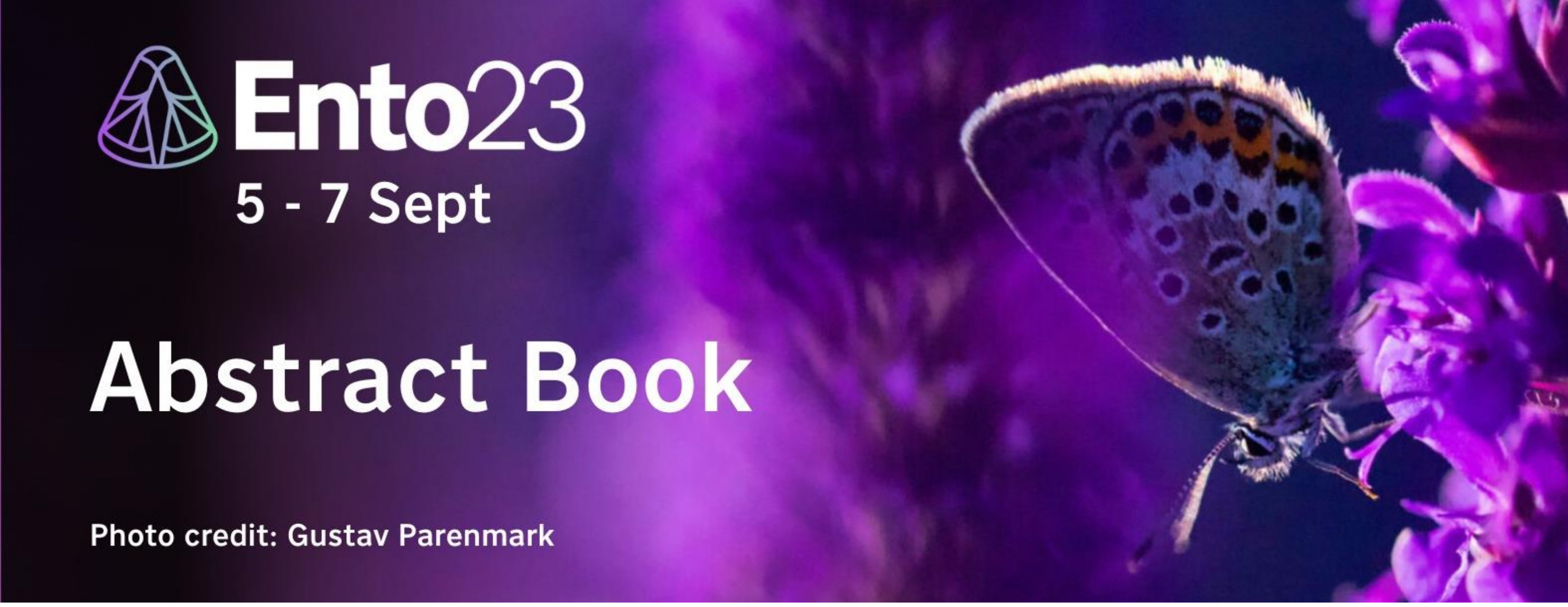

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Abstract Book

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Tuesday 5 September

- Movement and Migration

Lecture Theatre A

Chairs: Johanna Hedlund and Jason Chapman

10:45 – Shawan Chowdhury, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Insect migration and conservation

Globally, at least 3% of butterflies (568 species) show evidence of migratory movements, yet the taxonomic and geographic distribution of butterfly migrants remains poorly understood. About 62% of publications focus on the monarch, with nearly 50% of migratory butterfly species mentioned in a single paper. Several research methods have been applied to ascribe migratory status and to study the physiology, neurobiology, and ecology of migration; however, virtually all this research is on a handful of species. There remain hundreds of species for which we do not understand the comprehensive seasonal movement pattern, flight destinations, wintering, or breeding grounds. The conservation status of butterfly migrants also remains poorly understood. While protected areas safeguard different animal groups, nearly 85% of migratory butterflies are inadequately represented in the global terrestrial protected area system. Coordinated efforts across multiple countries are needed to conserve migratory butterflies.

11:15 – Toby Doyle - University of Exeter

Sex differences in insect migration

Migration is a widely observed phenomenon found across many lineages from large birds to small flies. The ability to undergo long-distance movement is underpinned by various morphological, physiological and behavioural traits, the genetic basis of which are poorly understood. Recently we have unpacked the genetic mechanisms underpinning migration in the marmalade hoverfly (Diptera: Syrphidae) by detecting differential gene expression between female summer and female migratory forms. Male hoverflies also migrate, but sex ratios change from approximately equal in northern Europe to >90% female in southern Europe suggesting males are poorer long-distance migrants. To elucidate the mechanisms underpinning this sex difference, we carried out a genome-wide transcriptomic comparison between active male and female migrants, caught as they flew through a high Pyrenean pass. We also looked at various morphological (wing area, wing loading, wing aspect ratio) differences between the sexes. Our analysis of differentially expressed genes revealed that males are metabolically very active but 'live fast and die young', spending their resources to mate on migration while not maintaining energy balance or the health of body tissues as seen in female migrants. Morphologically we found that female hoverflies had a larger wing area and lower wing loads when compared to males with no differences in aspect ratio. This highlights morphological differences potentially impacting migratory success rates. Finally, our study also highlights the role of a conserved cellular component that mediates energy allocation in this process and provides a wealth or testable hypotheses for future research.

Other authors: Karl Wotton, University of Exeter

11:30 – Fanqi Gao – University of Exeter

Mapping the potential Spatio-Temporal Distribution of Fall Armyworm in Europe

The fall armyworm (*Spodoptera frugiperda*) is a major migratory noctuid moth originating in the Americas. The caterpillars of this pest can damage over 180 species of plants. The fall armyworm’s preferred host plant (corn) suffers tremendous damage, and the yield can be reduced by up to 70%, potentially causing billions of dollars of economic loss. The fall armyworm has already invaded almost every country in Africa and Asia, even as far as Australia. According to the EPPO report, the fall armyworm was discovered in the Adana province of Turkey in 2022, significantly increasing the risk of dispersion in Europe. Therefore, predicting the invasion risk of fall armyworms in Europe is urgent. Insects sourced from Africa play a significant role in invading Europe. My PhD project involves conducting a risk assessment on two potential routes for African FAWs to invade Europe. To predict the seasonal invasion risk of fall armyworms in Europe, we will use species distribution modelling and trajectory simulation to create a Spatio-Temporal Distribution model. In this presentation, I will introduce my project and the main objectives of our research and share some preliminary results.

Other authors: Fanqi Gao1, Gao Hu2, Robert L. Meagher3, Regan Early1, Jason W. Chapman1, 1. University of Exeter, UK, 2. Nanjing Agriculture University, 3. US Department of Agriculture-Agricultural Research Service

11:45 – Karl Wotton – University of Exeter

Genetic pathways involved in active insect migration

Insects are capable of extraordinary feats of long-distance movement that have profound impacts on the function of terrestrial ecosystems. The ability to undertake these movements arose multiple times through the evolution of a suite of traits that make up the migratory syndrome, however the underlying genetic pathways involved remain poorly understood. Migratory hoverflies (Diptera: Syrphidae) are an emerging model group for studies of migration. They undertake seasonal movements in huge numbers across large parts of the globe and are important pollinators, biological control agents and decomposers. In this talk I describe our work characterising migration in this group and present the results of a genome-wide transcriptomic comparison of actively migrating hoverflies, captured from a high mountain pass as they flew south to overwinter, with the transcriptomes of summer forms which were non-migratory. Our analysis revealed the differential expression of genes with a remarkable range of roles in metabolism, muscle structure and function, hormonal regulation, immunity, stress resistance, flight and feeding behaviour, longevity, reproductive diapause and sensory perception. These results provide a powerful genomic resource for research, and I discuss new lines of investigation that have recently emerged from this work.

12:00 – Birgen Haest – Swiss Ornithological Institute

Aerial diel insect flight periodicity patterns across Europe

Most insects depend on flight for their movements during at least part of their life cycle, and each day and night, innumerable insects take to the skies. Diel timing of flight activities are not random, e.g., many insect species show peak flight activity at dawn, noon, or dusk. Quantification of these patterns in flight periodicity are mostly limited to small-scale single-species visual count or trapping studies. The advent of vertical-looking entomological radars has enabled studying diel flight periodicity at larger scales and at previously difficult-to-sample altitudes. The experimental nature of such radars has, however, limited the geographic extent over which flight periodicity patterns were assessed, to a few hundred kilometres. Here, we quantify patterns in diel flight periodicity across Europe with continuous measurements from March to October 2021 using a network of fifteen vertical-looking radars. The network consists of commercially available Birdscan MR1 radars that detect insects between 50 and 500m altitude and stretches along a southwest to northeast axis from southwest France to Finland in the northeast. We present patterns in diel flight periodicity across Europe, and how diel peak flight timing, absolute insect numbers, and the relative abundance of crepuscular, nocturnal, and diurnal insect numbers vary as a function of geographic location, season, altitude, and habitat. We then also show how the local environment, weather, and insect composition drive these observed patterns across Europe and across the year.

Other authors: Will L S Hawkes (Swiss Ornithological Institute), Felix Liechti (Swiss Birdradar Solution AG), Susanne Åkesson (Department of Biology, Centre for Animal Movement Research, Lund University), Jason Chapman (Centre for Ecology and Conservation and 4 Environment and Sustainability Institute, University of Exeter & Department of Entomology, Nanjing Agricultural University), Vincent Comor (Independent researcher), Fabian Hertner (Swiss Birdradar Solution AG), Anna Nesterova (Orade-Brèche), Judy Shamoun-Baranes (8 Theoretical and Computational Ecology, IBED, University of Amsterdam), Silke Bauer (Swiss Ornithological Institute)

12:15 – Johanna Hedlund – University of Exeter and Lund University

Migration in dragonflies and damselflies - a global overview

Most aspects of the migration of Odonata (dragonflies and damselflies) remains unexplored. We know very little about which species that migrate, where and how far they fly and what adaptations they have evolved to cope with the strains of e.g. open ocean flight and navigation. In this talk I will give a concise overview of the current knowledge of dragonfly migration based on an exhaustive literature review. The results include a biogeographical analysis, showing an overrepresentation of migrant species in the Palearctic, and a phylogenetic analysis, demonstrating that migration likely appeared at several points during odonate evolution. In addition, the diversity of this ancient order of insects, the first animals to fly on Earth, reveals a variety of migratory behaviours. The fact that dragonflies may travel hundreds of kilometres and form immense swarms emphasise their importance for the ecosystems they connect through migration and the need to remedy the current knowledge deficit of their movement ecology.

12:30 – Will Leo Hawkes – Swiss Ornithological Institute

The most remarkable migrant - Assemblage and quantification of migratory insect species across European flyways

Insects are perhaps the most remarkable of migrants. They move in their trillions and are known to travel thousands of kilometres using celestial cues and wind patterns to guide and power their migration. However, despite the impressive nature of this phenomenon, very little is known (when compared to knowledge of other migrants such as birds) about exactly which insect species migrate, how many they number, where they are going, and the ecological roles insect migrants play.

This talk is based on my PhD thesis and focuses on Europe, studying the assemblages and quantifying the numbers of migratory insects moving along European flyways.

I will touch upon my fieldwork in Cyprus and the Isles of Scilly focussing on the spring migration of insects, my autumn fieldwork in the Pyrenees as the insects’ stream south towards Spain and beyond, as well as underlying the lesser-studied but hugely important insect migrants - the Diptera.

- Pests, Biological Control and IPM I

Location: Lecture Theatre A

Chairs: Dave Chandler, Ben Raymond and Michelle Fountain

14:30 – Johan Stenberg – Swedish University of Agricultural Sciences

Optimizing IPM under climate change and upcoming low-input policies.

Integrated Pest Management (IPM) is an approach to prevent pest problems by using all available methods, with minimal applications of chemical pesticides. The aim is not to eradicate pests, but to manage them, maintaining their populations below Economically Injurious Levels (EIL). Until now, chemical pesticides have remained as a last and reassuring resort which conventional growers can utilize when pest populations approach the EIL. In fact, most growers feel compelled to reach for the pesticide sprayer most years. However, new global developments place new and radical demands on future pest management strategies. First, climate change implies that new pests will establish and that both old and new pests will reach the EIL more often. Second, policy developments around the world mean that the availability of chemical pesticides will radically decrease – for example, the upcoming EU Regulation on the Sustainable Use of Plant Protection Products (SUR) implies that the use of pesticides must decrease by at least 50 – 80 % until 2030. Thus, we can expect pest risk to increase, while pesticide availability will decrease dramatically. In light of these developments, it is necessary to radically improve IPM strategies to prevent pests from reaching the EIL – not just in perfectly managed display fields, but in real cropping situations.

I argue that significantly improved IPM strategies are not just necessary, but also within reach, provided that policy makers make the necessary funds available to facilitate the foreseen paradigm shift. Entomologists can contribute to important developments by, e.g., engaging in crop breeding for biological control, optimizing trophic interactions under climate change, employing all-new insects as dedicated vectors of beneficial microorganisms, and make better and more informed use of biodiversity for increased resilience.

15:00 – Alicja Witwicka – Queen Mary University of London and University College London

Unravelling the effects of insecticides on insect health: Insights from high-resolution molecular approaches.

The extensive use of pesticides puts insect pollinators under threat. Insects may experience varied pesticide exposure regimes, such as residual doses over extended periods or higher concentrations immediately after application. Yet, we have a limited understanding of to what extent different pesticides, concentrations, and exposure durations disrupt essential biological traits and processes in different insect species. We also do not fully understand how pesticides spread throughout the insect body and what processes they affect in different tissues. By examining gene activity changes, we can acquire valuable insights into the subtle and novel effects imposed by pesticides. Such knowledge is critical for enhancing pesticide safety assessments, development of new toxicity assays, and future in-field residual management. We examined gene expression profiles in the brains, leg muscles, and Malpighian tubules of *Bombus terrestris* bumblebees, and brains of *Osmia bicornis* solitary bees and *Vanessa cardui* butterflies. We first show that the same pesticide may cause contrasting effects between different species, showcasing why the use of surrogate species in pesticide safety assessment is deeply flawed. We further show that the effects of acute, short-term exposure and chronic, low-concentration exposure to the same pesticides determine fundamentally different gene expression responses. For example, acute exposure to acetamiprid and sulfoxaflor caused distinct metabolic changes, while we detected minimal effects in bees chronically exposed to these compounds, implying that acute effects may not translate to chronic harm. Moreover, although both acute and chronic exposure to clothianidin induced distinct transcriptomic changes, both treatments resulted in significant mortality, indicating varying molecular mechanisms underlying lethality. We also demonstrate that the effects of pesticides not only differ between distinct chemical compounds but also exhibit significant variation among different anatomical regions. We reveal that bumble bees possess a sophisticated molecular machinery capable of mitigating the detrimental consequences inflicted by pesticides. Importantly, this adaptive mechanism exhibits tissue-specific variations, underscoring the necessity of comprehending the unique responses of different tissues in future investigations on pesticide toxicity. Overall, our findings provide a mechanistic understanding of how insects respond to exposure to pesticides with different toxicity profiles and under varying exposure regimens. Our work demonstrates the transformative potential of high-resolution molecular approaches in enhancing our understanding of the unintended effects of insecticides on insect health. The novelty and importance of our results make a compelling case for regulatory bodies to consider our findings in their decision-making processes.

Other authors: Alicja Witwicka, Federico López-Osorio, Hannah Laila Chaudhry-Phipps, Yeahji Jeong, Courtney May, Yannick Wurm

15:15 – Rufus Isaacs – Michigan State University

Rebuilding blueberry IPM through advances in *Drosophila suzukii* control

The 2010 detection of *Drosophila suzukii* (Diptera: Drosophilidae) in the midwestern United States marked a rapid change for insect pest management in berry crops across this region. Responses to this invasive pest reversed years of progress towards the goals of IPM, led to greatly increased insecticide use, and has triggered outbreaks of multiple secondary pests. Over the last decade, a series of research projects explored chemical controls, evaluated cultural controls, developed fruit sampling methods to guide control decisions, and supported the recent release of a specialist biological control agent for this pest. This presentation will review the potential of these IPM components for integration into current fruit production systems, their current status within commercial fruit production, and the challenges to their adoption. I will report on the recent releases of *Ganaspis brasiliensis*, a Figitid parasitoid that has been recently approved for field release in the United States. Releases in 2022 and 2023 at multiple locations are being evaluated, serving as baseline locations for future comparisons as the parasitoid community of this pest changes. During 2022 sampling, we recovered *Leptopilina japonica* at multiple locations providing encouraging evidence for increased parasitism that we expect will reduce the amplitude of *D. suzukii* populations and may also reduce the need for insecticide applications in berry crops. Integrating biological control into intensively managed fruit crops is challenging, but the recent results are promising for returning blueberry IPM programs to dynamic management programs that support sustainable crop production.

15:30 – Peter Convey – British Antarctic Survey

***Eretmoptera murphyi*, an iconic sub-Antarctic insect and now a successful invader and ecosystem engineer into the more extreme core Antarctic region.**

The wingless and parthenogenetic midge, *Eretmoptera murphyi* (Chironomidae: Orthocladiinae) is one of very few native insects present in the wider Antarctic region. It is a palaeoendemic species endemic to the sub-Antarctic island of South Georgia in the South Atlantic sector of the Southern Ocean. Molecular phylogeographic studies link it with two related species of the genus Belgica (*B. antarctica*, endemic to the Antarctic Peninsula region, and *B. albipes*, endemic to Crozet Island in the Indian Ocean sector) and, potentially, to a further newly discovered relative in the Cape Horn Biosphere Reserve (southern Chile). These species appear to have diverged in concert with the final breaking of the connection between southern South America and the Antarctic Peninsula, and provide important support for the continued existence of suitable terrestrial habitat refugia within all of these regions from that time to the present day.

Eretmoptera murphyi was accidentally introduced to the more southern and environmentally extreme Signy Island in the maritime Antarctic, probably during plant transplant experiments in the 1960s, although it was first 'discovered' on the island in the early 1980s. Our recent studies on Signy have confirmed that, after a period of two to three decades of persistence, since the mid-1990s the midge has started to expand its local distribution rapidly. While the adults are non-feeding and short-lived, the detritivorous larvae inhabit moss peat, a common habitat on the island, and currently have a two-year life cycle. Larval population densities can approach 100,000 ind. m-2, with biomass considerably greater than the entire native micro-invertebrate community in these habitats. Decomposition is currently a rate limiting process in maritime Antarctic ecosystems, and rates achieved in the presence of high densities of *E. murphyi* larvae are almost an order of magnitude greater than those achieved by the entire native invertebrate community. Furthermore, the activities of larvae lead to a three- to five-fold increase in available nitrate in soils, comparable to levels found close to vertebrate aggregations on the island, and likely to influence both native plant community development and the ease with which further non-native species may establish. Distribution modelling studies indicate that, even under current environmental conditions in this rapidly warming region, *E. murphyi* would be capable of considerably increasing its distribution on the island, and also establishing in similar habitats along almost the entire length of the western Antarctic Peninsula, where it could come into competition with the native endemic *B. antarctica*. Ecophysiological studies also highlight the considerable salinity tolerance of the larvae, and potential for several weeks' survival in sea water facilitating transfer between islands via local seawater currents in the South Orkney and South Shetland Islands and western Antarctic Peninsula, as also recently hypothesised in population genetic studies of B. antarctica. Effective biosecurity measures are required to ensure that further human-assisted transfer beyond the species' current distribution on Signy Island and beyond is avoided.

Other authors: Jesamine Bartlett (British Antarctic Survey, UK; University of Birmingham, UK); Tamara Contador (Cape Horn International Center CHIC, Puerto Williams, Chile; Biodiversity of Antarctic and sub-Antarctic Ecosystems, Santiago, Chile; University of Magallanes, Punta Arenas, Chile); Claudia Maturana (Cape Horn International Center CHIC, Puerto Williams, Chile; Biodiversity of Antarctic and sub-Antarctic Ecosystems, Santiago, Chile); Scott Hayward (University of Birmingham, UK)

15:45 – Srinivasan Ramasamy – World Vegetable Center
Are we winning the tug-of-war with diamondback moth in tropical Asia? (Online talk)

Vegetable brassicas are an important group of crops, cultivated by the smallholder farmers in Asia because of their economic and nutritional values. However, their production is constrained by a plethora of insect pests including diamondback moth (*Plutella xylostella*), cabbage head caterpillar (*Crocidolomia pavonana*), cabbage webworm (*Hellula undalis*), cabbage butterfly (*Pieris spp.*) and flea beetles (*Phyllotreta spp.*). The World Vegetable Center (WorldVeg) introduced a guild of parasitoids such as *Diadegma semiclausum*, *Cotesia vestalis*, and *Diadromus collaris* for the biological control of diamondback moth (DBM) in South- and Southeast Asia from 1985-2005. Subsequent exploration in Syria and studies at WorldVeg in Taiwan during 2007-2008 indicated that the *D. semiclausum* strain from Syria was a heat tolerant strain, which could be exploited for successful management of DBM in the tropical lowlands. Although the DBM can be brought under reasonable control using these introduced parasitoids, the secondary lepidopterans and flea beetles rise to the level of primary pests in the absence of DBM and cause severe yield losses in vegetable brassicas. Since we do not have bio-control options for the secondary lepidopterans and flea beetles, the farmers predominantly rely on the use of chemical pesticides to manage them, but these harmful chemical pesticides also eliminate the introduced parasitoids of DBM and thus resurging DBM as the predominant pest in vegetable brassica production systems.

Hence, efforts have been taken at WorldVeg to develop viable alternatives for chemical pesticides to manage the secondary lepidopterans and flea beetles sustainably on vegetable brassicas. Evaluation of spider plant (*Cleome gynandra* L.) as a trap crop decreased the oviposition by DBM and other secondary lepidopterans and it reduced the fitness of these insect pests. Various *Bacillus thuringiensis* toxins such as Cry 1Aa, Cry 1Ab, Cry 1Ac, Cry 1Ba and Cry 1Ca were found to be effective against DBM and other secondary lepidopterans. Interestingly, lepidopteran-specific B. thuringiensis formulations were found to reduce the striped flea beetle (*Phyllotreta striolata*) and the bases for such a reduction were also elucidated. In addition, male-borne aggregation pheromone was identified from *P. striolata*. This pheromone formulation along with the host plant volatile attracted a significantly higher number of beetles in pheromone traps but it did not contribute to any yield improvement. Finally, an integrated pest management (IPM) package based on the combination of bio-pesticides significantly reduced the primary and secondary lepidopterans as well as flea beetles on brassicas in farmers' fields in Southeast Asia. Besides reducing the pest damage, the IPM package also reduced the use of hazardous chemical pesticides, increased the marketable yield and proliferated the natural enemies. Thus, the prospects and challenges of DBM and other secondary pests' management on vegetable brassicas in tropical Asia will be discussed.

- Genetics and Genomics I

Location: Lecture Theatre B

Chairs: Bartek Troczka and Angela Hayward

14:30 – Tom Mathers – Wellcome Sanger Institute

Decoding the sap-sucking "mosquitos" of plants

Plant-feeding insects are hyper diverse and ecologically highly successful. Much of this diversity is thought to be driven by co-evolution between insects and their plant hosts. Although plant-insect interactions appear simple and mechanical (i.e. chewing or piercing and sucking) they require complex molecular interactions between the insect and a potential host plant before, during and after feeding is established. As a result, plant-feeding insects are often highly specialised. However, despite the ecological and economic importance of plant-feeding insects, the genetic basis of insect host range is often unknown, even for important crop pests. Aphids – sap-sucking insects from order Hemiptera – are particularly important due to their role as vectors of plant disease agents. Over the last 150 million years, aphids have diversified into over 5,000 species. A few of these species have become highly invasive and damaging crop pests. In this talk I will show how we are using genomics to revolutionise our understanding of the emergence, evolution and adaptation of aphid crop pests.

15:00 – Nwamaka Akpodiete – University of Chester

Improvement of water quality for mass anopheline rearing: Dynamics of larval tray bacterial communities under different water treatments revealed by 16S ribosomal RNA ultra-sequencing

Background: The immature stages of anopheline mosquitoes develop in aquatic environments with varying physicochemical properties that contain a vast array of microorganisms. Under insectary conditions, where mosquitoes are reared in standing water, larval rearing trays can accumulate high ammonia levels, resulting in larval mortality. Bacteria in larval trays can impact ammonia levels via the nitrification and denitrification processes. Although studies have shown that internal bacteria are essential to nutrition, digestion, reproduction and immune responses in *Anopheles gambiae* s.l., none has characterised the tray microbial communities in relation to anopheline rearing.

Methods: Following up on a study testing the independent impact of ammonia-capturing zeolite and water changes on the rearing of *Anopheles coluzzii* larvae in the insectary using a 2x2 fully balanced experimental design, we characterised the bacteria communities in larval trays of the 4 treatment groups using 16S rRNA gene sequencing to highlight bacteria associated with mosquito survival and phenotypic quality. Functional filters were then applied to abundance data for 1031 Operational Taxonomic Units (OTUs) to identify bacteria species associated with ammonia nitrification and beneficial or detrimental to larval development. To validate the ultra-sequencing data, the 10 most important bacteria identified through multi-dimensional filtering were further quantified by qPCR.

Results: Treatments with water changes resulted in significantly lower bacteria diversity and abundance in *An. coluzzii* rearing trays, positively impacting adult mosquitoes' developmental success and phenotypic quality. Treatments without water changes resulted in a higher abundance and diversity of potentially toxic bacteria species, negatively impacting mosquito development. Where zeolite was applied, there was a higher presence of nitrifying bacteria with a positive impact on mosquito development and a lower abundance of potentially toxic bacteria. These trends from filtering of sequence OTUs were validated by qPCR. Amongst the top ten species validated by qPCR, 60 % showed strong correlations with sequencing data. Additionally, some species had significantly higher abundance in more challenging larval environments (detrimental species) and vice versa (beneficial).

Conclusion: The first in-depth analysis of bacterial communities in mosquito larval rearing water identified several candidate bacteria species significantly positively or negatively associated with the ammonia nitrifying cycle and mosquito rearing success. In future, following further validation experiments, such beneficial bacteria could contribute to the development of probiotics designed to improve larval rearing conditions, whilst novel toxic bacteria may provide novel candidates for vector control.

Keywords: *Anopheles coluzzii*, Bacteria communities, Malaria, Mosquito mass rearing

Other authors: Frédéric Tripet (Swiss Tropical and Public Health Institute, Kreuzgasse 2, 4123 Allschwil, Switzerland)

15:15 – Dominic Phillips – Natural History Museum, London (NHM)

Darwin Tree of Life: A Museum Perspective

The Darwin Tree of Life Project (DToL) is an ambitious initiative aimed at sequencing the genomes of all 70,000 eukaryotic organisms found in the British Isles. The project is a collaboration between numerous institutions in the UK and aims to generate a comprehensive dataset that will revolutionize our understanding of the evolutionary history and biodiversity of the region. This undertaking involves collecting and processing samples from a wide range of organisms. The molecular work involved in this project requires the extraction, sequencing, and assembly of millions of DNA base pairs from each organism.

The project is expected to provide a wealth of information about the genetic diversity of life and shed light on the evolutionary relationships between different species. It is also anticipated to have important implications for conservation efforts, as the data generated will help identify species that are particularly vulnerable to environmental change.

Despite the enormous scope of this project, progress is being made at a rapid pace thanks to advances in DNA sequencing technology and data analysis methods. However, the project does face many challenges for the collection and sequencing of both rarer and smaller organisms for which material may be difficult to obtain.

This talk will be an introduction to the main goals and outcomes of the Darwin Tree of Life Project so far from the Natural History Museum’s perspective, covering some of the methodology and challenges in attempting to sequence a huge range of species. At its current rate, the project is poised to make significant contributions to our understanding of taxonomy and species relationships.

Other authors: Inez Januszczak (NHM), Chris Fletcher (NHM), DToL consortium (Various)

15:30 – Julien Devilliers – University of Leicester
***Anopheles gambiae*, male vs female: single cell transcriptomic in the head of the malaria vector**

Anopheles gambiae, the vector of malaria, is responsible for half a million deaths each year. Being a species of human health interest, multiple studies aim to unravel the use of sensory modalities in host seeking. While males only feed on flower nectar, females seek human blood to extract enough energy to produce eggs. This behaviour mainly involves the detection of visual and odoural cues, as well as carbon dioxide, temperature, and chemicals detection. Here we use single-cell transcriptomic technologies to compare the cell composition of whole heads of mosquitoes between sexes. For each sex, cells of whole heads were dissociated, sorted and sequenced using the SPLiT-seq method. Cell atlases generated from male and female samples were then compared to identify differences in neuronal and sensorial cell composition of these mosquitoes. We hope this ongoing work will help to identify new specific targets for the control of *Anopheles gambiae*, but also mark a key start for comparisons with other work such as the yellow fever mosquito (*Aedes aegypti*).

Other authors: Judi Bagi (UCL), Ezio Rosato, Charalambos Kyriacou, Roberto Feuda (University of Leicetser)

15:45 – Louise McNamara – Teagasc
Understanding and managing Barley Yellow Dwarf Virus

Aphids are economically important cereal pests that reduce grain quality and crop yield through direct feeding and vectoring Barley/Cereal Yellow Dwarf Viruses (B/CYDV). Controlling aphids and therefore managing B/CYDV is increasingly difficult due to insecticide resistant aphid populations, climate change and fewer insecticide options. There is an urgent need for an enhanced understanding of BYDV epidemiology and BYDV detection in order to improve control decisions. Plant pathogens are constantly emerging and spreading and there are often limited (or none in case of B/CYDV) post diagnosis treatment options, making surveillance key to their control. Previous work indicated that BYDV-MAV was the most predominant species of B/CYDV in Irish cereal crops. The BYDV-MAV strain was either the only species of the virus found or the most common strain. However, these previous identifications were ELISA based which is not able to discriminate between BYDV-PAV and BYDV-PAS, and demonstrates cross reactivity between BYDV-MAV & BYDV-PAV. Advanced detection of B/CYDV is needed to determine if this observation still applies almost a decade later. A high-throughput sequencing survey of symptomatic barley plants collected around Ireland in 2021 and 2022 has identified a BYDV-MAV like species that was prominent and detected in all field sites sampled. However, we also identified many cases of co-infection with BYDV-PAS and BYDV-PAV like sequences, and one incidence of CYDV-RPS. These data were used to develop improved molecular surveillance tools for C/BYDV monitoring. To enhance our understating of resistance mechanisms in the major Irish vector, the grain aphid, we sequenced the complete genome of the partial pyrethroid resistant *S. avenae* clone. Our newly improved genomic resources (genome and viral sequences) has enabled us to develop molecular tools to investigate virus presence, aphid genetic diversity and insecticide resistance in national aphid monitoring network will help to improve the understanding and management of BYDV spread/outbreaks.

Other authors: Maximilian Schughart (Teagasc and UCD), Virgile Ballandras (Teagasc and Maynooth University), James Carolan (Maynooth University) and Stephen Byrne (Teagasc)

- Pests, Biological Control and IPM II

Lecture Theatre A

Chairs: Dave Chandler, Ben Raymond and Michelle Fountain

16:30 – Simranjit Kaur – Teagasc

Developing endophytes as biological solutions to manage BYDV & aphid vectors in spring barley (Online talk)

Entomopathogenic fungi (EPF) offer potential biological solutions to manage plant sap-feeding insect pests, such as aphids. The plant-colonization capability of notable endophytic EPF strains ensures their survival and confers plant protection and growth functions. This work is aimed to discover novel EPF candidates with the potential for effective management of Barley Yellow Dwarf Virus (BYDV) and the aphids that vector the virus in barley crops.

In this study, nineteen multi-genera endophytic fungal candidates were utilised, which were isolated from different plant niches such as seed, stem, leaf and root tissues of cereal plants. For the screening experiment, the synchronised adult aphids were exposed to endophytic fungal spores and then transferred to the plants. The results under controlled conditions have shown a promising reduction in the aphid population across different time points. There were up to two-fold reductions in the number of adult aphids and nymphs elicited by four different fungal candidates. Interestingly, >30% of the endophytic fungal candidates screened demonstrated the potential to suppress aphids and nymph numbers. Direct pathogenicity leaf assay confirmed decreased reproduction in aphids. Four endophytic fungi were observed to colonise the aphid surface. Two selected fungi were coated on seeds and tested for plant growth and pest reduction under field conditions this spring. The early growth stage plant data from the field indicated higher plant biomass as compared to control spring barley plants, this trial is still underway.

These preliminary findings suggest that diverse representations of endophytic taxa could potentially offer multi-choice effective biological control and growth-promoting agents for sustainable agriculture practices. Future work is focused on establishing a mechanistic understanding of aphid inhibition by best-performing endophytes.

Other authors: Simranjit Kaur, Diego Bianchi, Maximilian Schughart, Stephen Kildea, Trevor R. Hodkinson and Louise Mc Namara

16:45 – Maria-Rosa Paiva – NOVA University of Lisbon

Strategies for management of forest insects with semiochemicals (Online talk)

Insects depend on olfactory communication for survival and reproduction. Since immemorial times, humans attempted to control pests based on empirical knowledge of this mechanism. Yet, synthetic semiochemicals, comprising pheromones, feeding attractants, repellents and other behavioural, or physiological active chemicals, first became available in the 1970ies. This breakthrough gave rise to a new era of insect management, with semiochemicals for over 7,500. insect species being presently identified and mostly available. Pheromones, that is compounds that transmit intraspecific messages, constitute the overwhelming majority of these compounds. The management of forest insects poses specific problems, in part due to the environmental value and fragility of this type of ecosystems. Insecticides are thus generally banned in forestry, with rare exceptions, such as for the control of the invasive large pine weewil *Hylobius abietis*, in the UK. Strategies for the application of volatile semiochemicals include detection and monitoring, mass trapping, attract-and-kill, mating disruption, push-and-pull among others, E. g. sensors. Yet, their successful implementation can only be achieved within the framework of an

Integrated Pest Management (IPM) programme. This concept will be illustrated using three forest insect species, distributed in Southern Europe, as example. Management strategies for the native species pine processionary moth *Thaumetopoea pityocampa* (Lepidoptera, Notodontidae) and the flathead oak borer *Coroebus undatus* (Coleoptera, Buprestidae), as well as for the invasive species *Gonipterus platensis* (Coleoptera, Curculionidae), will be considered. State of the art results, regarding ongoing research for the control of these species and their integration into management strategies analysed and pros and cons for the different options considered weighted.

Other authors: Sofia Branco, Marco Gomes-da-Silva, Eduardo P. Mateus NOVA School of Science and Technology, NOVA University of Lisbon

17:00 – Daniel Leybourne – University of Liverpool

Cabbage stem flea beetle pest pressure in rapeseed fields is influenced by surrounding crop diversity, but can the surrounding landscape alter the insect microbiome?

Globally, oilseed rape is one of the most widely cultivated oilseed crops. Oilseed rape can be attacked by a range of agriculturally important herbivorous insects, and of these the cabbage stem flea beetle, *Psylliodes chrysocephala*, is of significant agricultural and economic importance. P. chrysocephala can cause high levels of crop damage, leading to severe yield losses. *P. chrysocephala* cause crop damage to young oilseed rape plants via adult feeding between July and October, where characteristic shot-hole damage can be observed. Generally, younger crops have a greater risk of *P. chrysocephala* damage as more vigorous crops are able to tolerate some feeding damage through compensatory growth. Additional crop damage can be caused by P. *chrysocephala* larva between October and February when they burrow into the plant stem, resulting in bushy plants and delayed crop maturation. Microbial diversity is a key driver of insect success, and phenotypic traits conferred by insect microbes have been well characterised in other insect groups (e.g., aphids). However, relatively little is known about the composition and diversity of the *P. chrysocephala* microbiome and how this might influence the pest status of *P. chrysocephala*.

Recent syntheses have indicated that the heterogeneity surrounding agricultural landscapes can directly affect the provision of ecosystem services, such as herbivorous insect suppression. It is becoming increasingly apparent that functional heterogeneity (i.e. the presence or absence of habitat types required for species feeding, reproduction, overwintering, or nesting) influences the ecosystem services provided to agriculture by the surrounding landscape. Recent studies have indicated that pest suppression services are influenced by the diversity of crops within the surrounding agricultural landscape. However, despite the importance of *P. chrysocephala* as an agricultural pest, the influence of the surrounding landscape, and abundance of important ecosystem service providers (i.e., composition and diversity of natural enemies), on *P. chrysocephala* pest pressure and subsequent level of crop damage has not been examined in great detail.

Here, we monitored 14 winter oilseed rape fields between September-November to determine whether *P. chrysocephala* pest pressure, crop damage, or *P. chrysocephala* larval abundance were affected by the surrounding landscape. Our results indicate that crop diversity in the previous season is a key driver of pest pressure, plant damage, and larval load in oilseed rape fields. With crop diversity in a 1 km circumference of the examined fields a significant spatial factor. We also collected P*. chrysocephala* from 18 winter oilseed rape fields (4 during summer, 14 during autumn) to examine whether the surrounding landscape might also influence the beetle microbiome. Our microbiome results indicate that Pantoea spp., Wolbachia spp., and Pseudomonas spp. are the most highly abundant microbial taxa within the *P. chrysocephala* microbiome. Ongoing analysis aims to determine whether the surrounding landscape, including the composition of natural enemy populations, might influence the structure of the *P. chrysocephala* microbiome.

Other authors: Antonia M C Pahl (Leinbiz University Hannover, Germany); Emily A Martin (University of Gießen, Germany)

17:15 – Gwenaëlle Deconninck – Institut de Recherche sur la Biologie de l'Insecte (IRBI, CNRS)
Fallen fruits: a back-up resource shaping fruit fly communities.

Most research on insect pests focuses on crops of interest for human consumption, and generally neglects the post-harvest period when decaying fruit lay on the ground. However, fallen fruit represent an important feeding and breeding substrate for insects, especially members of the family Drosophilidae. They could also represent a potential reservoir when primary host fruit become scarce, providing a seasonal refuge and potentially fueling pest outbreaks.

The seasonal dynamics of the Drosophilidae community has been poorly studied. Recently, two important invasive species, *Drosophila suzukii* and *Chymomyza amoena*, appeared in Europe. These two invasive fruit flies are expected to alter this community composition and could benefit from fallen fruit. In this study, we aimed to disentangle the relative roles of microclimatic, landscape and local factors driving the diversity of the Drosophilidae community in decaying fruit across seasons.

Each month, from September 2021 to April 2022, we collected fallen apples at 19 sites in the Amiens region in northern France. We used linear mixed models to investigate the effects of landscape, local biotic and abiotic variables, including microclimatic variables, as well as apple tree and fruit traits, on the number of emerging Drosophilidae adults.

Mean daily site temperature during the week preceding sampling and the proportion of rotten tissue on the apples had the strongest positive effects on Drosophilidae abundance and species richness, respectively. Drosophilidae diversity also increased with tree cover in a 100 m radius around sampled trees. Decaying apples were important breeding sites for *C. amoena* dominating the community in autumn, but they were a suboptimal substrate for *D. suzukii*, which were only present in late summer.

This research sheds light on the role of the Drosophilidae community in recycling agricultural waste, as well as the importance of unharvested fallen crop fruit in maintaining the diversity of an insect family, that are often neglected in field studies. Our data also show the importance of taking into account multiple scales and factors, from fruit characteristics to landscape composition and macro- and microclimatic variables, when studying the interactions between invasive species, native species and their shared trophic resources.

Other authors: Méghan Boulembert (EDYSAN, UMR7058), Patrice Eslin (EDYSAN, UMR7058), Aude Couty (EDYSAN, UMR7058), Françoise Dubois (EDYSAN, UMR7058), Emilie Gallet-Moron (EDYSAN, UMR7058), Sylvain Pincebourde (IRBI, UMR7261), Olivier Chabrerie (EDYSAN, UMR7058)

17:30 – John Banks – California State University
Spatial scale, predator behaviour, and pesticide sprays: Modelling interactions in IPM

Ecological field studies and theory over the past several decades have demonstrated that the spatial scale at which heterogeneous habitats are deployed can have a profound effect on the population dynamics of resident arthropods. Diversifying agroecosystems by establishing or retaining natural vegetation in and around crop areas has long been recognized as a potentially effective means of bolstering pest control by attracting more numerous and diverse natural enemies, though outcomes are inconsistent. Furthermore, increasing evidence from studies in agroecosystems reveals that landscape complexity affects different organisms in different ways. We use a simple mathematical modelling framework to address gaps in our understanding of underlying mechanisms potentially driving differences in species responses to spatial scale and agroecosystem diversity, exploring the linkages among non-crop vegetation, pesticide sprays, natural enemy behaviour, and pest suppression. In particular, by using a system of partial differential equations, which include population-level predator-prey interactions as well as spatial processes, we examine the dynamics of crop plants, herbivores, and generalist predators. We focus on differences in how important natural enemies (carabids and coccinellids) colonize crop fields where they forage for aphid prey, examining differences in how the predators move into the fields from adjacent vegetation as a potential driver of differences in overall pest suppression. Furthermore, we explore how differences in colonization behaviours may interact with spatial scale and exposure to pesticide sprays in determining the ability of predators to suppress prey in diversified agroecosystems. We show that colonization behaviour and spatial scale are important factors in pest suppression, and discuss the implications of our results in terms of habitat management for biological control in agroecosystems.

Other authors: Dr. Amanda Laubmeier, Texas Tech University.

17:45 – Vasthi Alonso Chavez – Rothamsted Research
Optimised Surveillance Strategies for the early detection of the Emerald Ash Borer in the UK

The Emerald Ash Borer (EAB; *Agrilus planipennis*) is a jewel beetle from the family Buprestidae, endemic to East Asia. In its native habitat, EAB colonises stressed ash (Fraxinus spp.) trees and causes minor damage to healthy ash. However, in Canada, USA and Russia EAB is arguably the most devastating insect pest of ash as it has killed millions of trees in those areas. The EAB devastation caused in North America and Russia is a warning for the UK and Europe to develop surveillance strategies to detect EAB before it is established in the environment. EAB's most likely entry pathway into the UK is through firewood trade from Europe. Dispersal then may occur from ports, firewood depots and households with wood-burning fires.

To determine how best to deploy surveillance efforts we have developed a risk map for the probability of EAB arrival and linked this to a model of the lifecycle and spread of EAB to account for the potential dispersal and establishment of the beetle. Through simulations, we have quantified the benefits of using an optimised surveillance strategy, as opposed to one purely based on perceived entry risk, for various scenarios related to entry biocontrol and efficacy of the surveillance method. Through this we then address the following questions: 1) How does better identification of entry points impact optimal surveillance strategies? 2) How does surveillance by landowners and managers impact optimal surveillance strategies?

By answering these questions, we provide a sound strategy to survey for EAB while accounting for most likely entry points, stakeholder surveillance behaviour and optimisation techniques to increase our chances to eradicate or successfully manage EAB if and when it arrives in the UK.

Other authors: Alice E. Milne (Rothamsted Research, UK), Nathan Brown (Forest Research, UK), Clare Hall (Forest Research, UK), Mariella Marzano (Forest Research, UK), Berglind Karlsdottir (Forest Research, UK), Liz O'Brien (Forest Research, UK), David Williams (Forest Research, UK), Alison Dyke (University of York, UK), Joanne Morris (University of York, UK), Stephen Parnell (University of Warwick, UK), Matt Combes (University of Warwick, UK), Frank van den Bosch (Curtin University)

- Genetics and Genomics II

Location: Lecture Theatre B

Chairs: Bartek Troczka and Angela Hayward

16:30 – Andrew Jones – Oxford Brookes University

An unusual nicotinic acetylcholine receptor from the honey bee, *Apis mellifera*, which is sensitive to the biogenic amine, serotonin

Nicotinic acetylcholine receptors (nAChRs) play an important role in signalling in the insect nervous system. They are the molecular targets of highly effective insecticides such as neonicotinoids. The actual nAChR consists of five proteins (subunits) that assemble around a central ion channel. Upon binding of acetylcholine or a neonicotinoid, the ion channel is opened allowing cations into the cell leading to the initiation of a nerve impulse. Insects commonly possess twelve different nAChR subunits, which are referred to as either alpha (which are essential for acetylcholine binding) or beta (contributes to the pharmacological characteristics of the nAChR). Analysis of protein sequences show the subunits are generally highly conserved between various insect species. There are, though, some interesting exceptions. In one example, the amino acid sequence of the alpha5 nAChR subunit from the honey bee, *Apis mellifera*, is considerably different to the alpha 5 subunit from Dipteran insects such as the fruit fly, Drosophila melanogaster. We expressed the honey bee alpha 5 nAChR subunit in the oocytes of the African clawed frog, *Xenopus laevis*. This allows for the application of two-electrode voltage-clamp electrophysiology to the frog's eggs to measure the functional/pharmacological properties of the A. mellifera nAChR. We found that the honey bee alpha 5 nAChR has unusual pharmacological properties in that it is insensitive to acetylcholine, instead being considerably more responsive to the biogenic amine, serotonin. Also, the receptor is insensitive to nicotine and does not respond to the neonicotinoids, imidacloprid and thiacloprid. It remains to be determined why a receptor that responds quickly to biogenic amines has evolved in the honey bee.

Other authors: Eleanor Mitchell (University of Leeds), Franco Viscarra (Oxford University), Isabel Bermudez (Oxford Brookes University), Joseph Hawkins (Syngenta), Emily Armstrong (Oxford Brookes University), Jim A. Goodchild (Syngenta) and Andrew K. Jones (Oxford Brookes University)

16:45 – Reuben James – John Innes Centre

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

Aphids (order Hemiptera) cause substantial crop damage worldwide. Some aphids are specialists, colonising specific hosts, whilst others, like the green peach aphid *Myzus persicae*, have a wide host range, affecting crop yields, often to the point that their growth becomes economically unviable. In addition to direct feeding damage, aphids are proficient vectors of plant viruses, further exacerbating their detrimental impact on agricultural productivity. Investigating aphids via gene editing approaches may lead to novel avenues for understanding aphid biology, such as identifying aphid 'Achilles heels' that could inform innovative pest management strategies.

Transformation and gene editing in insects have historically relied on microinjection of eggs. However, aphids rarely produce eggs and predominantly reproduce asexually, involving clonal lineages of aphid females giving birth to multiple live young (viviparity) that already have daughters developing inside them. This telescoping of generations enables aphids to quickly expand in population size. While gene editing of aphids by egg injection was shown to be possible, the process is challenging and time consuming. Hence, we wish to investigate whether aphids may be gene edited via a technology known as receptor-mediated transduction of cargo (ReMOT control). This involves injecting female insects with gene editing cargo that directly targets aphid early embryos that protrude into the hemolymph of the abdomen in female aphids. The cargo should include chimeric proteins consisting of Cas9 fused to peptide chaperones derived from vitellogenins or other yolk precursor proteins. This approach has successfully enabled gene editing in mosquitoes, parasitic wasps, and black-legged ticks, making it a promising method to obtain gene-edited clonal lineages of aphids with rapid reproductive rates.

Our investigation focuses on aphid vitellogenins, which are smaller compared to those of other egg-laying and sexually reproducing hemipterans. Despite this difference, the conservation of vitellogenin receptors between aphids and other hemipterans suggests potential cross-species functionality. Structural analysis using Alphafold indicates similarities in the vitellogenin domains involved in receptor binding among hemipterans. Moreover, we have successfully produced and purified chimeras of mCherry fused to a range of peptides obtained from vitellogenins of aphids and other insects. Microscopy analyses suggest that upon injection of adult aphid females, some of these chimeras migrate to early embryos, showing their potential for efficient cargo delivery to the germline in aphids. We have begun experiments to knock out M. *persicae* genes via ReMOT control.

Other authors: Amber S. K. Hall (John Innes Centre [JIC]), Sam T. Mugford (JIC), Wendy Harwood (JIC), Marcus Guest (Syngenta, Jeallot's Hill), Grant L. Hughes (Liverpool School of Tropical Medicine), Saskia A. Hogenhout (JIC)

17:00 – Ryan Brock – John Innes Centre
Breeding resistance to cabbage stem flea beetle

The cabbage stem flea beetle (CSFB; *Psylliodes chrysocephala*) represents an economically important oilseed rape (OSR; Brassica napus) pest that reduces crop establishment, growth, and yield through both adult and larval feeding. CSFB damage was previously limited using neonicotinoid and pyrethroid insecticides. However, the 2013 neonicotinoid ban coupled with increasing levels of pyrethroid-resistant CSFB populations has led to increased CSFB pressure, prompting a 60% reduction in UK OSR cropping area over the last decade. Hence, alternative strategies for CSFB control are urgently required to ensure the survival of the UK OSR industry. One promising strategy is through the characterisation of genetic resistance within B. napus, such that genes and traits associated with CSFB resistance can be made available to commercial breeding programmes. Using a captive CSFB population and recently developed feeding assays, we screened a B. napus diversity set comprising 96 genetically diverse lines and identified significant variation in CSFB resistance. Of particular interest were two lines that showed highly contrasting responses to CSFB herbivory (resistant vs susceptible). Follow up experiments found these differences to be highly reproducible, with the susceptible variety being twice as heavily fed on in both lab- and field-based feeding assays. Building on this work, we carried out RNAseq analyses on the two lines when challenged with CSFB herbivory, allowing the identification of multiple genes involved in CSFB resistance. Future assays using gene knockout mutants in the Arabidopsis model system are planned, helping to identify the function of various genes of interest. Ultimately, these findings should provide a better understanding of CSFB resistance traits, helping to inform future breeding of high-yielding, CSFB-resistant OSR varieties.

Other authors: Dr Emmanuel Solomon, John Innes Centre; Jessica Hughes, John Innes Centre; Professor Steven Penfield, John Innes Centre; Dr Rachel Wells, John Innes Centre

17:15 – Henry Youd – Liverpool School of Tropical Medicine
Identification of insecticide resistance mechanisms and associated genes in *Aedes aegypti* from Angola

Aedes-borne disease exerts an enormous public health burden worldwide, with an estimated 390 million cases annually from dengue alone. Having effective control options, particularly as a rapid response to disease outbreak scenarios, is imperative to limit infections. Insecticides have played an important role in such control during the last 60 years, but their effectiveness is being threatened by the rise of insecticide resistance in *Aedes aegypti* (Diptera: Culicidae). Understanding the resistance mechanisms present in this species can greatly assist with insecticide resistance management programs. However, our knowledge of these mechanisms and associated genes specifically in African *Ae. aegypti* populations is glaringly absent, with no published RNAseq datasets for these populations.

Thus, to provide greater insight *Ae. aegypti* from Angola underwent RNA extraction and sequencing of both insecticide-unexposed and fenitrothion-resistant mosquitoes, as well as two control susceptible laboratory strains. Quantification of sequenced reads was used to identify significantly up- and down-regulated genes in the resistant population compared to the unexposed and susceptible populations. Additionally, signatures of selection were used to determine genomic regions with high genetic differentiation which may be linked with the resistance phenotype. Upregulation of genes in enzyme families previously implicated in resistance were observed including cytochrome P450s (CYP450), glutathione S-transferases (GSTs), and carboxylesterases, as well as an abundance of cuticular-related genes. Among these were known resistance genes for example CYP9J24, CYP9J26, and CYP6BB2 but also numerous novel detoxification gene candidates, particularly in the CYP325 family. This was followed by in silico molecular docking and metabolism assays for novel candidate resistance enzymes against a panel of insecticides for further validation. Several single nucleotide polymorphisms (SNPs) present in the voltage-gated sodium channel (VGSC) gene which are known to confer insecticide resistance phenotypes were also examined and found to be at high frequencies.

These results contribute to a greater understanding of the resistance mechanisms present in African *Ae. aegypti* and it is concluded that further genomic and transcriptomic research within these populations would be of great value to global health.

Other authors: David Weetman - Liverpool School of Tropical Medicine, Liverpool, UK. Joao Pinto and Carla A Sousa - Global Health and Tropical Medicine (GHTM), Instituto de Higiene e Medicina Tropical (IHMT), Universidade Nova de Lisboa (UNL), Lisbon, Portugal. Xavier Grau Bove - Universitat Pompeu Fabra (UPF), Barcelona, Spain. Linta Grigoraki - Institute of Molecular Biology and Biotechnology, Foundation for Research and Technology Hellas, Heraklion, Crete, Greece.

17:30 – Laura Campbell – Durham University
The evolution of plant cultivation by ants – a case study using the genus Philidris

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 a minimum of 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 specialized ones—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, such as the expansion of the olfactory gene repertoires as well as genes related to aggressiveness. Strikingly, the evolution of obligate dependence on plants is not associated with large genome size reduction as is currently the case in microbial endosymbiosis. This suggests that dependence on partners is mediated by fundamentally distinct mechanisms in mutualisms between macro-partners.

Other authors: Prof. Guillaume Chomicki (Durham University)

17:45 – Liam Crowley – University of Oxford

The process and applications of sequencing the full genomes of the British and Irish arthropod fauna.

The Darwin Tree of Life (DToL) project is an ambitious attempt to sequence the complete genome of every species of Eukaryotic organism in Britain and Ireland. Approximately 40% of these species are terrestrial arthropods, therefore an effective sampling strategy for this group is essential. The unprecedented number and quality of genomes being produced provides an exciting opportunity for research, with applications across a wide range of areas including genomics, evolution, physiology and conservation. Arthropods also provide and especially interesting opportunity for genome-enabled research due to the huge diversity of species and biology exhibited within the group.

This talk will summarise the process involved in sampling the British and Irish arthropod fauna. This process includes compiling and reviewing the species lists; prioritising and collecting species for genome sequencing; handling methods to ensure that high-quality genomic DNA is preserved; and compiling standard operating procedures for processing specimens, verification and voucher specimen curation. This talk will also explore examples of ongoing genome-enabled research using DToL arthropod genomes, such as investigating the evolution of homeobox genes in Lepidoptera.

Other authors: Peter Mulhair, Owen Lewis and Peter Holland; University of Oxford.

Wednesday 6 September

- Symbionts and Microbes

Location: Lecture Theatre A

Chair: Ailsa McLean

10:45 – Anne Duplouy – University of Helsinki

Adding the microbial layers to a 30 year-long ecological monitoring project (Online talk)

The metapopulation of the Glanville fritillary butterfly in the Åland Islands in Finland, is a model system for the study of the ecology and evolution of species in fragmented landscapes. The long-term ecological monitoring of the abundance and habitat occupancy of this butterfly population has provided exceptional demographic and insights on the population dynamics and genomics of the species under habitat changes. My research group has taken up the challenge to revisit this research and investigate the diversity and functions of microbial species associated with this system. I will present a few of our projects.

11:15 – Jennifer Kate Upfold – INRAE

Interaction of the gut microbiota and immune response on host resistance to bacteria and fungal pathogens in *Galleria mellonella* larvae (Online talk)

Understanding the role of the microbiota in host resistance to pathogens is a key concept required to maintain insect health, but the extent to which the microbiota contributes to the immune response is not fully understood. The tripartite interaction of the gut microbiota, pathogen and host response is evaluated in *Galleria mellonella* larvae reared in sterile (=axenic) and non-sterile (=conventional) conditions. We conducted single inoculations using two pathogens with different modes of infection: oral infection with *Bacillus thuringiensis galleriae* (Btg, a gram-positive bacterium) and topical infection with Metarhizium anisopliae (Ma, Hypocrealean fungi). Conventional larvae infected with Btg had an increased percentage survival with an LC50 dose, compared to axenic larvae where the same dose resulted in 90-

100% mortality. Through a dual-analysis experimental design, we were able to identify changes in the relative abundance of the bacterial microbiota using 16S rRNA seq, as well as assess the level of immune-related gene expression in the gut of the same group of larvae. We found the microbiota was entirely dominated by four Enterococcus species, with all species present pre- and post- infection by both Bt and Ma. This relatively non-diverse microbiota was able to stimulate the immune response of AMPs and IMPI in the conventional larvae at basal conditions, in particular at 20 and 40 hours with an observed decline in the stimulation at 96 hours. During oral infection by Bt, a similar expression of immune genes was observed between axenic and conventional larvae, therefore when examining the fold-change expression from basal to infected state, axenic larvae exhibited significantly greater immune gene induction compared to conventional larvae during Btg infection, due to the lack of stimulation. In contrast, the topical Ma infection elicited different gene expression patterns compared to the oral Btg infection, with conventional larvae showing significantly higher expression levels of AMP Gallerimycin at 20- and 96-hours post-infection compared to the axenic larvae. These findings highlight the immune-modulatory role of the Enterococcus-dominated gut microbiota (an increasingly common outcome in laboratory populations of Lepidoptera), and its influence on the host's response to Btg and Ma infections. Further fitness experiments involving the generation of gnotobiotic larvae with a single *E. mundtii* isolated from the conventional larva gut will help assess its impact on the host’s immune system and ability to protect against or enhance susceptibility to these infections.

Other authors: Agnes Réjasse1, Christina Nielsen-leroux1, Annette Bruun-Jensen2, Vincent Sanchis-Borja1
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11:30 **– Michael Jardine –** University of Exeter

Managing antimicrobial resistance: How do burying beetles and microbes sustainably coexist in competition over shared resources?

The rise of antimicrobial resistant bacteria is one of the most serious issues facing human health. Antimicrobial resistance (AMR) is a widespread rapidly evolving phenomenon, with resistance to new compounds emerging quickly after they are introduced, heavily impacting their effectiveness. However, while we have struggled to manage the emergence of AMR in the last hundred years, many insect groups, who produce their own antimicrobial compounds, have been coping with the threat of AMR for much longer. One such group of insects are beetles of the family Silphidae (burying beetles). Members of this family raise their offspring on small animal carcasses that they bury in the soil and coat in a mix of antimicrobial peptides (AMPs) to prevent colonisation and decomposition by bacteria. Remarkably, not only does resistance to AMPs appear to be uncommon in soil bacteria, but fossil Silphidae from the mid-Cretaceous indicate that their unique lifecycle, which brings them into conflict with decomposing bacteria, has deep roots. Whatever strategies these beetles are using to manage AMR in their environment are effective and evolutionarily stable.

To investigate these management strategies, we have focused on the common British species *Nicrophorus vespilloides*, which produces 40 distinct AMPs. Five of these have been shown to be up regulated when females breed, indicating that these are especially important in controlling the bacterial community present on animal carcasses. Previous work has also found that *N. vespilloides* shows substantial plasticity in breeding behaviour. We find that this plasticity extends to the AMPs that are up regulated during breeding, with even closely related beetles expressing drastically different amounts of each peptide. The beetles are clearly actively reacting to and managing their environment to improve their breeding success, but precisely how they do this, or why is it able to curb the evolution of AMR, is currently unclear.

To resolve this, we are pursuing several lines of investigation: 1) sampling of the carcass microbiome to record the presence/abundance of bacterial species during breeding; 2) creating bacterial mutants that are resistant to key beetle AMPs to describe what mutations would be required for AMR to evolve in this system and quantify the fitness costs of resistance; 3) experimentally evolving beetles and soil bacteria to test how they co-evolve. Our findings so far, and the future questions we aim to investigate, will not only allow greater understanding of how this unique groups of insects have approached the issue of AMR management, but could also provide crucial lessons on how to manage AMR to improve human health.

11:45 – Loretta Mugo – University of Tours and University of Exeter

Diet-dependent virulence effects of gut microbiota: The symbiosis of *Enterobacter cloacae* and *Plutella xylostella*

Symbiosis describes a continuum of host-bacteria interactions that range from parasitism to mutualism depending on the ecological context. Mutualistic interactions however pose an evolutionary problem because of their ability to defect from mutualist to parasitic. This defection may occur due to several ecological factors among them diet quality. Enterobacter cloacae is a commonly occurring gut symbiont of the crop pest *Plutella xylostella* that was previously shown to be mutualistic on plant host diet, but parasitic on nutritionally rich artificial diet. Based on these findings but focusing only on artificial diet for better control of sterility, we investigated whether Enterobacater cloacae would benefit or parasitize axenic Plutella larvae depending on diet quality. We hypothesized that the host would pay a net fitness cost when fed on a nutritionally rich wheat germ diet, but gain fitness benefits when fed on nutritionally poor cellulose diet. We found parasitism to be more apparent in the rich diet as opposed to mutualism in the poor diet as measured by relative growth rate of larvae. In addition, diet quality did not affect the gut colonization rate of the host. In the rich diet, we found parasitism decreases with dose. However, even when larvae clear out the Enterobacter infection at low doses, their growth does not catch up with the control group, suggesting that effects on the immune system persist. Preliminary qPCR results show a dose-dependent expression of cecropin and lysozyme, which are antimicrobial peptides commonly found in insects against gram positive and negative bacteria. In summary, we see that Plutella larvae pay a net fitness cost for harboring a single Enterobacter symbiont when fed on nutritionally rich diet. We anticipate that ongoing transcriptomic analysis will shed more light on the effects on the host's immune system and bacterial mechanisms of virulence involved.

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12:00 – Cedric Aumont – Freie Universität Berlin

Harnessing near-chromosome level quality genomes to explore the evolution of termite immunity.

The phylogeny of the Blattodea boasts a wide degree of sociality spanning from solitary cockroaches to advanced ecosystem-dominating higher termite societies. The emergence of sociality in termites was associated with the acquisition of a diverse range of social structures. Previous work has found evidence for a caste-specific social defence system in termites leading to an immune system that may favour group over individual defence. While preliminary work suggests a correlation between social transitions and a reduction of immune gene family diversity, the lack of available high-quality termite genomes hampers complete knowledge of the true diversity of immune gene evolution across termite phylogeny. Here, we report on the sequencing and near-chromosome level assembly of 48 high-quality long-read-based genomes across major termite and cockroach sister-branch lineages. We investigate the diversity and evolutionary history of immune genes across genomes, focusing particular attention on correlations between immune gene evolution and transitions in sociality over termite phylogeny.

Other authors: Dino P. McMahon - Freie Universität Berlin

12:15 – Gabriele Gloder – KU Leuven

Parasitism by endoparasitic wasps alters the microbiome and body odours of a caterpillar host, with consequences for higher tropic levels.

Several factors influence insect multitrophic interactions. However, the contribution of microbes and microbial volatile organic compounds (mVOC) has been substantially ignored. mVOCs may be produced by microorganisms residing on or inside insects, thus contributing to the distinctive odour associated with these organisms.

The emission of mVOCs can act as a reliable signal for predators and parasitoids to locate their prey or host. The microbiome of a host may undergo modifications due to parasitism by parasitic wasps, thus affecting their interactions with hyperparasitoids. The olfactory cues emitted by parasitised caterpillars play a crucial role in aiding the location of parasitoid hosts by hyperparasitoids. However, the precise source of these olfactory cues and their correlation with the microbiome of the caterpillar remain unknown. This study involved the manipulation and analysis of the microbiome of unparasitised *Pieris brassicae* caterpillars and caterpillars parasitised by the parasitoid *Cotesia glomerata*, along with an analysis of their body odours. There were significant differences in the microbial communities and body odours between caterpillars that were parasitised and those that were not. Most likely, changes in the external microbiome and body odour after parasitism were driven by the resident internal microbiome of caterpillars. Particularly, the presence of the bacterium Wolbachia was exclusively detected in parasitised caterpillars. In order to investigate the potential impact of Wolbachia on higher trophic levels, non-parasitised caterpillars were injected with Wolbachia and subsequently subjected to a behavioural assay involving exposure to the hyperparasitoid *Baryscapus galactopus*. The introduction of Wolbachia resulted in an increased attraction of hyperparasitoids towards caterpillars as opposed to those that were not treated, while no differences were found compared to parasitised caterpillars. The results of our study demonstrate the importance of microorganisms as inconspicuous drivers of multitrophic interactions and highlight their contribution in insect food webs.

Other authors: Mitchel Bourne (Wageningen University and Research), Berhane Weldegergis (Wageningen University and Research), Marijn Slingerland (Wageningen University and Research), Andrea Ceribelli (Wageningen University and Research), Sam Crauwels (KU Leuven), Bart Lievens (KU Leuven), Hans Jacquemyn (KU Leuven), Marcel Dicke (Wageningen University and Research), Erik H. Poelman (Wageningen University and Research)

12:30 – Frank Jiggins – University of Cambridge

The population genomics of Wolbachia in *Aedes albopictus*

Wolbachia is a common endosymbiont in many insect species. The mosquito *Aedes albopictus* is naturally infected with two strains of Wolbachia, and they reduce the rate at which this species transmits dengue virus. We have sequenced the genomes of the symbionts from a collection of mosquitoes from across the species' range and reconstructed their phylogenetic relationships. This is a young infection, with the symbionts sharing a common ancestor a few thousand years ago. The phylogeny of the mitochondria and the two Wolbachia genomes are largely congruent, indicating that they have been maternally transmitted, with only very rare paternal or horizontal transmission events. Subsequently the symbiont has spread globally, and has largely followed the migration of the mosquito hosts. The density of the symbionts, which determines their antiviral effect, varies greatly between samples, with at least some of this variation being determined by the Wolbachia genome. this may be related to the loss of genes that has occurred in many lineages. Together, this dataset has allowed us to reconstruct the origins and evolution of a symbiont that is thought to reduce the burden of infectious disease in human populations.

Other authors: Tom Schmidt (University of Melbourne), Julien Martinez (University of Glasgow), Jon Day (University of Cambridge), and Jon Welch (University of Cambridge)

- Pollinators I

Location: Lecture Theatre A

Chairs: Juliet Osborne and Chris Kaiser-Bunbury

14:30 – Jessica (Jess) Knapp – Trinity College Dublin

A view across fields - Interdisciplinary perspectives on pollinators

Insect pollinators are vital for healthy ecosystems and human-wellbeing, yet their populations are under-threat – negatively affected by human-mediated stressors, such as habitat loss and pesticide use. My work focuses on these land management practices and mitigative conservation measures, exploring their complex socio-ecological drivers and consequences to identify win-win solutions for people and pollinators. My talk will describe this holistic approach to pollinator and pollination ecology through a lens of bees, flowers and pesticides in agricultural landscapes. I will draw on a mix of methods, including new insights into pesticide exposure and effects, that I have used to extend my perspective from a flower- field and individual-to-population scales to inform policy and practice. Throughout my talk, I will identify key challenges and opportunities– across literal and disciplinary fields- for improved pollinator conservation.

15:00 – Michael Thomas Smith – University of Sheffield

Exploring bumblebee foraging in the landscape using a novel Bluetooth tracking system

The significant, widespread and continuing declines in wild pollinators is impacting both wildflower and food production. In particular central-place foraging insects, such as bees, play a vital role in providing such pollination services. Conservation and agriculture would benefit from being able to record and understand foraging behaviour across real landscapes. Unfortunately, current methods for exploring this question are very limited.

We present a method in which a new low-energy Bluetooth (BLE) system-on-a-chip receiver is attached to the bee, using custom-made micro-batteries. A series of high-gain BLE transmitters are deployed across the landscape. The bee is allowed to perform its foraging flight, and after it returns to the nest, the tag is retrieved and the flight path reconstructed using the records saved on the BLE receiver.

We describe the development of this method for insect tracking and instrumentation, and demonstrate that can operate in a range of landscapes aimed specifically at central place foraging. We show a proof-of-concept application of this method to record and explore the structure of foraging flights of bees.

Understanding how bumblebees use the landscape will give insight into the reasons for their relative abundance or rarity. In particular we will explore their use of linear features (such as hedgerows), how they respond to the shape and distribution of various floral resources, and how this changes over the colony lifetime.

15:15 – Adam Vanbergen – INRAE

Landscape type & floral resources modify plant pollinator network structure and stability: implications for pathogen exchange.

Pollinators face multiple, potentially interacting threats from human activities. The Biodiversa VOODOO project (https://voodoo-project.eu/) seeks to understand how landscape-use, through its impact on floral resources, affects plant-pollinator communities and the transmission of viruses between pollinator species. We present initial results to show how the architecture of plant-pollinator networks varies among agricultural, habitat mosaic, and urban landscapes, with consequences for co-extinctions. We show how modification of floral resources can affect network structure to shape interspecific transmission of viral pathogens and we provide early results that show how niche overlap among species governs the degree of viral pathogen sharing among wild and managed bees.

Other authors: Willem PROESMANS (INRAE), Matthias ALBRECHT (Agroscope), Hajnalka SZENTGYÖRGYI (Jagiellonian University), Anna GAJDA (Warsaw University of Life Sciences), Peter NEUMANN (U of Bern), Maryline PIOZ (INRAE), Josef SETTELE (UFZ), Oliver SCHWEIGER (UFZ), Robert PAXTON (MLU Halle-Wittenberg) & the VOODOO CONSORTIUM

15:30 – Claire Carvell – UK Centre for Ecology & Hydrology
The UK Pollinator Monitoring Scheme: six years on

The UK Pollinator Monitoring Scheme (https://ukpoms.org.uk) was established in 2017 to understand how insect pollinator populations are changing across the UK. PoMS features two large-scale surveys: the Flower-Insect Timed Count (FIT Count) and the 1 km square survey, using a combination of volunteer and professional recorders to collect data on the abundance and species distribution of flower-visiting insects and floral resources from a wide range of habitats across the UK. Six years on, PoMS has generated data from more than 12,000 FIT Counts including over 133,000 insect-flower interactions to insect group level. Over 1,100 survey visits to a network of 80+ 1 km squares have been conducted, with 234 species of bee and hoverfly identified from pan traps. Data are made available for further academic research and to the wider conservation community through the NERC Environmental Information Data Centre. Further afield, the FIT Count app has been developed for use in seven EU member states and in Brazil, Argentina and Chile. This talk will feature the results and successes of PoMS so far, and highlight some of the challenges we face in continuing to document changing insect populations in the face of ongoing environmental change.

Other authors: the UK PoMS partnership

15:45 – Ritesh Kumar Gautam –Wildlife Institute of India
Pollinator diversity, distribution and pollination interactions along the elevational gradient in Western Himalaya, Uttarakhand

The Himalayan ecosystem is remarkably rich in biodiversity and endemism but also fragile and facing threats due to forest fragmentation, overexploitation, and climate change. Being part of the ecosystem, Himalayan insect pollinators are impacted by these menaces. Nevertheless, the diversity and ecology of wild pollinators are not well documented in this region. Our study is being conducted along the elevational gradient of Kedarnath Wildlife Sanctuary, and it aims to: (1) elucidate the diversity and distribution of wild insect pollinators (mainly bees) and association in their occupancy and different plant communities; (2) reveal their pollination inactions using flower visitation and pollen signature; (3) partake in their conservation through spreading awareness about their significance. We are developing forest-type-wise bee inventory using sweep nets and coloured pan traps on different elevations. For documenting the pollination interactions, we are using: (1) ocular observations, (2) CHDK-enabled Canon PowerShot® cameras on tripods as flower-pointed camera traps and (3) pollen signature by preparing pollen reference library. We found an association of pollinator diversity with forest types and elevations. The species diversity is highest in Moist temperate mixed deciduous forests of mid-elevation zones (1800m–2800m). In contrast, Alpine meadows of extremely high elevation zones (above 3600m) and gregarious pine forests of lower elevation zones (below 1800m) represent low species diversity. This coalition results in pollination interdependency between bees and the plants: the high-elevation plants (Bistorta, Potentilla, Taraxacum) are majorly (perhaps only) pollinated by bumblebees. We are disseminating our findings to the forest department, native people and tourists to explain bees' role in sustaining natural forests, agriculture and urban forests.

Other authors: Dr V P Uniyal Wildlife Institute of India, Dehradun

- Infection and Immunity I

Location: Lecture Theatre B

Chairs: Megan Wallace and Mark Hanson

14:30 – Sheena Cotter – University of Lincoln

Are you what you eat: how diet impacts body nutrients.

Many hosts respond to infection by changing their diet. Previous studies have assumed that the function of this response is to strengthen their immune response. However, for parasites, their host represents the nutrients available for their growth and reproduction. Perhaps hosts are exploiting this by changing their body composition in a way that is detrimental to parasite growth? To understand this potential, it is vital to understand how quickly dietary change can change the nutrient pool in the host. We reared caterpillars on different diets and categorised the nutrient pool in the blood in terms of macro- (carbohydrates, proteins, fats) and micronutrients (simple sugars, amino acids) 24 hours later. Whilst sugars and lipids were tightly controlled, proteins and major amino acids increased with protein intake. We discuss the implications for host-parasite interactions and self-medication.

Other authors: Robert Holdbrook, Joanna L. Randall, Yamini Tummala, Catherine E. Reavey (University of Lancaster), Geraldine A. Wright (University of Oxford), Judith A. Smith (University of Central Lancashire), Stephen J. Simpson (University of Sydney), & Kenneth Wilson (University of Lancaster)

15:00 – Shuyu Zhou – University of Cambridge

Natural selection has driven the recurrent loss of an immunity gene that protects Drosophila against a major natural parasite.

A fundamental question in infection biology is why some individuals are susceptible to infection but others are resistant. We have investigated why fruit flies vary in susceptibility to parasitoid wasps in natural populations. We genetically mapped a single locus affecting the susceptibility of Drosophila to the parasitoid wasp *Leptopilina boulardi*, and found a lectin gene to be modulating resistance. When we mutated the resistant allele, we found resistance dropped to similar levels as the susceptible allele. Here we show, the resistant allele is massively upregulated following parasitoid infection, but a cis-regulatory polymorphism upstream of the gene greatly reduces the expression of the susceptible allele. By creating transgenic flies carrying a fluorescent reporter construct, we dissected the promoter region of the lectin gene and identified a 21base pair deletion responsible for this difference in expression. In natural populations we also identified multiple other loss-of-function alleles in cis-regulatory and coding sequence, and in all cases the resistant allele was the ancestral state. Using population-genetic analyses we conclude that natural selection has driven recurrent loss-of-function in a gene that protects flies against an important natural enemy, likely due to the cost of maintaining resistance in the absence of parasitization.

15:15 – Ryan Imrie – University of Exeter

Exploring patterns and determinants of virus susceptibility across Drosophilidae hosts.

The outcome of any one infection can be influenced by an array of factors, including host and pathogen genetics, environmental and ecological conditions, microbiome compositions and the presence of coinfecting pathogens. Understanding the contribution of each of these factors to the patterns of susceptibility seen in nature can improve our knowledge of the evolution of host-pathogen interactions and the emergence of novel infectious diseases. To investigate the influence of these different factors on host susceptibility, we have performed experimental infections with two viruses – Drosophila C virus (DCV) and Cricket Paralysis virus (CrPV) – across a diverse panel of Drosophilidae host species and looked for changes in the ability of each virus to persist and replicate across our host phylogeny. Over multiple studies, we have shown varying contributions to host susceptibility, with host diet showing no detectable effects, temperature increasing the variance across host species, coinfection status increasing stochasticity, and virus genotype disrupting the rank-order of host species susceptibility. Together, these studies reveal the complex interplay of factors that can influence the outcomes of infection across host species.

Other authors: Katherine E. Roberts, Sarah K. Walsh, Ben Longdon (all University of Exeter)

15:30 – Eduardo Costantin – Universidade Federal de Viçosa and Lancaster University
Insect pathogenic fungi as a model system to study coinfections.

Animals and plants are commonly coinfected by more than one parasite species or strain in nature, which could have considerable implications for disease dynamics and pathogen evolution. Studies with multiple parasites can be challenging, however. For example, the outcomes of coinfections are largely affected by the identity of the parasites involved, and this dependence makes it difficult to understand other factors that may impact these infections. To address this problem, we report here the establishment of a model system composed of the beetle Tenebrio molitor and the entomopathogenic fungi *Beauveria bassiana* and *Metarhizium anisopliae*. These two fungi belong to the same taxonomic order (Hypocreales) and interact in a similar fashion with the host. This allows us to examine coinfections experimentally with limited impact of parasite identity and host exploitation strategy. Both fungi kill their host then sporulate, one white and one green, allowing simple and rapid visual collection of data on infection outcomes. When both fungi were inoculated at the same time and at the same place, coinfection did not affect virulence towards the host and *B. bassiana* was the only fungus to sporulate in 60% of the infected larvae, while only M. anisopliae sporulate in 12%, and both parasites in 28%. When both fungi sporulated in coinfections, they suffered a ten-fold reduction in the number of spores produced compared to single infections, which clearly represents a pattern of interference competition between them. We then tested whether the location of infection, order of parasite arrival and time between infections could modify this outcome. None of those variables impacted virulence substantially. Nonetheless, our results showed that the first parasite to arrive dominates the host, even the weak competitor Metarhizium. Curiously, time elapsed between infections did not alter this within-host priority effect. We also found that the location of infection altered the outcome of coinfection. When both fungi infected the host in separate locations of its body, the proportion of coinfected larvae increased, indicating that competition between parasites was alleviated by altering the location of infection. Our findings strongly support the use of the proposed system to study coinfections, since we successfully showed the impact of varying characteristics of infection for host and parasite life-history. Subsequent studies will investigate how external variables impact outocomes of coinfection. This line of investigation will help the understanding the basic aspects of coinfections and may contribute with biological pest control in agriculture, given the use of multiple pathogens in this setting and the possibility of coinfections.

Other authors: Simon Luke Elliot - Universidade Federal de Viçosa; José Augusto Martins Roxinol - Universidade Federal de Viçosa; Pablo Fernandes Braga - Universidade Federal de Viçosa

15:45 – Matt Tinsley – University of Stirling

How does parasite coinfection influence the virulence experienced by insect hosts?

Organisms are usually simultaneously infected by multiple parasites. Coinfecting parasites interact within the 'ecosystem' inside their host: competing for host resources, triggering or suppressing overlapping immune responses, and directly suppressing or facilitating growth of other members of the parasite community. Impacts of these interactions on the virulence experienced by the host are widely debated. We studied impacts of coinfection on virulence and the factors influencing virulence change under combined infection compared to a single infection. We used a literature survey and meta-analysis of insect coinfection studies, yielding over 1000 effect sizes. Strong reductions in virulence were rare; on average, mortality increased slightly during combined infections, an effect that was less than additive. The extent of virulence increase was strongly influenced by the phylogenetic distance between coinfecting parasites. We suggest that increases in infection-induced mortality under coinfection are most likely when coinfecting parasites exploit relatively independent niches inside an insect's body.

Other authors: Dr Lucy Nevard, University of Stirling; Dr Luc Bussiere, University of Gothenburg

- Pollinators II

Location: Lecture Theatre A

Chairs: Juliet Osborne and Chris Kaiser-Bunbury

16:30 – Elisa Rigosi – Lund University

A new in vivo approach to studying sublethal, neurophysiological effects of pesticides in non-model insect pollinators (Online talk)

Insect pollinators are important for natural ecosystems and the human economy, yet are threatened by common agrochemicals in both rural and urban environments. Most insecticides act as neurotoxins in the insect nervous system, however, their more subtle modulation of neural activity at sublethal concentrations are often overlooked. While navigating through the environment, flying insects rely mainly on visual information. Yet how the processing of this information is affected by neurotoxic insecticides is an open question. The majority of studies on this topic have focused on bees despite recent literature showing large variability in insecticide sensitivity across species. This highlights the importance of extending the analysis of sublethal insecticide effects to non-model organisms. Here, we introduce the pollinator fly *Eristalis tenax* as a new model to study sublethal neurophysiological effects in living individuals stimulated by relevant sensory stimuli for natural behaviour. We developed a new system to orally expose flies and then assess visually sensitive neurons in whole, living animals, viewing computer generated visual scenes. We performed electrophysiological recordings from visual neurons involved in motion detection and flight stabilisation. We compared their physiological responses in chronically exposed animals (and controls) in vivo at different timepoints after exposure. Our data show how the visual neuropils of Eristalis are physiologically resilient to field relevant, chronic exposure of imidacloprid, a widely used cholinergic pesticide. Our techniques could reveal new insights into the neurophysiological impact of virtually any neurotoxic pesticides and open the door for employing the same experimental approach to other insect species.

Other authors: Nicolas Nagloo, Department of Biology, Lund University; David C. O'Carroll, Department of Biology, Lund University

16:45 – Maxime Eeraerts – Ghent University

Pollination deficits and their relation to insect pollinator visitation are cultivar-dependent in an entomophilous crop (Online talk)

Insects contribute considerably to global crop pollination, yet pollination deficits are documented for multiple crops. With different and expanding cultivar availability being grown within and across production regions, it is essential to understand the cultivar variability of these deficits. Here, we used a dataset from 286 sites from multiple production regions to analyze pollination deficits in two northern highbush blueberry cultivars, Bluecrop and Duke. Additionally, we determined if bee visitation or bee richness can reduce pollination deficits. On average, neither cultivar showed significant pollination deficits for fruit set. However, in Bluecrop we found pollination deficits for berry weight and seed set, which was not the case for Duke. Increasing total bee visitation reduced both berry weight and seed set deficits for Bluecrop. These relationships were best predicted by a negative exponential model. We conclude that the extent of pollination deficits is variable between cultivars of a single crop and that pollination deficits are most likely to be mitigated when these deficits are high compared to when they are low. We highlight that assessments of crop pollination deficits and pollination services should be examined across different cultivars to improve management of pollination to enhance crop yields.

Other authors: Stan Chabert - Department of Entomology and Nematology, University of Florida, Gainesville, FL 32608, USA Lisa W. DeVetter - Department of Horticulture, Northwestern Washington Research and Extension Center Washington State University, Mount Vernon, WA 98273, USA Péter Batáry - ’Lendület’ Landscape and Conservation Ecology, Institute of Ecology and Botany, Centre for Ecological Research, 2163 Vácrátót, Hungary John J. Ternest - Department of Entomology and Nematology, University of Florida, Gainesville, FL 32608, USA Kris Verheyen - Forest & Nature Lab, Department of Environment, Ghent University, 9090 Melle-Gontrode, Belgium Rufus Isaacs - Department of Entomology, Michigan State University, East Lansing, MI 48824, USA

17:00 – Simeon Wilton – UK Centre for Ecology & Hydrology

Exploring the potential impacts of the Asian hornet, *Vespa velutina*, to wild pollinating insects in the UK.

Vespa velutina, also known as the Asian hornet, was first observed in France in 2005. This species was unintentionally introduced into France and has since spread rapidly within Europe and can be found in France, Belgium, the Netherlands, Germany, Italy, Spain, Portugal and the Channel Islands. It is included within the list of invasive alien species of Union Concern (EU Regulation 1143/2014[1] on Invasive Alien Species). Between 2016-2022 there have been 23 confirmed sightings of *V. velutina* in the UK. The rapid reporting of this species in the UK has underpinned the successful eradication. While *V. velutina*, is smaller in body size than the native European hornet, *Vespa crabro*, the nests of *V. velutina* frequently contain more workers and this could result in greater predation impact of other insect species than the native hornet. *Vespa velutina* is well documented as a predator of the European Honeybee, Apis mellifera, which unlike the Asian honeybee, *Apis cerana*, has not developed effective defences to *V. velutina*.

However, little is known about the impact of *V. velutina* on other insect prey, which include wild pollinators such as hoverflies and social wasps. Consequently, I am investigating which insect species could be most at risk if *V. velutina* were to become established in the UK. I have used a trait-based mixed effects model incorporating body size, seasonality, habitat and family of the insect prey. *V. velutina* captures prey in flight and then lands to process the prey item, removing all body parts except the thorax which is chewed to form a prey pellet to feed to hornet larvae in the nest. I have used data from published field studies in the Dordogne (France) which used morphological and DNA barcoding techniques to quantify the frequency of different prey within the pellets of *V. velutina* (Rome et al., 2021). By modelling diet from the Dordogne, I aim to predict potential UK prey species. This work will underpin my research on the robustness of plant-pollinator networks in the UK under varying invasion scenarios of *V. velutina*. Understanding the impacts of invasive non-native species, such as *V. velutina*, is critical to inform policy and guide management.

Other authors: Helen Roy (UKCEH), Dan Chapman (University of Stirling), Louise Barwell (UKCEH), Beth Purse (UKCEH), Olaf Booy (GB Non-native Species Secretariat)

17:15 – Joshua Moon Sammy – University of York

Dynamics of invertebrates in British anthropogenic habitats.

Humans have had increasingly large impacts on the world's ecosystems, generating a set of more-or-less human-modified (anthropogenic) environments with reduced local diversity. However, new environments, including human-created ecosystems, are then available for ecological colonisation and evolutionary adaptation, such that ongoing and future responses of species to different levels of human modification will determine how biodiversity adjusts to human-caused ecosystem change. Analysing 38,265,792 site-specific records of 1,509 invertebrate species from 14 taxonomic groups between 1981-2000 and 2001-2020, we find here that the geographic distributions of species that are positively associated with the highest levels of modification, such as with urban, suburban and arable habitats, have increased more than species associated with relatively unmodified ecosystems. Thus, 'human-associated' species in Great Britain have been increasing relative to 'human-avoiding' species, generating new ecological communities. Contrary to previous hypotheses, we find no evidence that human associated species are more likely to be habitat generalists. We also find strong links between the invertebrate fauna of some more and less human modified environments, suggesting that some of the most human modified environments may still provide benefits to less human associated species, and vice versa. These findings suggest that facilitating the expansion of species in human-modified landscapes may be as important to the future of biodiversity as preserving the least human influenced ecosystems.

Other authors: Dr. Jack Hatfield (University of York), Prof. Helen Roy (Centre for Ecology and Hydrology), Dr. Andrew Salibury (Royal Horticultural Society), Chris D. Thomas (University of York)

17:30 – Vera Kaunath – University of Potsdam

Does shape matter? An experimental design of Rolling Wildflower Blocks to increase insect diversity in agriculture.

Biodiversity and abundance of arthropods have declined dramatically in agricultural landscapes, so sown wildflower strips (WFS) have been implemented across Europe as part of the Agri-Environmental Schemes (AES) as a way to counteract reduced diversity by providing overwintering habitats and offer floral resources. Despite this, WFS have been subject to ongoing criticism regarding their effectiveness and suitability as a part of sustainable insect conservation. The is innovative concept of the Rolling Wildflower Blocks (RWB) seeks to improve the effectiveness of the AES by changing the shape of the traditional strip to a block shape and by combining several WFS of different successional stages. On the basis of this data, we are trying to promote an improvement of the AES, which would require a change in the subsidies in agriculture, as clustered WFS are explicitly not supported.

In addition to assessing the overall insect diversity, this research will focus on the diversity and abundance of carabids, which, with their diverse and often perennial life cycles, are often not considered well enough in the development of AES as part of insect conservation.

In the summer season of 2022, the first year of the implementation of the RWB, we set 200 pitfall traps in five arable fields in German agriculture (Havelland, Brandenburg) to investigate the effect of the two different shapes - a block shape (50m x 50m) and a traditional strip (15m x 150m) - on diversity, abundance and biomass of insects.

Unfortunately, the data collection is not yet complete, but will be finished in September. Preliminary data suggest that both higher abundance and richness of insects are higher in the traditional WFS, although this may be related to the larger border area towards the adjacent uncultivated field margins in the WFS compared to the block elements. However, we have not yet found difference in the insect diversity.

A larger border to the adjacent uncultivated fields may be advantageous for colonisation of WFS, but does not guarantee adequate quality of WFS as suitable habitats for insects. The full data analysis will allow a first assessment of the comparison of differently shaped flowering elements as a way of improving AES.

Other authors: Jana A. Eccard, University of Potsdam, Animal Ecology

17:45 – Ayman Asiri – Cardiff University

Does infection change the smell of honeybees?

Honeybees are one of the world's most important pollinators, but they are under threat worldwide by the emergence and persistence of infectious diseases. In several human and livestock systems, both infectious and non-infectious diseases change the volatile organic compound (VOC) profile of the organism.

Currently, beekeepers monitor infection in colonies by manually inspecting hives. This is a labour-intensive process and often when symptoms are visible it is too late to treat. Monitoring VOCs of honeybees may provide a non-invasive alternative to traditional disease monitoring in apiculture with the potential to alert beekeepers to infection prior to the onset of visual symptoms.

We performed a meta-analysis by screening four databases for papers reporting headspace compounds associated with infected honeybees, resulting in 1190 papers of which 22 met our inclusion criteria and were analysed.

We obtained 280 compounds representative of 5 treatments: Uninfected, infected, lab killed, lab killed (infected), and in vitro pathogens.

A network-based approach was used to assess if VOCs clustered according to treatment; i.e. if there was a unique smell of infection, or not, using a bipartite network to link compounds according to treatment. Community detection algorithms were subsequently used to detect compounds associated with one another. The analyses formed seven communities, of which three were highly characteristic of American foulbrood, Varroa mite and Chalkbrood infections.

These preliminary findings provide support for our hypothesis that VOCs may act as suitable targets for detecting infection in colonies.

Future investigations will study VOCs empirically in a range of pathogens and include behavioural manipulation studies to see whether honeybees use VOCs to regulate social immunity, and whether smell is a mechanism underlying disease transmission.

Other authors: Carsten Muller, Sarah Perkins (Cardiff University)

- Infection and Immunity II

Location: Lecture Theatre B

Chairs: Megan Wallace and Mark Hanson

16:30 – Bengisu Subasi – Freie Universität Berlin

How frequently are insects wounded in the wild? A case study using *Drosophila melanogaster*

Studies in the field of immunity have increased our general knowledge about infections and immune responses, yet wounds, i.e., a route via which pathogens could theoretically enter the body, are rather understudied in nature. The insect cuticle is one of the defence mechanisms against the invasions of pathogens and parasites. Abrasions or deep cuticular scratches could result in opportunistic pathogens entering the body cavity and initiating an immunological response. In insects after the injury the haemolymph coagulates at the injured area to clot the injury. After clotting the damaged area, prophenoloxidase cascade activation starts and leads to the melanization of the clot to form a hard clot which is observable as brown to black pigmentation. Despite the fact that injuries may be a potential entry point for pathogens and have significant ecological and evolutionary implications, little is known about the prevalence and consequences of injuries in model organisms like Drosophila. Injuries are thought to be common in the wild and can result from various causes such as predator attacks, intra- and inter-specific competition over food, territory or mating, and environmental factors. Injury rates can differ depending on the species, sex, and geographic location, and can have various effects on the host, such as decreased mobility, impaired reproduction, and increased susceptibility to pathogens. With this study, we aimed to investigate the prevalence and possible causes of injuries in wild-collected D. melanogaster. We systematically collected D. melanogaster in three different seasons and locations. We found 31% of individuals (in a total of 1174) had at least one type of damage to the external cuticle (head, leg, thorax, or abdomen) and the most abundant injury was found on the abdomen. Furthermore, females were significantly more likely to have damage to their abdomens (44 %) compared to males (8 %). D. melanogaster is a species with traumatic mating, i.e., where the male routinely wounds the female during copulation. Our data showed that 52 % of females showed genital wounding, suggesting that a large proportion of them were virgins. Not only this but Drosophila species are also known to host a variety of ectoparasitic mites and endoparasitoid wasps. We observed that in 11 % of flies a melanised parasitoid egg was visible through the adult cuticle. Moreover, 0.7% of Drosophilidae species (54 out of 8085) were captured with a mite attached to their body, which is remarkably consistent with another published study. Mites could perforate the host cuticle with their chelicerae to feed on the heamolymph which might cause a breach on the cuticle leading to a possible infection route for opportunistic pathogens. Therefore, we are investigating the implication of the damage induced by mites on the fly cuticle. This is the first systematic study that has been done in wild D. melanogaster to examine their injuries. Our results show that D. melanogaster are injured in the wild and injuries might be an important selective pressure.

Other authors: Veit Grabe2, Martin Kaltenpoth2, Sophie A.O. Armitage1. 1 Institute of Biology, Freie Universität Berlin, Germany, 2 Max Planck Institute for Chemical Ecology, Germany

16:45 – Aleksei Belyi – University of Cambridge

Genotype-specific interaction of Drosophila melanogaster and its parasite sigma-virus

Host-parasite interactions guide the evolution of both sides, determining levels of host resistance and parasite infectivity. These traits often show high levels of genetic variation maintained in the interacting populations, which may be explained by negative frequency-dependent selection (NFDS). In this study, we carried out a controlled laboratory experiment using a wide range of *Drosophila melanogaster* lines infected with isolates of its natural vertically transmitted parasite, sigma virus, to measure the genetic variation in viral transmission rates. We found that virus transmission rates varied considerably depending on both the host and virus genotypes. In particular, flies carrying resistant alleles of the genes ge1, CHKov1 and ref(2)p had lower transmission rates for the majority of the virus genotypes. Furthermore, there was a sex-specific interaction between the Drosophila and the virus genotypes on the transmission rate, such that flies that are adapted to one sigma virus genotype might be maladapted to other genotypes. This genotype-specific interaction has the potential to generate NFDS within both insect and parasite populations.

Other authors: Frank Jiggins (University of Cambridge), Ben Longdon (University of Exeter)

17:00 – **Hongbo Sun –** University of Exeter

Susceptibility to bacterial pathogens across host phylogeny

Host shifts are the main cause of emerging infectious diseases and cross-species transmission is an important source of bacterial and viral pathogens. Our current work uses Drosophila species as a model system to examine how species vary in their susceptibility to pathogens. By infecting 36 species of Drosophilidae with four bacterial pathogens (two Gram-positive and two Gram-negative) we examine whether the host phylogeny is an important determinant of bacterial load and virulence across host species. we then look at the correlations in susceptibility to G+ and G- bacteria to examine if susceptibility is specific or more general. we also investigate the correlations between host survival and host within bacterial load. This study will provide insights into the emergence of bacterial pathogens in novel hosts.

17:15 – Jingbo Liu – University of Bath

Terminal Investment encoded by immune gene expression.

The fields of Innate Immunity and Eco-Immunity research are stuck on the same problem: it's difficult to explain how defence against infection evolves. As the expression of canonical innate immune genes is costly for survival, even in the presence of systemic infection, it is not clear how immune genes would be maintained. The solution might to study defence against infection under the low-dose and sexually transmitted infections though to be the most prevalent insect diseases. We developed novel topical inoculation methods in fruit flies, Drosophila melanogaster, as host for an indigenous fungus. We found that our modes of low-dose topical infection alter reproductive output in a pattern that matches the dynamic threshold model of terminal investment. We found evidence for trade-offs between survival and reproduction that are not evident under high-dose infections. And, using immune gene knockdown assays, we find that a canonical immune gene, Dif, facilitates fitness trade-offs between survival and reproduction in response to low-dose sexually transmitted infections. These findings suggest that innate immunity genes evolve in conjunction with reproductive output, which provides an ecoevolutionary solution to why defence against infection is maintained.

17:30 – Alessandro Roman – University of Exeter and Wageningen University

Effects of *Asaia* bacteria on mosquito fitness for improvement of SIT programs

Arboviruses are responsible for many diseases in both humans and animals. The well-known yellow fever mosquito, *Aedes aegypti*, is the primary vector of yellow fever, dengue, chikungunya and Zika virus. Currently disease-control strategies strongly rely on mosquito population management through insecticides and larvicides. However, the threat of insecticide resistance is rising, bringing to a less effective vector control outcome. The sterile insect technique (SIT) is method that have been recently developed for insect population management. To successfully apply SIT, healthy and competitive mosquito colonies are required, to better allow sterilised males to successfully compete with their wild counterparts.

It has been shown that mosquito microbiota could play an essential role in larval development and fitness. Bacteria of the genus Asaia were identified as hypothetical actors in paratransgenesis techniques and as probiotic. Notwithstanding, little is known about the effects of Asaia spp. on adult fitness, in Ae. aegypti and in other mosquito species of public health interest. Here, we inoculated first instar larvae of *Ae. aegypti*, *Ae. albopictus*, *Culex pipiens* biotype molestus and *Anopheles coluzzii* with different species of Asaia. Fitness parameters were analysed. Ongoing efforts include exploring potential microbiome manipulations on male attractiveness and competitiveness in laboratory and semi-field contexts and vector competence. Our findings underline the importance of understanding host-microbe interactions. In addition, improving mosquito fitness can be beneficial for large-scale sterile male production.

Other authors: Paula Luikens (Wageningen University and Research, Laboratory of Entomology, The Netherlands); Constantianus JM Koenraadt (Wageningen University and Research, Laboratory of Entomology, The Netherlands); Ben Raymond (University of Exeter, Science and Engineering Research Support Facility (SERSF), Penryn, United Kingdom)

17:45 – Jenny Regan – University of Edinburgh
Sex and death: dimorphisms in host-pathogen interactions in Drosophila melanogaster (Online talk)

The sexes show profound differences in responses to symbionts, parasites, and pathogens, and these immune dimorphisms are found across taxa, in both arthropods and vertebrates. *Drosophila melanogaster* demonstrates sex differences in immune responses and survival to infection with a range of different pathogens. The mechanisms underpinning these sex differences are not well-understood, particularly the role for individual tissues, including phagocytes. We are asking how sex differences in immune function are regulated: how does the sex of individual immune tissues impact host-pathogen interactions to determine the outcome to infection? Are sex dimorphisms in immunity present at all life stages? Does adaptation to pathogens at one life stage carry through ontogenesis? How do sex and genotype influence immune ageing? Using viral and bacterial models of infection and genetic manipulation of sex, we are uncovering sex differences in immune tissue function that will have implications for host-microbe interactions in insects throughout the life course.

Other authors: Rebecca Belmonte, Mary-Kate Corbally, Julia Aleksandrovic (University of Edinburgh); David Duneau (Toulouse)

Thursday 7 September

- Conservation and Declines

Location: Lecture Theatre A
Chair: Alan Stewart

09:15 – Charlie Outhwaite – University College London
Understanding insect biodiversity change at the global scale

The global state of insect biodiversity is the subject of mounting concern. A growing body of evidence has reported declines in insect abundance, richness, and density across various regions of the world. However, the available evidence is rather patchy, both in terms of geographical coverage and in taxonomic coverage. As a result, we do not have a complete picture of how insects are faring at the global level, particularly in how they are responding to major anthropogenic drivers of change. We know that insects are facing multiple pressures including land use change, land use intensification, climate change and pollution to name just a few. However, the specific contributions of these pressures have yet to be quantified at a global scale. Furthermore, the impact of these pressures will vary among different insect Orders, owing to the vast array of insect species, their varied forms, habitat preferences, and life histories. It is unlikely that all insects will exhibit identical responses. In this talk, I will present recent work looking at global responses of insects to the interaction of land use and climate change, assessing both the global average and the variation in responses of different insect Orders. I will also share some insights into the ongoing research of the GLiTRS project, a large collaborative project aiming to get a better handle on the state of insects globally by bringing together different forms of evidence to assess the responses of insects to a range of anthropogenic drivers.

Other authors: Kyra Smith (Università di Bologna), Tim Newbold (UCL), Joe Millard (NHM), Andrew Bladon (University of Cambridge), Rob Cooke (UKCEH), Nick Isaac (UKCEH)

09:45 – Marcus Rhodes – University of Exeter
Feeling the heat: can microclimate & behaviour buffer insects against climate change?

Species’ responses to climate change are typically predicted using seasonally aggregated, spatially coarse climate data that often fails to reflect the thermal environments of organisms. Small animals, such as insects, inhabit microclimates that can be highly heterogeneous and markedly different from ambient conditions. By exploiting favourable microclimates and altering their posture in order maximise or minimise heat exchange, insects have considerable capacity to alter their body temperature through behavioural thermoregulation. We have developed a biophysical model for predicting the body temperature of a Common Blue butterfly (*Polyommatus icarus*) as a function of its basking posture and microclimate. Using this model, we predict the range of body temperatures that a butterfly can achieve at each hour throughout the year, across sites in Cornwall and central Spain. We demonstrate that behavioural thermoregulation is necessary for achieving optimal body temperature under current climate conditions and that fifty years’ worth of climate change is theoretically within the capacity of behavioural thermoregulation to absorb.

Other authors: Richard ffrench-Constant (University of Exeter), Jonathan Bennie (University of Exeter), Adrian Spalding (Spalding Associates (Environmental) Ltd) & Ilya Maclean (University of Exeter)

10:00 – Eleanor Slade – Nanyang Technological University
Addressing the taxonomic and capacity impediment in tropical entomology: Mobilising data on the dung beetles of Malaysia and Singapore

A crucial but often overlooked part of being able to predict biodiversity responses to environmental change is the collation and curation of the variety of data documenting species occurrences, distributions, traits, and natural history. For temperate regions and common groups such databases exist and have allowed ecologists and conservationists to map species distribution changes over time and space, to determine their conservation status, and predict their future response to environmental change. Dung beetles are an ecologically important insect taxa providing many ecosystem functions and services. They are also an excellent model taxon for biodiversity research as they respond rapidly to environmental changes and can be sampled cost-effectively. However, in Southeast Asia little is documented about their natural history and distributions, many species are still undescribed, and there are few taxonomists, guides or keys for the region.

In this presentation we will discuss how we have addressed these taxonomic and capacity impediments through:

1. Collating data into open access databases, such as GBIF, to act as a repository for functional traits, species distributions, high-resolution photographs, and literature.

2. Working with taxonomists to describe unidentified species and resolve morphospecies codes among existing studies.

3. Creating useable keys and photographic guides to species.

4. Generating molecular barcodes in Genbank for each species that link to the database and new species descriptions.

5. Training students and stakeholders in SE Asia in species identification and curation, databasing, digitization, and preparation of keys and identification guides.

Our Taxonomic Checklist and Occurrences of the Dung beetles (Coleoptera: Scarabaeidae: Scarabaeinae) of Sabah, Malaysia is now available on GBIF and documents 192 records from over 10,000 occurrence records from all available taxonomic and ecological literature on the dung beetles of Sabah. We have documented 154 taxonomically accepted species names, and are working to create a morphospecies database with associated barcodes to help enable the description of new species. We have developed a user-friendly key and guide to the dung beetles of the region in both English and Bahasa Malaysia, and provided training and capacity building workshops to both increase understanding of the importance of insects and to build in identification and surveying skills.

There is both a taxonomic and capacity impediment preventing the use of insects in biodiversity monitoring and conservation assessments, particularly in the tropics. This project presents an example of how data can be mobilized to help address these gaps and facilitate the use of insects as bioindicators of environmental change.

Other authors: Ong, Xin Rui (NTU); Zann Teo (NTU); Chiew, Li Yuen (NTU); Marx Yim (NTU)

10:15 – Helen E. Roy – UK Centre for Ecology & Hydrology

Citizen science reveals the distribution patterns of native ladybirds in the presence of invasive alien ladybird, *Harmonia axyridis*

The harlequin ladybird, *Harmonia axyridis* (Coleoptera: Coccinellidae), is native to Asia but has been introduced intentionally and unintentionally to many countries worldwide. *Harmonia axyridis* has been used as a biological control agent of aphids but as a generalist predator it poses a threat to other insects. Many studies have demonstrated the adverse effects of *H. axyridis* on other aphid predators including ladybirds. In 2012 we published a study comparing the distribution and abundance of formerly common and widespread native ladybirds in Europe before and after the arrival of *H. axyridis*. This study provided evidence of *H. axyridis* displacing native ladybirds with high niche overlap. Volunteer contributions through citizen science initiatives in Belgium, Netherlands and UK have provided a further ten years of ladybird observations and an opportunity to repeat analyses assessing distribution trends of ladybirds. The rapid declines evident for native ladybird species in the presence of *H. axyridis* resulted in range contraction for a number of species. Most notable was the distribution decline of 2-spot ladybirds, *Adalia bipunctata*; in the UK this species experienced a decline in distribution of 44%. The repeat analysis, using ladybird observations up to 2020, highlight that although the declines have stabilised there is little evidence of recovery. Here we provide an overview of ladybird distribution trends and discuss the implications of sustained reduction in occupancy of previously common and widespread species on biodiversity conservation. We also highlight the invaluable role of volunteers in this research and the ongoing need to encourage biological recording to provide datasets to assess the effects of global environmental change on insects. The ladybird observations accrued through citizen science over many decades have made a huge contribution to our understanding of the ecology of ladybirds.

Other authors: Tim Adriaens, Research Institute for Nature and Forest (INBO), Brussels, Belgium; Peter M.J. Brown, Anglia Ruskin University, Cambridge; Vincent Kalkman, Naturalis Biodiversity Center, Leiden, Netherlands; Gilles San Martin, Centre wallon de Recherches agronomiques (CRA-W), Gembloux, Belgium; Dirk Maes, Research Institute for Nature and Forest (INBO), Brussels, Belgium and Radboud Institute for Biological and Environmental Sciences (RIBES), Radboud University, PO Box 9010, NL-6500 GL Nijmegen, The Netherlands; Thierry Onkelinx, Research Institute for Nature and Forest (INBO), Brussels, Belgium

10:30 – James R. Bell – Rothamsted Research
Spatial synchrony: A useful concept to manage insect populations?

Spatial synchrony is arguably a useful concept to manage insect populations and has been used for both insect conservation and insect pest management. Spatial synchrony indicates whether population fluxes are coincident across space or are instead heterogenous, resulting in idiosyncratic site-specific responses. Often the driver of spatial synchrony is caused by a synchronous response to changes in their environment (aka the Moran effect). Examples of environmentally-driven synchrony include the introduction of a novel technique to agriculture, or widespread habitat enhancement for nature conservation. The utility of this technique will be discussed in the context of i) host-plant genetic modification, and, ii) deployment of insecticides at scale. I will conclude with thoughts regarding its use for decision support in agriculture and reversing insect declines for nature conservation.

10:45 – Mahtab Yazdanian – University of Oulu
Ecological and life-history traits predict temporal trends in biomass of boreal moths (Online talk)

Dramatic insect declines, and their consequences for ecosystems globally, have received considerable attention recently. Yet, it is still poorly known if ecological and life-history traits can explain declines and whether insect decline occurs also at high latitudes. Insects' diversity and abundance are dramatically lower at high latitudes compared to the tropics, and insects might benefit from climate warming in high-latitude environments.

We adopted a trait- and biomass-based approach to estimate temporal change between 1993 and 2019 in Finnish macro-moth communities by using data from 85 long-running light traps. We analysed spatio-temporal variation in biomass of moth functional groups with Joint Dynamic Species Distribution Models while accounting for environmental variables.

We did not detect any declining trends in total moth biomass of moth functional groups, and most groups were stable over time. Moreover, biomass increased for species using coniferous trees, lichens, or mushrooms as hosts, multivoltine species, as well as monophagous and oligophagous species feeding on trees. We found that length and temperature of the growing season, winter climatic conditions, and habitat structure all partially explained variation in moth biomass.

Although boreal moth communities are rapidly changing due to species turnover, in terms of total biomass they seem to contradict the trend of dramatic insect declines observed globally. This may lessen the immediate possibility of negative bottom-up trophic cascades in boreal food webs.

Other authors: Tuomas Kankaanpää, Juhani Itämies, Reima Leinonen, Thomas Merckx, Juha Pöyry, Pasi Sihvonen, Anna Suuronen, Panu Välimäki, Sami M. Kivelä

11:00 – Robert J. Wilson – Museo Nacional de Ciencias Naturales MNCN-CSIC

Turnover in space and time of mountain butterfly communities over four decades of environmental change

Understanding how landscape heterogeneity could increase ecological resilience to global change by providing diverse habitats or communities is important for insect conservation. Here, we assess how butterfly communities varied over space (beta diversity) and time using repeat surveys from 166 localities in four mountain ranges in the Iberian Peninsula between 1985 and 2022. Spatial turnover in butterfly community composition was primarily related to elevation both historically (1985-2005) and more recently (2017-2022), whereas beta diversity among the mountain ranges reduced over time. The changes appear to be driven in part by colonizations of generalist and hot-adapted species, and local extinctions of specialist and cool-adapted species, implying community homogenization and thermophilization. In contrast, local (alpha) and functional diversity appeared to be maintained at mid-elevations in the most structurally diverse habitats, suggesting that habitat and microclimatic heterogeneity could play a role in buffering communities against environmental change.

Other authors: Guim Ursul, Mario Mingarro, Hugo Alejandro Álvarez (all Museo Nacional de Ciencias Naturales MNCN-CSIC)

- Behavioural and Evolutionary Ecology

Location: Lecture Theatre B

Chairs: Jeremy Field and Jodie Gruber

09:15 – Thomas Schmitt – University of Würzburg

Cuticular hydrocarbons as chemical cues for recognition in insect antagonistic interactions

All insects investigated so far exhibit a complex blend of hydrocarbons (CHCs) on their cuticle. These CHC profiles are often species- and sex-specific and play a crucial role in intra- and interspecific recognition and communication. Although CHC composition and function is studied intensively, our knowledge of the evolution of this ubiquitous trait is rather scarce. In order to understand the factors shaping CHC profiles, we studied antagonistic interaction networks of solitary wasps and bees (Hymenoptera). The interactions involve chemical mimicry, because CHCs of brood parasites may be recognised by the hosts, and, consequently, the parasites are under selection to avoid being recognised. In my talk I will discuss strategies of chemical deception and conditions that facilitate the evolution of chemical mimicry. I will focus on how interactions between hosts and their parasites impact the composition of complex CHC profiles and thus potential recognition processes. Finally, I will show how our research sheds light on the co-evolutionary processes selecting for ubiquitous chemical cues in Hymenoptera.

09:45 – Jim Galloway – University of Exeter

Testing behavioural thresholds of nocturnal moth acuity under day and night conditions.

While there is significant research into the acuity of a variety of animals including in insects, there are still gaps in taxonomic groups, and with the context of visual environments. On such taxonomic gap is in nocturnal moths, especially noctuid and geometrid species. There is increasing evidence these species play an important role in pollination, and there is a significant visual component in this process. In addition, there's evidence that acuity shifts with light levels. How these factors interact is equally unknown. This experiment is part of a wider project investigating the impact of light pollution on nocturnal pollinators and aims to catalogue the day and night behavioural thresholds of various British crepuscular and nocturnal moths as well as the degree to which changing light levels affects acuity. Using an open source optomotor set up, we will measure the behavioural thresholds of acuity in wild caught moth species under both daylight and night conditions. Following this, moths will be light adapted and then have their acuity remeasured to test for any evidence of circadian rhythms independent of light levels. This will provide baseline data to inform follow-up experiments investing the flight behaviour of moths in response to artificial light sources, as well as testing contrast sensitivity thresholds. Our predictions based on previous work examining the responses of moth visual pigments to light, and the understanding of compound eye acuity, are that moth acuity will deteriorate under low light conditions especially in nocturnal species possessing superposition eyes, and after sufficient adaptation under light, acuity will return to daylight levels.

Other authors: Dr Emmanuelle Briolat, Dr Jon Bennie, Professor Kevin Gaston, Dr Jolyon Troscianko

10:00 – Emmanuelle Sophie Briolat – University of Exeter
Hide and seek - how artificial lighting affects activity, background selection and camouflage in nocturnal moths

Artificial light at night, or ALAN, is a widespread and growing source of anthropogenic disturbance, that fundamentally alters the night-time lighting environment, and has a wide range of impacts of the physiology and behaviour of nocturnal species. Behaviours involving vision, underpinning crucial ecological interactions such as foraging, signalling and evading predators, are especially likely to be disrupted. Even without involving visual processes, artificial lights are thought to increase mortality in nocturnal Lepidoptera, as attraction to lights can itself be fatal and predators may take advantage of aggregations of moths around lights, yet lighting may also affect moths' ability to protect themselves from more visually-guided predators. While at rest in the daytime, moths are at risk from diurnal predators such as birds, and most undefended species will rely on concealment and crypsis to avoid detection. Previous research has shown that many moths are indeed capable of selecting backgrounds that more closely match the brightness of their wings, while some bark-dwelling species can even adjust their position to better suit the pattern of the background. Yet this ability evolved under natural night-time lighting conditions, and ALAN-related changes to the moths' visual environment may cause them to choose less appropriate backgrounds, leaving them more visible to diurnal predators. In this study, we used choice tests and visual modelling to test both the ability of a range of UK moth species to select backgrounds against which they are better-camouflaged, in terms of both luminance and colour, and the impacts of artificial lights on this behaviour. Moths were placed in individual choice chambers containing artificial backgrounds varying in colour and brightness, under natural night-time conditions or artificial lights. We used time-lapse photography to record the activity and background selections of each moth throughout the night, and digital photography and image analysis to quantify visual contrasts between their wings and the backgrounds they preferred, as perceived by the visual system of a model bird, the blue tit *Cyanistes caeruleus*. Traditional light types, that typically emit narrow-band long-wavelength orange lights, are progressively being replaced by more broad-spectrum energy-saving LEDs, so we tested the impacts of several light types that could reasonably be deployed in public lighting, including broad-spectrum white LEDs, narrow and broad-spectrum amber LEDs, and RGB LEDs. Preliminary results suggest that moths do select backgrounds against which they are better matched, especially in terms of colour, under natural night-time lighting, compared to narrow-band amber LEDs, which are predicted to block their colour vision. These findings suggest that light pollution may not only affect moth behaviour at night, but also have knock-on effects on their camouflage and predation risk in the daytime.

Other authors: James Galloway (Centre for Ecology & Conservation, University of Exeter), Jonathan Bennie (Environment and Sustainability Institute, University of Exeter), Kevin Gaston (Environment and Sustainability Institute, University of Exeter), Jolyon Troscianko (Centre for Ecology & Conservation, University of Exeter)

10:15 – Mabel Sydney – University of East Anglia
Nutritional insensitivity to mating in male fruit flies

Animals can adjust their consumption of different nutrients to match their physiological state and account for variation in social and sexual experience. For example, reproduction can trigger a dramatic change in nutritional needs. Female *Drosophila melanogaster* fruit flies change their diet preference after a single mating to consume more food and a higher proportion of protein to support egg production. In contrast, male fruit flies do not adjust their diet preference after a single mating. This is consistent with the idea that mating has little physiological impact on males, as sperm is 'cheap' to produce. However, a single mating may not capture the true effect of mating on male diet choice because males are able to mate multiply in quick succession in natural scenarios, which can have cumulative impacts on male ejaculate reserves and fertility. Male nutritional demand as a result of mating might then only be exposed after sustained reproductive effort, rather than a single mating. We tested this idea by measuring the effect of multiple matings on the diet choice of male D. melanogaster fruit flies. Males were assigned to three mating treatments – unmated, mated once or mated five times consecutively – and then allowed to feed freely on diets of protein and carbohydrate. We found that males that mated five times did not alter the amount, nor the proportion of protein and carbohydrate consumed, in comparison to unmated or once-mated males. This occurred despite fewer offspring sired from each consecutive mating. The results suggest that males remain on a strict feeding trajectory even when mating close to their daily maximum, and do not increase nutrient intake to account for their reduced ability to transfer ejaculates. These results reveal a lack of plasticity in male feeding behaviour according to mating status, despite substantial potential fitness costs, and highlight the differences in dietary regulation between males and females.

Other authors: Tracey Chapman (University of East Anglia, UK) Jennifer C Perry (University of East Anglia, UK & St. Francis Xavier, Canada)

10:30 – Mia Graham – University of Stirling
Rapid evolution of resistance to a parasitoid wasp used in horticultural biocontrol.

Pathogens and parasites can exert strong selection pressures on host populations in natural ecosystems and drive rapid evolutionary change. Pesticide resistance evolution is a continual agricultural concern, causing reduction in crop protection efficacy and economic losses. Environmental impacts of chemical pesticides are motivating a shift towards sustainable pest control using biocontrol agents. Whilst risks of resistance evolution to chemical pesticides are well understood, threats of pest resistance evolution to the pathogens and parasites used as agricultural biocontrol agents are underappreciated. One serious pest of protected horticulture is glasshouse whitefly (*Trialeurodes vaporariorum*). In European horticulture, this species is most commonly controlled using fungal biopesticides and parasitoid wasps.

We assessed the extent to which *T. vaporariorum* may be able to evolve resistance to the parasitoid wasp *Encarsia formosa*. We also assed the potential for resistance trade-offs with a second parasitoid wasp species. In a laboratory experiment we imposed experimental selection for parasitoid wasp resistance in T. vaporariorum against *E. formosa*. Twenty replicated selection lines rapidly evolved resistance over ten generations of selection to E. formosa. Larval survival probability increased by 80% during ten generations in the selected lines. When selected lines were exposed to *Eretmocerus eremicus*, we found that they were also resistant to this second parasitoid wasp species. This suggests that *T. vaporariorum* has relatively general defence mechanisms against these parasitoids and that there is no specificity of resistance. This rapid evolution of resistance could threaten the effectiveness and longevity of these ecologically sustainable biological control agents.

10:45 – Ginny Greenway – University of East Anglia

Crossing boundaries: interspecific preferences drive frequent reproductive interference in Tribolium flour beetles

One of the most crucial decisions an animal makes over its lifetime is who it chooses as a reproductive partner. Selecting a compatible mate can maximise offspring production, whilst making a mistake can cost individuals dearly, leaving them with no or low fitness. However, this decision is often not straightforward. When choosing, individuals must typically navigate a complex social environment, containing both males and females of their own species as well as individuals from other species. This can lead to instances of reproductive interference, or costly mating interactions between individuals of different species. This phenomenon is the subject of much speculation; is reproductive interference a rare case of mistaken identity? Or a spill-over of adaptive within-species mating processes and preferences?

In this study I examine the frequency and drivers of reproductive interference across three species of *Tribolium* flour beetles. Using *Tribolium castaneum* as the focal species, I determined both male and female mating patterns and preferences by simultaneously presenting individuals with a gradient of four related options (*T. castaneum* from the same population, *T. castaneum* from a different population, *T. confusum* and *T. freemani*). These species are all stored grain pests with a cosmopolitan overlapping global distribution. Replicates of these group compositions (either 1 focal male and 4 females or 1 focal female and 4 males) were continuously recorded for 30 minutes and all contact, mounting and mating interactions were recorded.

Focussing first on trials with focal *T. castaneum* males, individuals mated indiscriminately with females of their own species, regardless of population, and directed very few mating attempts towards *T. confusum* females, despite their visual similarity. Contrary to expectations, focal males showed a marked preference for the considerably larger *T. freemani* females, mounting them more frequently than females of their own species. In trials with focal *T. castaneum* females, the only mating activity they were observed engaging in was with conspecific males. However, these trials also contained very frequent male-male interactions. Indeed *T. castaneum* males directed higher levels of mating effort towards the larger *T. freemani* male in their respective experimental arenas than the focal *T. castaneum* females present. Given that focal female observed mating activity was correlated with subsequent offspring production, this raises the intriguing possibility that male heterospecific mating attempts may limit conspecific female reproductive output under these conditions.

Overall, the systematic preference of *T. castaneum* for *T. freemani* individuals of either sex implies that reproductive interference in this context is not an occasional error or the result of an absence of discrimination. Instead it may reflect a preference for large body size, for instance, which may maximise partner fecundity when expressed in conspecific settings but be costly in mixed species environments. Continuing to examine drivers of reproductive interference in this group will shed further light on within-species mating dynamics and how these may be impacted by changes in species compositions in the future.

11:00 – Rebecca (Becky) Boulton – University of Stirling

Do asexual females get the best of both worlds in the sexually polymorphic aphid parasitoid *Lysiphlebus fabarum*?

Why sexual reproduction evolved from more efficient asexual reproduction is a long-standing question in evolutionary biology. Individuals that reproduce asexually should have higher fitness than sexual individuals for several reasons, but most notably because of genome dilution and the costs of producing males. Despite the costs of sex, it has evolved from an asexual ancestor to become the predominant reproductive strategy in nature. Moreover, in species that are sexually polymorphic (with individuals that reproduce either sexually or asexually) there is no clear and consistent evidence that asexuality always increases in frequency or that asexuals outcompete their sexual rivals. The general consensus is that sex predominates as it increases genetic diversity and evolutionary potential when selection pressures change. In particular sex has been proposed to help hosts keep up with their faster reproducing pathogens in evolutionary arms races. The aim of this study is to test whether this extends to co-evolution between a parasitoid and its more rapidly reproducing host. We use the parasitoid wasp *Lysiphlebus fabarum* which reproduces sexually (arrhenotokous haplodiploidy) and asexually (thelytoky via central fusion automixis) on cyclically asexual aphids (*Aphis fabae*). In *L. fabarum* asexual reproduction appears to be obligate but we have observed that asexual females from many populations commonly accept matings with males produced by sexual females. We test whether sexual or asexual females which either have, or have not mated, are more able to overcome host defences and achieve higher parasitism success and fitness. The results of this study improve our understanding of the dynamic economy of sex, shedding light on whether it can modify the balance of power in evolutionary arms races beyond hosts and pathogens.

- Poster presentations

Behavioural and Evolutionary Ecology

P1 – Arianna Chiti – University of Stirling

Sexual conflict and population dynamics: a dung fly story

Sexual reproduction generates selective pressure over traits and strategies that favour individuals in acquiring mates and fertilizations and, therefore, increase their fitness. In some circumstances, mating strategies that are advantageous to one sex may be costly for the other, thus generating asymmetries in reproductive success. This gives rise to sexual conflict between the sexes.
The mating rate is the most often cited example of sexual conflict, as higher rates are generally better for males than females. While multiple matings maximise male reproductive success, accepting or resisting too many mating attempts often reduces female fitness and can ultimately result in reduced offspring production and smaller populations.

The sex ratio (the proportion of males to females in a population) is one factor that affects sexual conflict: the higher the proportion of males, the more mating attempts each female must accept or reject. Mating conflicts can also vary with population density, as high densities increase the rate at which individuals encounter mates and mating competitors.

While the costs of sexual conflict on individual female fitness have been widely documented, little evidence exists on its ultimate demographic consequences and potential as a regulatory mechanism for population dynamics.

In this study, I investigated the effects of sexual conflict on the population reproductive output of the dung fly *Sepsis punctum*, where sexual conflict over mating is well-known. By manipulating sex ratios and population densities to create different scenarios of sexual conflict, I assessed whether (i) individual female fitness and population reproductive output varied with sex ratios and (ii) whether such changes were population density-dependent.

I found clear evidence for a decrease in female fitness and population reproductive output with increasingly male-biased sex ratios. However, the effects of sex ratio did not depend on population density. In fact, the population reproductive output increased with population density, suggesting that, in this study system, the effects of sexual conflict might depend more on the relative number of flies per sex rather than the total number of flies per population. These findings provide compelling evidence for the demographic consequences of sexual conflict and encourage further investigation into its potential role as a regulatory mechanism of population growth.

Other authors: A. Bradley Duthie (University of Stirling), Luc Bussière (University of Gothenburgh), Rebecca Boulton (University of Stirling)

P2 – Mukta Mala – University of Oxford

Warming with temperature oscillation alter critical thermal maximum and metabolic rate of pea aphid

Study of insect thermal physiology is predominantly biased towards the effects of changing mean temperatures, whereas the effects of fluctuating, extreme climatic events have been largely overlooked. Exposure to extreme temperatures affects insects' thermal tolerance capacity, such as critical thermal maximum (CTmax), and metabolic rate, which may influence a population's ability to survive under elevated fluctuating microclimatic conditions. This study assesses the impacts of warming and oscillating temperatures on the CTmax and metabolic rate of the pea aphid, *Acyrthosiphon pisum* using thermolimit respirometry. We use nine temperature regimes as treatments: four fluctuating temperature regimes (base temperature from a field-recorded, fluctuating base temperature increased by +0 °C, +2 °C, +4 °C and +5 °C) and five constant temperature regimes (19 °C, 21 °C, 23 °C, 24 °C and a control temperature of 25 °C). We find that the CTmax of both aphid species is significantly higher at elevated fluctuating temperatures compared with its corresponding constant temperature, and that metabolic rates increase with temperature, peak, and then drop at the highest temperatures. This study demonstrates that aphids develop metabolic plasticity through physiological adjustments to raise their CTmax to better cope with temperature changes, which is of significant importance for comprehensive planning in informed pest management decision-making.

Other authors: Prof. Dr. Nigel Andrew Chair of Discipline (Science), Faculty of Science and Engineering, Southern Cross University, Australia. E-mail: nigel.andrew@une.edu.au http://insectecology.une.edu.au

Conservation and Declines

P3 – Yoann Bourhis – Rothamsted Research

Explainable neural network for trait-based multispecies distribution modelling

Using species traits for community wide modelling of occupancy can be very helpful. Traits allow environmental drivers to affect species differently, as a function of their trait values. Such trends, learnt across the taxonomic dimension, helps poorly recorded species to build on others, hence improving the prediction of their occupancy.

This is called trait mediation and it is aptly captured with Bayesian hierarchical models (e.g. Hmsc). However, machine learning approaches do not easily conform to this hierarchical nature. Here we propose a novel artificial neural network (ANN) architecture that supports trait mediation, by building on a time distributed (TD) layer. Thanks to the non-linear and interactive nature of ANN, it reaches much higher accuracies than existing alternatives, while being also faster to train.

By coupling it with a novel method called SHAP, aimed at explaining machine learning models, we also show that our model is explainable. This is key to species distribution modelling, as explaining why a species is present is often as important as predicting correctly its presence.

We demonstrate our model capabilities on two data sets resulting from national insect survey: the UK butterfly monitoring scheme (UKBMS) and moths collected by the Rothamsted Insect Survey (RIS) light trap network.

Other authors: James Bell (Rothamsted R.), Chris Shortall (RR), Bill Kunnin (University of Leeds), Alice Milne (RR)

P4 – Sam Rogerson – University of Stirling

Are beetles colonising created woodland?

Invertebrates comprise a substantial portion of earth's biodiversity, of which beetles represent the most diverse group. Their various ecological roles underpin important ecosystem functions and human-derived benefits, including nutrient cycling, pest control, and waste disposal. Responses of beetles to woodland creation are driven by complex interacting factors, including colonisation ability, habitat preference, and local (e.g. patch size, age, and tree density) and landscape (e.g. amount and configuration of surrounding habitat) characteristics. Given the UK's recent focus on habitat restoration, we require further understanding of how and where to target woodland creation to maximise biodiversity gains. The WrEN (Woodland creation & Ecological Networks) project is a long-term, large-scale natural experiment investigating the colonisation of 106 UK secondary woodlands across an age gradient of 10 -160 years. Utilising WrEN species data, I will use Structural Equation Modelling to determine the relative and combined effects of local and landscape characteristics on beetle abundance and diversity in created woodlands.

Other authors: Professor Kirsty Park (University of Stirling), Ben Woodcock (UK Centre for Ecology and Hydrology), Elisa Fuentes-Montemayor (University of Stirling), Kevin Watts (Forest Research), Emily Waddell (University of Stirling)

P5 – Hannah Risser – UK Centre for Ecology & Hydrology

Varied effects of atmospheric nitrogen deposition on GB butterflies

Atmospheric nitrogen deposition has been linked with an overall loss of plant species richness and homogenisation of semi-natural habitats both in GB and elsewhere. We expect that nitrogen-induced changes in plant communities will impact invertebrate species through the loss of reproductive habitat, food plants and suitable microclimatic conditions caused by the shifts in composition of plant communities. Butterflies are often used as indicator species due to their sensitivity to environmental change, our comprehensive understanding of their ecology, and the existence of long-term datasets on their abundance and distribution. We performed a spatio-temporal analysis on data from the UK Butterfly Monitoring Scheme using generalised additive models to understand the complex and often non-linear relationships between butterfly trends and their drivers. We demonstrate that butterflies vary in their relationships with nitrogen deposition and highlight both species-level and trait level differences.

Other authors: Ed Rowe (UK Centre for Ecology & Hydrology), Susan Zappala (Joint Nature Conservation Committee), Susan Jarvis (UK Centre for Ecology & Hydrology) & Carly Stevens (Lancaster University)

P6 – Stephen Gillanders – University of Aberdeen

Invasive European earwigs in the Falklands: How big is the threat?

European earwigs (*Forficula auricularia*) have become an established introduced species in the Falklands Islands and may be classified as an Invasive Non-Native Species with implications for agriculture, native biodiversity, human health and the economy. There are concerns that their presence could disrupt natural and agricultural ecosystem functions, exclude endemic species, and cause trophic changes in established food webs, but at this time, there is insufficient data to draw conclusions.

While in some production environments (namely orchard systems) *F. auricularia* has been recognised as a beneficial predator of pest species, in others it has the potential to become a plant pest itself, particularly in canola, wheat, barley, oat, and lupin growing systems – although in some grain-growing systems has also been reported as beneficial. This, in combination with the generalist feeding strategy, which can impact rare or sensitive native species, has resulted in *F. auricularia* becoming a species of concern for Falkland Islands government where it has become successfully established.

Considering invasion biology theory, the earwig has appeared to enjoy in Falkland Islands several of the factors which allow for successful establishment outside its home range; absence of natural predators and pests, capacity to exploit its new environment, competitive exclusion of native species occupying the same niche. Certainly, the earwig has managed to overcome common issues faced by introduced species on numerous occasions. In Australia in particular, several endemic threatened species' decline has been attributed to *F. auricularia* including endangered Coleoptera (beetles) and Lepidoptera (butterflies and moths).

The project will compare invaded and non-invaded areas, using various sampling techniques to assess invertebrate diversity and determine the impact of earwigs on native species. Additionally, the project will develop a DNA fingerprint database of native species in the study areas and relate that to the faeces of earwigs to determine their diet.

The impact of earwigs on native camel cricket (*Parudenus falklandicus*) and other endemics will be of particular concern, and the project will assess the camel cricket's diet to determine if it has a comparable diet to earwigs and hence vulnerable to competitive exclusion.
Through the main objectives of determining the impact of earwigs on native species in the Falkland Islands and informing effective control measures, this project will help to preserve the native biodiversity of the Falkland Islands and contribute to the protection of the ecosystems from the negative effects of this pest species. By researching the extent of earwig invasion and their impact on native invertebrates, we can inform the government's efforts to identify policy and legislative gaps related to invasive species.

P7 – Xin Rui Ong – Nanyang Technological University

Impediments and proposed solutions towards Southeast Asian insect conservation in the 21st century

Monitoring of insect populations and developing regional conservation status assessments enables the development of targeted conservation actions. Prioritizing areas for conservation can only be achieved with sufficient data on species distributions, of which the majority is available only for vertebrates and plants. For insect groups in Southeast Asia, there remains a high proportion of undescribed species, with the taxonomy of many groups being in flux. Knowledge on the research trends and expertise in insect taxonomy and ecology across Southeast Asian countries is required to inform future collaboration efforts, increase local capacity to conduct insect studies, and establish platforms for resource sharing in the region.

Through a thorough examination of Southeast Asian insect occurrence data and primary literature gathered since 2001, our research aims to identify knowledge gaps and biases toward certain taxa, localities, and research topics and to determine cross-boundary collaboration efforts based on publication metrics and funding data. We obtained Southeast Asian insect occurrence data from the Global Biodiversity Information Facility and primary literature records from Scopus and Web of Science. Occurrence records were mapped to identify taxonomic and locality bias across Southeast Asia. For literature records, we created co-occurrence matrices to visualise the relationships between study countries, taxon orders and research topics. We also developed authorship and funding networks to determine the status of regional collaboration and funding efforts.

For insect records, we identified taxonomic biases towards well-studied groups, and locality biases towards more technologically advanced countries. For primary literature, insect conservation and ecology studies are still lacking in most countries, which is likely attributed to low political prioritization and a larger focus towards economically and medically important research topics. Regional collaboration and funding efforts remains limited, but we found an increasing trend in host-nation authorships in recent years and higher proportions of local funding in certain countries.

We suggest potential solutions such as public engagement initiatives, integrative taxonomic approaches, and regional collaborations to address the existing data and knowledge gaps, and stress the need for political will and funding to overcome the impediments towards insect conservation efforts in Southeast Asia.

Other authors: Eleanor Slade, Nanyang Technological University

P8 – Daniel Schläppi – University of Bristol

Synergistic effects of Flupyradifurone and *Metarhizium brunneum* in black garden ants (*Lasius niger*, Hymenoptera: Formicidae)

Insect populations have declined dramatically over the past few decades due to a combination of environmental stressors, such as agricultural pesticides and diseases, whose impact may be exacerbated when acting simultaneously via synergistic interactive effects. Despite a recent surge of research on pesticide-disease interactions in bees, little is known about such interactions in other beneficial arthropods such as ants. Here we investigated how chronic exposure to a novel butenolide insecticide, Flupyradifurone affects the survival of black garden ants (*Lasius niger*) simultaneously challenged with the entomopathogenic fungus *Metarhizium brunneum* to test for potential interactive effects. First, a susceptibility test was performed to establish sublethal flupyradifurone doses, which were subsequently used in a fully crossed experiment with the fungus to investigate interactive effects. Concentrations exceeding 50 ppm resulted in increased in worker mortality, and the pesticide's concentration-dependent effects could not be explained by reduced food intake. At lower concentrations, flupyradifurone exposure alone did not affect survival, but when combined with exposure to *M. brunneum*, increasing flupyradifurone concentrations led to a rise in mortality. These results indicate synergistic effects of the two stressors, with chronic pesticide exposure apparently increasing pathogen susceptibility. This is the first report of synergistic effects between flupyradifurone and pathogens in ants, raising concerns about the long-term impacts of novel pesticides on the health of beneficial insects.

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P9 – Lucia Chmurova – Buglife, The Invertebrate Conservation Trust

Important Invertebrate Areas – supporting future invertebrate conservation.

Important Invertebrate Areas (IIAs) are nationally or internationally significant places for the conservation of invertebrates and their habitats. They are a vital tool for the conservation of our most threatened species and sustainable populations of declining species, identifying a network of sites to direct the future focus of invertebrate conservation and initiatives.

Since their launch at Ento 17, Buglife has been progressively fine-scale mapping the IIA network, including completing Wales. In 2023 a new online IIA webmap was launched that shows the full suite of IIAs, including fine-scale networks and provides information on understanding and using IIAs. Users are able to explore the maps and download the fine-scale files for completed IIAs, alongside a profile document that characterises its landscape, key species, notable assemblages and their habitat associations. They also identify locally relevant threats and opportunities to improve landscape and guide management decisions for invertebrates.

IIAs aim to support invertebrate conservation by making complex information understandable, useable, and readily accessible. This will ensure that everyone is able to better understand key habitats and landscapes for invertebrates and make better decisions to support their conservation – whether they are members of the public, ecologists, planners, local authorities, statutory bodies, eNGOs, land managers or other decision makers.

We will provide a valuable update on IIAs, how they are being rolled out and how a completed suite of IIA maps and profiles will support and further invertebrate conservation.

Other authors: Jamie Robins (Buglife- The Invertebrate Conservation Trust), Tom Thomson (Buglife- The Invertebrate Conservation Trust)

P10 – Harry Brindle – University of South Wales

Ants as pets: How the recent increase in trading ants as pets could affect naive environments.

The pet ant trade is an up-and-coming industry that has gone largely ignored by governments and the scientific community. With a lack of specific regulation, monitoring, and research this industry may cause devastating impacts on ecosystems across the globe. The entirety of the exotic pet trade (including the pet ant trade) is currently estimated to be worth $5 billion, with the ant trade worth just over $1 million. Currently, 1000 ant species are available to purchase online, covering great diversity of ecological roles. The removal of these species from host countries could pose devastating impacts to the ecosystems they help to maintain and thrive. Whilst the transport and keeping of species could open gateways for biological invasion. Here, the way host and destination countries may be affected are investigated with links to the trading of: rare species, invasive species and species classified as ecosystem engineers. Information was gathered from a variety of sources including journal articles, websites and books, along with data harvested from a variety of ant trading websites, helping to conclude that the ant pet trade was a growing industry. It was determined that the threat to ant ecology may not be globally present, however, localised harvesting of wild ants and the trade of rare species could impact the health of ecosystems on a small scale. Ant pet trade-linked invasiveness is expected to rise, leading to potential damage to destination ecosystems such as a monoculture like presence. The impacts of the ant pet trade have the potential to spiral out of control if the ant pet trade persists to go unmonitored and unregulated. It's proposed that the ant pet trade is further investigated to mitigate these potential impacts, and research is used to inform much needed regulations.

Other authors: Anthony Caravggi & Luis Cunha

Genetics and Genomics

P11 – Rebecca Evans – Aberystwyth University

Epidemiological and genetic variation between a resident and invasive population of *Colletes cunicularius* bees

Colletes cunicularius, or the spring mining bee, which is a solitary, polylectic burrowing species, is associated with nesting in areas of mature coastal sand dunes and sandy soil. This species was previously recognised by the Natural History Museum as of conservation concern and in 1995 as a globally threatened species. While it is now currently recognised by the IUCN as of 'least concern' in terms of conservation, solitary bees are still of higher extinction risks compared to their hive-dwelling counterparts due to extreme genetic load over small populations. As well as this, recent developments in range shifts of *C. cunicularius* in Wales and newly England could challenge the health and overall fitness of this species, bringing to question its future as a viable species in the UK.

Records support the view of an established 'resident' population of *C. cuncicularius* within Western Coastal areas of Wales and across to Cumbria, presumably cut off from European mainland conspecifics. However, in recent years, recently established populations, presumably of European origin, have been observed in the Southeast of England.
The purpose of this research was to determine if there were any genetic differences between these resident and invasive groups. To test this, samples of *C. cunicularius* were taken from both groups and population genetic analysis performed using a combination of mtDNA and nuclear markers. The results provide new insight into the demographics of the UK native population, and the invasive population which can be considered to represent the leading edge of the range expansion of the European population. This information is relevant for conservation of these species in the UK and beyond.

Other authors: Supervisor, Dr Niall McKeown, Aberystwyth University.

P12 – **Ko-Fan Chen** – University of Leicester

A novel neural pathway underlying daylength-compensated sleep homeostat in *Drosophila melanogaster*

Sleep is a quiescence state widely observed in insects. It is well established that environmental factors such as light and temperature modulate the sleep homeostat. Adjusting sleep profile against varying daylength at different time of the year to achieve sleep homeostat is particularly important in the mid to high latitude habitats. However, the sleep relevant light or visual cues in this context as well as the underlying neural-circuital pathway remains largely elusive. Drosophila is a diverse Diptera genus including species across latitudes and habitats. Among them, D. melanogaster has been a forerunner in insect neurogenetics with decades of research using it as a powerful experimental model to provide mechanistic insights into sleep. Importantly, recent research advances in identifying both neural sleep centres and their potential connections to visual system in D. melanogaster have set the stage for investigating the functional neural pathway by which visual inputs modulate sleep. Against this background, we have previously identified a mutant in D. melanogaster showing sleep variation across daylengths. Further investigation then revealed that the mutation in the gene called Neurocalcin in this mutant underlies the alteration of sleep homeostat across daylengths. To identify the underlying neural pathways responsible for this daylength-compensated sleep homeostat, we therefore used the latest behaviour and genetic tools to observe sleep variation upon introducing Neurocaclin mutation in various part of the visual/sleep system. So far, we have evidence that the mechanism underlying sleep homeostat across daylength involves a novel neural pathway linking the compound eye and a deep brain structure called Anterior Optic Tubercle. Further imaging experiments are required to elucidate the neural activity of this pathway under different daylengths. With the increasing accessibility to neurogenetics in wider insect taxa, the finding will be a useful framework ready to expand into investing other non-cosmopolitan Drosophila species, whose adaptation in variable daylength are crucial for their success in high latitude habitats.

Other authors: Taranjit Kaur Ahluwalia, Nichan Memet, Deekshitha Sanaboina, Yu-Chien Hung, Department of Genetic and Genome Biology, University of Leicester

Infection and Immunity

P13 – **Christopher Sanders** – The Pirbright Institute

Studying the activity of Culicoides midges under laboratory conditions to understand virus – vector interactions.

Culicoides biting midges (Diptera: Ceratopogonidae) are abundant small haematophagous insects with an almost worldwide distribution. Some species of Culicoides act as vectors of viral livestock diseases with substantial welfare and economic impacts including bluetongue, Schmallenberg and African horse sickness. Although previously thought to be apathogenic in the vector, viral infection may result in physiological and behavioural changes. Infection-associated changes in behaviour may represent adaptive manipulation of the vector by the virus or be due to neural and sensory pathway damage sustained during viral infection and dissemination. Evidence for reduced attraction to UV light in bluetongue virus-infected Culicoides in the field suggests viral infection results in changes in normal vector behaviour that may have implications for virus transmission and vector surveillance. To understand the impact of virus infection on Culicoides activity and behaviour, we first established methods for the study of the behaviour of non-infected Culicoides using a Drosophila Activity Monitor, a device which uses infrared beams to detect motion. Laboratory reared and field collected individual Culicoides were monitored for up to 10 days at 25 °C and 40 % relative humidity with a 16:8 L:D cycle. A dimmable light was provided to mimic dusk and dawn periods, as decreasing light intensity is favourable for crepuscular midge activity. For laboratory reared Culicoides, activity was greater during dawn than dusk, whereas dusk activity was greater in field collected Culicoides. Survival of individuals was greatest for field Culicoides and lowest for blood engorged females. Further work will use this technique to compare diel activity of virus-infected Culicoides with non-infected individuals.

Other authors: Zoe Langlands, The Pirbright Institute, Marc Guimera The Pirbright Institute, Richard Bomphrey Royal Veterinary College

P14 – Ivan Canada Luna – University of Exeter

Developing *Galleria mellonella* as a replacement model for bacterial infections.

Larva of the greater wax moth (Fig. 1), *Galleria mellonella*, is acquiring an important role as a replacement model organism, especially for infection studies. The system offers multiple benefits, such as short lifecycle, easy and unexpensive maintenance and an observable melanisation of the body in response to infection.

G. mellonella has been reported to be a suitable model to study virulence of several pathogenic bacteria and fungi, including intracellular pathogens such as *Burkholderia pseudomallei* and *Coxiella burnetii*. Despite these advantages, the infection readouts are merely observable and the methods for its analysis are quite limited.

In the *Galleria mellonella* Research Centre (GMRC), we are aiming to improve the tools of this promising replacement model organism. At GMRC we are working to improve our understanding of the *G. mellonella* immune response to pathogenic organisms. We are keen to collaborate with researchers and institutions, and we offer consulting to any facilities interested in starting their research with this emerging model.

We have established a permanent research-grade colony in the Living Systems Institute at the University of Exeter. We are also proud to say we are the first research facility to have developed novel tools in the study of *G. mellonella*, such as genetic tools and quantitative readouts on phagocytosis of alien particles.

Other authors: James Pearce, Jennie Campbell, Isobel H Norville & James Wakefield

P15 – Mark Hanson – University of Exeter

Ecology-relevant bacteria drive the evolution of host antimicrobial peptides in Drosophila.

Antimicrobial peptides are host-encoded immune effectors that combat pathogens and shape the microbiome in plants and animals. However, little is known about how the host antimicrobial peptide repertoire is adapted to its microbiome. Here we characterize the function and evolution of the Diptericin antimicrobial peptide family of Diptera. Using mutations affecting the two Diptericins (Dpt) of Drosophila melanogaster, we reveal the specific role of DptA for the pathogen *Providencia rettgeri* and DptB for the gut mutualist Acetobacter. Strikingly, presence of DptA- or DptB-like genes across Diptera correlates with the presence of Providencia and Acetobacter in their environment. Moreover, DptA- and DptB-like sequence predicts host resistance against infection by these bacteria across the genus Drosophila. Our study explains the evolutionary logic behind the bursts of rapid evolution of an antimicrobial peptide family, and reveals how the host immune repertoire adapts to changing microbial environments.

Other authors: Lena Grollmus, Bruno Lemaitre, both from Ecole Polytechnique Federale de Lausanne (Lausanne, CH)

P16 – Laura Ann Jones – The Pirbright Institute

Investigating the utility of *Culex pipiens* pupal exuviae as a non-invasive method of form differentiation.

Culex pipiens (Linnaeus, 1758) are important vectors of arboviral diseases such as West Nile virus and Usutu virus that causes zoonotic disease in the Palearctic and Nearctic regions. The species consists of two morphologically indistinguishable forms, pipiens (L.) and molestus (Forskål, 1775) that differ in behaviours such as host preference and the expression of autogeny. Hybridisation between these forms has been reported from several European countries, including the UK, with rates of up to approximately 26%. Hybridisation may allow gene flow of form-specific characteristics with hybrids hypothesised to possess intermediate behaviours that are key drivers of disease transmission. Due to the lack of morphological identifiers, identification of these forms plus hybrid specimens is reliant on molecular methods.

Pupal exuviae have been utilised as a source of trace DNA for use in molecular speciation in other insect species and may provide a non-invasive method of differentiating the *Culex pipiens* forms. Here different extraction methods are compared for use in field and colony-derived pupal exuviae from *Culex pipiens* to assess nucleic acid concentration and PCR amplification success. Genomic DNA was extracted from 300 individual *Culex pipiens* pupal exuviae with an overall PCR amplification success of 79% across all experiments. Time of processing post-eclosion significantly influenced *Culex pipiens* form identification as nucleic acid concentration and PCR amplification success decreased with increased time elapsed between eclosion and processing. While PCR amenable DNA was obtained from all processing methods tested, the efficiency of these varied, with methods involving the prior extraction of DNA yielding superior results. Application of these methods for field collected *Culex pipiens* exuviae resulted in an average amplification success rate of 66.25% across the different processing methods. Finally, the method was used to successfully create ‘pure’ form colony lines from a mixed *Culex pipiens* colony population. This study presents a non-invasive technique for differentiation of the *Culex pipiens* forms which is accessible to a range of projects and resource levels through the use of different processing methods.

Other authors: Christopher Sanders, The Pirbright Institute; Marion England, The Pirbright Institute; Simon Carpenter, The Pirbright Institute; Mary Cameron, London School of Hygiene and Tropical Medicine

P17 – James Pearce – University of Exeter

Improving the greater wax moth, *Galleria mellonella*, as a human disease model through development of a molecular and cellular toolkit

There is a rapidly growing list of publications validating the use of the larval stage of the greater wax moth’s (*Galleria mellonella*) use as an in-vivo animal partial replacement model in the fields of infection, immunology, and inflammation. This is because Galleria larvae exhibit an easily identifiable, but qualitative, biological read-out of such challenges – they produce melanin pigment, turning the larvae from cream-coloured to black. They possess broad susceptibility to microbial pathogens, with pharmacodynamics of drug clearance showing remarkably similar patterns of drug clearance to humans. Moreover, individual larvae can be precisely dosed by injection, their maintenance is straightforward and, in contrast with competing non-mammalian systems, such as zebrafish, C. elegans and Drosophila, they can be reared at 37°C, facilitating research into both normal cellular kinetics of biological processes and host-pathogen interactions.

Unlike these other model organisms however, Galleria is not currently genetically tractable and lacks detailed protocols for molecular and cellular tools which is limiting it’s uptake amongst the wider infection community. In this talk we describe the steps taken to develop a set of robust and reproducible protocols for this moth, including transgenic and cell sorting techniques, and how these are applicable to research on human relevant pathogens. This work is being used to create a database of tools and techniques for other Galleria researchers to enable wider uptake and more reproducible data (*Galleria mellonella* Research Centre - GMRC UK) and will likely be of use to entomologists looking to develop similar tools for different species.

Other authors: Jennie Campbell (University of Exeter), Masanori Asai (Imperial College London), James Wakefield (University of Exeter

P18 – Hannah-Isadora Huditz – Wageningen University and University of Exeter

Isolation and separation of the tsetse fly viruses: *Glossina morsitans* morsitans iflavirus (GmmIV) and *Glossina morsitans* morsitans negevirus (GmmNegeV)

The importance of mass-reared insects is constantly growing, as they are used for food and feed, biopesticides, and wild insect population control through Sterile Insect Technique (SIT) programmes. In all these cases and specially for SIT, the mass-reared insects need to be healthy and competitive with the wild type populations. One major threat for the health of mass-reared insects are covered viruses. These viruses might switch from a covert infection to an overt infection and cause the collapse of entire insect colonies. In the case of the tsetse fly, different viruses have been discovered but only the Salivary gland hypertrophy virus (SGHV) has shown severe consequences for the reared colonies of *Glossina pallidipes* species, thus far. Nevertheless, it is utterly important to understand the impact of other viruses on the teste fly to anticipate any further outbreaks. The Glossina morsitans morsitans iflavirus (GmmIV) and Glossina morsitans morsitans negevirus (GmmNegeV) are two positive-stranded RNA viruses. So far, these viruses were only studied in combination as they naturally coinfect the flies. In this project we aim to study the viruses independently. However, traditional separation methods via sucrose gradient ultracentrifugation were unsuccessful due to the similar size and density of both viruses. Therefore, we aim to obtain pure viral stocks through a combination of cell culture techniques and molecular biology methods. We infected the fall armyworm Sf9 cell line and the mosquito C6/36 cell line with the GmmIV and GmmNegeV mixture. After two passages, only GmmIV was present in the Sf9 cell line as well as in the C6/36 cell line at detectable levels, as indicated by RT-PCR. This result will allow us to isolate a pure stock of the Iflavirus by passaging on Sf9 and C6/36 cells. Furthermore, we are constructing infectious clones of both viruses, using RT-PCR and molecular cloning techniques. We will assemble the full-length viral sequences in an expression plasmid for further viral characterization and future tsetse fly in vivo studies.

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P19 – Megan Wallace – University of Exeter

Variation in the activity of viral suppressors of RNAi across *Drosophila* host species

RNA interference is a key mechanism by which insects defend themselves against infections – acting to degrade double stranded RNA (dsRNA) in a sequence specific manner. Proteins that act as suppressors of this response - viral suppressors of RNAi (VSRs) - have been described in the genomes of many insect-associated viruses. In *Drosophila melanogaster* and its sister species, some of these VSRs show high host specificity. However, the action of VSRs has never been tested across >3 insect species. This is despite evidence that the susceptibility to several viruses varies across the Drosophila phylogeny, the mechanistic basis of which is unknown.

We analysed variability in the suppression of RNA silencing when multiple species of Drosophila are infected with Drosophila C virus (DCV). DCV encodes a VSR, DCV-1A, which primarily acts to reduce the efficiency of the RNAi response of Drosophila melanogaster by sequestering dsRNA and preventing the action of Dicer2. However, the action of DCV-1A has not been assessed in other Drosophila species, and, based on the varying virulence of DCV by species, Dicer2 activity could be suppressed inefficiently in other species. Alternatively, DCV-1A may differentially suppress the RNAi response at a different stage, such as preventing formation of the RISC complex.

To identify the true scenario, we first used small RNA sequence data to analyse the distribution of vsiRNAs produced on infection with DCV across 32 Drosophila host species. We then used in vitro assays to investigate how the presence of the 1A protein affects the activity of Dicer2, and RISC complex formation, in multiple host species. Finally, in ongoing molecular work we are attempting to investigate whether the outcome of infection with DCV, and its relative Cricket Paralysis virus, in multiple species, is differentially affected by the presence or absence of the VSR proteins in vivo.

Other authors: Katherine Roberts (University of Exeter), Gijs Overheul (Radboud University, Nijmegen), Matthew Chisnall (University of Exeter), Steinike van Houte (University of Exeter), Ronald van Rij* (Radboud University, Nijmegen), Darren Obbard* (University of Edinburgh), Ben Longdon* (University of Exeter), * - Equal Contribution

P20 – Ellie Jarvis – University of Bath

Can *Drosophila melanogaster* self-medicate STIs with alcohol?

In recent years, the concept of self-medication in animals has gained increased attention, shedding light on the phenomenon of animals using natural substances to alleviate health challenges. *Drosophila melanogaster* fruit flies, a widely studied model organism, exhibit intricate behaviours and physiological responses that offer a unique opportunity to investigate self-medication in the context of their innate chemical preferences.

D. melanogaster has a well-established relationship with Metschnikowia yeast species that grow on rotting fruit, providing necessary dietary protein. Metschnikowia yeasts are also known for producing 2-phenylethanol (2PE), an aromatic compound used in wine and fragrance production. D. melanogaster are famous for their attraction to alcohols, and 2PE appears to be no exception. But, does consuming these yeasts and their alcohols provide any other fitness advantages to flies?

My PhD investigates the potential self-medication benefits of the consumption of *M. pulcherrima* and 2PE to *D. melanogaster* suffering from a sexually transmitted infection caused by pathogenic *Aspergillus austwickii* fungi. I investigate the effects of consumption on survival and fecundity, as well as nutritional choice during infection. I intend to support this with further work on the physiological mechanism of the interaction between 2PE and *A. austwickii* infection, and determine whether this relationship fulfils the four criteria of self-medication behaviour.

Further to studying this in the lab, I utilise and evaluate citizen science by taking my experiments directly to the public for them to participate in and influence. I am particularly interested in investigating the role of citizen science in highlighting the nature of science, the research process, and overall public trust in science.

Other authors: Nicholas Priest (University of Bath), Jingbo Liu (University of Bath)

Movement and Migration

P21 – Oliver Poole – University of Exeter

Exploring evolved solutions to muscle and age modification

Ageing is a fundamental biological process that involves the progressive loss of vitality as organisms grow old. A typical consequence to ageing is reduced muscle mass, quality, and strength. The ageing process itself is flexible and there are some natural systems where environmental and genetic factors cause variation in phenotypic expression of ageing. The leading causes of illnesses are all associated with ageing, making the discovery of novel approaches to control its rate and quality a major goal of global healthcare.

Episyrphus balteatus (the marmalade hoverfly) is a multigenerational migrant playing key roles in crop pollination, pest control and nutrient transfer. This species exhibits long distance flight and variable ageing across its different seasonal phenotypes, with its autumn form living the longest by fivefold. The extreme endurance capacity and variable life span highlights this as a model species for investigating the modification of age-related muscle decline at a fundamental level.

Utilising lab reared and wild caught specimens I aim to demonstrate how muscle decline can be modified at the structural and functional level and identify the underlying genetic pathways that enable this. I will quantify structural changes to muscle cells over time using a histological approach. This method will be preceded by tethered flight tracking to record muscle functional capacity. Coupled with this will be genetic sequencing of muscle tissue to show the up- and down-regulated genes involved in the observed changes to muscle ageing between phenotypes.

In this poster I will present the results from the first part of this project and discuss ideas for the following parts.

Pests, Biological Control and IPM

P22 – James Hourston – Eden Research plc

Investigating terpenes as novel bioinsecticides

Plant terpenes are secondary metabolites and are one of the many ways plants have evolved natural defence against insect herbivory. We have been developing these plant derived secondary metabolites into a range of biopesticides. Typically, a terpene's direct mode of action when encountering the cells of an insect or pathogen, is to rapidly alter lipid profiles, causing cell leakage through cell membranes, cell collapse and finally irreversible changes to the permeability of cell membranes. Therefore, a key challenge when using these actives is formulating and applying terpenes in such a way as to ensure effectiveness against the target insect whilst ensuring that there is no phytotoxicity to the plant you are aiming to protect.

We investigated a range of terpenes as potential actives as part of a botanically derived bioinsecticide. This work focused on geraniol, thymol and eugenol and their impact on sucking pest targets (aphids, whitefly and spider mite). We conducted a range of lab-based screens on *Myzus persicae*, *Trialeurodes vaporariorum* and *Tetranychus urticae* followed by two years of independent field trials in both the US and EU. We will share results of this work from both the lab and field.

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P23 – Ranjeet Kumar – Bihar Agricultural University, India

Bio activities of Diatomaceous Earth against *Sitophilus oryzae L., Rhyzopertha dominic F*. and *Tribolium castaneum H*. in stored wheat and their effect on germination attributes

The experiment Experiments were conducted for bio activities of Diatomaceous Earth (DE) against *Sitophilus oryzae* L., *Rhyzopertha dominic* F. and *Tribolium castaneum* H. in stored wheat in plastic jars and their effect on germination attributes to find out alternative of aluminium phosphide. The DE is natural amorphous silica powder and act as physical poison for stored product insects and also environmentally safe for human. The all experiments were conducted on untreated and graded wheat seed variety HD-2967. The experiments were conducted in plastic jars each of which were filled with 10 Kg wheat seed and plastic jars were arranged in completely randomized design on the floor of the laboratory. The fifty pairs of adults of *S. oryzae*, *R. dominica*, and *T. castaneum* were released in each plastic jars to ensure infestation of stored wheat seed, after a week release of insects measured quantity of Diatomaceous Earth (food grade) mixed in each jar after which jars was sealed for six months. The all treatments which were replicated thrice and untreated seed were used as control. After six months of storage sample was taken at bimonthly interval from each jar. The samples were drawn from different depth of the jars and after mixing them a measured volume 250 g per treatment were analyzed to record percent inhibition, infestation, weight loss and germination attributes in treated seed. The food grade of Diatomaceous Earth completely inhibits the feeding and breeding of *S. oryzae*, *R. dominica*, and *T. castaneum* at 1.25g and 1.50g per kg of seeds as compared to untreated control in which 56.00, 38.40 and 12.30, adults were emerged respectively after six month of storage. After twelve months of storage very few adults were emerged in treated jars as compared to untreated control in which 58.62, 29.62 and 26.21 of *S. oryzae*, *R. dominica*, and *T. castaneum* respectively. There are no significant differences of percent infestation and percent weight losses were found in all treated jars as compared to untreated control in which 23.64 and 26.21 percent infestation and 4.37 and 5.43 percent weight losses were observed after six and twelve months of storage respectively. The 96.48 and 95.78 percent germination were recorded in untreated control which is similar to all treated seeds and vigour index, significance of viability statistically similar to all treated seeds in plastic jars. The food grade of Diatomaceous Earth inhibit the population build-up of *S. oryzae*, *R. dominica*, and *T. castaneum* and do not affect the germination attributes of stored wheat seed in plastic jars for twelve month of storage.

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P24 – Susmita Aown – University of Sussex and NIAB

Do 'frog(hoppers)' like wine? Grapevines as host plants of *Philaenus spumarius* Meadow spittlebug, insect vector of *Xylella fastidiosa*

Froghoppers are sap-sucking insects that feed solely on plant xylem. *Philaenus spumarius* Meadow spittlebug is one of the most widespread spittlebugs in the UK. It feeds on over 100 dicot plants. Meadow spittlebug is the most important vector of *Xylella fastidiosa*, a bacterial pathogen that causes disease symptoms in plants, such as leaf scorch and plant dieback. *Xylella fastidiosa* and their insect vectors are high priority in research as the bacteria caused an epidemic in Italian olive orchards in 2013, which incurred a loss of €6.3 billion a year. *X. fastidiosa* has not been found in the UK yet but there is a high chance that it might come to the UK from Europe.

My research is focussed on understanding the feeding behaviour of *P. spumarius*, specifically the host plant preferences of the insect in the UK. *P. spumarius* feeds mainly on olives and grapevines in continental Europe and the USA respectively, in California the economic losses were estimated to be $104.4 million in a year. Grapevines are a major commercial crop in the UK. However, we do not yet know whether the insect feeds on vines in the UK. In my project, I am working with vineyards in South England to study the host plant preference of *P. spumarius*, study the probing and feeding behaviour of this sap-feeding insect in real time using electrical penetration graph, and determine if there are any natural enemies that might be affecting the distribution of the insect in vineyards.

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P25 – Anusha Mohan – Kumar – Rothamsted Research Institute and University of the West of England
Semiochemical-based alternative concepts for the management of wireworms

Wireworms, the larval stage of click beetles (Elateridae: Coleoptera) are highly diversified, soil-dwelling, polyphagous pests of cereals and various root vegetables in Europe and North America. They mainly feed on roots and seeds, causing seedling mortality, and harvestable plant parts such as tubers, leading to quality and yield loss. Due to environmental considerations, agricultural practices are changing to more sustainable methods, such as minimal tillage and live mulches, which could exacerbate wireworm infestations. Insecticides, including neonicotinoids, are currently used for controlling wireworms, although the ban on existing insecticides and the registration of new insecticides is uncertain, making wireworm management problematic. Hence, there is a need for developing alternative, more sustainable management practices.

One alternative strategy is the use of semiochemicals; naturally occurring development and behaviour-modifying compounds produced by a range of organisms, which could provide an environmentally benign alternative for wireworm management. In the rhizosphere, wireworms and other soil insects are attracted to semiochemicals including low molecular weight volatile organic compounds (VOCs) released by plant roots. While CO2 serves as a general attractant, its role in precise host location by these wireworms in a mixed community of plants is uncertain. In addition, very little is known how VOCs change temporally and spatially due to the herbivorous insect damage, the age of the plants and other biotic and abiotic factors.

This project aims to investigate the influence of VOCs produced by a range of crops on wireworm behaviour. The behavioural and neurophysiological response of wireworms will be determined through bioassay methods (soil olfactometry, soil mesocosms, and electroantennography). The identity of behaviour-modifying VOCs will be determined by Gas Chromatography (GC)/coupled GC-Mass Spectrometry. Additionally, the project will utilize Near-infrared spectroscopy (NIRS) and selected ion-flow tube – mass spectrometry (SIFT- MS) to effectively monitor rapidly changing volatile emissions in real-time. The preliminary data from the SIFT-MS coupled with NIRS system demonstrates the potential of this system for real-time continuous monitoring of volatiles over extended periods, without the need for discrete sampling. Findings from this work will help to identify behaviour modifying VOCs produced by plant roots, creating the basis to develop push-pull management systems for wireworms, which will reduce the need to apply insecticides.

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P26 – Mark Bridges – John Innes Centre
The entomology and insectary platform at the John Innes Centre

The main aim of the Entomology and Insectary Platform is to support and promote excellent entomological research within the John Innes Centre, but we are also seeking to engage in national and international collaborations with academic and commercial partners. The platform has a quarantine insectary with several controlled environment rooms and rearing chambers and holds a Defra licence to import, rear and work with over forty species of prohibited invertebrates, following high-quality quarantine standards. The Entomology team is highly experienced in establishing colonies of a wide range of invertebrate species. We are specialised in small-scale, highly-controlled experimentation, usually involving the development of standard operating protocols from scratch using innovative approaches. Our main focus is on the study of plant-invertebrate and plant-pathogen-invertebrate interactions, but we also carry out research into the discovery of invertebrate-associated natural products of interest and conservation of endangered invertebrate species. The platform is unique in its capability to generate and analyse invertebrate genomic resources using evolutionary approaches. In particular, we are interested in using genomic data to learn about genetic diversity, population structure, migration dynamics of pests, and to understand genotype-phenotype interactions of traits of interest. We are also working towards integrating data of herbivorous invertebrates by developing information hubs that enhance re-usability and support plant health-related entomological research.

P27 – Benjamin Hunt – University of Exeter

Sublethal insecticide exposure impacts epimutation rate and transposable element activity in the peach potato aphid *Myzus persicae*

The peach potato aphid *Myzus persicae* is a global crop pest, its impact due in part to its enormous parthenogenetic reproductive capacity. While such asexually reproducing organisms have been referred to as ‘evolutionary dead ends’, research has shown that they nonetheless accumulate spontaneous mutations and we have previously conducted work showing the ability of a clonal lineage to adapt to selection pressures within a few generations. To investigate the potential for such adaptation we conducted a long term mutation accumulation experiment over dozens of generations.

We first aimed to calculate the genome-wide spontaneous mutation rate of *M. persicae* in the absence of selection and document the relative frequency, and genomic location, of mutational events. In a second arm of the experiment we studied the effects of an environmental stressor (the insecticide Imidacloprid) on the rate of mutation. Using whole genome bisulfite sequencing we examined changes in DNA cytosine methylation, a transgenerationally inheritable phenomenon linked to gene expression changes in many species, and which may be particularly relevant for adaptation in the absence of genetic diversity. We further investigated gene expression differences between start and end points and between the two arms of the experiment using RNA-seq, and performed pre- and post-experiment assays to assess fitness impact and the possible emergence of insecticide resistance.

We found no loss of reproductive fitness or change in insecticide sensitivity in either arm of the experiment. The mutation rate in *M. persicae* does not appear to be impacted by imidacloprid exposure, but the epimutation rate in exposed lines is significantly slower. Exposed lines also exhibited downregulation of genes involved in neuronal development and function, and a striking bias towards upregulation of transposable element activity.

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P28 – Jaimie Barnes – University of Exeter

Influence of tobacco host plant on success of *Episyrphus balteatus* predation on *Myzus persicae nicotianae*

Myzus persicae is a polyphagous, globally, and economically important pest aphid species with over 400 host plant species. The agricultural industry relies heavily on neonicotinoids to control the pest. *M.*

persicae has recently host shifted to tobacco, forming a subspecies *M. persicae nicotianae* which exhibits adaptations to feeding on tobacco. Notably, the subspecies overexpresses a nicotine detoxification enzyme, the cytochrome p450 CYP6CY3. This overexpression is thought to have been the driver allowing for the host shift and subsequent subspeciation to occur. The host shift allows the aphid to exploit a new food resource, therefore reducing competition. This provides an explanation for the cost-benefit trade-off of overexpressing an enzyme just to tolerate tobacco as a food plant. The subspecies, as well as successfully host-shifting to tobacco, due to its nicotine tolerance is also consistently more tolerant of neonicotinoid insecticides designed to control the aphid pest populations.

The insecticide and nicotine tolerance are well established in *M. persicae nicotianae*. However, the influence a host plant has on predators in a plant-aphid-predator system are less explored. The tobacco adapted *M. persicae* have been shown to excrete nicotine in their honeydew despite having enzymes to breakdown the xenobiotic. Suggesting that for a predator that feeds on the aphids, they may be indirectly consuming and accumulating nicotine which is a potent insecticide. *Episyrphus balteatus* (the marmalade hoverfly) is a key pollinator species and is used as biological pest control as the aphidophagous larvae are voracious. It is important to understand how the aphid host plant influences their success as pest control. Moreover, as key pollinators, it is important to determine if the host plant may inadvertently negatively affect their populations. Finally, this system also provides the opportunity to investigate the influence of adaptation to new host plants on established tri-trophic systems, linking evolution and ecology.

This poster will present experimental results investigating if nicotine consumption in *M. persicae nicotianae* reduces fitness and/or increases mortality in *E. balteatus* larvae. *M. persicae nicotianae* reared on different concentrations of nicotine in an artificial diet will be fed to lab populations of *E. balteatus*. The fitness and mortality of the hoverfly larvae then measured. A second experiment will be conducted using tobacco plants. *E. balteatus* larvae will be reared on tobacco plants infested with *M. persicae nicotianae*. Two treatments will be set up, one with uncut tobacco plants and one with cut tobacco plants. Cutting the tobacco plants should induce greater nicotine production in the tobacco. The fitness/mortality of the hoverfly larvae will be measured. The results will show how adapting to a new host plant may provide additional benefits such as changing the predator-prey dynamic. More broadly, it will also demonstrate if nicotine bioaccumulates through a tri-trophic system and therefore, the effect host plants may have on pollinators and biological pest control efficiency.

P29 – Bolajoko Bolarinwa Adewoye – Yaba College of Technology, Yaba Lagos

Entomotoxicity and Chemical characterization of the extracts of *Zanthoxylum zanthoxyloides* and *Anarcadium occidentale* on *Sitophilus oryzae*

Sitophilus oryzae is a major storage insect pest of rice mostly managed with synthetic insecticide. Synthethic insecticides has been flawed due to the adverse effects on human health, the environment, and insect resistance while safer alternatives are considered. This study assessed the toxicity effect of powders and oil extracts of *Zanthoxylum zanthoxyloides* and *Anacardium occidentale* on S. *oryzae*. Plant powders were tested at 1.0g, 1.5g, and 2.0g (w/w) concentrations at different time intervals 24, 48, 72, and 96 hours. Oil extracts were tested at 0.625ml, 0.125ml, 0.250ml, and 0.500ml (v/w) concentrations at 24, 48, 72, and 96 hours intervals respectively. The result showed that after 96 hours of exposure, 1.5g powder of Z. zanthoxyloides evoked 100% mortality while A. occidentale evoked 80% mortality after 96 hours of application. Similar trend was also observed in the oil-treated grains. Mortality was observed to increase with concentrations and time of exposure for both powder and oil treatments. From the GCMS profiling 5-Hydroxymethylfurfural, 9, 17-Octadecadienal, (Z)- Sopranone, and Piperonal were identified from Z. zanthoxyloides while 9,12-Octadecadienoic acid (Z,Z)- Hexadecanoic acid, and Octadecanoic acid were also identified from *A. occidentale*. The findings of this study showed that both powders and extracts of *Z. zanthoxyloides* and *A. occidentale* were effective in the control of *S. oryzae*. Both plant contains chemical components that exhibited entomocidal activity which can be incorporated into the management of *S. oryzae*.

Keywords: Anarcardium occidentale, Entomocidal, GCMS, Sitophilus oryzae, Phytochemicals, Zanthoxylum zanthoxyloides

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P30 – Octavia Brayley – University of Birmingham (in partnership with the British Antarctic Survey)

The effects of a non-native insect in Antarctica on soil biogeochemistry

Terrestrial biodiversity in Antarctica is relatively low compared to temperature and tropical regions, giving rise to 'simple' and nutrient-limited ecosystems. This means that the establishment of just one species can have a large impact on the resident organisms. Accidentally introduced to Signy Island (South Orkney Islands, maritime Antarctic, 60°43'0"S,45°36'0"W) in the 1960s, the flightless midge, *Eretmoptera murphyi*, is a detritivore that inhabits the soil. Where it occurs on Signy, it can be found at densities far greater than all the other native microarthropod species combined (the numbers of larvae can be as high as 150,000 m2). Previous studies have shown that high population densities of *E.murphyi* are associated with significant increases in soil nitrates - up to five times greater than 'background' levels (similar to the high levels found near giant petrel colonies). This may have profound effects on the native flora and fauna, as well as potentially providing more favourable conditions for future non-native plant species to become established. This is of particular concern in Antarctica as growing human activity around the continent is increasing the chances of non-native species introductions, combined with climate change increasing the likelihood of successful establishment. Antarctic soils are characterised by nitrogen limitation, and therefore, anything affecting nutrient cycling processes could have profound consequences for ecosystem functioning. For example, increase in available nitrogen can boost microbial growth, respiration, and associated decomposition rates of soil organic carbon, releasing carbon dioxide into the atmosphere.

This PhD project (2022-2026) aims to understand the effects of *E. murphyi* on soil biogeochemistry. Chemical analyses have already documented levels of soil carbon, nitrogen (including ammonium and nitrate), and phosphate in different locations around the island. This project seeks to understand the underlying mechanisms by which *E. murphyi* can alter soil nutrient levels, as well as the wider ecosystem impacts of this introduced species. More broadly, this research is important for human health and food security. Understanding soils from extreme climates- where the effects of changing variables can more easily be deconstructed, makes them an ideal model for comparison with temperate and tropical soil systems.

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P31 – Melanie Nicholls – The Pirbright Institute

The effect of dietary components on larval and pupal development in the stable fly, *Stomoxys calcitrans*

The Stable Fly, *Stomoxys calcitrans*, is an important pest of many animals worldwide and a potential vector of a variety of diseases. Maintaining colonies in the laboratory is important for providing a means of studying these insects in greater depth. A variety of methods and diets exist for rearing this species in numerous laboratories. A colony of Stomoxys has been reared at The Pirbright Institute on a mixture of grass meal, corn meal and yeast for the past ten years, but the colony has occasionally been subject to unexplained crashes. Investigations into the reasons behind these colony crashes have revealed that manipulating the amount of water in the diet impacts the successful development of larvae into pupae, and on the successful emergence of pupae into adults. There are also effects on the size of the pupae and resultant adults, and furthermore, the exact formulation of corn meal used also seems to have an effect on development to a certain degree. A better understanding of the effects of diet components on larval development will not only give a better understanding of this species' biology, but will also help ensure a reliable colony of insects for research into their status as vectors of disease.

P32 – Emma Weeks – University of Florida

Does clustered egg laying enhance survival in the common bed bug, *Cimex lectularius*?

The common bed bug is a global public health pest with a rapid reproductive cycle. The aim of this study was to determine if there is clustering in egg laying, and if multiple females are contributing to egg clusters. Further studies attempted to understand the benefits of this behaviour.
In a preliminary study, bed bug egg positions on colony papers were measured and clustering was observed. In a second experiment females were fed, paired with males, and placed into arenas. After week one, half were removed, fed, and placed back into their dishes; the other half were removed and replaced with new bugs. After week two, egg position was analysed, and it was determined that egg clustering was occurring between conspecific females. Then, in three experiments we tested the physically fitness of first instar nymphs hatched from clustered eggs or individually. Nymphs from both groups had similar hatching and survival data. When nymphs were manually flipped onto their backs, nymphs that had hatched from clustered eggs were more successful at flipping back onto their legs than those hatched alone. Finally, nymphs hatched from clustered eggs were more likely to survive and moult following a blood meal than those hatched individually. Experiments were replicated three times.
Our results indicate that bed bugs lay eggs in conspecific clusters to promote survival of offspring. Furthering our understanding of bed bug survival, oviposition, and aggregation can help us develop tools and techniques to manage challenging infestations in urban areas.

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P33 – Christopher David Williams – Liverpool John Moores University

Exposure of the Large Pine Weevil (*Hylobius abietis*) to entomopathogenic fungi stimulates and inhibits feeding depending on the fungal strain and LT50

Some pathogens inhibit feeding, whilst others stimulate it, in their herbivorous hosts. We investigated this phenomenon in 12 entomopathogenic fungi (EPF) when they infected the Large Pine Weevil (*Hylobius abietis),* the most serious insect pest of commercial forestry in Europe. EPF were collected from soil from eight nature reserves in the Merseyside area. Two depths of soil were taken (10cm and 20cm below the surface, respectively) from a 5m x 5m grid in nine equidistant points using a screw auger. Each soil sample was split and then baited with five wax moth larvae (*Galleria mellonella)* and five mealworm larvae (*Tenebrio molitor).* The best 12 EPFs, as assessed by speed of kill and characteristic growth morphology, were used in the experiments. These twelve EPF were identified in the following way: DNA was extracted from mycelia; 50-100 mg of fungi in 1.5 ml Eppendorf tubes were quick-freezed in liquid nitrogen, then thawed at 60oC on a hot plate and immediately frozen again prior crushing with a micro-pestle. Following this the DNeasy Plant Pro kit protocol was followed. To measure DNA concentration we used a microvolume UV-Vis spectrometer (NanoDrop™ One, Thermo Scientific) and samples were standardized to 5ng µl-1 for PCR. The fungal internal transcribed spacer (ITS) region was amplified using forward and reverse primers. Following PCR, the amplified sequences were visualised using an agarose gel electrophoresis, obtaining 11 out of the 12 amplicons. Confirmed sequences were purified using QIAquick® PCR Purification Kit (Quiagen) and sent for Sanger sequencing (Eurofins). One of the 12 isolates was *Beauveria bassiana*, one was Metarhizium anisopliae, and 9 were Metarhizium sp. Spores were extracted from the 12 shortlisted candidates and counted using a haemocytometer placed in a light microscope (400 x magnification). Ten adult *H. abietis* were exposed to 108 spores/ml of each EPF isolate treatment (120 treatments + 10 controls = 130 total individuals). The best 2 isolates were further tested at lower concentrations (107 and 106 spores/ml) on another 10 adult weevils (40 treatments + 10 controls = 50 total individuals). Prior to experiments, weevils were starved for 48h, and their individual weight was recorded on the day of the experiment (t = 0). Each weevil was submerged for 5s in its treatment and placed in a 9cm petri dish each containing an 8cm long fresh Scots pine (*Pinus sylvestris*) twig and a 2cm diameter damp paper filter ball to provide access to clean distilled water. Insect mortality was recorded daily for 21 days to obtain the LT50, whereas weight variation and area consumed was recorded for 14 days (on days 4, 7 and 14). The amount of bark consumed from each twig was copied using transparent acetate and scanned with a scale to be analysed using the image analysis software ImageJ to obtain feeding areas in mm2. Mortality analysis was carried out in OASIS. Results show that some fungal strains stimulate feeding in infected hosts whilst others inhibit it. The relationship between an EPF's LT50 and the level of feeding inhibition / stimulation is discussed.

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P34 – Laura Reeves – University of Reading

Functional and behavioural responses of the natural enemy *Anthocoris nemoralis* at elevated summer temperatures

Anthocoris nemoralis is the dominant predator of pear sucker (*Cacopsylla pyri*) in the UK. It is estimated that *C. pyri* causes £5 million worth of losses to the pear industry, highlighting the importance of an effective control strategy. *A. nemoralis* migrates into orchards in spring or is introduced as a biocontrol agent, reaching peak population levels in July-August. This contributes to effective control of summer pear sucker populations. However, due to temperature dependent development and metabolism there are concerns that *C. pyri* populations or feeding rates may increase due to changing climatic conditions. Thus, how *A. nemoralis* responds to temperature, impacts its ability as a biocontrol agent. This presentation will discuss the efficacy of anthocorids as biocontrol agents under elevated temperatures, based on functional response experiments and novel behavioural assays. Behavioural assays using Ethovision XT tracking software, were used to monitor anthocorid velocity, distance travelled and behaviour demonstrated (feeding, moving, cleaning, stationary and antennating). Whilst functional response experiments monitored the attack rate and handling time of anthocorids when consuming *C.pyri* nymphs. Behavioural and functional responses were monitored at three temperature regimes (18 °C, 21 °C and 23) selected based on current mean July-August temperatures and mean temperatures predicted for July-August by RCP 4.5 and RCP 8.5 emissions scenarios for 2080. Results indicated sex specific differences in functional responses; with female anthocorids demonstrating a shorter handling time and attack rate than males. Males also showed longer prey handling times at 18 °C compared to 23 °C. Heatmaps from behavioural assays indicated that anthocorids preferred *C. pyri* nymphs over eggs, spending significantly more time feeding in nymph compared to egg treatments. Results from this study are applicable to the wider scientific community, behavioural and functional response assays demonstrated can be easily adapted for other pest and natural enemy species.

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P35 – Norbertas Noreika – Estonian University of Life Sciences and Nature Research Centre, Vilnius, Lithuania

Pesticide-caused food and macronutrient deficiency in beneficial predatory beetles

Pesticide usage is claimed as the main cause of insect declines. Pesticides can directly eradicate beneficial predatory beetles, but they are also exposed to indirect pesticide effects arising from reduced prey (as well as plant-based food) availability and quality in agroecosystems. The main aim of the current study was to investigate if higher food and macronutrient deficiency levels in carabid beetles are related to conventional agricultural practices (especially pesticide usage).

Individuals of different carabid species were collected by hand from 8 conventional and 8 organic oat fields scattered around Tartu, Estonia (three times). In the laboratory beetles were served with three semi-artificial diets: lipid-rich, protein-rich, and sugar-rich. Consumption of each diet was evaluated after 24 hours (=test1). Afterwards, beetles were fed ad libitum for a week until full satiation. Then the procedure of test1 was repeated (=test2). The differences of consumed diets among two tests showed the level of food and macronutrient deficiencies in carabids within assemblages. Separately, pesticide residue analyses in beetle bodies were performed.

No pesticides were detected in beetle bodies from organic fields, while seven different pesticides were detected in beetles from conventional fields. Several carabid beetle species weighted less in conventional than in organic fields. Double-test experiment revealed that carabids tended to be more food as well as sugar and lipid deficient with the presence of neonicotinoid insecticide and less so in organic fields. Finally, beetles were less protein-deficient in organic fields. We conclude that organic farming and reduced pesticide usage would improve beneficial carabid nutrition and fitness thus leading to higher efficiency in providing biocontrol service.

Pollinators

P36 – Victoria Buckle – Anglia Ruskin University

Mitigating the impact of beekeeping on wild pollinators: Conservation guided solutions for co-existence

Mitigating the impact of beekeeping on wild pollinators: Conservation guided solutions for co-existence.

The falling abundance of pollinators in the UK [1] has increased the focus on beekeeping with Defra implementing the Healthy Bees Plan 2030 [2]. Managed honeybees are utilised on farms to enhance crop pollination and apiculture is becoming an increasingly popular activity with more people taking up beekeeping as a hobby.

Although increased beekeeping may benefit honeybees and pollination services, it is likely to add to the problems already affecting wild pollinators, which compete with managed honeybees for limited floral resources. A key driver of this is floral resource overlap, with evidence of exploitative competition revealed in many studies [3]. Additional issues are behavioural shifts, impacts on fitness and the potential for pathogen-crossover.

Whilst current research demonstrates the impact of managed honeybees on other pollinators, experimentally proven solutions so far remain untested. This project aims to find a compromise, working with beekeepers and exploring ways to reduce the potential for competition between managed bees and wild pollinators so they may coexist. The project will take place in Cambridgeshire (a county where beekeeping is very popular), with sites split into high and low honeybee density areas based on known hive proximity.

The objectives include assessing the impacts of managed bees on wild pollinators in honeybee-dense areas, determining the nature of the competition and factors affecting it, and whether timing of hive placement is a factor. The final goal is to reduce competition through tailoring of experimental floral compositions.

Flower mixes will be selected and piloted, then adjusted based on first year results. Raised flower beds will be erected on sites containing selected floral resources and the behaviour of the pollinators monitored. In addition to the experimental flower plots, members of the public participating in a citizen science element of the study will be supplied with the tailored seed mixes to apply and carry out surveys in areas where there are hives.

It is expected that by testing the effectiveness of identified flower composition treatments, the negative impacts of interspecific competition between managed honeybees and wild pollinators can be reduced and recommendations made for optimal floral resources in areas where honeybees are kept.

1. Biesmeijer, J.C., Roberts, S. P., Reemer, M., Ohlemüller, R., Edwards, M.,Peeters,T., Schaffers, A.P., Potts, S.G.,Kleukers, R. and Thomas, C.D., Settele, J., Kunin, W.E. (2006) ‘Parallel declines in Pollinators and Insect-Pollinated plants in Britain and the Netherlands’, Science, 313 (5785), pp. 351-354.

2. Department for Environment, Food and Rural Affairs (DEFRA), (2020). Available at: https://www.gov.uk/government/news/defra-launches-the-healthy-bees-plan-2030-to-help-protect-honey-bees (Accessed 03 October 2022).

3. Iwasaki, J.M., Hogendoorn, K. (2022) ‘Mounting evidence that managed and introduced bees have negative impacts on wild bees: an updated review’, Current Research in Insect Science, 2, 100043, available: https://dx.doi.org/10.1016/j.cris.2022.100043.

P37 – Clare Boyes – Manchester Metropolitan University

A bee’s eye view of landscape change

Pollinator declines are linked to landscape change affecting the availability of nesting sites and flowers. Most pollinator research focuses on social bees. Less is known about how solitary bees respond to landscape change, despite increasing evidence of their importance in pollinator systems. Historic pollen records for Bedfordshire gave a unique opportunity to analyse changes in the diet of two species of Andrena bees, from the same sites almost 80 years apart; and to examine potential links between landscape change and the bees’ diets.

In 2021, sites visited during the 1940s were revisited and pollen collected from bees as they returned to their nests. The species studied were *A. flavipes*, nesting at a roadside in Tingrith; and *A. barbilabris* nesting in a conifer plantation at Aspley Heath. Both bees take a wide range of pollen and are thought to have foraging ranges of less than 300m. To provide a direct comparison with the historic data, pollen was collected and identified using methods described by Chambers (1946). The 1940s data was collated from Chambers’ notebooks.

For both species, there were significant differences in the pollen families used by the bees between the two periods although this was more marked for *A. barbilabris*. The proportion of pollen from woody plants increased significantly. Both species had a narrower diet in 2021 demonstrated by a reduced species richness. Other notable findings were that in 2021, there were significantly more types of pollen per load for *A. flavipes*; and that most pollens used by *A. barbilabris* were found over 575m from the nest site.

The Bedfordshire landscape has changed significantly since the 1940s, with a reduction in flower-rich grassland by conversion to arable. This was the case at Tingrith; however, Aspley Heath showed little apparent change at the landscape scale. However, it is possible that recreational pressures have negatively impacted the ground flora at this site

Our analysis demonstrates that both species exhibited dietary flexibility, taking a wide range of pollens from different families; however, the pollen load composition differed over time. Changes in the diet of both bees reflect changes in land-use, particularly the loss of grassland and associated wildflowers as agriculture has intensified. Although landscape changes were less marked at Aspley Heath, the bee's-eye view highlights local changes which are not readily apparent at the landscape scale and highlights the importance of understanding how species respond to such change. The fact that these species persist at sites at which they have been recorded for almost 80 years, even though the floral resources appear suboptimal, suggests the importance of familiar nesting sites may be underestimated, and further research is needed.

Chambers, V.H. (1946) 'An Examination of the Pollen Loads of Andrena: The Species that Visit Fruit Trees', The Journal of Animal Ecology, 15(1), pp. 9–21. Available at: https://doi.org/10.2307/1621.

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P38 – Chris Wyver – University of Reading
Climate-driven phenological shifts in emergence dates of British bees

Climate change has a diverse range of impacts on wild bees, including their phenology, or timing of life history events. Climate-driven phenological shifts can not only impact individuals at species level but also threaten the vital pollination service that wild bees provide to both wild plants and cultivated crops. Despite their involvement in pollination, for most bee species, especially in Great Britain, little is known about phenological shifts. This study makes use of 40 years of presence-only data for 88 species of wild bees to analyse shifts in emergence dates, both over time and in relation to temperature.

The analyses reveal widespread advances in emergence dates of British wild bees, at an average rate of 0.40 ± 0.02 days per year since 1980 across all species in the study dataset. Temperature is a key driver of this shift, with an average advance of 6.5 ± 0.2 days per 1°C warming. For both change in emergence dates over time and in relation to temperature, there was significant species-specific variation, with 14 species showing significant advances over time, and 67 showing significant advances in relation to temperature.

Species' life-history traits did not appear to explain variation in individual species' responses, with overwintering stage, lecty, emergence period and voltinism considered as possible explanatory traits. Pairwise comparisons showed no differences in sensitivity of emergence dates to increasing temperature between trait groups (groups of species which share all four traits) that differed by only one trait. These results highlight not only a direct impact of temperature on the phenology of wild bees themselves but also the species-specific shifts highlight a possible impact on the temporal structure of bee communities and the pollination networks for which the wild bees are so crucial.

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P39 – Joanna Brebner – University Paul Sabatier, Toulouse III
Can honey bees communicate multi-destination routes?

Honey bees are impressive navigators, able to form efficient multi-destination routes within single foraging trips. Returning foragers actively communicate the distance and direction of foraging locations with other bees in the hive using a 'waggle dance'. This dance is commonly understood to indicate one single location or flower patch. However, honeybees frequently forage on large patches or on several distinct locations within one foraging route. We trained our bees to fly to one, then five feeders within two different environments (farmland, UK, and rice paddies, Spain) and recorded the dances of foragers who were tracked feeding on our feeders. We examined the differences between dances to single feeders and to five feeders, and how they related to the bees' routes. Specifically, we found that when dancing for five feeders, the variation between dances and the variation between waggle runs within each dance is greater than when dancing for one feeder. Interestingly, we observed that when landmarks were available, bees frequently deviated their dances towards these features. From this evidence, we suggest first that the variation within a waggle dance can indicate patch size, and second that landscape features outside the food source can influence this behaviour.

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Symbionts and Microbes

P40 – Onur Erk Kavlak – Freie Universität Berlin Institute of Biology
The effect of gut microbiome size on the evolution of bacterial resistance

The gut microbiome of holometabolous insects undergoes significant changes during metamorphosis, brought about by the secretion of immune effectors. A recent study found that *Galleria mellonella*, a holometabolous insect, upregulates three different antimicrobial peptides (AMPs) and lysozyme at the onset of pupation. These AMPs cause a significant reduction in the gut microbiome abundance, and this is believed to constrain the evolution of resistance in opportunistic pathogens due to the lower mutation supply in smaller populations. However, there is a lack of information on how much the gut microbiome fluctuates during metamorphosis and whether there are differences in resistance evolution among different population sizes.

We used *Galleria mellonella* as an insect model to investigate changes in bacterial population size in the gut during different developmental stages using CFU counting. We also analyzed the gut microbiome composition using 16S metabarcoding. Finally, we conducted an experimental evolution study with different population sizes of gut bacteria based on the range of observed microbiome sizes.

We found high variability in bacterial abundance among individuals at each developmental stage. The population size range measured between 10^5 – 10^8 CFU/gut, which varied as much as 1000 fold. Significant variation may be caused by technical errors in dissection success, differences in insect size, and food intake of larvae, but not in gut length. Gut microbes experienced a reduction in population size at the onset of metamorphosis. At the gut replacement stage when the AMPs are highly upregulated, the gut microbiome abundance declined from 10^7 to 10^6 CFU/gut. 16S metabarcoding showed the symbiotic Enterococcus genus was the most abundant bacteria through all stages as expected (~56 % of all amplicon sequence variants). During experimental evolution, all populations went extinct, possibly due to the doubling cecropin-A concentration at each transfer cycle. Additionally, there might be evidence for the inoculum effect: larger populations have higher minimum inhibitory concentrations (MIC). Similarly, we found that the largest population size (10^8 cells) seems to have a higher MIC level.

Our results indicate that the gut microbiome abundance varies among and experiences a reduction during metamorphosis. Nevertheless, we were unable to observe the effects of AMPs on resistance evolution due to the rapid extinction of all populations. Loosening selection pressure for the next trials may trigger resistance evolution, particularly in larger populations. This study will provide more insight into how population size reduction can constrain resistance evolution against host immune effectors.

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P41 – Veronika Pavlasova – Newcastle University

Characterising amino acid transporters in aphid endosymbiosis

Many hemipteran insects feed exclusively on phloem sap despite it being deficient in key nutrients such as essential amino acids. To overcome these nutritional deficiencies, such insects maintain symbiotic partnerships with specific, co-evolved microbes. For example, the aphid *Acyrthosiphon pisum* houses its obligate prokaryote partner, *Buchnera aphidicola*, as an endosymbiont in specialised aphid bacteriocyte cells. Within these cells, each Buchnera is individually surrounded by a host-derived symbiosomal membrane. Sap-derived and aphid-derived non-essential amino acids are provided to Buchnera which utiltise them to synthesise the essential amino acids required by the aphid. The amino acid metabolic pathways within the aphid host and the endosymbiotic bacteria are complex and integrated, with many being encoded by a combination of both endosymbiont and host genomes. To sustain this integrated metabolism, non-essential and essential amino acids must be moved selectively across the cell membranes of the aphid gut, bacteriocyte (plasma membrane and symbiosomal membrane) and Buchnera. Such amino acid transport will be the function of a multitude of different, as yet uncharacterised, transporter proteins. To predict the function of putative aphid amino acid transporters we use comparative sequence analysis and structural homology modelling against mammalian, insect and bacterial transporters of known function. Function of individual aphid transporters is characterised following heterologous expression in *Xenopus laevis* oocytes using both electrophysiology (two- electrode voltage clamp) and measurements of radiolabelled amino acid flux. These experiments allow substrate specificity and mode of action of these proteins to be characterised. Comparing function to published metabolic analysis of aphid and Buchnera enables prediction of the physiological roles of such transporters within the endosymbiotic relationship.

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Adeyemi Daniel Adetimehin – University of Cape Town

Diversity, abundance, and successional patterns of insects on an adult pig carcass (*Sus scrofa domesticus L.*) in Cape Town, South Africa: preliminary investigation in the summer season

In forensic entomology, the estimation of the age of the oldest immature insects and analysis of the successional patterns of insects found in, on, or around decomposing vertebrate remains are the two principal ways through which forensic entomologists can generate information relating to the minimum time since death. Recent studies have shown that considerable differences exist in the insect assemblages associated with decomposing vertebrate remains in different geographical areas or localities within the same region. In the Western Cape Province of South Africa, especially in the Table Mountain region, no published studies exist on the activities of insects on human-sized vertebrate remains. Therefore, we investigated the abundance, diversity, and successional patterns of carrion-associated insects on a decomposing adult pig carcass within the vicinity of the Table Mountain National Park located in Cape Town. A 60kg adult pig carcass was used for this study and it was deployed specifically in the summer seasonal period (December – January). A total of 2,132 adult insect individuals comprising of 4 orders, 14 families and 24 species were recorded. The order Diptera was the most abundant as it accounted for 68.15% of the entire insect population followed by the orders Hymenoptera (15.9%), Coleoptera (15.85%), and Hemiptera (0.1%). Members of the family Piophilidae (Diptera) were the most abundant, followed by *Chrysomya chloropyga* (Diptera: Calliphoridae), and *Crematogaster cf. liengmei* (Hymenoptera: Formicidae). Within the order Coleoptera, members of the family Histeridae were the most abundant followed by the families Dermestidae and Cleridae. In this study, egg masses of *Ch. chloropyga* were seen on the pig carcass as early as Day 2, while the first and second instar larvae of *Chrysomya albiceps* (Diptera: Calliphoridae) were seen on Day 4. Only the members of the family Dermestidae utilized the pig carcass as a breeding site, and their larvae were seen on the carcass on Day 18. In conclusion, this study revealed that *Ch. chloropyga*, *Ch. albiceps* and Dermestidae gen. sp. are insects that can provide useful information relating to the estimation of the minimum time since death of adult human cadavers found within the Table Mountain region in the summer seasonal period.

Keywords: Forensic Entomology, Insect Succession, Decomposition, Summer, South Africa

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Aparna Kalawate – Zoological Survey of India, Western Regional Centre

An environment cleaner: the secret earth boring beetles of India.

Earth borer beetles are members of the scarab group. Scarab are present on all continents except Antarctica. Generally, dung beetles are an incredibly diverse and are categorised into four ecologically distinct groups: dwellers (Endocoprids), tunnellers (Paracoprids), stealers (Kleptocoprids) and rollers (Telecoprids). 'Dwellers' spend their life inside the dung pad, 'tunnellers' spend more time beneath the pad, burrowing below to build brood chambers and burying dung for their larvae to feed on. 'Stealers' often take advantage of tunnellers by occupying tunnels for the development of their own larvae and stealing the already buried dung. 'Rollers' roll the dung pads into round balls, which are used as a food source or breeding chambers. The Earth-boring Scarabs are Paracoprids and tunnels and dig the soil.

These are tiny to large round and bulbous earth-boring scarabs, tank-like beetles with bulbous orange extensions on their antennae. As their name suggests, they dig into the ground, and sometimes upto 2-3 meters deep. Female lay a single egg at the end of each long tunnel and food is left there for the growing grub. Larval food sources include fungi, dung, compost and decaying plant material. The grub eats its food, come out of the tunnel to the surface, and pupate.

In general, species of Bolboceratinae occur on all continents except Antarctica, but almost none are found on oceanic islands. Recently Bolboceratinae has been raised to Bolboceratidae. Further the Bolboceratinae divides into two tribes: Athyreini and Bolboceratini. The Athyreini occur in South America, Africa, and in a narrow band to northern India. The Bolboceratini are essentially worldwide and are found mostly in areas with sandy or light clay soils.

How to recognize earth borers? Earth¬borer beetles resemble other scarab group beetles in general form (short, domed body, spiny legs and short antennae with terminal clubs) but can be distinguished by the following combination of characters: Antennae terminating in relatively large, subspherical clubs formed of three segments. Pronotum strongly developed and, viewed from the side, extending lower than lateral margin of wing case or 'elytron'.

The adult emerges only after dusk and only after heavy rain when the soil is damp. They are strong and "musician beetles," (termed by Howden) and tend to be attracted to lights. This is when they are most likely to be seen. Most of the time, they remain hidden in burrows in the ground. The burrows are always circular in cross section and, if they extend to any depth, leave a noticeable pile of soil at the entrance. Usually if the beetle burrow is open, it indicates that the beetle has left, but occasionally the beetle has an open burrow and is near the top and slightly to one side of the burrow. The depth of the burrow depends both on the soil type and the size of the beetle. Due to their soil tunneling habit they are termed as environment cleaners and play important role in providing the nutrients in the soil.

Bianca Greyvenstein – North-West University

What we know about the magnificent Mantodea of South Africa

Despite human fascination with the Mantodea or praying/preying mantids over millennia, very little is known about of their diversity, biology and ecology, especially in South Africa. Praying mantids are not only important because of the ecosystem services they provide, but they have a "mystical‟ status and are regarded as a kind of oracle in some cultures. Due to the cultural value associated with Mantodea, these insects could be used as a flagship or gateway species to advance peoples' awareness of insects and increase their appreciation which can ultimately increase conservation efforts. The literature regarding South African Mantodea is very limited and the most recent species list was compiled 20 years ago. In this study, we used data from approximately 4000 historic museum records as well as from citizen science platforms such as iNaturalist to update the checklist of the Mantodea of South Africa. The updated checklist reports 148 species, 64 genera and 14 families of Mantodea in South Africa. The distribution and biology under captive rearing conditions of *Galepsus lenticularis* (Tarachodidae), *Popa spurca* (Mantidae), *Sphodromantis gastrica* (Mantidae) and *Harpagomantis tricolor* (Galinthiadidae) were also described. This study provides a glimpse into a group of insects that has never been studied in South Africa.

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Dawn Morgan – University of Wolverhampton

Post-Feeding larval behaviour of the forensically relevant blow fly *Calliphora vomitoria* in the UK.

Blow flies are the primary colonisers of a body, and can arrive at a cadaver within minutes, they are therefore acknowledged as the most important insects in determining the post-mortem interval (PMI), or the minimum amount of time the body has been exposed, and available for insect interaction. For the PMImin to be as accurate as possible it is essential to collect the oldest insect specimens associated with the body.

The oldest specimens are not often found on the body itself but have dispersed away to find a suitable site to pupate. This suitable site may be some distance away from the body on which they were feeding. The dispersal stage occurs after the feeding stage of the final, third instar. The literature that is available for this stage reveals that there is very little known, and what is known is very contradictory depending on which piece of literature is read.   Obtaining a better understanding of this understudied stage can help predict the locations where dispersing larvae and developing puparia are most likely to be found, therefore maximising collection at crime scenes.

A series of experiments have been conducted to investigate dispersal behaviour in one species of UK forensically relevant blowfly. Post-feeding *Calliphora vomitoria* were used in experiments that studied distance dispersal, depth dispersal and dispersal within a residential property.

Results found that in an experimental setting *C. vomitora* can disperse a distance horizontally of 800 cm, vertically to a depth of 24 cm, and over 800 cm within a residential setting, this included dispersing down two flights of stairs and under two closed doors. Dispersal via ceiling spaces was also observed.

Enrique A. Mundaca – Universidad Católica del Maule

New insights of seasonal fluctuations and distribution of *Notiothauma reedi* Maclachlan, 1877 (Mecoptera: Eomeropidae) a rare living fossil from the Chilean hotspot

Notiothauma reedi is the only living member of the Eomeropidae family (order Mecoptera) and is considered a living fossil. This species is endemic to central Chile occurring in humid and forested locations. During its larval stage under roots and leaf litter. The adult inhabits shaded and humid places in the Chilean Winter Rainfall – Valdivian Forests, which belong to one of the world's biodiversity hotspots. The insect exhibits a saprozoic behaviour, feeding on decaying carcasses. Within that biome, in the remaining patches of the coastal Maulino forest, we established two sampling plots (at the localities of Pelluhue and Cobquecura, central Chile). Specimens were collected using 5 pitfall traps for a whole year. Traps were partially concealed within the substrate and were monthly emptied. Samples were transported to the laboratory to carry out specimen identification and counts. Seasonal variation and abundance of individuals of *N. reedi* were registered and plotted to identify flying periods and abundance peaks. In terms of its distribution, this study represents the first record of the species for two localities in the coastal range of Chile, and confirms its association with native forests, although at present heavily fragmented. We discuss the importance of our findings, in terms of the conservation status of the species and its occurrence in an endangered forest type threatened by logging, forest fires, and lack of natural regeneration. Regarding the scant knowledge of the species, it is important to highlight that many aspects of its biology remain unknown, preventing a proper assessment of its current conservation status. Finally, we reflect on the importance of deepening the ecological understanding of the species and revealing the still unknown aspects of its life cycle, its ecological role, and the importance of its conservation.

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Ezequiel González – Instituto Multidisciplinario de Biología Vegetal (CONICET, UNC)

Insect communities and ecosystem processes in fragmented Chaco forests: summarizing 20 years of studies in central Argentina.

Habitat loss and fragmentation are landscape transformations with profound impacts on biodiversity. Insects are particularly affected by these processes, with consequences for ecosystem services. In the Neotropics, the Chaco forest is one of the largest phytogeographic regions and has suffered critical deforestation rates in recent decades. For 20 years, we have studied the impact of these modifications on insect communities in Córdoba, Argentina, and the interaction between forests and adjacent crops. Here, we review 25 empirical studies of the influence of fragment area, forest cover, and edge habitats on different insect functional groups, ecological processes, and ecological networks in fragmented Chaco forests in central Argentina. Small fragments and landscapes with low proportions of forest cover were generally linked to impoverished insect communities across most functional groups. Fragment area reductions negatively affected above-ground processes such as herbivory and parasitoidism, whereas leaf litter decomposition and most network parameters were not affected. Edge effects were variable, favoring some insect groups (i.e., ground-dwelling arthropods and parasitoids) and parasitoidism rates. Moreover, intense insect movement between forests and crops increased ecosystem service provision near the forest. Our results indicate that the fragmentation of Chaco forests has clear implications for insect communities and ecosystem services. Maintaining forest remnants and promoting native forest plantations should be prioritized to guarantee insect biodiversity conservation.

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Jakovos Demetriou – University of Athens, Joint Services Health Unit Cyprus and Enalia Physis Environmental Research Centre

Alien bees, wasps and ants of Cyprus: current knowledge, gaps and what's next

Thousands of alien insect species have been introduced to Europe, with a subset negatively affecting biodiversity and ecosystem functions, economies as well as human, animal and plant health. Island ecosystems are particularly susceptible to biological invasions, with invasive alien species impacting their evolutionary histories and even leading to the extinction of native and endemic island species. Situated at the heart of the Eastern Mediterranean, Cyprus lies at the biogeographic crossroad of Asia, Africa and Europe. The island's geographic position, as well as the increasing movement of people and goods, have led to the introduction of more than 1,200 alien species.

Hymenoptera represent one of the most species rich insect orders within alien species databases, with more than 300 species being introduced to Europe intentionally as biological control agents or unintentionally as stowaways or contaminants through plant trade, stored products and alongside their hosts as parasitoids or hyper-parasitoids. The latest checklist of alien Hymenoptera on the island of

Cyprus recorded 74 species, most of which being tiny wasps in the superfamily Chalcidoidea (53 species = 71%), followed by Ichneumonoidea (10 species = 14%), and ants (9 species = 12%). One bee species and one yellow-jacket wasp are considered to be of “questionable” status. More than one-third of alien Hymenoptera have been intentionally introduced as biological control agents. The rest, have most probably been unintentionally introduced alongside their host- insects/plants as contaminants of plant material or soil.

Despite ongoing efforts, the number of alien Hymenoptera on the island is presumed to be severely underestimated, as evidenced by the constant detection of novel alien species. In addition, the distribution, introduction pathways and impacts of alien Hymenoptera are largely unknown. Updated resources (e.g. identification keys) are necessary to raise awareness and support biosecurity strategies. Future studies would benefit from integrating classical methods, citizen science and molecular tools. Additionally, it is important to ensure rapid and open access to data relating to imports, release, and utilization of new biological control agents.

Within the efforts of two Darwin Plus Fellowships (DPLUS200 and 202) we will further investigate the biodiversity of ants and chalcid wasps in Cyprus as well as the environmental and socio-economic impacts of alien species. Checklists and websites for the island’s fauna will be created, with special reference to the Akrotiri Peninsula. All data will be included within the Cyprus Database of Alien Species (CyDAS - https://ris-ky.info/cydas), an online database including more than 1,200 alien species, ensuring the accumulation, availability and transparency of data on alien species in order to assist monitoring and research efforts.

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Srikrishna Narasimhan – Museum and Institute of Zoology, Polish Academy of Sciences

Problem-solving through individual cognition in invasive social insects

Biological invasions currently pose one of the major threats to ecology and economics, but they also offer valuable insights into evolutionary processes in a short time because species must adapt to solve new problems in the introduced environment. Problem-solving is usually addressed by behavioural plasticity, but it was proposed that in social species such as ants, the costs of individual plasticity might outweigh its benefits. We analysed behavioural and neuroanatomical variability in one of the most widespread invasive ant species, the Argentine ant (*Linepithema humile*), to unravel whether individual behavioural differences might be sufficient to reach colony-level solutions or exposure to problems is the factor shaping individual behaviour and brain. We exposed 173 age-controlled callow workers from five different colonies to sets of three behavioural tests conducted every day over five days. We tested ants’ exploration in an empty arena, reaction towards a neophobic element (encounter with an unfamiliar object) and maze-solving ability. The maze was composed of six bilateral choices branching one after the other in a chiral manner. Repeated behavioural testing allowed us to analyse personality, predictability, repeatability, memory and learning. The brains were extracted with a fixed protocol; subjected to antigen staining to focus on the micro glomeruli density of the Mushroom Bodies calix and then correlated with the behavioural variables. Initial results suggest callow workers' personalities when considering exploration, time spent moving, and use of the central part of the arena (most vulnerable). Surprisingly, our results showed that the individuals' explorative value, the use of the new item, and the number of errors avoided in maze solving increased with each successive test with the time spent on exploration remaining constant. Our results suggest that ants can use new resources and solve new problems without modifying their behavioural patterns. Future analyses will unravel how *Linepithema humile* behaviour is linked to neuronal development.

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Wilmari Uys – University of Cape Town

Utilising micro-computed tomography in age estimation during the puparial period of the forensically relevant blowfly, *Chrysomya chloropyga*

Age estimation of the immature life stages of blowflies can be useful in determining minimum post-mortem interval (minPMI). Changes in morphological features related to the age of blowfly larvae have been extensively investigated; however limited research has been conducted on minPMI determination from puparial specimens. Additionally, methods utilised in age estimation usually require the destruction of the specimen. Micro-computed tomography (micro-CT) has emerged as an alternative method for assessing morphological changes in insects. In this study, we evaluated the use of micro-CT to identify age-related morphological changes during the puparial period of the forensically relevant blowfly, *Chrysomya chloropyga. C. chloropyga* were reared under controlled conditions at 25°C, 65% relative humidity and a 14:10 photoperiod. Once pre-pupation occurred, pre-pupae were collected and observed at age intervals of every 6 hours for the first 2 days and then every 12 hours until adult emergence. Specimens were stained in a 1% Lugol's iodine solution for 14 days and rinsed in ethanol an hour prior to scanning using a Nikon XT H 225 system. The resulting projections were reconstructed with a voxel size of 9.73 µm in CT-Pro 3D and slice stacks were rendered, reorientated, and visualised using VG Studio Max 2023.1. Development of structures was assessed over time, including changes in the volume of the adult midgut, rectal pouch and indirect flight muscles. Pre-pupal morphology corresponded significantly with post-feeding larvae, but as the pupal period progressed, the pupal body and organ systems changed to that of an adult fly. In the head, the lamina started as a bulb shape at 42 hours post-pupation and progressed into a horseshoe shape by 48 hours post-pupation before it started to unfold at 84 hours post-pupation, lying parallel to the retinular cells. Equally, the cornea was visible 18 hours post-pupation, but the layer of crystalline cones only became apparent 96 hours post-pupation. The larval midgut was swiftly replaced by the adult midgut which continued to change in shape, with the final portion of the midgut clearly coiled by 60 hours post-pupation. Similarly, the adult hindgut was first observed as a thin tube 30 hours post-pupation with the rectal pouch and rectal papillae visible 36 hours post-pupation. Both the adult midgut and hindgut showed a continued change in shape and size until adult emergence. Volume measurements of the adult midgut showed a decline in volume from 18 hours post-pupation until the end of the intra-puparial period. In contrast, the indirect flight muscles and rectal pouch volumes, measured from 30- and 36 hours post-pupation, respectively, increased greatly until the conclusion of the puparial period. Micro-CT can be a useful tool in estimating pupal age, providing both qualitative and quantitative data on several key morphological features, without destruction of the specimen.

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