects are vital to ecosystems, providing services like pollination, pest control, and nutrient transfer, contributing significantly to the global economy. However, rapid environmental changes are causing significant declines in insect populations, termed the Insect Apocalypse. Major threats include habitat loss, fragmentation, and diseases, which confine populations to small, isolated pockets, increasing extinction risk. Genetic drift in small populations reduces genetic diversity, fitness, and adaptability. Conservation efforts have historically focused on vertebrates, necessitating urgent action for insects.

Our study explores assisted migration in genetic rescue by introducing immune-primed migrants to enhance fitness and pathogen resistance. We compared migrants for genetic diversity and immune-primed individuals. While genetic diversity alone improved fitness, it did not protect against pathogens. Immune-primed migrants showed significant disease resistance, increased survival, and higher offspring production. Delivering heat-killed bacteria to migrants enhanced transgenerational disease resistance, tripling survival rates compared to unprimed migrants. Although immunity-reproduction trade-offs were noted, hybrid vigor in target populations mitigated these effects. Our findings highlight the importance of disease-focused conservation strategies, particularly through immune priming of migrants to strengthen population resilience.

Other authors: Matt Wallace, Ruth Hufbauer

16:45 – Pedro Vale, University of Edinburgh (Online Talk)

IMD-mediated innate immune priming increases *Drosophila* survival and reduces pathogen transmission

*Invertebrates lack the immune machinery underlying vertebrate-like acquired immunity. However, in many insects past infection by the same pathogen can 'prime' the immune response, resulting in improved survival upon reinfection. Here, we investigated the mechanistic basis and epidemiological consequences of innate immune priming in the fruit fly *Drosophila melanogaster* when infected with the gram-negative bacterial pathogen *Providencia rettgeri*. We find that priming in response to *P. rettgeri* infection is a long-lasting and sexually dimorphic response. We further explore the epidemiological consequences of immune priming and find it has the potential to curtail pathogen transmission by reducing pathogen shedding and spread. The enhanced survival of individuals previously exposed to a non-lethal bacterial inoculum coincided with a transient decrease in bacterial loads, and we provide strong evidence that the effect of priming requires the IMD-responsive antimicrobial-peptide Diptericin-B in the fat body. Further, we show that while Diptericin B is the main effector of bacterial clearance, it is not sufficient for immune priming, which requires regulation of IMD by peptidoglycan recognition proteins. This work underscores the plasticity and complexity of invertebrate responses to infection, providing novel experimental evidence for the effects of innate immune priming on population-level epidemiological outcomes.*

17:00 – Simon Kiplimo, International Centre of Insect Physiology and Ecology**Unlocking the Secrets of Tsetse Flies: Exploring Olfaction and Innovations in Trypanosome Eradication**

Trypanosomiasis is a neglected tropical disease transmitted mainly by tsetse flies and remains a major problem of public health importance in Sub-Saharan Africa. We delve deep into how tsetse flies locate hosts and transmit the deadly trypanosomiasis disease. Despite the reported low numbers of infected tsetse flies in nature at 5%, the economic impact of trypanosomiasis is still a problem to the livestock sector. Infection of tsetse flies with trypanosomes impact their odor perception and subsequent host seeking and feeding behavior.

Understanding what promotes or inhibits parasite development, and transmission in a disease vector such as tsetse fly can result in effective control strategies. We are using RNA sequencing among other omics techniques to understand molecular and cellular basis driving tsetse fly-trypanosomes coevolutionary relationship which might reveal genes or pathways, a basis in designing novel trypanosomiasis blocking or control strategies.

Trypanosomes infected animals are more attractive to tsetse flies compared to trypanosome free livestock. Understanding tsetse fly olfactory changes during feeding and infection is crucial since these are two key stages in disease transmission. Use of targeted approach focusing on attracting and killing infected tsetse flies reducing the number of infected disease vectors in nature which is key in integrated vector management (IVM).

Other authors: Christopher Weldon, Merid Getahun, Daniel Masiga

17:15 – Sara Rooney, Liverpool School of Tropical Medicine**USUV and *Wolbachia***

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 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.*

*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.*

Other authors: Grant Hughes (Liverpool School of Tropical Medicine)

17:30 – Idalba Serrato, MIVEGEC, IRD

Multiple flaviviruses secrete a viral non-coding RNA in mosquito salivary vesicles to enhance saliva infectivity by reducing early IFN response

*West Nile (WNV) and Zika (ZIKV) viruses are endemic in tropical and subtropical regions and have recently appeared in temperate areas of Europe and North America. There are no effective treatments or preventive measures, and vector control strategies have limited success. Understanding the initial steps of bite-initiated transmission can lead to new interventions. Orthoflaviviruses produce a subgenomic flaviviral RNA (sfRNA) with immune inhibitory properties within mosquitoes. This study shows that multiple orthoflaviviruses secrete sfRNA in the saliva of various mosquito species to enhance transmission by inhibiting innate immunity. First, sfRNA was detected in saliva from *Culex quinquefasciatus* mosquitoes infected with WNV and *Aedes aegypti* mosquitoes infected with ZIKV. Oral infection is not required for salivary sfRNA secretion. Second, WNV and ZIKV salivary sfRNA were resistant to RNase degradation unless treated with detergent, indicating packaging inside a lipid-based vesicle. Third, infection of human cells with saliva containing different sfRNA concentrations showed increased infection, replicated by transfecting synthetic sfRNA. Fourth, sfRNA increases infection by reducing early innate immune response in a RIG-I independent manner, as shown by RNAseq analysis. Finally, we determined the effect of salivary sfRNA on transmission by using a mouse transmission model. This study identifies a conserved salivary transmission enhancer across orthoflaviviruses and elucidates its mechanism.*

Other authors: Idalba Serrato-Pomar, Quentin Narpon, Jim Zoladek, Felix Rey-Cadilhac, Solena Rossi, Rodolphe Hamel, Oleg Medianikov, Dorothée Missé, Sébastien Nisole, and Julien Pompon.

17:45 – Christida Estu Wastika, Liverpool School of Tropical Medicine

A single-sugar-fed modulates *Aedes aegypti* vectorial capacity

*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 zikense (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.

Other authors: Tara S. Joseph (Liverpool School of Tropical Medicine), Samiksha Venkatesan (Liverpool School of Tropical Medicine), Grant L. Hughes (Liverpool School of Tropical Medicine)

- Pollinators

Location: Lecture Theatre 3 (LT3)

Session Chair: Jane Stout

16:00 – Stella Shackel, University of Liverpool

Effectiveness of Nature-based Solutions for the diversity and abundance of insect pollinators in urban and sub-urban Liverpool

A variety of Nature-based Solutions were implemented in urban and sub-urban areas of Liverpool as part of the Horizon 2020 funded Urban GreenUP project (<https://www.urbangreenup.eu/>). This international project demonstrated how green interventions could be introduced into urbanised areas to provide multiple benefits, such as flood prevention, improving air and water quality, thermal cooling, carbon storage and sequestration, as well as biodiversity benefits in terms of habitat and foraging provision.

Insect populations are declining due to various factors including habitat loss and fragmentation. This research aimed to determine if the addition of extra habitats and availability of flowers would create more opportunities and a positive change in insect pollinator species populations.

Flower-Insect Timed count surveys determined numbers and types of flowers together with related pollinator visits. These surveys were based on the established UK Centre for Ecology and Hydrology and UK Pollinator Monitoring Scheme citizen science data methodology.

Overall, strong positive increases in pollinator abundances and diversity were observed. The resulting data provide an assessment of the importance and effectiveness of various green interventions and flower types in order to provide evidenced guidance for the improvement of biodiversity options within urban landscapes.

Other authors: Presenting on behalf of the partner organisations (Mersey Forest, Liverpool City Council and University of Liverpool) and the Urban GreenUP project

16:15 – Sarah Arnold, NIAB, East Malling

Insect ecosystem services in protected soft-fruit – influence of landscape composition

Landscape effects on pollinators and natural enemies are widely studied in various crops, but how landscape influences ecosystem services (e.g. pollination, pest management) in protected soft-fruit crops like strawberries has not been studied as closely.

We are surveying 18 soft-fruit farms across England to understand how the surrounding landscape influences the beneficial insect community in and around strawberry crops. Spring and summer surveys are recording bee pollinators (crop/margin) and parasitoids emerging from aphids. We are using DNA barcoding to support traditional taxonomic identification. Additionally, parallel analysis is considering landscape complexity in space and time.

*So far, we found that human judgements of landscape complexity are a reasonable proxy for more accurate analysis of landscape metrics. Our surveys found various common bumblebee and a range of solitary bee species (> 7 genera) present in and around the crop. There were a range of aphid species hosting various parasitoids, including hyperparasitoids and species not present in commercial biocontrol mixes. Notably, *Lysiphlebus testaceipes*, an invasive parasitoid with no previous UK records, was found at nearly half the sites across England. Our findings will provide insight into the relative importance of landscape and local factors in influencing beneficial insect communities in soft-fruit.*

Other authors: Francis Wamonje[1], Celine X Silva[1], Marco Bascietto[2], Luigi Orru'[3], Michelle T Fountain[1] 1NIAB East Malling, UK 2Research Centre for Engineering and Agro-Food Processing, CREA, Italy 3Research Centre for Genomics & Bioinformatics, CREA, Italy

16:30 – Cedric Maforimbo, University of Greenwich

More Bees for More Beans: Harnessing Pollination for Promoting Yield in Common Beans (HaPPY Beans)

Common beans (Phaseolus vulgaris L.), an important source of protein for millions in East Africa, rely on insect pollinators for 50% of their yields. Bees, the largest group of insect pollinators, are attracted to bean agri-systems by pollen resources provided by field margin plants. However, farmers in Northern Tanzania typically cut or cultivate their field margins. The impact of this practice on bee pollination of beans is unknown. To address this gap, bees visiting bean plants in fields subjected to varying field margin management were collected, identified and had pollen extracted from them. The same was done for margin plants. Bee and plant pollen samples were analysed using liquid chromatography-mass spectrometry (LC-MS) and the data was compared. Matches inferred a bee's visitation of a specific plant. The majority of bee pollinators of common beans were Apis mellifera whilst a minority came from the Xylocopa, Pachymelus, Macrogalea, Amegilla, Megachile, Acunomia, Crocispaspida, Trinomia, Ceratina, Gronocera, Lasioglossum, Lipotriches, Macronomia and Plebeina genera. LC-MS results suggest that Apis mellifera utilise the field margin plants Acalypha fruticosa and Harrisonia abyssinica whilst Xylocopa nigrita utilise Sesamum indicum and Harrisonia abyssinica. Seladonia jucunda bees utilise Tithonia diversifolia. Determination of field margin management effects is underway.

Other authors: Dr. Sarah E.J. Arnold (National Institute of Agricultural Botany East Malling Research, UK), Dr. Steven J. Harte (University of Greenwich, UK), Dr. Angela G. Mkindi (Nelson Mandela African Institution of Science and Technology, Tanzania) and Prof. Philip C. Stevenson (University of Greenwich/Royal Botanic Gardens, Kew, UK)

16:45 – Cassandra Uthoff, Helmholtz Centre for Environmental Research GmbH - UFZ

Impact of Acute Pesticide Exposure on Honeybee Worker (Apis mellifera) Behaviour and Gut-Brain Molecular Changes

Honeybee colonies, as superorganisms, depend on effective communication and coordination that can be disrupted by pesticides on multiple levels. To understand this, we studied the molecular changes in the gut and brain of workers, along with in-hive behaviour investigations. We found effects of worker behaviour after one-day exposure in an in-hive feeding experiment to SIVANTO® Prime (Flupyradifurone), Cantus® (Boscalid), and Click Pro® (Terbutylazine and Mesotrione) at environmentally relevant concentrations. SIVANTO® Prime significantly decreased colony maintenance behaviours, but increased allo-grooming shortly after exposure. Cantus® increased resting behaviour, whereas Click Pro® decreased brood care, mainly by reducing larval feeding. To unravel the mechanism by which pesticides affect the brain, we analysed the global proteome and amino acid and biogenic amine levels of exposed bees from the same colonies. We found significant changes in levels of neurotransmitters such as GABA and serotonin. Furthermore, a multi-omics approach was used to investigate structural and functional changes in the gut microbiome and lining to better understand the sub-lethal effects of pesticides on the microbiome-host relationship. Together, this gives us insight into structural and functional changes in the gut microbiome and brain function of worker bees pre- and post-exposure, while also examining behavioural phenotypes in nucleus colonies.

Other authors: Abdulrahim T. Alkassab, Julius Kühn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Bee Protection, Braunschweig, Germany; Beatrice Engelmann, Department of Molecular Toxicology, Helmholtz-Centre for Environmental Research – UFZ GmbH, Permoserstraße 15, 04318,

Leipzig, Germany; Ulrike Rolle-Kampczyk, Department of Molecular Toxicology, Helmholtz-Centre for Environmental Research – UFZ GmbH, Permoserstraße 15, 04318, Leipzig, Germany; Sven-Bastiaan Haange, Department of Molecular Toxicology, Helmholtz-Centre for Environmental Research – UFZ GmbH, Permoserstraße 15, 04318, Leipzig, Germany; Jens Pistorius, Julius Kühn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Bee Protection, Braunschweig, Germany; Andreas S. Thum, Leipzig University, Institute for Biology, 04103 Leipzig, Germany; Nico Jehmlich, Department of Molecular Toxicology, Helmholtz-Centre for Environmental Research – UFZ GmbH, Permoserstraße 15, 04318, Leipzig, Germany; Martin von Bergen, Department of Molecular Toxicology, Helmholtz-Centre for Environmental Research – UFZ GmbH, Permoserstraße 15, 04318, Leipzig, Germany

17:00 – Lydia Thompson, University College Dublin
Impacts of Non-Lethal Sampling Behaviour on Bumblebee Foraging

*Recent advances in genetic technology have allowed for the ability to sequence whole genomes with only a single leg sample from a bumblebee. The ability to sample non-lethally is incredibly important when it comes to working with rare species. This study investigates how non-lethal sampling behaviours including chilling, tarsal removal and full leg removal impact commercial *Bombus terrestris* ability to forage. Behaviours evaluated include how many flowers they visit, the length of time between flowers, and whether they start to forage at all again after treatment. This study will show how these sampling behaviours impact the foraging behaviour, which could have major implications for those working with whole genome sequencing especially individuals working with rare species who want to confirm they are not doing damage to the populations.*

Other authors: Moya Owens, Catriona Barry, Dara Stanley (University College Dublin)

17:15 – Morgan Morrison, Royal Holloway
Alarms Buzzing: Pathogen Spillover from Honeybees to Wild Bees European Protected Areas

The question of whether to keep honeybees in protected areas has been debated within conservation science. Advocates of this practice highlight the enhanced pollination services, improved local biodiversity and healthier honeybee colonies as benefits. Conversely, opponents argue that honeybee colonies could result in disease transmission to wild species and the negative impacts to wild bees this transmission could entail.

Despite this recognised risk and evidence of pathogen spillover from honeybees in agricultural areas, whether disease transmission occurs in protected areas has not been established. To address this pivotal yet unanswered question, we collected honeybees and wild bees from a protected calcareous grassland from four countries in Europe. Using these bees, we identified widespread pathogen spillover of a key virus from honeybees to wild bee species in protected areas. Furthermore, we have assessed the relevance of different factors potentially driving the likelihood or severity of pathogen spillover.

Given that emerging pathogens pose a significant threat to bee species today, our research provides key evidence for the transmission of honeybee pathogens in areas designated for the conservation of wild pollinator species across Europe. This research brings to light a new issue for land managers and, ultimately, provides evidence for policymakers in decision-making on honeybee colony management.

Other authors: Mark JF Brown (Royal Holloway)

17:30 – Christopher Noroozi, University of Sheffield
Developing and deploying a novel bluetooth tracking system to reconstruct bumblebee flight paths using probabilistic machine learning

Critical to conservation is understanding how animals use landscapes, but we know very little about how central place foragers such as bumblebees learn about & use their surroundings. Current landscape-scale insect tracking methods have limitations in accessibility and efficacy in cluttered environments. We are developing a novel method for landscape pollinator tracking using rotating Bluetooth low energy transmitters placed across a hive's foraging range.

We have designed small tags (>40mg) placed on a bee to receive packets from each transmitter containing their angle of rotation, time and ID. To keep the tag weight low its power source has a constrained capacity so sampling packets is done very infrequently. The unique 3 offset antenna design of the transmitters allows the probable bearing of the tag from the transmitter to be inferred from one sample via the difference between the signal strength of packets from each different antenna.

To model the bee's probable flight path from infrequent, probable bearings across time a Gaussian process is used, allowing for encoding of existing knowledge on flight behaviour and capturing the uncertainty of the predicted flight path. To perform inference of the non-gaussian likelihood of the flight path, doubly stochastic variational inference is used.

Other authors: Michael Smith (University of Sheffield)

17:45 – Sarah Scott, University of Cambridge

Potential exposure routes and bioaccumulation of trace metals in social bees

*Metal pollution is a byproduct of many industrial and urbanization processes and is ubiquitous across the landscape. Bees are exposed to metals while foraging, yet exact exposure routes remain unknown. We identified how metal content and concentration varies across Cambridgeshire, UK, a patchy, metal contaminated landscape and between *Bombus terrestris* and *Apis mellifera* species. We used Inductively Coupled Plasma- Mass Spectroscopy to sample metal concentrations within bumblebee and honeybee adults, bee collected pollen, and nectar from pollinator forage plants. The results of this study will be used to identify the relationship between soil metal contamination, floral resources, and metal bioaccumulation within bees, and identify if honey bees serve as a proxy for metal exposure in other social bee species. The results will be compared against current lethal metal exposure limits for bees to identify landscape areas that pose elevated risk for bees. Additionally, the data will be used to inform best management practices in polluted areas targeted for habitat establishment, and to contribute to understanding the quality of urban lands for bee populations.*

Thursday 12 September

- Vector surveillance and control

Location: Lecture Theatre 1 (LT1)

Session Chair: Lisa Reimer

09:45 – Luigi Sedda, Lancaster University

Optimising mosquito surveillance: Adaptive Designs Tested in Mozambique and Ghana

For an entomological survey to provide unbiased information on species occurrence and abundance while detecting the spatio-temporal relationships between species and environment, a degree of spatial spread of sample locations including areas where these relationships are weaker is required. In absence of prior knowledge, a spatially balanced design provides more uniform coverage over the study area than random sampling. However, when previous data are available sampling can be based on a target function. In this

case adaptive designs allow selection of locations based on a specific criteria.

This talk describes the adaptive sampling framework and its components used in two entomological surveillance trials respectively in Ghana and Mozambique under the project 'Equipping countries for evidence-based malaria intervention strategies' (funded by Bill & Melinda Gates Foundation, INV-024346). We evaluated the effect of spatial adaptive sampling designs in terms of fit of the models and robustness in their estimations. In both countries uncertainty around the estimated means is lower in post-adaptive than in the pre-adaptive phase, although in general the model's goodness-of-fit is still not optimal. This is a very important result since provides support and operational guidance on the use of adaptive sampling and the deployment of new surveillance sites.

10:00 – Sylvester Coleman, Liverpool School of Tropical Medicine

Mosquito Dynamics in beneficiary Communities of the Shire Valley Transformation Project (SVTP) in Chikwawa District, southern Malawi: Insights and Implications for Vector Control

The Shire Valley Transformation Project (SVTP), sponsored by the World Bank, is transforming agriculture in southern Malawi with a 40,000-hectare irrigation scheme. While promising socioeconomic benefits, it may also reshape disease vector ecologies. Recognizing this, we began a baseline study in July 2023 to understand mosquito population dynamics before the irrigation canals are completed. This data is crucial for designing pre-emptive control strategies in the SVTP catchment area.

*Preliminary results based on 1,493 trap nights from three sentinel sites using CDC light traps and Prokopack aspiration identified a dominance of *Anopheles gambiae* s.l. (941 out of 1,089 mosquitoes; 86%), with significant presence of *An. pretoriensis* (122; 12%) and *An. funestus* s.l. (2%).*

Variations in mosquito biting rates and resting densities suggests that proximity to breeding sites and livestock availability influences mosquito distribution and behavior. Residential design, like eaves presence, influences vector entry and resting, offering household-level control opportunities.

The ongoing study will guide SVTP's development to incorporate vector control measures, ensuring agricultural progress aligns with health security. Our findings will form the basis for strategic mosquito-borne disease control, promoting sustainable development that harmonizes agricultural and public health goals.

Other authors: Rex B. Mbewe-MLW, Olivia Wetherill-LSTM, Eggrey Kambewa-LSTM, Christopher Jones-LSTM

10:15 – Elsie Isiye, South East Technological University (SETU)

A DNA-based approach to surveillance of *Culicoides* vectors Bluetongue (BTV) and Schmallenberg (SBV) viruses in Ireland.

**Culicoides* biting midges serve as vectors for Bluetongue (BTV) and Schmallenberg (SBV) viruses, which impact the well-being and productivity of livestock. Outbreaks of these viruses highlight the urgent need for precise and efficient vector surveillance. The aim of this work is to conduct to develop species-specific qPCR assays for the rapid detection of *Culicoides* vectors in pooled samples.*

*Adult *Culicoides* were captured using OVI traps at 12 livestock farm locations in Ireland from May 2022 to December 2023. Individual specimens were barcoded using PCR amplification and sequencing of cytochrome oxidase subunit 1 (CO1) and internal transcribed spacer (ITS) gene regions. qPCR tests were designed to discern specific *Culicoides* vectors.*

A total of 354 midges belonging to 12 species were barcoded from six sites (Co. Dublin, Co. Waterford, Co. Galway, Co. Laois, Co. Kilkenny, and Co. Cork).

qPCR assays were designed to detect vectors including C. obsoletus, C. scoticus, C. chiopterus, C. dewulfi, C. pulicaris, C. lupicaris, C. punctatus, and a specific assay for detecting C. impunctatus in pools of 100 midges.

The molecular techniques established in this research provide a valuable tool for the efficient surveillance of Culicoides vectors essential for preventing and managing the transmission of viruses to livestock.

Other authors: Elsie Isiye 1, Angela Valcarcel 2, Thomas Curran 1, Annetta Zintl 2, David O'Neill 1, Theo De Waal 2, Aidan O'Hanlon 4, James O'Shaughnessy 5, Gerald Barry 2, Nicole Keohane Mc Carthy 1, Audrey Jenkinson 3, Akke Vellinga 2, Alan Johnson 3, Damien Barrett 3, Tim Ashmore 6, Bruce Thompson 7, Nick Berry 7 and Denise O'Meara 1 1. South East Technological University, Waterford, Ireland 2. University College Dublin, Ireland 3. Department of Agriculture, Food and the Marine - Government of Ireland 4. National Museum of Ireland-Natural History, Merrion Square West, Dublin 2, Co., Dublin, Ireland 5. Central Veterinary Research Laboratory, Backweston Laboratory Campus, Celbridge, Co. Kildare 6. Teagasc, Kildalton Agricultural College, Ireland 7. Camcloon Dairy Limited, Ireland

10:30 – Riona Walsh, University of Galway

Predicting Ixodes ricinus abundance in the west of Ireland.

Lyme borreliosis (LB) is a vector borne zoonotic disease caused by bacteria of the Borrelia burgorferi sl. complex. LB is the most prevalent vector-borne disease in Europe, and Ixodes ricinus is the main vector in Europe. The pathogen is transmitted to humans via the bite of an infected tick. Nymphal tick abundance in an area is an important predictor of tick bite risk in the area, and some studies suggest that tick abundance is also an important predictor of LB incidence in an area. As the genospecies of the pathogen, the species of the tick vector, the availability of wildlife host species, and the abiotic and habitat factors affecting the tick vector differ between regions where LB is endemic, factors predicting tick bite and LB often differ between regions. Ireland represents a region of the range of I. ricinus in which the climate, habitat structures, and availability of vertebrate hosts differs to other regions. The current study presents data collected over the course of three years, in tick habitats in Ireland, answering questions on how abiotic factors, habitat factors, and vertebrate host dynamics may be used to predict nymphal tick abundance in sites in the west of Ireland.

Other authors: Mike Gormally, University of Galway; Christopher Williams, Liverpool John Moores University; Caitriona Carlin, University of Galway.

10:45 – Lesley Bell-Sakyi, University of Liverpool

Insect cell lines: research tools from the Tick Cell Biobank

Continuous insect cell lines are valuable tools for many aspects of research on insect biology and insect-borne pathogens of medical, veterinary and agricultural importance. The Tick Cell Biobank, originally founded as a repository and source of tick cell lines (which are particularly challenging to generate and maintain), has recently expanded into generation, storage and supply of insect cell lines. We focus particularly on developing cell lines from neglected insect vectors and the more challenging beneficial insects such as honey bees and ladybirds. In addition to tick cells, we maintain cell lines derived from mosquitoes, biting midges, sand flies, tsetse flies, fruit flies, honey bees and triatomine bugs (most generated in-house). We supply cells and training in their maintenance to institutes worldwide; our Outposts in Malaysia and Brazil facilitate access to these valuable research tools and technologies for lower- and middle-income country scientists. We also maintain a growing collection of obligate intracellular arthropod-borne bacteria including multiple strains of Wolbachia. For added value, we generate nuclear and mitochondrial genomes, transcriptomes and proteomes from selected insect and tick cell lines, and screen all lines for symbiotic or contaminating bacteria. Cell lines are distributed subject to Material Transfer Agreements; for

for further information, contact tickcellbiobankenquiries@liverpool.ac.uk.

Other authors: Catherine Hartley, Jing Jing Khoo, Youseuf Suliman, Alistair Darby and Benjamin Makepeace, University of Liverpool

11:00 – Martyn Wood, IMBB FORTH

Discovery and screening of novel insecticidal bacteria, their sonicates and their solvent-extracts against *Culex pipiens molestus* larvae.

*Mosquito transmitted disease kills over 700,000 people each year. Availability and efficacy of traditional insecticides continues to decline, driving the search for environmentally friendly alternatives. Disparate habitats in Crete were surveyed extensively and 797 live bacterial isolates were coarsely screened against 3rd and 4th instar *Culex pipiens molestus* larvae, of which 39 caused LT100 values <3 days. These 39 were assessed intensively using 10 mL of sonicated liquid cultures in 90 mL distilled water containing 10 *Cx. pipiens* larvae (n = 90). Liquid cultures of the 39 were also extracted into hexane and ethyl acetate and re-assayed in parallel to gain insights into the relevant metabolite characteristics. Several bacterial isolates showed potent larvicidal activity, with four key species - belonging to the genera *Pseudomonas* and *Chryseobacterium* - demonstrating significant potential for biopesticide development, achieving LT100 in as little as 24 hours. Solvent extract assays showed that non-polar extractions contained the majority of larvicidal actives, but not for all isolates, while pupation delay was found to be common in polar extracts. Data show that several species of terrestrial bacteria from the island of Crete, alongside their specific metabolites, are highly promising candidates for future development as novel biopesticidal agents.*

Other authors: Juan J. Silva (IMBB FORTH), Katerina Kanelli (IMBB FORTH, University of Crete), Joel Couceiro (IMBB FORTH), Andronikos Papadopoulos (IMBB FORTH, University of Crete), Maria Mazavli (IMBB FORTH, University of Crete), Stefanos Mastis (IMBB FORTH, University of Crete), Inga Sidren-Kamos (IMBB FORTH), John Vontas (IMBB FORTH, Agricultural University of Athens), George Dimopoulos (IMBB FORTH, John Hopkins University)

11:15 – Vishaal Dhokiya, Liverpool School of Tropical Medicine

Towards the Use of Novel High Density Anopheles-Specific *Wolbachia* Strains for Anopheles Vector Control

*The use of the widespread bacterial endosymbiont *Wolbachia* as a novel vector control strategy has been highly successful, demonstrating a significant impact on disease prevalence in field trials targeting *Aedes* mosquitoes. Long thought to be absent from natural populations of *Anopheles* mosquitoes, the highly effective malaria vectors, *Wolbachia* based interventions have proven challenging. Our recent discovery of natural high density *Wolbachia* strains in populations of *Anopheles moucheti* and *Anopheles demeilloni* has reinvigorated efforts to create transinfections in medically relevant *Anopheles* mosquitoes. Here we present our work demonstrating high density maternally transmitted strains of *Wolbachia* in *Anopheles moucheti* and *Anopheles demeilloni* from sub-Saharan Africa, providing concrete evidence for resident *Wolbachia* strains in this genera. In addition, we report on our recent endeavours generating a tractable source of these novel *Wolbachia* strains for further experiments. We discuss our findings in the context of developing novel *Wolbachia*-based control approaches in *Anopheles* to reduce the burden of malaria.*

Other authors: Janvier Bandibabone, Centre de Recherche en Sciences Naturelles (CRSN/LWIRO), Maurice Marcel Sandeu, Centre for Research in Infectious Diseases (CRID), Christophe Antonio Nkondjio, Organisation de Coordination pour la lutte contre les Endémies en Afrique Centrale (OCEAC), Thomas Walker, The University of Warwick, Grant Hughes, Liverpool School of Tropical Medicine

11:30 – Walter Leal, University of California-Davis
In my hands, DEET performs better than Picaridin

*Insect repellents are crucial to integrated vector management (IVM) as the first line of defense against the transmission of vector-borne diseases. Travelers and people living in endemic areas of malaria, dengue, encephalitis, and other vector-borne diseases often use repellents as a preventive measure. During arbovirus outbreaks, authorities recommend regularly using the oldest synthetic repellent in the market, DEET, or a second-generation synthetic alternative to DEET, Picaridin. DEET is more affordable than Picaridin, which, in turn, is more pleasant to the skin and less reactive with plastic in watchbands and eyeglass frames than DEET. But about protection? Which of these two repellents is more effective in repelling mosquitoes? Using a hand-in-cage assay modified from the standard WHO protocol, we compared these repellents against mosquitoes, including *Aedes (Stegomyia) aegypti* and *Aedes (Stegomyia) albopictus*. Initially, we prepared our formulations of DEET and Picaridin at 20%. Then, we compared 20% DEET and 20% Picaridin from the same supplier. The surprising results suggest that DEET remains the “gold standard” of insect repellents.*

We acknowledge funding support from the Pacific Southwest Center of Excellence for Vector-Borne Diseases, funded by the U.S. Centers for Disease Control and Prevention (agreement # 1U01CK00649-02).

Other authors: Sunny An

- Monitoring and controlling pests

Location: Lecture Theatre 3 (LT3)

Session Chair: Jordan Cuff

09:45 – Katharine Preedy, Biomathematics and Statistics Scotland

How do diverse vector life-history traits and transmission rates interact to affect BYDV infection in cereal crops?

*Crop infections by Barley Yellow Dwarf Viruses (BYDVs) can have a significant impact on cereal yields. Cereal aphids, including *Rhopalosiphum padi* and *Sitobion avenae*, are the primary vectors of BYDV in the UK and Europe. These vector species have contrasting life-histories, behavioural patterns and disease transmission rates which potentially influence the efficiency with which they transmit BYDV. There are multiple strains of BYDV, with BYDV-PAV and BYDV-MAV being of greatest agricultural concern in Europe. The transmission efficiency of different BYDV strains varies between vector species; *R. padi* is a more efficient vector of BYDV-PAV, and *S. avenae* a more efficient vector of BYDV-MAV. Recently, it has been shown that diversity within vector species (i.e., genetic variation in aphid populations) can influence BYDV transmission efficiency. However, the extent to which BYDV transmission efficiency and other life history traits in vector populations (e.g. development time, reproductive output, flight patterns) interact to influence virus incidence and spread across agricultural fields is unknown. Here, we use mathematical models to synthesise current monitoring and experimental data to explore the impact of the between- and within-species differences on BYDV spread in summer and winter cereal crops.*

Other authors: Daniel Leybourne, University of Liverpool; Lawrence Bramham, Rothamsted Research; Maximilian Schughart, Teagasc; Louise McNamara, Teagasc

10:00 – Sophie-Leigh Claassen, University of Johannesburg**A review on ecology, alternative methods of control and distribution of the brown locust, *Locustana pardalina* Walker 1870**

*The brown locust, *Locustana pardalina* Walker 1870, is considered a national pest in South Africa, posing a threat to the livelihoods of rural and farming communities as well as the country's food security. The review has compiled information on the locusts' lifecycle, behaviour, feeding preferences, and predators. The current method of control in South Africa involves chemical control, which is costly and has negative ecological impacts. Alternative and less ecologically harmful methods were reviewed, and physical traps were highlighted. Designs for traps using lights, pitfalls and physical barriers were proposed. The distribution of the locust is presented in maps created in QGIS, made using proxy location data, with the influencing weather factors presented in a similar format to demonstrate the relationship between the distribution and weather. QGIS and MaxEnt were used to produce niche-modelled predictions of future distribution based on varying climate change severities.*

Other authors: Supervisor: Professor J. Francois Durand, Department of Zoology, University of Johannesburg

10:15 – Jack Perry, Teagasc & Harper Adams University**Comparing aphid monitoring tools for BYDV, what we've learnt after year one**

Aphids reduce grain yield and quality in cereal crops via direct feeding and vectoring viruses. The most economically important aphid vectored virus in cereals is barley yellow dwarf virus (BYDV), which can cause up to 80% yield losses. Managing aphids is becoming increasingly challenging due to (i) reduced insecticide availability, (ii) insecticide resistance, (ii) lack of robust thresholds and (iv) climate change. Navigating these challenges requires robust monitoring programmes that account for both the spatial and temporal distribution of aphids.

We have established a multi-year national aphid-trapping programme in Ireland, to validate the use of different monitoring tools (suction tower network, in-field water traps and in-field aphid searches) to forecast aphid populations and BYDV incidences. All aphids captured with the monitoring tools are tested for BYDV, alongside leaf samples collected from barley crops. The first year of this study has been completed and includes data from three suction towers and 18 winter barley crops across Ireland. Our results from year one provide initial insights into the species of aphids and incidence of BYDV-infected aphids present in Ireland using different monitoring tools and how this links to BYDV incidence with barley crops.

Other authors: Liam Sheppard, Teagasc; Dr. Joe Roberts, Harper Adams; Dr. Tom Pope, Harper Adams; Dr. Stephen Byrne, Teagasc; Dr. Louise McNamara

10:30 – Carolyn Mitchell, James Hutton Institute**Getting to grips with a new pest: choosing crop varieties for blueberry aphid**

*Over recent years, Scottish growers have reported increased abundance of aphids on blueberry crops. The blueberry aphid is native to North America but has been introduced to Europe, with the first UK sighting recorded in the 1970s. Blueberry aphid is thought to form a species complex containing *Ericaphis scammelli* and *Ericaphis fimbriata*. The main host is *Vaccinium* species (blueberry) with blueberry production in the UK worth £72 million. The main concern about the increasing abundance of this aphid is that it vectors the Blueberry scorch virus. While the virus has not yet been reported in the UK, infections can remain latent in the plant for 2 years and cause serious declines in yield, ultimately leading to plant death. To future-proof the blueberry sector against potential virus appearance, we have investigated varietal differences in aphid infestation. Insect surveys were carried out in 2019 and 2023 comparing nine*

blueberry varieties grown within a tunnel and open field. The results reveal differences in variety susceptibility to the blueberry aphid and differences in natural enemy abundance between tunnel and open field conditions. We will indicate how these findings can be used to reduce aphid pest problems in blueberry production.

Other authors: Gaynor Malloch, James Hutton Institute, Ailsa Smith, James Hutton Institute, Zsuzsanna Revesz, James Hutton Institute and Alison Karley, James Hutton Institute

10:45 – Muhammad Saeed, University of Swabi

Assessment of Antixenosis Properties and Toxicity of Selected Indigenous Plant Extracts against *Lasioderma Serricorne* (Fab.)

Lasioderma serricorne (F) is a perilous pest of stored goods. The utilization of botanical extracts is considered the most secure and eco-friendly approach for managing this insect/pest. This research investigated the impact of seven different plant species on *L. serricorne*, focused on factors such as fecundity, developmental time from egg to adult, growth index, incubation period, adult emergence, weight loss, repellency, as well as contact and fumigant toxicity. The *L. serricorne* showed significantly lowest fecundity (0.673 ± 0.106), lowest growth index (-0.846 ± 0.431), longest incubation duration (mean 1.785 ± 0.004) on *Parthenium hysterophorus*, whereas *L. serricorne* had the highest fecundity (2.371 ± 0.002), highest growth index (1.376 ± 0.052), and shortest incubation duration (1.500 ± 0.012) on *Nigella sativa*. At larval stage, essential oils (EOs) of some plants exhibited higher repellent effect on cigarette beetle after 48 hours for example, *P. hysterophorus* (RD50 = 2.406%), *D. vescosa* (RD50 = 1.649%), and *V. jatmansii* (RD50 = 1.137%). The maximum contact toxicity at the larval stage of beetle was observed on *P. hysterophorus* after 24h exposure (LD50 = 3.762 μ l/ml insect), followed by *D. vescosa* and *V. jatmansii* (LD50 = 3.551 and 2.678, respectively). *P. hysterophorus* provided the highest fumigant toxicity to beetle after 24h exposure (LC50 = 4.262 μ l/ml air), followed by *D. vescosa* and *V. jatmansii* (LC50 = 3.669; 3.274, respectively). The cigarette beetle was least hazardous to *N. sativa*, with just 1.295 mortality noted at 50% of the utilized concentration (LC50). The *P. hysterophorus* essential oil exhibits the best repellency contact and fumigation toxicity against *L. serricorne* larvae and adults, supporting the potential for commercial use of plant essential oils, as environmentally friendly insect control agents.

Other authors: Abdul Latif, University of Swabi; Abid Farid, The University of Haripur; Mukhtar Alam, University of Swabi; Hidayat Ullah, University of Swabi; Fazal Ullah, University of Swabi

11:00 – Arthy Surendran, SRUC - Scotland's Rural College

Unseen Threat in Peat-Free Growing Media: Sciarid Flies

Currently the UK horticulture is moving toward peat-free, due to the various environmental issues with the peat extraction. Various peat alternatives such as wood chips, bark, coir etc. have been identified and substituted peat in the plant growing media. One issue that has been noted anecdotally, is the increase in the prevalence of sciarid fly (Diptera; Sciaridae) infestations, particularly under protected environments.

Hence Scotland Rural University College with Royal Botanical Garden, Edinburgh is currently surveying various stakeholders across the UK and reviewing the available evidence to explore the links between the peat-free growing media and the emergence of sciarid fly as a pest in the UK environment. The ongoing study reveals:

- Most of the stakeholders identified an increase in sciarid fly populations in the peat-free growing media
- 263 species of sciarid fly were identified in the British Isles some of them are identified as economically important pests around the world. Sciarid flies are direct and indirect pests to horticulture crops.

As a part of this study, we have identified a knowledge gap, recommendations and integrated pest management practices (IPM) to control this emerging economically important pest.

Other authors: Matt Elliot, Royal Botanical Garden, Edinburgh.

11:15 – Simranjit Kaur, Teagasc

Exploring role of fungal endophytes for aphid management and host growth functions

*Entomopathogenic fungi (EPF) are potential biological control tools to develop an integrated pest management (IPM) approach to manage plant pests, such as aphids. The endophytic EPF strains are known for their potential to confer plant protection and growth functions. This work aims to discover EPF candidates with the potential for effective management of aphids and Barley Yellow Dwarf Virus (BYDV) virus in barley crops. In this study, sixteen multi-genera endophytic fungal isolates were tested for aphid management along with one commercial biocontrol, *Beauveria bassiana*. In this experiment, the adult aphids were exposed to endophytic fungal spores and then transferred to fresh plants. The selected endophytes from the screening experiment were further used to inoculate the plants to test their indirect biocontrol efficacy in managing aphids. The results have shown up to a two-fold reduction in the total number of aphids elicited by different endophytes. Interestingly, more than 30% of the endophytes demonstrated the potential to suppress aphids. The plants inoculated with, particularly two endophytes, *Penicillium sp.* and *Beauveria sp.*, showed a significant reduction in the total number of aphids as compared to the control and also improved root growth and biomass. Field trials are underway to test the biocontrol impact of endophytes in controlling BYDV-aphids. This study investigates whether these endophytes could have future applications in biological control and growth-promoting agents for IPM and sustainable agriculture practices.*

Other authors: Simranjit Kaur¹, Steven Kildea¹, Diego Bianchi², Maximilian Schughart¹, Trevor R. Hodgkinson² and Louise McNamara¹ ¹Teagasc, Crops Research Centre, Carlow, Ireland, ²School of Natural Sciences, Trinity College Dublin, Dublin 2, Ireland

11:30 – Helen Hesketh, UK Centre for Ecology & Hydrology

Applying Ecotoxicology Principles to Understand mixed Stressor Interactions to improve Biocontrol of insect pests

*Insect pathogens play a crucial role in the microbial control of insect pests in agriculture and horticulture, forming a key component of integrated pest management (IPM) programmes aimed at sustainable food production and environmental protection. IPM combines multiple control methods to enhance reliability and resilience of pest control strategies. The co-application of chemical and pathogen mixtures presents promising opportunities, but understanding interactions between insect pathogens and other stressors, and predicting their combined effects based on mechanisms of action remains a challenge in insect pathology. Here, we apply an ecotoxicological mixtures model (MIXTox) to describe interactions between pathogens and chemicals and their effects on insect hosts. Existing methods generally determine overall patterns of additivity, synergism, or antagonism but the MIXTox model can be used to assess more intricate response patterns, such as time or dose dependency. We discuss the use of this model for understanding outcomes of mixture applications of microbials and chemicals for control of Lepidoptera and whitefly plant pests. Additionally, we explore extending the model to understand interactions between insect pathogens and other stressors in mass-reared yellow mealworms, *Tenebrio molitor*. Through this research, we highlight important considerations for advancing the understanding of multiple stressors and their impact on insects.*

Other authors: Eleanor Dearlove, RSK ADAS Ltd.; Pascal Herren, UKCEH, Claus Svendsen, UKCEH

- Poster presentations

Behavioural and evolutionary

P1 – Marta Potrzebska, University of Silesia in Katowice

Is a hemimetabolous insect a useful model for studying effects of high-sugar diet and tryptophan pathway mutation? House cricket, *A. domesticus* as an alternative to the fruit fly, *D. melanogaster*.

*High - Sugar Diet (HSD) can contribute to the onset of various diseases, including type II diabetes. The high evolutionary conservativeness of carbohydrate metabolism systems in the animal kingdom allows it to be investigated using non-human species. The most popular invertebrate model for diabetes research is fruit fly, *Drosophila melanogaster*. It plays a key role in genetic, developmental, and physiological research. Research related to the effects of HSD at various levels of development and using multiple research models opens new paths in understanding the problem of the impact of metabolic disorders. As part of the research project, it was decided to check whether the house cricket, *Acheta domesticus*, could be used as an alternative invertebrate organism for research into diseases caused by HSD. Compared to the fly, this insect is characterized by incomplete development, which makes it more developmentally similar to mammals. Research indicates that carbohydrate metabolism regulation affects the tryptophan metabolism pathway. White-eyed fruit flies with altered eye color (resulting directly from disruptions in this pathway) are also used as a model. As part of the research project, both wild phenotype crickets and white-eyed mutants were used to compare the described research models.*

Other authors: Jacek Francikowski, Monika Tarnawska, Agnieszka Babczyńska; University of Silesia in Katowice

P2 – Matthew Sparks, Swansea University

How do Urban flies view their environment?

*Filth flies are a strong mechanical vector for over 100 pathogens and therefore of key importance to human and animal health. Urban environments are a preferred habitat due to abundant feeding and oviposition opportunities and warm temperatures. My poster explores current understanding of the visual ecology of filth flies and what remains to be discovered about their visually guided behaviour in urban environments in terms of illumination, object detection and recognition, and interaction with polarised light. I then demonstrate my work that uses visible, ultraviolet and polarisation panoramic photography, image processing and visual modelling of filth fly vision to investigate how flies perceive urban environments. Analysis of resulting images representing a 'fly's eye view' can be used to understand the information content and structure of urban environments to flies. Analyses incorporate differences in the visual performance of filth flies including the common house fly, *Musca domestica* and urban Blowflies, *Calliphoridae*. Findings will allow for better understanding of flies' visually-guided behaviour in urban environments and potential for manipulation of environmental cues to influence behaviour and limit the spread of pathogens.*

Other authors: Matt Green, Rentokil Initial. Tariq Butt, Swansea University. William Allen, Swansea University

Conservation and diversity

P3 – Imogen Cockwell, Swansea University

The role of spatial scale in structuring aquatic invertebrate assemblages and connectivity across peatland pools

Castell Nos Habitat Restoration Area, located near Maerdy, South Wales, is a Lost Peatlands Project Site undergoing restoration to remove artificial drainage. The installation of dams has created numerous pools that allow investigation into how communities develop within a close network. The aim is to analyse how local connectivity between pools shapes aquatic invertebrate community structure, with the hypothesis that synchrony between neighbouring pools decreases with increasing distance from a source population. Between June and August, aquatic invertebrates will be sampled from 160 peatland pools grouped into clusters of four, allowing assemblages to be compared within and between clusters. Additionally, a more established 'source' pond will be sampled as well as terrestrial invertebrates with an aquatic life stage. Using the concept of Dark Diversity, it can be determined whether there are species present in the surrounding environment that have failed to colonise the pools. Exploring aquatic invertebrate metacommunity dynamics on the Castell Nos site will allow greater understanding into how these species colonise new areas in response to large-scale peatland restoration. The Dark Diversity concept can also be useful to understand patterns of diversity and may help to develop conservation methods with regards to invertebrates.

P4 – Aoife Crowe, University of Galway

The comparison of three trapping methods and the effects of surrounding environmental variables for saproxylic and other woodland using beetles.

Saproxylic beetles depend on dead, decaying, and live wood for a part of their lifecycle. The abundance and diversity of these beetles promote the healthy functioning of woody ecosystems. Furthermore, these beetles provide an array of beneficial ecosystem services including; pollination, decomposition, and nutrient cycling. Like many insect groups, these beetles are declining in Europe due to the change and loss of their associated woody habitats. Despite these declines and their ecological importance, saproxylic beetles are understudied and knowledge gaps remain regarding their conservation status and ecological requirements. This is particularly the case in Ireland. Thus, to ensure the future conservation of the insect group in Ireland more targeted, scientific research on the ecology of saproxylic beetles is required.

This talk discusses the results from a robust sampling of saproxylic and other woodland using beetles in one of Ireland's most important ancient woodlands. Three different trapping methods, each targeting different woodland layers, were used and compared to collect a full suite of beetle species. The effects of surrounding environmental variables on beetle abundance and diversity were also quantified.

Other authors: Authors: Crowe, Aoife¹, O' Hanlon, Aidan², Carlin, Caitriona¹, Williams, Christopher³ and Gormally, Mike¹ :¹ Applied Ecology Unit, Earth & Life Sciences, School of Natural Sciences, University of Galway, Ireland ² National Museum of Ireland, Merrion Street, Dublin 2, Ireland ³ School of Biological & Environmental Sciences, Liverpool John Moores University, Liverpool L3 3AF, UK

P5 – Matthew Darbon, Liverpool Hope University

An investigation into the lichen host preference of Footman moth *Eilema* spp. larvae in urban green spaces in Liverpool

*Footman moth (*Eilema* spp.) larvae are lichenivorous and are known for being polyphagous of multiple lichen species. However, little is known about which species of lichen are preferred in the UK by these larvae, with only a small amount of literature covering this subject in Finland. With the exponential increase in abundance and their distribution shifting further northwards in the UK of the Footman moths, it is im-*

portant to work out reasons for these changes. This project aims to investigate which lichens are most favoured by the Footman moth larvae and, if possible, discover what role urban green spaces in Liverpool may play in this shift northwards in their distribution.

P6 – Elen Griffith, Manchester Metropolitan University

Gully blocking restoration efforts increase invertebrate abundance and improve water quality in the Peak District

Functional peatlands are crucial for biodiversity preservation and carbon storage. However, the Peak District has faced intense degradation, primarily caused by drainage for agriculture and forestry, pollutants, burning and tourism which have severely impacted its ecological health. Understanding the effectiveness of restoration can inform future conservation efforts and global peatland restoration. This study explores the potential for biodiversity gain through restoration efforts focussed on gully blocking, which aims to heighten the water table and reduce soil erosion at Dove Stone, Peak District, which has experienced degradation and loss of water holding capacity. Data was collected biannually (April and August) from 2022 to 2024, August 2024 data collection is still forthcoming. We are utilising sweep netting and colonisation traps to collect aquatic invertebrates and assessing water quality parameters of the ponds. So far, we have seen a significant increase in overall invertebrate abundance (282%) and Diptera (80%) and Coleoptera (6%) abundance between 2022 and 2023. Water quality measurements are variable, with initial peaks in water pollutants and nutrients levels which reduced in 2023. Our research shows that water quality measures improve, and invertebrate abundance and diversity can very quickly increase when gully blocking is employed to create new ponds.

Other authors: Scott Pedley, Manchester Metropolitan University; Matthew Sparrow, Manchester Metropolitan University; Lauren White, Manchester Metropolitan University

P7 – Jane Hill, University of York

Conservation and diversity of woodland insects: connectivity benefits most taxa, but the benefits for individual species vary greatly

Large-scale woodland creation is taking place, to meet the UK's commitments on nature recovery and achieve net-zero carbon emissions. Improving woodland connectivity is often assumed to be beneficial for biodiversity, but connectivity studies generally only consider benefits for single species or taxa, and so the generality of the biodiversity benefits of connectivity is unclear. We quantify the benefits of woodland connectivity for 15 invertebrate groups (including 12 insect taxa). We analyse a large citizen science dataset of > 3000 species (> 48 million records) to test whether the occurrence of species increases with the connectivity of woodland within landscapes (1 km grid resolution across GB and NI). Overall, we find that occurrence of woodland species increases with woodland connectivity, even after accounting for the stronger positive effect of woodland cover on species occurrences. However, there is considerable variation among species and taxa in terms of the importance of connectivity, and connectivity benefits are greatest in landscapes where woodland cover is very low. We conclude that increasing woodland cover is most important for insect diversity, but that increasing connectivity is also important, especially in regions where woodland cover is low.

Other authors: Charles A. Cunningham, University of York; Diana E. Bowler, UK Centre for Ecology & Hydrology; Michael J.O. Pocock, UK Centre for Ecology & Hydrology; Robin Hutchinson, UK Centre for Ecology & Hydrology; Colin M Beale, University of York; Piran C. L. White, University of York; Lisa Emberson, University of York; Merryn Hunt, UK Centre for Ecology & Hydrology; Lindsay Maskell, UK Centre for Ecology & Hydrology

P8 – Gail Jackson, University of Edinburgh**How is carabid beetle abundance and community structure influenced by sustainable farming practice?**

*The Centre for Sustainable Cropping at Balruddery Farm (James Hutton Research Institute, Dundee) was established in 2009 to test the long-term impacts of an integrated cropping system on whole-system sustainability. By conserving arable habitats, diversifying field margins and beneficial in-field weed communities, and applying IPM strategies to reduce reliance on crop protection chemicals, the aim is to enhance biodiversity, improve ecosystem resilience and promote the delivery of ecosystem services. A split-field design is used to compare conventional commercial practice with integrated practice. Pitfall traps are used to assess changes in carabid beetle abundance and community structure between fields. Monitoring has been continuous between 2011 and 2017, with a further data set collected this year (spring 2024). Initial results suggest that carabid abundance is most strongly determined by crop type and that the effectiveness of management practice varies according to crop type. Key predatory species such as *Nebria brevicollis* show a preference for cereal crops and oilseed rape and are more abundant in integrated compared with conventional fields. These findings demonstrate that the implementation of IPM measures, can successfully increase carabid abundance in commercial crops and therefore the potential they have for enhancing natural pest control.*

Other authors: Cathy Hawes (James Hutton Research Institute), James Reid-Thomas (University of Edinburgh), Emily McClay (SRUC).

P9 – Fabio Leonel, Rentokil Initial**Optimising Fly Traps: Comparing the Efficacy and Efficiency of LED and Fluorescent Lamps**

Visual stimuli plays a crucial role in fly behaviour, however, designing effective light traps remains challenging due to the complex ways insects respond to different wavelengths and light intensities. Light emitting diode (LED) lamps are due to entirely replace fluorescent lamps in the next few years, with new production now halted. As such, it is important that new trap designs are optimised for this new technology. In this study, a simple but effective and flexible assay is used to compare fly traps with LED and fluorescent lamps. Our results show the LED traps keep a similar capture rate than the fluorescent lamps, however, they are also more efficient, having approximately 60% of energy saving and a durability of more than 30.000 hours. Utilising LEDs technology brings new features and more possibilities for trap designs in addition to being more efficient and reducing carbon emissions.

Other authors: Matt Green, Gregory Murray

P10 – Rosie McCallum, Newcastle University**How can post-industrial land restoration in the North-East contribute to Biodiversity Net Gain in England?**

Restoration of former mining sites often aims to enhance biodiversity. Habitat restoration and offsets have been proposed to compensate biodiversity losses, however few studies provide empirical evidence of success, and technical challenges exist to effectively measure losses and gains owing to mining. Emerging mechanisms and policies aim to both advocate for and enforce effective conservation action, including Biodiversity Net Gain (BNG), which could help to fund restoration targets in England. However, as a habitat-driven approach, there are concerns that BNG could neglect important components of ecosystems, such as invertebrates, and will not be effectively monitored or enforced. This PhD will assess whether the project-level management, monitoring, enforcement, and proposed reporting of BNG are sufficient and achievable. Biodiversity variability will be examined on former open-cast mining sites at different stages of restoration in Northumberland. Invertebrate surveys, including pollinator surveys, and soil analysis will be conducted to measure above and below ground health, and habitat surveys and remote sensing will be used to measure changes in vegetation structure. This PhD will contribute to our understanding of how effective

the current methodologies are for achieving BNG on former mining sites, helping to strengthen the achievability of conservation goals in England.

Other authors: Dr Elisa Lopez-Capel, Dr Mark Goddard, Dr Katherine Baldock, Dr Miranda Pendergast-Miller, Dr Ankush Prashar, Lee Rankin (Agricultural Production Systems, School of Natural and Environmental Sciences, Newcastle University)

P11 – Sarah Meredith, Royal Entomological Society

Collecting the evidence and applying the science to further the conservation of *Phengaris arion* in the UK

*Since the 1970's, Large Blue science has underpinned the conservation of this endangered and iconic butterfly. Surveys undertaken include the distribution and abundance of, the Red ant *Myrmica sabuleti*, Large blue butterfly eggs, foodplant/s (Thyme and Marjoram), soil temperature recording and adult timed counts. Data collected is analysed and used to inform the management advice which we give on an annual basis to landowners and sites managers on over 50 sites. The data also helps us to write management plans, to give bespoke grazing advice and to both justify and prioritise future reintroductions.*

Other authors: Professor Jeremy Thomas, University of Oxford, David Simcox FRES, Royal Entomological Society

P12 – Moses Musonda, University of Zambia

The effects of physicochemical parameters of water on the abundance of Anopheles mosquito larvae in various breeding sites of Kapiri mposhi district Zambia

*Malaria is a global public health problem, caused by malaria parasites transmitted by a vector female Anopheles mosquitoes, belonging to the order Diptera. Their developmental cycle under goes a complete holometabolous with the larval stages associated with aquatic habitats. It is envisaged that the larval control measures are intended to reduce malaria transmission when vector development is prevented. This due to the fact that for some reasons, most drug treatments coupled with other bed net insecticide treatments of adult mosquitoes are increasingly failing. In this study, it was important to determine whether the abundance of Anopheles mosquito larvae in different water sites was associated with the following parameters: (i) particular pH level, (ii) particular temperature (iii) the Total Dissolved Solids (TDS) (iv) or a particular electrical conductivity of water (IV). It was also essential in this study to establish the species composition of adult Anopheles mosquitoes in Kapiri Mposhi district of Zambia. Both larvae and adult mosquitoes were identified using a morphological key. To achieve relevant results, a variety of qualitative and quantitative analytical methods were involved, inclusive of Polymerase Chain Reaction (PCR) and numerous multivariate statistical analyses involving SPSS statistical package version 21.0. Out of the total of 489 Anopheles larvae that were collected from breeding sites and reared in the insectary, only 45% emerged into adults. It was observed that the Anopheles larvae was absent in Rivers and dam breeding sites. Further molecular results revealed that the most abundant mosquito species in Kapiri Mposhi were *An. gambiae* (60%) and breeds well in temporal water ponds, followed by *An. arabiensis* Paton (35%) and 5% were no amplified results. A positive significance was recorded on Pearson Correlation for physicochemical parameters of electrical conductivity ($p = 0.003$), Total Dissolved Solids (TDS) ($p = 0.004$), temperature ($p = 0.001$) and pH ($p = 0.000$). Consequently, it was, concluded that electrical conductivity, pH, temperature and Total Dissolved Solids (TDS) of water in various mosquito breeding sites of Kapiri Mposhi has an effect on the abundance of Anopheles*

Other authors: Sichilima Alfred, Copperbelt University

P13 – Anna Platoni, Forest Research**If you go down to the woods today - the surprises and the routine of monitoring woodland insects at Forest Research**

Entomologists at Forest Research (FR) coordinate and support many UK-wide monitoring programmes for forest insects. Our monitoring programme is made up of surveillance trap networks, monitoring on known pest outbreak sites and surveillance traps at high-risk locations such as at ports and wood-processing plants. We also monitor tree pests using citizen science as part of a free advisory service called “TreeAlert”. Combined, information from this surveillance: informs plant health policy, alerts authorities and scientists to new pests of UK concern at borders and inland, prompts outbreak response, and produces scientific data for further study. This presentation will introduce insect monitoring at FR and present some of the day-to-day management of these large-scale networks, including interesting recent findings and their impact to UK tree health security.

Other authors: Sarah Facey 1, Jason Sumner-Kalkun 1, Alice Walker 1, Max Blake 1 (1= Forest Research)

P14 – Giorgos Stavrianakis, University of the Aegean**Does biodiversity affect Olive fly population? Evidence from different understorey treatments**

*The agricultural industry is intensifying production methods to increase crop yields. Olive cultivation, the prevalent permanent crop in Europe and the Mediterranean area, involves intense practices with heavy agrochemical use. This significantly impacts agroecosystem biodiversity and its ecosystem services. In this study, we explore how biodiversity influences the adult olive fly (*Bactrocera oleae* (Rossi)) population in Lesvos Island, Greece, under different understorey management practices in olive groves. Our findings show that increased plant and arthropod abundance and diversity negatively affect the olive fly. The results suggest that maintaining undisturbed plant cover enhances olive grove biodiversity, ecosystem services, and biological control of the olive fly. Moreover, this practice is in line with Integrated Pest Management principles and Conservation Biological Control approach.*

Other authors: Efstratios Sentas, Department of Geography, University of the Aegean. Thomas Tscheulin, Department of Geography, University of the Aegean. Thanasis Kizos, Department of Geography, University of the Aegean.

P15 – Daniel Turk, University of York**Digging Deeper: Exploring ants as beneficial ecosystem engineers**

*Greater plant diversity provides many ecosystem benefits and is promoted by increased habitat heterogeneity. Habitat heterogeneity is increased by the presence of ant mounds, which have altered abiotic soil properties relative to the surrounding soil. These altered soil properties often result in distinct plant communities on mounds compared to the surrounding soil, increasing overall landscape biodiversity. A widespread UK mound-building species is the yellow meadow ant, *Lasius flavus*. *L. flavus* creates long-lasting mounds that can reach densities of over 50 mounds/100 m², yet the relationship between plant diversity and meadow ant mound density is unknown. I have compared plant diversity and plant community composition between landscapes with three mound densities: ‘Absent’, ‘Standard’, and ‘High’. Species diversity is similar between ‘Standard’ and ‘High’ mound densities; however, overall plant community composition across landscapes is different. I have taken soil cores to quantify the soil properties of mounds, and to determine how far altered soil properties extend from the mound boundary. I have also translocated mounds and ‘fake’ mounds to mound-absent landscapes, to compare their effect on landscape biodiversity. This work will help inform our understanding of the best use of these ecosystem engineers for restoration work and more sustainable land management practices.*

Other authors: Dr Kelly Redeker, University of York; Carl Hawke, National Trust; Professor Elva Robinson, University of York

Genetics and genomics

P16 – Virgile Ballandras, Teagasc

Identifying various aphid species from bulk insect samples using Mito-Metagenomics

One of the principal obstacles in our ability to respond rapidly to insect pest infestation is correct and timely species identification and quantifying incidence of migrating aphids carrying B/CYDV in the autumn and spring. Identification of insect species can be difficult and dependent on taxonomic expertise (becoming less accessible); particularly in the identification of groups such as aphids. The major bottleneck for a monitoring/forecasting scheme is now the manual processing of hundreds to thousands of insect specimens collected in bulk samples directly from the field (e.g. pan-traps) or in proximity of crops (e.g. suction-traps).

In this context, we are currently evaluating the use of metagenomics for the identification of aphids, after their separation from other insects. For this work, we are focussing on samples from 6 meters suction traps that typically trap 100s to 1000s of aphids each week. We are also preparing aphid mock communities of different complexity and using these to evaluate metagenomics for both measuring relative aphid abundance in a sample, and for tracking a species abundance across samples. The move towards greater 'automation' in processing of bulk collected material from insect traps will remove a major bottleneck and open the possibility for long-term longitudinal studies of insects.

Other authors: Dr. Stephen Byrne, Teagasc Crops Science Department; Dr. Louise McNamara, Teagasc Crops Science Department; Dr James Carolan, Maynooth University

P17 – Isabela Begnami, Universidade Estadual de Campinas

Using de novo transcriptome analysis to identify RNAi machinery in the spittlebug *Mahanarva spectabilis* Distant, 1909 (Hemiptera: Cercopidae)

Mahanarva spectabilis spittlebugs are a limiting pest to Brazilian forage production, but there are few viable and ecological alternatives for controlling them. RNA interference (RNAi) technology enables insect control in an ecologically sustainable way. We aimed to provide molecular information to explore the RNAi silencing mechanism in this species. We extracted total RNA from eggs, nymphs and adults, prepared cDNA libraries and sequenced them on a NextSeq 550. Data quality was checked; reads were trimmed and filtered for rRNA. A de novo transcriptome was assembled and filtered for redundancies, resulting in 197,003 contigs with an N50 of 853 bp. 96.6% of transcripts were found among Hemiptera orthologs and 90.59% of reads were aligned to this reference. Transcripts were annotated and RNAi mechanism genes were searched, leading to the identification of over 30 genes involved in five major RNAi pathways. Multiple sequence alignment of six key genes with their homologs in eight other insects was performed and a phylogenetic tree was constructed. *M. spectabilis* sequences are most similar to planthopper *Nilaparvata lugens* Stal and honey bee *Apis mellifera* Lin. This indicates *M. spectabilis* has an active RNAi mechanism, and the transcriptome is suitable for searching targets for silencing.

Other authors: Gustavo Fernando Ferreira Gonçalves, Universidade Federal de São Carlos; Wilson Malagó Júnior, Embrapa (Brazilian Agricultural Research Corporation) Southeastern Livestock; Marcos Rafael Gusmão, Embrapa (Brazilian Agricultural Research Corporation) Southeastern Livestock; Anete Pereira de Souza, Universidade Estadual de Campinas; Bianca Baccili Zanotto Vigna, Embrapa (Brazilian Agricultural Research Corporation) Southeastern Livestock

P18 – Stewart Rosell, Agri-Food and Biosciences Institute**Testing eDNA sampling methods to detect plant pests using the Light Brown Apple moth, *Epiphyas postvittana***

*Non-native herbivorous insects can be introduced on plants via horticultural trade and pose a threat to plant health. Environmental DNA (eDNA) can be used to detect these pests on foliage. This method is sensitive and can detect pests from frass or partial specimens, which are challenging to diagnose using traditional inspection methods. Pests can be introduced via a variety of plant types so eDNA sampling methods applicable to a range of plants and plant products would be required to apply this method to biosecurity. In this study I am using Light Brown Apple moth (*Epiphyas postvittana*) to test eDNA sampling on types of plants important for plant health. *E. postvittana* is polyphagous, feeding on over 100 plant families and it is easy to rear making it suitable for experiments on a very wide range of plant species. *E. postvittana* is taxonomically and ecologically similar to other plant pests such as the tortricid genera *Choristoneura*, *Acleris*, *Archips*, and *Grapholita*. The findings from this study are likely to be relevant to surveillance for similar pest species, which can be difficult to detect or identify using morphology.*

Other authors: Dr. Archie Murchie, Agri-food and Biosciences Institute, Dr Neil Warnock, Agri-food and Biosciences Institute, Dr. John Baird, University of Aberdeen

Host microbiome interactions

P19 – Kerry Barnard, University of Surrey**The microbiome of the honeybee hive as an indicator of hive health**

We recently found that honeybee hives possess their own distinct microbiomes (Santorelli et al. 2023). 16S rRNA sequencing of honey DNA showed a high diversity of bacterial communities that derive from bees, plants, soil, and water. Microbes of the honeybee gut are well described and have been proposed as a key driver of immunity against pathogens; however, their presence in honey, and the role that honey plays on immune protection is poorly understood. Our research aims to use DNA from honey to fully characterize the microbiome of the entire beehive. This approach is expected to reflect the complex social behaviour and interactions of honeybees within the colony and their surrounding ecosystem.

Currently we are testing the antimicrobial activity of honey from different hives against bee pathogens and commensal gut bacteria to correlate the presence or absence of activity with the type of microbiome observed for each hive. Comparison with hives known to be diseased will then determine microbiota associated with healthy or diseased hives. Floral origins of the honey and apicultural practices, such as antibiotic use, are also being tested. Consequently, we will better understand how these factors affect the overall microbiome and the associated antimicrobial properties, for future use as hive health indicators.

Santorelli, L. A., Wilkinson, T., Abdulmalik, R., Rai, Y., Creevey, C. J., Huws, S., and Gutierrez-Merino, J. 2023. Beehives possess their own distinct microbiomes. *Environmental Microbiome* 18 (1).

Other authors: Dr Jorge Gutierrez-Merino, William Wilkinson, Dr Elizabeth Nicholls, Dr Claudio Avignone-Rossa

P20 – Andrea Ceribelli, University of Liverpool**The role of protective symbionts in mediating aphid interactions with beneficial rhizobacteria and parasitoids on barley**

Aphid pests are increasingly being managed via biological control agents, such as parasitoid wasps or entomopathogenic fungi. In addition, rhizobacteria inoculation of plants to boost plant defences against insect pests also has strong potential for sustainable agriculture. However, aphids host facultative bacterial

*endosymbionts that can provide protection from natural enemies, reducing biocontrol effectiveness, with unknown effects in response to rhizobacteria-inoculation of host plants. Protective symbionts often impose a fecundity cost to the aphid, leading to cost-benefit trade-offs and variation in symbiont infection rates within aphid populations. We present data on aphid symbiont prevalence from a field trial where we inoculated barley plants (*Hordeum vulgare*) with two different rhizobacteria (*Acidovorax radialis* and *Bacillus subtilis*). We also present data from preliminary experiments using field-collected aphid lines (*Sitobion avenae*) with different symbionts, that vary in population growth and susceptibility to parasitoids. Future work will create experimental aphid lines differing in symbiont infection status using a microinjection protocol for artificial symbiont transmission. This project aims to shed more light on the role of aphid protective symbionts in a community wide context and inform the development of effective biocontrol strategies.*

Other authors: Sharon Zytynska, University of Liverpool; Daniel Leybourne, University of Liverpool; Julia Ferrari, University of York

P21 – Stephen Oware, University of Exeter

A Comparative Study on Infection Routes of DCV Across Fruit Fly Species.

*This study investigates how the infection route of DCV affects the mortality of different fruit fly species. Understanding the infection routes of DCV, an important pathogen in *Drosophila* research, is pivotal in grasping host-pathogen interactions.*

*DCV was administered to 4 species of fruit flies, *Drosophila melanogaster*, *D. persimilis*, *D. pseudoobscura* and *D. virilis* via two methods: an oral infection, where virus was on the food, and systemic infection, where the virus was injected directly through pricking. The mortality was monitored and recorded over a given period.*

The results indicated a distinct difference in mortality rates of flies. Oral infections resulted in a much slower rate of mortalities as compared to systemic infections. This suggests that when the virus is ingested, there is a gradual spread of the virus as it has many defensive barriers to go through while on the other hand, in the systemic infection, the virus has immediate access to the haemocoel of the fly. These findings emphasize the importance of infection route in studying pathogenicity of DCV and potentially other viruses in fruit flies.

Other authors: Ben Longdon (University of Exeter)

P22 – Robert D. Pienaar, CNRS & Université de Tours & Universitat de València

A novel Solinviviridae that can infect black soldier flies (*Hermetia illucens*)

*The current focus on entomopathogens in black soldier flies (BSF) is on bacteria, fungi and nematodes, highlighting the need for monitoring entomopathogenic viruses in BSF. In recent work, we described historical interactions between BSF and multiple viral families, however, viral surveillance, characterization, and testing is a gap in mass-reared insect models such as BSF. Samples were received from a BSF rearing company with reports of early mortality in adults and reduced fecundity. A metatranscriptomic-based approach was taken that yielded a mostly complete genome for a virus candidate which displayed high coverage (147 343x) in the dead adult samples. Characterization of the virus candidate showed a close relation to other Solinviviridae, thus we named it *Hermetia illucens solinvivirus 1* (HiSvV1). Alongside this, we developed bioassays and RT-qPCR protocols to test for viral replication in BSF. We found evidence of HiSvV1 replication in adults infected after the larval stage and detected HiSvV1 in all tissues investigated. Furthermore, cross-exposure experiments suggest horizontal transmission between male and female adults. These findings indicate that HiSvV1 is related to viral pathogens of arthropods and has been demonstrated to reinfect BSF and undergoes natural transmission between individuals. Remarkably, this is the first study of a virus isolated from diseased BSF, in mass-rearing conditions.*

Other authors: Pablo Garcia-Castillo (Universitat de València), Harmony Piterois (CNRS - Université de Tours), Herniou, Élisabeth (CNRS - Université de Tours), Salvador Herrero Universitat de València)

P23 – Shonnette Premchand-Branker, University of Oxford

The Dipteran microbiota as a reservoir of antimicrobial resistance in clinical settings across Africa

*Antimicrobial resistance (AMR) is a global health crisis in which arthropods may be playing a key role as reservoirs of AMR bacteria. The synanthropic nature of Dipteran filth flies such as *Musca domestica*, facilitates their persistence in many hospitals in low- middle-income countries (LMICs) across Africa where climate and limited resources are permissive to fly invasion.*

The Arthropods as Vectors of Infection and Antimicrobial Resistance (AVIAR) study seeks to determine the contribution of arthropods to the burden of AMR. This study aims to specifically screen flies captured in clinical settings for the carriage of bacteria with antibiotic resistance genes (ARG). 2059 flies were collected from 11 hospitals in five countries across the African continent: Chad (n=425), Egypt (n=169), Mauritania (n=403), Nigeria (n=662), and Sierra Leone (n=400). Microbiological culture and molecular detection methods revealed a high diversity of Gram-negative Enterobacterales and Gram-positive Staphylococcus species carrying ARG conferring resistance to commonly used beta-lactam antibiotics in flies sampled across Africa. Many of the bacterial species isolated are common components of the fly microbiota but also cause nosocomial infections and are associated with transmission of ARG within clinical settings. These findings implicate the Dipteran microbiota as a source of AMR in clinical settings.

Other authors: Edward A.R. Portal (IOI), Chioma Achi (IOI), Kirsty Sands (IOI), Teresa Iannetelli (IOI), Tim Beard (IOI) Kate Cook (IOI), Katherine Ansbro (IOI), Claudia Orbegozo Rubio (IOI), Tim Walsh (IOI), The AVIAR study collaborators

Outreach

P24 – Stephanie Glendinning, University of Sheffield

EntoBites: Communicating Entomology

We are a group of early-career entomologists currently setting up EntoBites, part of the ScienceBites collective (<https://sciencebites.org/>). Through our blog we aim to communicate insect science and research to a general public audience, and provide graduate students with the opportunity to develop their writing skills by contributing accessible and jargon-free articles. We would greatly appreciate the opportunity to promote our website at Ento'24 and recruit graduate students as authors.

Other authors: Wendy Harris, Swansea University; Madeleine Fabusova, University of Exeter

P25 – Mark Hanson, University of Exeter Penryn

The strain on scientific publishing

Publish or perish. Scientists are increasingly overwhelmed by the volume of articles being published. In our dataset (the intersect of Scopus and Web of Science), total articles grew exponentially in recent years: in 2022 the article total was 47% higher than in 2016. This article growth has outpaced the limited growth, if any, in the number of practising scientists. In short: our collective publication workload is demanding more and more time. We define this problem as "the strain on scientific publishing." We present five data-driven metrics on publisher growth, processing times, and citation behaviours. This work involved web scraping millions of articles, requests for publisher data, and publicly-available publisher material. This strain is generated by the ecosystem as a whole, driven by a universal mission by publishers to promote growth of their product. Specific groups have disproportionately contributed to this strain. Indeed, some publishers ena-

bled immense growth by adopting a strategy of hosting "special issues," which publish articles more rapidly, feeding into the publish or perish mantra. We also analyse citation metrics (e.g. Impact Factor, Scimago Journal Rank) and find evidence that some publishers systematically enable gaming of these "quality" signals, helping their journals entice more submissions. This immense growth cannot be sustained. The metrics we define here help enable this evolving conversation reach actionable solutions to address the strain on scientific publishing. Find out more at: <https://the-strain-on-scientific-publishing.github.io/web-site/>

Other authors: Pablo Gomez-Barreiro (Kew Royal Botanic Gardens), Paolo Crosetto (INRAE, CNRS), Dan Brockington (ICREA, ICTA)

P26 – Craig Perl, Insect Welfare Research Society

Identifying trends in reporting on the ethical treatment of insects in research

It is common for many scientists to report on the ethical treatment of their research animals. This serves multiple purposes, first to generate reproducible science, second to safeguard animal welfare, and third to foster public trust. However, reporting on the ethical treatment of research animals is uncommon practice among entomologists, as insects have not historically been considered plausibly sentient and thus are unprotected by laws that have mandated minimal reporting standards for other taxonomic groups. Wherein the alternative norms of entomology may pose a threat to 1) public trust, 2) animal welfare, or 3) reproducible science, entomologists may wish to review their norms and establish new best practices for the field. To aid this reappraisal, and establish a baseline for historical entomological reporting practices, we surveyed 15 entomology journals over 20 years to collect data on reporting related to the ethical treatment of insects in research, including: animal reduction methods, statements on anaesthesia prior to traumatic manipulation/handling, and information regarding sacrifice practices. After surveying historical practices, which suggest areas of greater strength and areas that need improvement, we present a methodology for improving transparent reporting on the ethical treatment of research insects, with the goal of improving reproducibility, animal welfare, and public trust.

Other authors: Bob Fischer - Department of Philosophy, Texas State University, San Marcos, TX // Meghan Barrett - Department of Biology, Indiana University Indianapolis, Indianapolis, IN

Pests, biological control and IPM

P27 – Frankie Amanesih, University of Greenwich

Fungal-derived technology for control of the invasive pest, *Drosophila suzukii*

*First recorded in the UK in 2012, *Drosophila suzukii* (Matsumura), also known as Spotted Wing *Drosophila* (SWD) is a significant invasive worldwide pest, threatening horticultural production in the UK, Europe, and the US. Currently, control of SWD primarily involves insecticide spraying fruit crops and labour-intensive hygiene practices. Laboratory studies have established that entomopathogenic fungi (EPF) can kill SWD, but current fungal formulations have not been effective in field trials.*

*We combine fundamental study of fly behaviour with aspects of fungal ecology and biochemistry to understand how *D. suzukii* resist EPF infection with the aim of developing new sustainable technologies for crop pest control.*

We have established EPF infectivity by conducting a series of mortality assays using four commercial EPF products previously proven effective against SWD in the laboratory. The fungal formulation with the most promising results will be used in a series of behavioural assays, consisting of two parts: identifying the interactions of SWD with fungal volatiles and discovering their species-specific behaviours following fungal

infection. Finally, the secondary metabolites of EPF will be identified to develop novel EPF-derived technologies, enhancing its efficacy through the combination with botanical extracts and adjuvants.

Other authors: Daniel Bray - University of Greenwich/Natural Resources Institute, Sarah Arnold - NIAB EMR, Steven Harte - University of Greenwich/Natural Resources Institute, Christina Supramaniam - University of Greenwich/School of Science, Mandela Fernández-Grandon - University of Greenwich/Natural Resources Institute

P28 – Nikoletta Foskolou, Harper Adams University

Enhancing biological pest control: olfactory conditioning of parasitoid wasps

Parasitoid wasps are used in biocontrol programmes to suppress pest populations below economic thresholds. However, parasitoids can be slow to establish following release. It is suggested that current mass-rearing systems do not account for the cognitive processes affecting host location, and recognition.

Host-searching behaviour is vital for female parasitoid fitness and relies on chemical cues from their environment following a three-level process: (1) host habitat location using herbivore-induced plant volatiles (HIPVs), (2) host location using HIPVs and other host-originating chemical cues and (3) host discrimination and acceptance using cues directly derived from the host. Parasitoid behavioural responses to chemical cues can be either innate or learned. Learning usually takes the form of an association between a particular odour and a successful oviposition experience. There is strong evidence for adult stage learning through laboratory-based studies. However, the extent to which parasitoid learning is important in determining their efficacy as biocontrol agents under semi-field conditions has not been demonstrated.

This project aims to characterise parasitoid learning in relation to chemical cues associated with host-searching. Parasitoid olfactory conditioning will be studied to investigate whether it can be incorporated into parasitoid mass rearing systems to improve the efficiency of parasitoids as biological control agents.

P29 – Shannon Goldberg, Northumbria University

Monitoring and detecting invasive species in anthrobiomes: bees on the Faroe Islands.

The Faroe Islands are an archipelago of islands located in the Atlantic Ocean. Because of the cold, windy climate, bees have been noticeably absent from the landscape. In the past seventeen years, however, sightings of some bumblebee species have been recorded, resulting from a combination of climate change, importing goods, and increased human transportation. This presents a unique opportunity to explore the effects of bumblebee invasions on native flora and fauna, particularly in island ecosystems which are sensitive to invasions because of high rates of endemism and specialism.

Several tools will be used to build a plant-pollinator network, allowing predictions to be made with the addition/removal of species resulting from bumblebee invasion. Plant-pollinator surveys will make up the bulk of data collection. Environmental DNA (eDNA) will be used to explore contemporary and historical landscapes of the Faroe Islands. The presence of 'bee pollinator-adapted' flowers in pollen records suggest that honeybees have been introduced previously. Peat cores will be taken in areas where Viking settlers may have kept apiaries, and ancient eDNA and pollen records will be used to explore historical presence of honeybees. A spatial modelling software will be used to predict impacts of future distributions of bumblebees.

Other authors: Dr Rinke Vinkenoog, Northumbria University, Dr Matthew Pound, Northumbria University, Anni Djurhuus, University of the Faroe Islands, Rosie Everett, Scotland's Rural College

P30 – Laura Haynes, University of Greenwich**Lethal and sub-lethal effects of naturally-derived pesticides on hoverflies**

Synthetic pesticides can have negative impacts on non-target agroecologically beneficial insects, but controlling insect pests is important for marketable quality and yield of crops. The use of biopesticides such as entomopathogenic fungi (EPF) and botanical insecticides, with naturally derived active components could be a more sustainable option. However, individual compound efficacy can be compromised in the field due to slow EPF infection rates and only temporary paralysis and recovery of botanical insecticide exposure. With combined use, shortfalls such as these could be negated.

*I examined the toxicity of individual and combined use of the botanical insecticide pyrethrum and the EPF *Beauveria bassiana* on the European migrant hoverfly *Eupeodes corollae*. This species is both an efficient pollinator as an adult, as well as producing aphidophageous larvae which are effective in Integrated Pest Management.*

I have identified dose-dependent lethal effects, with combined exposure at lower doses not increasing mortality rates. Sub-lethal behavioural and physiological bioassays have revealed no negative effect on oviposition and development of offspring. Laboratory foraging behaviour and greenhouse trials into effects of these treatments on fruit quality are also discussed.

P31 – Neil Hobbs, Swiss Tropical and Public Health Institute**Simulating the dynamics associated with insecticide resistance fitness costs in mosquitoes.**

A key assumption of many insecticide resistance management (IRM) strategies is the presence of fitness costs associated with resistance when compared against. Fitness costs are frequently measured for many life-history traits across a diverse range of insects. For mosquito control, the rotation IRM strategy is frequently highlighted as recommended strategy. However a key requirement for the rotation strategy to be effective is the presence of fitness costs when evaluated in simulation models. These models include fitness costs as a global composite. Here we present a coupled population dynamics and population genetics model. The model allows for the specification of fitness costs to directly to life-history traits (including egg batch size, survival rates, growth rates, and mating success). We simulate the impact fitness costs associated with resistance have on the rate at which susceptibility returns to the population, considering the life-history trait affected, the magnitude of the fitness cost, the frequency of resistance in the population and the fitness of the heterozygote. We demonstrate the fitness costs can show complex dynamics as a result of these interactions. The results presented will help inform the use of the rotation IRM strategy and also help in the design of fitness cost evaluation studies.

Other authors: Nakul Chitnis, Swiss Tropical and Public Health Institute

P32 – Diligent Oboho, University of Uyo**Gas Chromatography-Mass Spectroscopy analysis and Histopathological Effects of Methanolic Leaf Extract of *Lasianthera africana* P. Beauv. in the midgut of maize weevil, *Sitophilus zeamais* L.**

*Alternative methods for pest control have been widely used to mitigate challenges arising from pesticide applications in agriculture. This study investigated Gas Chromatography-Mass Spectrum (GC-MS) in the identification of bioactive components in methanol leaf extract of *Lasianthera africana* and examined its impact on the midgut histopathology of maize weevil, *Sitophilus zeamais*. The existence of eight (8) phytochemical substances with various therapeutic actions were shown by the GC-MS analysis : Thiirane (2.0); 1,1 dimethylhydrazine (2.8); L-aspartic acid (2.6); N-methyl-3,4-methylene dioxyphenylpropan-3-amine (1.7); 1-hydroxyimino-1-(4-methylphenyl) propan-2-one (2.3); Mercaptoethanol (1.6); 1,3-bis -t-butylperoxy-phthalan (1.3); 2-amino-4-(2-methylpropenyl)-pyrimidin-5-carboxylic acid (2.5) and other minor compounds, as the main constituents. Comparing the plant extract-treated *S. zeamais* specimen to the*

control, the histological section demonstrated a mild reorganization of the respiratory, secretory, and gastrointestinal layers along with the destruction of the muscular layer. In conclusion, the midgut histology of *S. zeamais* may be affected by the bioactive chemicals present in *L. africana*, which have a variety of biological functions. Thus, farmers are encouraged to use botanicals which are practical, ecologically friendly instead of synthetic insecticides with high residual effects to preserve their stored grains.

Other authors: Innocent Edagha², Akwaowo Nelson³, Rosemary Essien⁴, Akaninyene Akpan¹ Sulaimon Aina⁵, Affiong Edeke⁶, Basil Ita⁷, Sunday Ita⁸, and Joseph Eyo⁹ ¹Department of Animal and Environmental Biology, University of Uyo, Uyo Nigeria ²Department of Human Anatomy, University of Uyo Akwa Ibom State, Nigeria ³Department of Animal Sciences, Federal Polytechnic Ugep Cross River State, Nigeria ⁴Department of Crop Science, Akwa Ibom State University, Obio Akpa campus, Nigeria ⁵Department of Zoology and Environmental Biology, Olabisi Onabanjo University Ago-Iwoye Nigeria ⁶Natural Products Unit, Department of Chemistry University of Uyo, Nigeria ⁷Department of Physiology, University of Uyo Akwa Ibom State, Nigeria ⁸Department of Chemical Sciences, Topfaith University Mkpatak Nigeria ⁹Department of Zoology and Environmental Biology, University of Nigeria, Nsukka

P33 – John Owen, Harper Adams University

To me, to you - developing a push-pull system for sustainable management of aphid pests in seed and ware potato crops

'Stimulo-deterrent diversion' or 'push-pull' is a pest management strategy that utilises a variety of behaviour modifying cues, both visual and olfactory, to divert pest species away from their target ('push') and towards a trap area where they can be more easily controlled ('pull'). Push-pull has proved effective in the control of medical, veterinary and crop pests. Several potential components for a push-pull strategy to control aphid vectors of potato viruses have been identified, including repellent companion plants, essential oils and attractive trap plants. This study investigates the potential use of paints to produce a visually attractive 'pull' crop and test its ability to divert aphids from a potato crop. Initial experiments examine the effects of the paint on the settling behaviour of both alate and apterous aphids as a precursor to flight cage and small plot landing experiments. Once identified, successful pull crops will ultimately be trialled in conjunction with a variety of visual and olfactory 'push' strategies.

Other authors: Tom Pope (Harper Adams University), Joe Roberts (Harper Adams University), Matthew Back (Harper Adams University), David Almond (CUPGRA)

P34 – Nishi Pandya, The Maharaja Sayajirao University of Baroda

The neurophysiological effect of deltamethrin in the nesting behaviour of *D. gazella* (Fabricius, 1787)

To investigate the impact of pyrethroids on dung beetle, *Digitonthophagus gazella* (*D. gazella*) (5-♂, 5-♀) were exposed to deltamethrin treated dung at concentrations ranging from 0.005 ppm to 1 ppm. LC50 value (0.275 ppm) was determined, and sub-lethal doses were assessed for neurophysiological and behavioural effects. Results revealed a significant ($p < 0.01$) dose dependent decrease in the broodball count, brain somatic index along with neurotransmitters [acetylcholine esterase (AChE), nitric oxide (NO), dopamine (DA), and serotonin (5-HT)] and its biosynthesizing enzyme's gene expression [choline acetyltransferase (*cat*), dopa decarboxylase (*ddc*), 5-hydroxytryptophan (*5-HTPDC*), and nitric oxide synthase (*nos*)]. Further, oxidative stress was indicated by a significant ($p < 0.01$) dose and time-dependent increase in fluorescence intensity (dcfda staining) and a decrease in oxidative stress markers: superoxide dismutase (SOD), catalase (CAT), and glutathione (GSH). Additionally, a decline in *cyp4g7*, *cyp6bq9*, and *cyp4q4* gene expression was also recorded. Moreover, histomorphological alterations in brain tissue suggested potential functional disturbances, however, no sex dependent differences were observed. Our results confirmed that *D. gazella* retained the insecticidal effects, altered neurophysiology with noteworthy pathological consequences, thereby reducing the reproductive rate. These findings highlight the significant ecological and economic risks associated with deltamethrin exposure for non-target dung beetles.

Other authors: Ankita Salunke, The Maharaja Sayajirao University of Baroda; Pankaj Sharma, The Maharaja Sayajirao University of Baroda; Parth Pandya, Navrachana University; Pragna Parikh, The Maharaja Sayajirao University of Baroda

P35 – Antoine Pichon, Teagasc

A survey of *Bruchus rufimanus* incidence and damage in faba bean crops in Ireland

*The broad bean bruchid beetle (*Bruchus rufimanus*) is a major pest of faba bean in Europe. Only the larvae are harmful to the crop. They enter inside the young bean pods and consume the seed. The beetle will spend all his larval cycle protected inside the seed. The young adults will emerge from the seeds delivering a characteristic round hole. Following the European market rules, a batch of seeds exceeding 0 to 3% of damages cannot be sold for human consumption, and 10% for animal consumption.*

*The first specimen of Irish *B. rufimanus* was identified in 2003 in herbage in county Clare. Teagasc identified the first specimen in Irish fields with faba bean plants in 2016. At the same time the Irish production of faba bean increased from 17600 tonnes in 2014 to 65900 tonnes in 2015. The goal of our project aims to study the bruchid beetle population spreading over 3 years, and estimate the incidence on Irish faba bean production.*

Other authors: Eamon Nolan, Sheila Alves, Louise McNamara

P36 – Filip Vukajlović, University of Kragujevac

Trojan Female Technique for the biocontrol of the seed beetle *Acanthoscelides obtectus*: mitochondrial haplotype has negative male-specific effect on fertility across different nuclear backgrounds

*The seed beetle *Acanthoscelides obtectus* is one of the most economically important pests of stored legume seeds worldwide and is traditionally controlled with synthetic pesticides. However, the frequent use of these toxic compounds leads to environmental and health damage and the evolution of resistant insect populations. The Trojan Female Technique (TFT) is a novel species-specific, transgenerational biocontrol method for pest management. Sustained population control is achieved by releasing of Trojan females (TF) that carry naturally occurring mitochondrial DNA mutations (TFT mutation) that impair male fertility, but have no effects on females. TF and their female offspring could continuously, over multiple generations, produce males that sire fewer offspring than their wild-type counterparts. A candidate TFT mutation that causes male-only subfertility was recently described in *A. obtectus*. However, the applicability of TFT depends on mitochondrial TFT mutations whose male-sterilizing effects are general across different nuclear genomic contexts. We tested this assumption by expressing the candidate TFT mitochondrial haplotype alongside a range of three nuclear backgrounds and comparing its fertility in males with that of control haplotypes. We found that the fertility of males harbouring the candidate TFT mutation is consistently lower in all three nuclear backgrounds.*

Other authors: Filip Vukajlović¹, Uroš Savković², Sanja Budečević², Biljana Stojković³, Lea Vlajnić³, Mirko Đorđević² ¹ Faculty of Science, University of Kragujevac, Kragujevac, Serbia ² Department of Evolutionary Biology, Institute for Biological Research 'Siniša Stanković' – National Institute of the Republic of Serbia, University of Belgrade, Belgrade, Serbia ³ Institute of Zoology, Faculty of Biology, University of Belgrade, Belgrade, Serbia

P37 – Alice Walker, Forest Research
The Forest Trapping Network 2023

The Forest Trapping Network (FTN) is a rolling programme that surveys forests across Great Britain for a broad range of quarantine and priority Coleopteran tree pest species identified in the new EU Exit Regulations 2020, over a five-year cycle.

In each year of the five-year cycle, we will select 20 forests across GB. 4-6 insect traps will be installed at each forest in blocks of different species (spruce, fir, pine, oak and other mixed-broadleaf). Individuals caught from major families/subfamilies which contain the target pest species (including Cerambycidae, Scolytinae and Molytinae) will be identified to species level.

*Rarefaction-extrapolation curves showed good sampling coverage across GB. The FTN yielded a new record for the quarantine species *Ips typographus* in the wider environment in Scotland, and other records from SE England, but no other quarantine species were detected. 26,814 individuals from target families/subfamilies were sampled in total, revealing patterns in native and established species distributions across GB, including new county records and trends in recently-established species which must be closely monitored.*

The broad-spectrum trapping employed by the FTN will aid early detection of invasive forest pests across GB, which are likely to become a greater threat as climate change facilitates range expansions.

Other authors: Thomas Kendall, Max Blake

Pollinators

P38 – Safinatu Ameen, University of Greenwich
Hoverfly use for pollination of commercial soft fruit

The global decline in wild pollinators causes significant losses to soft fruit growers through malformed fruits and the need for commercial pollination interventions (hand pollination and the purchase of managed pollinators). Mitigating this requires improved ecosystem services from existing wild pollinators, such as hoverflies, which have the additional benefit of providing biological control and are increasingly valuable as a range of permitted plant protection products are becoming limited or are no longer available to growers. This greater pollination efficacy can be achieved with a more significant odour attraction within the crop by semiochemical lures. However, most research in hoverfly attraction has focused on ovipositional behaviour for biocontrol.

Therefore, we are identifying attractive semiochemicals using gas chromatography and mass spectrometry to create an attractive odour blend focused on improving pollination efficacy by both wild and reared hoverflies. Odour blends are being trialled for efficacy via Y-tube and cage trial bioassays. This will be further confirmed with electroantennography, wind tunnel behavioural assays and eventual field trials on commercial crops. Eventually, we aim to produce a semiochemical lure that can be used in crops to improve pollination services and crop yield in commercial soft fruits.

Other authors: Dylan Hodgkiss, Pollinator and Orchard Management, Ltd T/A Olombria, United Kingdom, Tashia Tucker, Pollinator and Orchard Management, Ltd T/A Olombria, Daniel Bray, Natural Resources Institute, University of Greenwich, Sarah Arnold, NIAB East Malling, Kent, United Kingdom, Mandela Fernandez-Grandon, Natural Resources Institute, University of Greenwich, United Kingdom and Steven Harte, Natural Resources Institute, University of Greenwich, United Kingdom.

P39 – Eiry Sian Bateman, University of South Wales**A novel approach to non-invasive pollen sampling from Hymenoptera and Lepidoptera, providing insights into pollinator preferences in a restored wildflower meadow**

Loss of the world's Pollinating insects in the current climate of ecological challenges may have devastating effect on our ecosystems and severe consequences for global food production. Analysis of current data suggests significant declines in many pollinating insect families, including Lepidoptera, Hymenoptera, Coleoptera, Hemiptera and Diptera.

This study tests a novel minimally-invasive sampling strategy to uncover pollinator preferences and wildflowers use, using Scanning Electron Microscopy (SEM). Novel methodologies of pollen collection from insects were developed with the aim of successfully releasing all insects without detrimental impact on foraged resources.

Of 75 insects sampled in this study, pollen was successfully collected from 73% of samples, representing 37 species in six families. Pollen from sampled insects was identified from a wildflower reference collection of SEM images, using morphometric analysis of pollen micro-characteristics at 7.00kx magnification. Weather conditions were determined to be a limiting factor in successful pollen collection. In this study most pollinator species were found to be polylectic foragers with pollen from an average of 2.14 (± 1.15) plant families per sample. Species of the Asteraceae were those most frequently identified.

This study demonstrates a new strategy in pollinator preference analysis which provides valuable insights without detrimental impacts on fragile insect populations.

Other authors: Dr Amelia Grass, University of South Wales

P40 – Elena Couper Coombs, University of Bristol**The combined impact of poor nutrition and novel insecticides on bumblebee colony initiation**

*Wild bees, such as bumblebees, are important pollinators of both crops and wildflowers, yet many species are in decline. Intensive agriculture reduces floral resources and increases agrochemical exposure in agricultural environments. Synergistic interactions between pesticides and poor nutrition may exacerbate individual effects; diets with low concentrations of sucrose may weaken pesticide resistance, or increase sucrose consumption, and consequently, pesticide intake. However, our understanding of the effects of environmental stressors across the whole bumblebee life cycle is limited. The initial solitary foraging stage of newly emerged bumblebee queens is vitally important, yet, the impact of poor carbohydrate nutrition and insecticide exposure at this stage is poorly understood. Here, we assessed the impact of lower carbohydrate intake and long-term exposure to a novel insecticide, flupyradifurone, on colony initiation and ovary development of wild-caught bumblebee (*Bombus terrestris*) queens. Using a fully crossed design, queens were provided bees with field-realistic concentrations of flupyradifurone (1.6ppm) at high (50%(w/w)) or low (15% (w/w)) sucrose levels, representing high or low quality diets respectively. We hypothesized that a low-quality diet will exacerbate the effects of insecticide exposure to negatively impact ovary development and colony initiation.*

Other authors: Dr Harry Siviter, University of Bristol

P41 – Sarah J. Larragy, Trinity College Dublin

Investigating colony growth dynamics in lab-reared wild and commercial lines of *Bombus terrestris* (ssp. *audax*)

*Domestication, an evolutionary process that occurs in captive-bred populations, can alter many organism traits, from genetic to behavioural. *Bombus terrestris*, a generalist bumblebee pollinator, is an insect species that has been domesticated for use in commercial crop pollination, and therefore may exhibit traits consistent with a ‘domestication syndrome’. Consequently, potential escape of individuals from these colonies could disrupt ecological balance and impact wild pollinator fitness e.g. through competition, pathogen spillover and introgression. In this study, we examine growth rates of colonies established from wild-caught and commercial *Bombus terrestris* (ssp. *audax*) queens, reared under the same lab conditions, to investigate distinctions between wild and commercial bumblebees during this key stage of the colony lifecycle. Several measurements were taken during colony rearing, including daily worker production rate, eclosed worker size, first worker developmental time and colony sucrose consumption. We found that colonies founded by commercial *B. t. audax* queens grew, in terms of worker production, at faster rates and had higher colony foundation success rates than wild-founded colonies. Our findings display potential evidence of domestication syndrome in commercial *B. terrestris* and have critical implications for risk-assessment of commercial bumblebee colony use, even when used within the native species, and subspecies, range.*

Other authors: Cian D. White, Jane C. Stout, James C. Carolan

P42 – Daniel Lim, University of Cambridge

Effects of Riparian Buffers on Pollinator Activity in Oil Palm Plantations

In Southeast Asia, a major driver of insect declines is habitat degradation due to oil palm agriculture, yet paradoxically, oil palm is heavily reliant on insects for ecosystem services such as pollination. Oil palm management thus needs to become more sustainable, such as by restoring riparian buffers (riverside conservation areas).

Here, I present the impact of riparian buffers on pollinator species in Indonesian oil palm plantations, part of the Riparian Ecosystem Restoration in Tropical Agriculture (RERTA) Project, a large-scale, long-term BACI (Before-After-Control-Impact) experiment.

Specifically, I used baited sticky traps and direct pollination measurements to assess the efficacy of three different riparian buffer management strategies and a control. Unexpectedly, my results indicate no major difference in pollinator abundance between the three buffers and control but show differences in pollinator diversity. Furthermore, pollination success was unchanged between buffers and control, indicating no ecosystem disservices.

My results highlight the importance of conserving insect diversity in agriculture. Specifically, I have shown that conservation areas may not immediately affect yield in palm oil plantations, but could improve resilience of pollination services through greater pollinator diversity. These findings have implications within and beyond academia as the oil palm industry supports millions of jobs in Southeast Asia.

Other authors: Edgar Turner, University of Cambridge; Becky Heath, University of Cambridge

P43 – Daisy Scott, University of Bristol**Winter-active parasitoids and pollinators: using a metabolomic approach to uncover potential resource competition between *Aphidius ervi* and *Bombus terrestris***

*Climate change is leading to milder winters in temperate areas, causing several insect species such as the parasitoid wasp *Aphidius ervi* and the bumblebee *Bombus terrestris* to become winter-active. As floral resources are typically low during winter, implementing strips of winter-flowering plants provides supplementary resources for beneficial insect populations, which are declining rapidly: 76% of insect biomass has been lost in the last 26 years. This loss is particularly pronounced in agroecosystems, which has ramifications for food production: pollinators are crucial to 35% of world crop production and biological control species, such as parasitoid wasps, provide pest regulation services worth approximately \$417 billion worldwide. However, competition over resources between different beneficial insects can occur. Due to being nectar-feeding insects, novel competition between parasitoids and bumblebees over floral resources could impact their nutritional status and parasitism rate. This project involves using cage experiments to investigate whether *B. terrestris* presence impacts the parasitism rate of *A. ervi* under winter conditions. Two floral treatments from winter-flowering species are being used to investigate how sugar composition could impact parasitism rate. Through employing metabolomic profiling and cameras, the project will determine the potential for exploitative and interference competition between the two species over floral resources.*

Other authors: David Renault (University of Rennes), Harry Siviter (University of Bristol), Martin How (University of Bristol), Lucy Alford (University of Bristol)

P44 – Alice Walker, University of Edinburgh, SRUC**Assessing Scotland's Pollinator Strategy: Taking a "Real-World" Approach**

Wild insect pollinators provide an essential ecosystem service, regulating crops and wild plant species, thereby encouraging ecosystems to be more resilient to disturbance. Continued pollinator population declines threaten this service, thus increasing the importance of utilising effective management strategies. However, despite considerable pollinator conservation effort, research identifying strategy effectiveness within the 'real-world', where practical problems, local farm differences and cost trade-offs are recognised, is still scarce. Outcome-based or Results-based payment schemes, a promising type of conservation scheme, attempts to address these trade-offs. By focusing on hedgerows and field margins, two key agroecosystem habitats, this project assesses these schemes effectiveness on pollinator communities, diversity and ecosystem function within South-East Scotland. Its findings should provide future policy recommendations and, through suggesting potential adjustments, ultimately improve the current schemes.

Other authors: Dr Gail Jackson (University of Edinburgh), Dr Lorna Cole (Scotland's Rural College), Dr Cathy Hawes (James Hutton Institute), Dr Graham Begg (James Hutton Institute)

Taxonomy and diversity

P45 – Joshua Clarke, Independent**Ecology and first description of a new-to-science hidden-snout weevil (Cryptorhynchinae) found in Northern Ireland, *Xenosacalles irlandikos* Stüben, Clarke & Anderson 2024**

*Discovered on wooden fences in damp woodland glen habitats, a new genus and species of hidden-snout weevils, *Xenosacalles* gen.n. *irlandikos* sp.n. are described from Northern Ireland with unknown origin. This species is distinguished from other Cryptorhynchinae in the Western Palaearctic by morphology and the mtCO1 barcode. The ecology of this introduced species is investigated, with discussion of how it was introduced and where it may originate. With increased global trade, further species may arise that are described from populations outside a place of origin.*

Other authors: Dr. Peter Stüben (Curculio Institute), Dr. Roy Anderson (independent), Stewart Rosell (AFBI / University of Aberdeen))

P46 – Jirui Wang, Zhejiang Agriculture & Forestry University
A taxonomy study of the whitefly (Hemiptera: Aleyrodidae) from China

Aleyrodidae belongs to order Hemiptera, suborder Sternorhyncha, there are 1707 species of whiteflies placed in 197 genera known worldwide, of which 273 species in 55 genera known from China, accounting for 15.9% of the world's total. As the taxonomy of whitefly is based almost entirely on the puparial stage, and adults offer so few characters to aid species definition, the adult characteristics of most species have not yet been described. We study and describe 48 known species of whitefly mainly based on adult characteristics, which is much enriches the information of adult characteristics of whiteflies. By comparative the adult morphology of these species, we mine some new stable taxonomic characteristic of adults, which can build the morphological systems for the systematic classification and identification of Aleyrodinae. Here we combine existing whitefly slide specimens with a large number of original descriptions, handdrawn drawings and ecological photos systematically compiles the taxonomic classification of Aleyrodinae in China: identification and description of Aleyrodinae in China, which includes 52 genera covering 12 tribes including 7 genera that have never been mentioned before, and we transfer 7 genera through the study.

Vector borne diseases

P47 – Katerina Athanasiou, Enalia Physis Environmental Research Center & Joint Services Health Unit, British Forces Cyprus
Surveillance of native and non-native ticks and tick-borne diseases at the Sovereign Base Areas of Cyprus

Ticks are major vectors of pathogens that cause disease to animals and humans. They can spread pathogens such as Rickettsia spp., Borrelia spp., Anaplasma spp. and etc. There are 19 tick species of five different genera known from Cyprus to date and all of them have been found on animals. Thus, studies on unengorged questing/hunting ticks their seasonality and associated pathogens are missing from the literature. Our project "Capacity building for the surveillance of native and non-native ticks and tick-borne diseases at the Sovereign Base Areas of Cyprus (Tick Alert)" looks at applying different surveillance methods (dragging, flagging, CO2 trapping) to collect questing and hunting ticks and study their seasonality since May 2023. The aim of the project is to improve our knowledge on tick biodiversity and associated impacts within the UK-SBAs in Cyprus and to raise awareness about ticks and tick-borne diseases among the local population. So far, we have recorded three species Ixodes ventaloji, Ixodes ricinus/inopinatus and Rhipicephalus turanicus s.l.. Adult ticks are the predominant tick developmental stage collected and this is the first report of a presumably established I. ricinus/inopinatus from Cyprus. Ticks are currently undergoing molecular analysis for a variety of pathogens. Moreover, to raise awareness regarding ticks we have created dissemination and educational material for children and adults.

Other authors: Angeliki F. Martinou, Laboratory of Vector Ecology and Applied Entomology, Joint Services Health Unit Cyprus, BFC RAF Akrotiri BFPO 57, Akrotiri, Cyprus / Anastasios Saratsis, 3Veterinary Research Institute, Hellenic Agricultural Organization-Dimitra (ELGO-DIMITRA), 57001, Thessaloniki, Greece

P48 – Kate Cook, University of Oxford

The vector potential of insect pests *Musca domestica* and *Blattella germanica* in the dissemination of resistant and pathogenic bacteria in a resource-limited Nigerian hospital

Insect infestation of hospitals is common in countries with tropical climates and limited infrastructure. Flies and cockroaches are known to carry antimicrobial-resistant (AMR) bacteria in Nigeria. The extent to which they are able to disseminate these bacteria in hospitals is unknown. The relative bodily localisations of different bacterial species may elucidate the possible vector mechanisms by which insects can disseminate different bacterial pathogens.

Houseflies and cockroaches were collected from Murtala Mohammed Specialist Hospital in Kano, Nigeria. They were washed and dissected to produce pooled samples representing bodily surface and gut microbiota. Bacterial culture, molecular and metagenomic experiments were conducted to assess the presence of AMR and pathogenic bacteria.

*Antimicrobial resistance genes (ARGs) against multiple classes of antibiotics were detected in bacteria cultured from all sample types at varying prevalence. Relative abundances of bacterial species varied between houseflies and cockroaches, and between gut compared to surface bacterial communities. Clinically relevant bacteria were abundant, including blaCTX-M-15-positive *Escherichia coli* and blaDHA-positive *Morganella morganii* in houseflies, and blaNDM-positive *Citrobacter* spp. and aminoglycoside ARG-positive *Serratia marcescens* in cockroaches.*

This work highlights the potential involvement of insect pests in pathogenic and AMR transmission networks in clinical settings – a critical issue that requires further investigation.

Other authors: Kate Cook, Ineos Oxford Institute for Antimicrobial Research, Department of Biology, University of Oxford. Maryam Yusuf Ahmad, Murtala Muhammad Specialist Hospital, Kano, Nigeria; Department of Microbiology, Bayero University. Firdausi Said Mohd, Murtala Muhammad Specialist Hospital, Kano, Nigeria. Aminu Aliyu, Department of Medical Microbiology, Aminu Kano Teaching Hospital, Kano, Nigeria. Abdulrazak Muhammad, Department of Microbiology, Bayero University. Shonnette Premchand-Branker, Ineos Oxford Institute for Antimicrobial Research, Department of Biology, University of Oxford. Chioma Achi, Ineos Oxford Institute for Antimicrobial Research, Department of Biology, University of Oxford. Kenneth Iregbu, National Hospital Abuja, Nigeria. Timothy Walsh, Ineos Oxford Institute for Antimicrobial Research, Department of Biology, University of Oxford. Kirsty Sands, Ineos Oxford Institute for Antimicrobial Research, Department of Biology, University of Oxford.

P49 – Sanam Sewgobind, Animal and Plant Health Agency

Assessing vector competence of West Nile virus in *Culex pipiens* mosquitoes

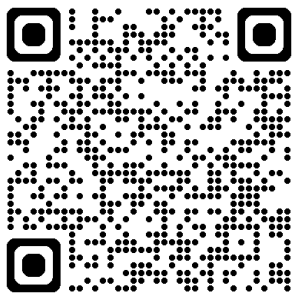
*West Nile virus (WNV) is a mosquito-borne virus causing disease in humans and horses. Vector competence (VC) is the potential of an arthropod vector to transmit a pathogen. A component of VC is the extrinsic incubation period (EIP), defined as the time between virus ingestion and the capability to onwardly transmit virus via saliva. We fed UK *Culex pipiens* mosquitoes with a WNV-infectious bloodmeal (GenBank accession number MH244511; 107 PFU/ml). After 10- or 14-days post-infection (DPI), mosquito tissues and saliva were collected and assessed using RT-qPCR for infection, dissemination, and transmission. Mosquitoes showed evidence for infection, dissemination and transmission at 10 DPI suggesting the EIP to be ≤ 10 days. However, the transmission efficiency was low (3.3%). Additionally, a sub-group of mosquitoes were fixed, sectioned and immunolabelled with anti-flavivirus envelope monoclonal antibody. Virus antigen within the mosquito midgut was visualised confirming viral replication. Furthermore, next generation sequencing from WNV-infected tissues showed evidence for non-synonymous mutations (T888I, I1047V, F1056S and C1995R). These changes in the genome consensus sequence suggests virus evolution during the infection process within the mosquito midgut. These results confirm *Culex pipiens* is competent for WNV transmission and WNV undergoes mutations that alter protein translation potentially contributing to*

mosquito infection.

Other authors: Ben Jones, Animal and Plant Health Agency; Insiyah Parekh, Animal and Plant Health Agency; Estela González-Fernández, Animal and Plant Health Agency; Luis M Hernández-Triana, Animal and Plant Health Agency; Edward Wright, University of Sussex; Nicholas Johnson, Animal and Plant Health Agency; Karen L Mansfield, Animal and Plant Health Agency

- Online posters

We are pleased to welcome a selection of online posters from delegates joining virtually. We encourage all in-person delegates to take the time to view these posters using the QR code below and contact presenters with any questions you have about their research.



royensoc.co.uk/ento24-posters

Ioanna Angelidou, Joint Services Health Unit, Enalia Physis Environmental Research Centre, Ionian University

Understanding of the ecology and trophic interactions of Eleonora's Falcon (*Falco eleonora*) with flying insects at the Akrotiri peninsula in Cyprus

*Insects are dominating the land biota in terms of numbers, biomass, and diversity, and constitute the largest food base for terrestrial carnivorous animals. Eleonora's falcon (*Falco eleonora*) is an aerial predator that feeds on large flying insects and switches its diet to primarily small passerine species during nesting, and needs continuous monitoring, especially because insect feeding grounds of the species are subject to intensive anthropogenic pressures. This study aims to evaluate the effect of land use type on foraging areas of Eleonora's falcon at their breeding grounds, as well as the human-induced pressures that affect spatial distribution of the species across the area of Akrotiri, in Cyprus. Spatiotemporal activity and correlation of Eleonora's falcon presence with the prevailed insect prey along with the significance of habitat characteristics in relation to food resources are examined within the framework of Darwin Plus. In total 15 plots (three per land use type) were selected, all used by Eleonora's falcon as foraging areas in the recent past according to telemetry tools. This study aims to increase our understanding regarding Eleonora's falcon trophic interactions with insects by adopting the following insect sampling methods: (i) Malaise traps, (ii) transect counts, (iv) Cicadas' surveys.*

Other authors: George Karris, Ionian University, Anastasios Saratsis, Veterinary Research Institute, Alexander Kirschel, University of Cyprus, Helen Roy, UKCEH and University of Exeter, Thomas Hadjikyriakou, Akrotiri Environmental Education Centre, Angeliki F Martinou, Joint Services Health Unit, Enalia Physis Environmental Research Centre, The Cyprus Institute

Chara Apostolidou, Enalia Physis Environmental Research Centre and Laboratory of Vector Ecology and Applied Entomology, Joint Services Health Unit

Environmental education and Raising awareness about pollinators and beneficial insects

Insects support many functions and services essential to the life of humans, animals and ecosystems. Climate change, degradation and fragmentation of natural habitats, urbanization, agricultural intensification with extensive use of pesticides negatively affect insect biodiversity globally and Cyprus is no exception to the rule. Cyprus is considered a biodiversity “hotspot” rich in insect biodiversity and endemism. Our work focuses on safeguarding insect biodiversity by filling educational gaps regarding beneficial insects and pollinators in particular. We will create a database for beneficial insects for the UK Sovereign Base area in Cyprus, promote environmental education through tools such as children’s stories and interactive group games) to primary schools so that foundations are built from an early age. Several workshops and citizen science outreach activities including BioBlitz and recordings using the FIT Count app are applied to motivate the public to record and protect beneficial insects.

Anton Bilsen, KU Leuven

Evaluation of a lepidopteran in vitro model of interactions between extracellular vesicles and viruses

Our project aims to develop an insect-derived cell line as an in vitro model to study the interactions between insect viruses and endogenous extracellular vesicles (EVs). EVs are membrane-bound nanostructures secreted by all pro- and eukaryotic cells, often facilitating intercellular communication. Recent research suggests a role of EVs in antiviral and other immune responses, including in insects. However, isolating EVs from live insects entails substantial challenges, including co-isolation of contaminants such as lipoproteins and differences in EV characteristics among organs and tissues within a single individual. EV studies in non-model species are also hampered by refractoriness to genetic and biochemical manipulations. Here, we use a variety of techniques to characterize EVs from a lepidopteran cell line (Sf9) and thereby evaluate its suitability as an in vitro EV study system.

Other authors: Simon Remans, KU Leuven; Stijn Van den Brande, KU Leuven; Dulce Cordeiro dos Santos, KU Leuven; Jozef Vanden Broeck, KU Leuven

Magda Bohus Hományi, National Centre for Biodiversity and Gene Conservation, Institute for Farm Animal Gene Conservation

Effect of carbamide-water-saccharose solution on honeybee in laboratory experiments: sublethal effects and concentration dependence of mortality rate

Carbamide (urea) is widely used as biostimulant and component of various fertilizer fluids. Urea is stable in aqueous solution, but it is considered to be readily biodegradable. It is known that urea is present in the bee gut, as a nitrogen content product of the protein metabolism of honeybees. However, we don’t have enough information about its potential toxicity to honeybees. Our aim was to get more information about the role of urea molecule in honeybee physiology.

Different amounts of carbamide was feed orally in 50% saccharose syrup (100-6400 µg a.i. /bee for acute and 5-40 µg/ml for chronic examinations). Our results show that in acute oral tests mortality in healthy adult bees increased slightly after 24 hours compared to the untreated control group. Mortality showed a small but further increase after 48 hours, depending on the urea concentration of the test solution. Sublethal effects observed on the treated groups were: restless, apathy, falling over and inability to fly; higher rate at higher concentrations of urea consumed. The chronic test led to similar results.

The practical utility of the knowledge gained from this experiment may help with the correct application of carbamide solutions in field crop production

Other authors: Edit Zajác, National Centre for Biodiversity and Gene Conservation, Institute for Farm Animal Gene Conservation

Jakovos Demetriou, Laboratory of Vector Ecology and Applied Entomology, Joint Services Health Unit Cyprus, National and Kapodistrian University of Athens, Enalia Physis Environmental Research Centre
The “Ants of Cyprus” website: online resources on the ants of a biodiversity hotspot

Ants are crucial components to ecosystems and their functioning, although the impact of some invasive alien species has been estimated to cost billions of dollars annually, on a global scale. The island of Cyprus is situated at the heart of the eastern Mediterranean, a global biodiversity hotspot and rarity centre for ants. Nevertheless, the myrmecofauna of Cyprus is considered understudied with online resources and scientific publications synthesizing a checklist of just 65 native and ten alien species. However, an important number of new alien and native species have been identified within the last few years. In the framework of the Darwin Plus Fellowship (DPLUS200) “Biodiversity and spatiotemporal patterns of ants in the Akrotiri Peninsula” the “Ants of Cyprus” website (<https://sites.google.com/view/ants-of-cyprus>) has been developed, aiming to (1) raise awareness and increase local knowledge on the biodiversity and importance of ants, (2) provide ecological data and (3) enhance conservation and management efforts for native and alien species, respectively. The website is intended for use by both the scientific community and the wider public, has been designed to be dynamic and user-friendly, and will be regularly updated throughout the project’s duration.

Other authors: Christos Georgiadis, 1 Museum of Zoology, National and Kapodistrian University of Athens, 15784 Athens, Greece, 2 Section of Zoology and Marine Biology, Department of Biology, National and Kapodistrian University of Athens, 15784 Athens, Greece; Sebastian Salata, University of Wrocław, Department of Biodiversity and Evolutionary Taxonomy, Myrmecological Laboratory, Przybyszewskiego 65, 51-148 Wrocław, Poland; Helen E Roy, UK Centre for Ecology & Hydrology, Benson Lane, Crowmarsh Gifford, Oxfordshire, United Kingdom; Angeliki F Martinou, 1 Laboratory of Vector Ecology and Applied Entomology, Joint Services Health Unit Cyprus, BFC RAF Akrotiri BFPO 57, Akrotiri, Cyprus 2 Enalia Physis Environmental Research Centre, Akropoleos 2, Aglantzia 2101, Nicosia, Cyprus 3 Climate and Atmosphere Research Centre/ Care-C, The Cyprus Institute, Athalassa Campus, 20 Konstantinou Kavafi Street, 2121 Aglantzia, Nicosia, Cyprus

Subrata Goswami, Banaras Hindu University

Comparative assessment of the in vitro insecticide degradation abilities of diverse gut bacteria associated with rice stem borer complex

*Gut symbionts provide several physiological advantages including the ability to withstand xenobiotics in insects. The present study aimed at characterizing the culturable gut bacteria from three stem borers attacking rice (*Scirpophaga incertulus*, *Sesamia inferens* and *Chilo suppressalis*) morphologically, biochemically, and genetically (based on 16S rDNA sequences). Their abilities to degrade two commonly used insecticides, i.e., chlorantraniliprole and thiamethoxam were quantified in vitro through minimal media study using HPLC. There was a great variation in the gut bacterial composition of these three borers despite belonging to the same guild and being collected from the same host (Varshadhan: CRLC-899) at the same time from ICAR-NRRI farm, Cuttack, India. It suggested that apart from the host plants, the gut microbiome is also significantly influenced by the respective insect species and their ecological requirements.*

Chlorantraniliprole and thiamethoxam were degraded to the tune of 10.52 to 74.38% and 14.30 to 33.61%, respectively as compared to the control. The differential ability of the bacterial fauna to utilize these insecticides as carbon sources provides insights into their possible role in insecticide detoxification in the rice SBs and future research can open up pathbreaking avenues for sustainable management of these most notorious pests of rice.

Other authors: S.B. Das, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur-482004; P.C. Rath, ICAR-National Rice Research Institute, Cuttack-753006

Ankita Gupta, ICAR-National Bureau of Agricultural Insect Resources

Braconid species complex (Hymenoptera: Braconidae) associated with plant galls from India

Braconids exhibit phytophagy, sequential predatory cum phytophagy and completely predatory behaviour apart from being parasitoids. During 2022-2024, an attempt was made to document braconids from various host associations under SERB funded project CRG/2021/001523 in India. Several plant galls from various genera viz. Ficus, Terminalia, Carissa, Garuga and Cinnamomum etc. mostly induced by psyllids and mites were collected. Among the collected galls, 10 morpho species of Braconinae and two species of Cheloninae with interesting host associations were observed. Leaf galls induced by psyllids on Ficus recemosa L., where braconid wasp larvae with sclerotised mandibles feeding on psyllid nymph by clinging on the back showed a typical predatory behaviour followed by phytophagy. Same behaviour was noticed in leaf galls of Carrisa spinarum L. Bracon garugaphagae Ranjith & Quicke (sequential predatory and phytophagy) from leaf galls of Garuga pinnata Roxb. and Bracon predatorius Ranjith & Quicke (complete predatory from Cinnamomum sp.) was reported from Southern and Northern India. Phanerotoma sp. from leaf galls of G. pinnata and Chelonus sp. from stem galls of Terminalia sp. were reared. Many other braconids were observed and collected from the leaf rolls of Attelabidae, Ficus tictoria G.Forst. syconia, Cassia pods, Phyllanthus reticulatus Poir. and Leucas sp. inflorescence.

Other authors: Rohit Pattar (ICAR-National Bureau of Agricultural Insect Resources), Hemanth Kumar H. M. (ICAR-National Bureau of Agricultural Insect Resources, S. N. Sushil (ICAR-National Bureau of Agricultural Insect Resources))

Aparna Kalawate, Zoological Survey of India, Western Regional Centre

India a Biodiversity rich treasure: Moths classical example

India is a megadiverse country with infinite diversity of insects holding in it. Lepidoptera is the second rich group in terms of species count. There are currently more than 13000 known species of moths in India. Museums in India are also rich in terms of specimen holdings. Zoological Survey of India, Kolkata and its regional stations located across India harbors rich diverse specimens. Moths are considered to be an important ecological indicator. They are the secondary source of food for higher animals like: Bats, frogs, birds, etc. The larvae of some moths are being consumed as a protein rich source. Some moths for instance, sphinx moths are the pollinators of the night blooming flowering plants in the wild. There are many important moths for instance silk moths which is source of livelihood for many farmers. The scientific taxonomic studies on such an important component of our ecosystems were largely neglected by the scientists and citizens of India. In this present study, an attempt has been made to shed lights on the diversity pattern of the moths. Also, the ways are discussed to increase the awareness about popularisation of moth's studies in India.

Other authors: Aparna Sureshchandra Kalawate

Mario Leto, Meiji University

Fostering positive worldviews: An ecolinguistic study of the discursive representations of insects and arachnids in online media

Insects and arachnids play a vital role in ecological maintenance but there are indications that populations are in decline worldwide. And while a few species enjoy high-profile consideration, most are maligned as pests and intruders, as is evident in the discourse of online media. These media representations, with the potential to affect worldviews in both positive and negative ways, are the focus of this linguistic study.

The theoretical framework for the study is ecolinguistics (Stibbe 2021), chosen for its potential to reveal in discourse the underlying worldviews about the natural world. In particular, I used four analytical tools: framing theory (Lakoff, 2010; 2014), appraisal patterns (Martin and White, 2005), erasure (van Leeuwen, 2008), and transitivity patterns (Halliday and Matthiesen, 2014). The overall goal was to identify the semiotic resources (van Leeuwen 2005) with the potential to alter the way that humans perceive and act toward the non-human-animal world.

The results of the study indicate that online media contributes to negative representation of insects and arachnids; that some attempts at positive representations still contribute to and perpetuate negative representations; and that wholly positive representations do exist, foregrounding the importance of the natural systems that support all life.

Jose I. Martinez, Florida Museum of Natural History, University of Florida

A new molecular phylogeny of Noctuoidea reveals robust family-level relationships

The monophyly of the moth superfamily Noctuoidea is robustly supported by both morphological and molecular evidence. However, relationships among families of Noctuoidea remain uncertain. We created a comprehensive phylogenomic dataset comprising of 676 loci from 623 sequenced Noctuoidea species, built from AHE data, transcriptomes, and genomes. Taxon sampling spanned all seven noctuid families, approximately 50 noctuid subfamilies, and 27 outgroups. Utilizing both maximum likelihood and multi-species coalescent approaches, we conducted a phylogenetic analysis that yielded robustly supported relationships among higher-level groups within Noctuoidea. Our results demonstrated more stable phylogenetic relationships, prompting us to propose the reclassification of at least 13 subfamilies (Arctiinae, Bagisarinae, Calpinae, Cobubathinae, Diphtherinae, Dyopsinae, Eulepidotinae, Eustrotiinae, Hypeninae, Hypocalinae, Lymantriinae, Pantheinae, and Plusiinae) as families to ensure the monophyly of existing Noctuoidea families. Additionally, we identified putative morphological apomorphies that support these family-group clades.

Other authors: Jose I. Martinez, Florida Museum of Natural History, University of Florida. Nicholas Homziak, Florida Museum of Natural History, University of Florida. David Plotkin, Florida Museum of Natural History, University of Florida. Christian Couch, Florida Museum of Natural History, University of Florida. Taylor Pierson, Florida Museum of Natural History, University of Florida. YiMing Weng, Okinawa Institute of Science and Technology. Jacqueline Y. Miller, Florida Museum of Natural History, University of Florida. Akito Y. Kawahara, Florida Museum of Natural History, University of Florida.

Sebastián Pita, Universidad de la Republica

Reconstructing *Sordida* subcomplex (Triatominae, *Triatoma*) phylogeny across species distribution range

*The conformation of the *Sordida* subcomplex (Hemiptera, Reduviidae, Triatominae) has been a topic of prolonged debate, with diverse methodological approaches employed to discern its constituent species. Up to now, *Triatoma sordida*, *T. garciabesi* and *T. rosai* comprise part of this subcomplex. Distinguishing and identifying these three species poses significant challenges due to their pronounced morphological similarity, overlapping distributions, and presence of natural hybrids. This study aims to uncover the genetic diversity and geographic spread of these three species by analyzing a mitochondrial cytochrome b gene fragment and supplementing this with chromosomal studies across natural populations from an extensive geographical range, including Argentina, Bolivia, Brazil, and Paraguay. Phylogenetic analyses reveal genetic distances that would suggest the presence of at least six putative species, rather than the three currently recognized. The present findings underscore the potency and significance of molecular analyses from natural populations for species identification and highlight the limitations of morphology in classifying Triatominae species.*

Other authors: Julieta Nattero, Universidad de Buenos Aires; Romina Valeria Piccinali, Universidad de Buenos Aires; Ana Laura Carbajal-de-la-Fuente, Centro Nacional de Diagnóstico e Investigación en Endemo-Epidemias (CeNDIE); Antonieta Rojas de Arias, Centro para el Desarrollo de la Investigación Científica (CEDIC); Catarina Macedo Lopes, Laboratório Interdisciplinar de Vigilância Entomológica em Díptera e Hemiptera- Instituto Oswaldo Cruz; Francisco Panzera, Universidad de la República

Dachena Romain Gracia, Mohammed VI Polytechnic University

Quinoa insect pests: an exploratory survey and screening for resistance to its major insects

Quinoa (Chenopodium quinoa) is an annual herbaceous plant, native to the Andes of South America. The FAO stresses the importance of promoting the cultivation of quinoa for its high natural and nutritional value, as well as for sustainable global food security. It has recently been introduced in Morocco, where it has shown excellent adaptation and drought tolerance in arid areas. Previously unknown agronomic, biotic, and abiotic problems may arise when a new crop is introduced into a new geographic region. When pests are not studied, inappropriate pest management techniques are applied. The main objective of this research is to identify the predominant insect pests of quinoa in the different regions of Morocco and to measure their severity, study their population dynamics and determine the type of damage caused to the plant at different stages. Also, we screened several quinoa ecotypes from UM6P collection for resistance to the main insect pests. The first observation from the survey in Rhamna and North part of Morocco, there is a wide range of chewing and sucking insects from different orders that cause damage to quinoa plants. Also, the preliminary screening results showed a notable variability in the insect's resistance in different quinoa ecotypes.

Other authors: Karim El FAKHOURI, Mohammed VI Polytechnic University; Manal MHADA, Mohammed VI Polytechnic University; LAMIRI Abdeslam, Hassan I University; Mustapha El Bouhssini, Mohammed VI Polytechnic University

Cristhian Rossi, Universidad Nacional Mayor de San Marcos

Spatial and temporal variation in the community structure of insects and its relationship with vegetation and hydroperiod in a coastal wetland of the South American Pacific

Ventanilla Wetlands Regional Conservation Area is a coastal wetland, located in the Ventanilla district, constitutional province of Callao, Lima department, Peru. It is amid a highly anthropogenically impacted area, therefore, it is necessary to conduct studies on its effect on the biological communities that develop there. To this end, the variation of the insect community structure in the ecosystem was evaluated at the spatial and temporal level, and the influence of vegetation and hydroperiod on these changes was defined. The richness and abundance of plants and insects were evaluated in eight sampling stations for six months, from February 2016 to February 2017, and changes in the composition of trophic guilds were also evaluated. It was observed that diversity is greater in the stations located in the inner part of the wetland; the anthropogenic impact is more evident in the external stations. The richness of vegetation and the hydroperiod influence the increase in the richness and structural changes of the insect community, which will move and concentrate in certain areas of the wetland favored by the presence of resources. Better management plans and awareness-raising campaigns should be implemented to reduce the impact on the wetland's border areas.

Mamta Sharma, Banaras Hindu University

Buzz Pollinator Niche Responses Under Climate Change in India

Pollinator losses are a major threat to global food security. In recent decades, there has been a growing concern regarding the decline of global pollinator populations. As climate change has been established to cause severe biodiversity loss especially in tropical areas, pollinator populations are expected to be at risk.

However, there is scarcity of research on this issue in tropical regions. Some pollinating groups such as buzz pollinators are vital contributors to specialized plant pollination need. Their loss may translate into decrease in agricultural productivity of supported plants. For agriculture dependent developing economy like India, the implication can be substantial on the health of growing population and economic stability. The study thus utilizes Species Distribution Modelling to assess the susceptibility of buzz pollinator habitat to climate change in Indian region. The purpose of the study is to contribute to a broader understanding of climate change impacts on pollinators in tropical ecosystems and aid in the development of targeted conservation strategies for protecting vital ecological services provided by these pollinators.

Other authors: P. C. Abhilash, Institute of Environment and Sustainable Development, Banaras Hindu University

Christian von Trotha Taylor, Open University

Emergence of niche space in rotting wood through fungal-insect interactions

*The paedogenetic cecid *Brittenia fraxinicola* exploits narrow sub-cortical niches of dead hazel (*Corylus avellana*) wood that has been colonised by the fungi *Hypoxylon fuscum* and *Vuilleminia comedans*. The insects specifically inhabit interaction zones containing areas of pseudosclerotial plate (PSP). The presence of cecids influences the interaction between fungi, causing an expansion of the PSP zone. Fungal interactions in turn cause changes in cecid behaviour, as well as increased larval size and enhanced cecid population growth. We conclude that the interaction between insects and fungi is an example of niche construction in which *B. fraxinicola* promotes the formation of its own habitat.*

Other authors: Alan D.M. Rayner, University of Bath, UK; Stuart E. Reynolds, University of Bath, UK

Maria C. Tocora, University of Toronto

Hymenoptera: Diversity of the second most species-rich animal order in the Galapagos Islands

The Galápagos Islands are a well-known biodiversity hotspot, yet the diversity of Hymenoptera, one of the most species-rich insect orders, remains poorly understood. Here, we combined data from museum collections, literature reviews, and extensive fieldwork across ten major islands to address the diversity of the order in the archipelago. We sampled different vegetation zones over latitudinal gradients using hand nets and different insect traps (e.g., pan, Malaise, pitfall, bait, and Winkler traps). We identified over 22,303 specimens from 41 families (not including Formicidae) within Hymenoptera. We document 664 morphospecies differentially distributed across islands and habitats. Accumulation curves indicate near completion of sampling. As for the family Formicidae, we identified 382,000 specimens corresponding to 50 species, 8 endemic and 42 introduced. Based on DNA metabarcoding, we also found high genetic variation across endemic ant species in the archipelago. This study provides critical insights into the ecological dynamics and diversification of the order Hymenoptera in the Galápagos. Also, we offer pioneering baseline information for future research and conservation efforts of insects in the islands.

Other authors: Patricio Picon (Escuela Superior Politecnica de Chimborazo); José M Avendaño (Escuela Superior Politecnica de Chimborazo); Fernando Fernández (Universidad Nacional de Colombia); Andrés Sánchez Restrepo (CONICET/FuEDEI); John M. Heraty (University of California); Carlos Sarmiento (Universidad Nacional de Colombia); Henri Herrera (Escuela Superior Politecnica de Chimborazo)

Zsófia Varga-Szilay, ELTE Eötvös Loránd University

Improving biodiversity in Central and Eastern European domestic gardens needs regionally scaled strategies

Amid ongoing urbanization and increasing anthropogenic activities, domestic gardens, while they cannot replace natural habitats, play a crucial role in enhancing urban biodiversity by supporting green areas and

ecological corridors. Moreover, these biodiversity-friendly gardens also improve human well-being and foster a connection between nature and people. We circulated a questionnaire to investigate how the garden parameters, the gardening motivation of garden owners, their knowledge about insects, and their pesticide use habits depend on each other in nine Central and Eastern European (CEE) countries and explore the differences and similarities between gardens and gardening practices with a potential for maintaining high biodiversity. Our findings reveal significant variability among participating countries, and even within them on a smaller scale, highlighting the need for region-specific approaches rather than unified regulations across European countries to maximize the gardens' conservation value for insects. Our study underscores the potential of domestic gardens in designing eco-networks and informs strategies to optimize their environmental benefits. Additionally, our findings suggest that effective environmental educational programs and tailored strategies should be developed to meet local needs and provide comprehensive biodiversity-related information, reaching all strata of society. This is especially important in CEE, where such initiatives are currently under-emphasized.

Other authors: Arvīds Barševskis - Daugavpils University; Klára Benedek - Sapientia Hungarian University of Transylvania; Danilo Bevk - Warsaw University of Life Science; Anton Krištín - Institute of Forest Ecology SAS; Jana Růžicková - ELTE Eötvös Loránd University; Lucija Šerić Jelaska - University of Zagreb; Eve Veromann - Estonian University of Life Sciences; Silva Vilumets - Estonian University of Life Sciences; Kinga Gabriela Fetykó - Independent researcher; Gergely Szövényi - ELTE Eötvös Loránd University; Gábor Pozsgai - University of the Azores

Bobika VK, University of Calicut

Red is safer: influence of gall traits on parasitism in *Garuga pinnata* Roxb.

*Plant galls induced by gall inducers (hereafter GI) can manipulate plant development in accordance to their own needs. Gall traits like volume and colour are influenced by the continuous stimuli from the GI. Though these traits safeguard the gall inducers, they are not refrained from top—down forces. We studied the role of gall inducer (*Phacopteron lentiginosum* Buckton) in manipulating gall size on the leaf galls of *Garuga pinnata* Roxb. Apparent change in phenotypical selection of galls for oviposition by parasitoids is also studied. Galls were inspected for the inhabitants, associated parasitoids (braconids, encyrtids) and their relation with phenotypical traits like gall volume and colour. Gall volume was positively related to number of gall inducers which highlight the role of incessant GI's stimuli. Though gall volume was found to be a positive driver of parasitism, Bracon parasitisation did not have any significant effect on gall volume. On the contrary, number of GI showed a positive indirect influence on the Bracon parasitisation. The significance of gall colour on parasitism was proved in the present study wherein parasitoids avoid red coloured galls. Biochemical analyses also showed the higher concentration of proteins, phenolics and anthocyanin in red coloured galls which may deter parasitoids. Way forward, this study acts as a first line research which depicts the influence of colour in galls wherein parasitoids eschew red coloured galls over green coloured galls.*

Other authors: K Manjusha (University of Calicut), M Nasser (University of Calicut), AP Ranjith (Chulalongkorn University)