Programme

#StudentForum23 @RoyEntSoc

Thursday, 30 March 2023 (all times UK Timezone)

09.00 - 10.00	*Refreshment and registration (in-person only)*
10.00 - 10.15	Welcome from the current Student Representatives
10.15 - 11.00	Invited speaker Ashleigh Whiffin National Museum Scotland Curating & Communicating: on a mission to advocate for insects
11.00 - 11.30	*Break and Poster Session*
11.30 – 11.45	**Thomas Pagon** - The Impact Of Connectivity On Aquatic Invertebrate Community Ecology In Recently Created Ponds
11.45 – 12.00	**Kate Graydon** - Investigating egg size plasticity in *Apis mellifera* as a potential strategy to cope with anthropogenic land use change
12.00 – 12.15	**Ritabrata Chowdhury** - Physical defences and insect-plant co-evolution: How do specialised heliconiine caterpillars cope with Passiflora trichomes?
12.15 – 12.30	**Dawn Morgan** (Online Talk) - Worst Game of Hide and Seek Ever - Larval Dispersal Within a Residential Setting
12.30-13.30	*Lunch and Networking (In-person only)*
13.30-14.15	Invited speaker Dr. Seirian Sumner University College London Endless Forms: Reasons to Love Wasps
14.15 -14.30	**Parvez Khan** (Online Talk) - Status of Firefly in India
14.30 -14.45	**Mayumi Madhushani** (Online Talk) - Citizen scientists on the move: A success story of citizen scientist's involvement in sand fly vector surveillance using DIY light traps in Sri Lanka
14.45-15.30	Invited workshop Francisca Sconce Royal Entomological Society Insect specimen curation
15.30 -16.00	*Break*
16.00-17.00	***Poster session**, wine reception and **Ento-fashion contest** (In-person only)*
	Voting for the best ento-fashion outfit
19.00	*Pub Quiz in The Woodville (In-person only)*

Programme

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Friday, 31 March 2023 (all times UK Timezone)

09.30 – 10.00	*Welcome & Refreshments (In-person only)*
10.00 - 10.45	Invited speaker Dr. Peter Graystock Imperial College London A hitchhikers guide to parasite dynamics in pollinator communities
10.45 - 11.15	*Break and Poster Session*
11.15 – 11.30	**Monika Yordanova** - Bee pathogens across the foraging landscape
11.30 -11.45	**Ciaran Harris** - Phenological imbalance in the supply and demand of floral resources
11.45 - 12.30	Invited workshop Emilie Aimé Royal Entomology Society How to get published in entomology
12.30 - 13.30	*Lunch and Networking (In-person only)*
13.30 - 14.15	Invited speaker Dr. Nathalie Stroeymeyt University of Bristol Social network plasticity decreases disease transmission in the ant Lasius niger
14.15 – 14.30	**Laura Campbell** - The evolution of plant cultivation by ants
14.30 – 14.45	**Adeyemi Daniel Adetimehin** (Online Talk) - Flowing with the stream: unidirectional dispersal of blow fly larvae following decomposition fluids from an adult pig carrion
14.45 – 15.00	**Laura Martinez-Chavez** - Potato aphid (*Macrosiphum euphorbiae*) clonal variation determine its susceptibility to *Aphidius ervi*
15.00 - 15.30	*Break, Poster Session and voting (last chance to see posters and vote for talks and posters)*
15.30 - 16.15	Invited speaker Dr. Jordan Cuff University of Newcastle PhD to postdoc in a pandemic: COVID, conflict and other conundrums
16.15 - 16.40	Prize announcements and event wrap up (from Student Rep)

RES Student Representatives Ayman Asiri, Ava Searles and Vera Kaunath look forward to welcoming you to Cardiff



Poster abstracts from page 13

Abstracts

Thursday, 30 March 2023 (all times GMT)

Invited speaker Ashleigh Whiffin

National Museum Scotland

Curating & Communicating: on a mission to advocate for insects

Ashleigh is a museum-based entomologist, working with National Museums Scotland for the past 8 years to care for, curate and develop the collection of 2.5 million insect specimens. A key element of this role is ensuring accessibility to the collection, which can take many forms. From hosting in-person visits and delivering tours or public talks, to sending specimen loans around the world, digitizing the collection, creating new public displays, or promoting the collection online. It's a varied and rewarding job.

As a keen science communicator, Ashleigh is passionate about disseminating entomology to the wider public. Alongside her museum work she is actively involved with a variety of organisations, to further this mission, including The Royal Entomological Society, The Biological Records Centre, and The Entomological Collections Network.

A thread running through all the various elements of her work is social media. It's a powerful tool that any entomologist can use to promote insects and infect others with this obsession! In this talk, Ashleigh will reflect on some of her experiences (both good and bad) and share some of her top-tips for advocating for insects via social media.

Thomas Pagon - Royal Agricultural University, UK

The Impact Of Connectivity On Aquatic Invertebrate Community Ecology In Recently Created Ponds

Several schemes have incentivised the creation of ponds in agricultural landscapes, aiming to reverse a historic decline. A key reason for this is to support aquatic invertebrate populations, which are key in many food webs and ecosystem services, including pollination and pest regulation.

A key aspect of conservation ecology is connectivity between habitats and aquatic invertebrates have been shown to have complex dispersal strategies that rely on a range of structural and functional connectivity within the landscape. However, like most aspects of pond ecology and management, connectivity for aquatic invertebrates has received little study, particularly in new ponds which are distinct habitats for aquatic invertebrates in their own right.

Considering this a study was conducted to examine the impact of a greater level of structural connectivity (specifically direct water connectivity to another aquatic habitat) on aquatic invertebrate community ecology in ponds. Data was gathered over three surveys on 9 newly created ponds, all spatially close but with 4 having a direct connection to a river and 5 having no direct connection.

Field data was collected with aquatic invertebrates collected using kick sampling followed by identification to family level alongside measurements of key abiotic factors. Diversity indexes, family richness and the similarity between the connected and unconnected ponds were calculated and tested statically for difference, with abiotic measures tested for significance and correlation.

These results showed that the ponds with direct connectivity were more diverse (0.87 vs 0.82 using Simpson's index of diversity), richer (11 vs 7) and notably distinctive (71.56% using Jaccard's similarity coefficient); however, unlike findings from the literature, none of the abiotic factors (pH, Nitrate, Phosphate and Electroconductivity) were significantly different between the ponds with a direct connection and those without. Phosphate and conductivity had a negative correlation with aquatic invertebrate diversity but was not statically significantly affected by the direct water connection.

A further analysis was undertaken with all aquatic invertebrates found being classified into either flying dispersers or nonflying dispersers, It was found that, as the literature suggested that flying dispersers dominated the ponds with no direct connection, whereas those with a direct connection were predominately inhabited by swimming/drifting disperses through flying disperses still contributed a substantial contribution.

These results illustrate that ponds with a direct connection are more diverse and distinctive in comparison to those without a direct connection but that even those without a direct connection are valuable habitats for aquatic invertebrates at the early stages of pond establishment. The results showed that both types of ponds are distinctive habitats for aquatic invertebrates, and while the connected ponds had a greater diversity and richness, having both within a landscape would maximise aquatic invertebrate diversity at the early stages of pond establishment.

Kate Graydon – University of Bristol, UK

Investigating egg size plasticity in Apis mellifera as a potential strategy to cope with anthropogenic land use change

Honeybees (Apis mellifera) provide crucial services to humans, accounting for approximately half of all crop pollination activities (Kleijin et al., 2015). Humans depend upon honeybees to provide many of the fruits and vegetables currently available in our supermarkets. Paradoxically human-induced environmental change is a key challenge for honey bees as colonies might struggle to find enough food in some modern environments (Naug, 2009; Potts et al., 2010; L'Anson Price et al., 2019). In urban areas, honey bee populations are supported by allotments and gardens that host a diverse range of floral resources and give steady access to pollen and nectar throughout the year (Baldock et al., 2019). On the other hand, monoculture farmland can strain honey bees by creating "bloom or bust" environments where floral resources are only available during a single season (Goulson et al., 2015). Honey bee queens manipulate the size of eggs to provision their offspring with more food during times of nutritional stress (Amiri et al., 2020). Yet, exactly the relationship between land-use type and honey bee egg size is unknown.

Here, we aim to characterize the manipulation of egg size in the honey bee Apis mellifera across 24 sites in the south-west of England, to show how egg size varies in different landscapes. Egg size in rural areas was significantly larger than those in urban areas, indicating that: honey-bees are more

nutritionally stressed in rural areas, and therefore, honey bees receive more nourishment in urban areas. Our work may provide more information on how A. mellifera bees respond to fluctuations in floral resources. Here, we show further evidence of the detrimental effect of monoculture farmland on the health of honey bees, in comparison with more urban landscapes. Our results suggest that egg size may be used as an indicator of colony health on a short time scale. Emerging from the results of this study are further research opportunities, including the long term consequences of egg size on the health of a colony- how egg size affects worker size, worker behaviour and worker longevity.

Other authors: Christoph Grueter, Socail Insect Research Lab at the University of Bristol

Ritabrata Chowdhury - University of Cambridge, UK

Physical defences and insect-plant co-evolution: How do 5pecialized heliconiine caterpillars cope with Passiflora trichomes?

Plants protect themselves against herbivory by chemical and physical defences, whereas some insects have evolved counter-adaptations to feed on these plants. So far, however, little is known about the mechanisms underlying physical plant defences and insect counter-adaptations. In this study, we investigated the role of hooked trichomes in Passiflora adenopoda as a physical defence against Heliconiini caterpillars and how certain caterpillars can cope with these trichomes. Behavioural assays and high-resolution videography showed that hooked trichomes arrest the movement of Heliconius melpomene and Heliconius erato caterpillars, by piercing their cuticle and causing wounds in the soft cuticle near the prolegs in large caterpillars and on the main body in small caterpillars. However, Heliconius charithonia and Dryas iulia caterpillars were able to easily walk on the leaves with hooked trichomes due to a thicker and more robust cuticle. Moreover, penetrometry measurements confirmed that the cuticle of H. charithonia and D. iulia caterpillars is more puncture-resistant. However, only H. charithonia caterpillars were able to feed and survive on P. adenopoda with hooked trichomes. We also discovered that H. melpomene caterpillars sometimes accepted P. adenopoda leaves as food, but they died after ingesting the leaves, but surprisingly always survived eating P. adenopoda leaves when the trichomes had been ""shaved"" off. This study adds an important but as yet little-explored aspect to our understanding of the evolutionary arms-race between Passiflora and Heliconius and is also one of the first studies on insect counter-adaptations to physical plant defences.

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

Dawn Morgan (Online Talk) – **University of Wolverhampton, UK**

Worst Game of Hide and Seek Ever - Larval Dispersal Within a Residential Setting

Forensic entomology is the use of insects/other arthropods in a legal context. Insects as evidence has been used in criminal cases for many years, with the main use of estimating the post-mortem interval (PMI), or the minimum amount of time the body has been exposed, and available for insect

interaction. While insect evidence is used in cases of violent and unexpected deaths, it can also be helpful and used where the deceased has died from either natural causes or accidently in their own home.

For an accurate estimation, the oldest specimen at a scene should be found. But where in a residential setting should be searched?

Using published case studies and reputable news sources, two areas within a residential setting were identified as being where deceased persons are typically found. University of Wolverhampton's dedicated crime scene house was utilised, with larvae bought from a local bait shop. Larvae were placed within the set areas and allowed to disperse naturally.

Preliminary results show that larvae will cover more ground than anticipated, they will go under not one, but two closed doors, as well as migrate to different floors using ceiling spaces.

Invited speaker Dr. Seirian Sumner
University College London
Endless Forms: Reasons to Love Wasps

There's a lot more to wasps than your stripy picnic friend: wasps matter to you and the world. There are five times more species of wasps than bees; there are wasps that have sex inside plants; there are wasps that turn cockroaches into zombies. Wasps taught us how to make paper; wasps are architects, guardians of microorganisms, invaders, pollinators, seed dispersers and predators. They are nature's pest-controllers; their endless forms are windows into evolution's most remarkable inventions; they are pharmacists; they might even hold a cure for cancer. I guarantee that a journey into the secret world of wasps will blow your mind.

Parvez Khan (Online Talk) – **Ballygunge Science College, University Of Calcutta, India**

Status of Firefly in India

Fireflies that once were abundant in the backyard of houses, shrubs, open wild green patches are today a rare sight in India. Due to rapid urbanization and habitat destruction, currently fireflies are hardly come-crossed even in thick green foliage and patches. Fireflies are soft bodied, carnivorous, beetles (Lampyridae: Coleoptera), indicators of climax vegetation and green biomass. These beetles are abundantly found in evergreen tropical forest and vegetation such as Western Ghats and Coffee estates in South India. They lit-up the green valleys with synchronous flashes of light during rainy season. In urban areas, beetles and their larvae are usually found hidden under bushes and small to medium - sized trees in soil. Lampyrid beetles spend most of their time (80-90%) in the larval stage. The larvae may spend the life either in soil or in water or bark of old trees. The adults live for short period (3-4 weeks) and are nocturnal in habit. Fireflies are flagship species for biological conservation and rank among the most charismatic beetles, with distinctive bioluminescence and

courtship behavior. They are also indicators of climax vegetation but are poorly studied in India. Further, they are not included in the Schedules of Wildlife Protection Act, 1972 of government of India. The populations of fireflies are drastically declining due to rapid urbanization and habitat destruction across the country. Studies on fireflies are also important to understand impacts of climate change. In India, fireflies are of great attraction to tourist because they emerge in massive numbers with synchronous colorful flashes of light. There is an urgent need to conserve such spots and declare them as protected area.

Other authors: Dr. A.K Chakravarthy and Amlan Das

Mayumi Madhushani (Online Talk) – **Rajarata University of Sri Lanka, Sri Lanka**

Citizen scientists on the move: A success story of citizen scientist's involvement in sand fly vector surveillance using DIY light traps in Sri Lanka

Introduction: Phlebotomine sand flies (Diptera, Psychodidae) are a medically important group of insects transmitting various arboviruses including Leishmania sp. Leading to more than one million deaths each year. Despite such significance, the updated information regarding the local sandfly fauna is inadequate in Sri Lanka. Available data shows that these vectors appear to increase their geographical distribution under the influence of climate change and other ecological factors. Therefore, continuous entomological surveillance is required to monitor the spread of sand fly vector expansion and the possible consequences of their spread. In Sri Lanka, Cattle baited trap is the only Entomological tool used for sand fly surveillance by Disease control campaigns. This method is both labor and time-intensive and limits the number of sites monitored and the frequency of monitoring. Citizen scientists' projects involving medical entomology enhance the public understanding of early identification of leishmaniasis disease symptoms, distinguishing sand fly vectors, and their control measures. This project aims to upscale entomological surveillance by interconnecting citizen scientists in the study area and using 'do-it-yourself' (DIY) light traps which assist to minimize the costs and enhance the frequency of surveillance with available limited resources.

Methods: The pilot study area was the Medawachchiya PHI area in Anuradhapura district, Sri Lanka. We created a citizen scientists' program in this area and selected volunteers were trained for delivering the sand fly entomological surveillance. Then provided five DIY light trap models and encouraged them to carry out entomological surveillance by themselves. Respective volunteers work under our guidance at specified GND areas. The study was carried out from January to April 2022. The collected samples were morphologically identified at the reference lab. Molecular identification using CO_I, and CO_II genes further supported species confirmation. Leishmania parasite species-specific primers (ITS-I) were used to confirm the infection prevalence of sand flies. The frequency of sand fly surveillance and expenses were properly recorded. Finally, a cost analysis was carried out for the whole process with the number of samples collected.

Results: During the study period, a total of 113 sandflies (male=71, female= 42) were collected from the traps placed in nine different locations, and among them 8 were blood-fed. All the sandflies were identified as Phlebotamus argentipes and 19.04% (n=8) of female sand flies were positive for

the Leishmania parasite while representing 100% from blood-fed females (n=8). Cost analysis data revealed that the total cost applicable to this study was nearly four times (3.6) lower than the cost of routine vector surveillance implemented by government health officials. The efficiency and sustainability of sand fly control are also promising compared to previously recorded routine field data in the same site.

Conclusion: DIY Light traps with a combination of citizen scientists are a cost-effective alternative for middle-income countries such as Sri Lanka for generating data on sand fly vectors and Leishmaniasis disease which is also a great path for community-based vector control approaches. Further, this approach could be used to minimize the drawbacks and barriers to approaching marginalized populations having limited access to health settings.

Other authors: N.D.A.D.Wijegunawardana , P.Kandegedara

Invited workshop Francisca Sconce
Royal Entomological Society
Insect specimen curation

This workshop will discuss the importance of entomology specimen collections, cover the key preservation techniques, highlight labelling and data, and summarise storage and digitisation.

Friday, 31 March 2023 (all times GMT)

Invited speaker Dr. Peter Graystock
Imperial College London
A hitchhikers guide to parasite dynamics in pollinator communities

Parasites are considered to be one of the leading causes of species extinction and population declines. This is particularly true in pollinators but our reliance on a handful of managed bees for agriculture has created some blind-spots in our understanding of parasite risk to wild bees. Here I present a summary of my work which has explored the parasite dynamics between managed and wild bees, the routes of transmission between bee species, and a wider view of pollinator community dynamics on pollinator health. Along with discussing my work and its impact, I will recount my fears of litigation during my PhD when publishing work that called out companies for poor practices, and the trials and tribulations of moving myself and partner around 6 different universities/cities and 2 continents over a 5 year period in various postdoc/fellowship roles, before finally getting a lectureship.

Monika Yordanova – Imperial College London, UK

Bee pathogens across the foraging landscape

Bees are essential pollinators; however, a variety of factors have contributed to their losses – one of these being increased disease incidence and pathogen spillover. As bees forage, they can disperse harmful pathogens upon flowers which subsequent foraging pollinators can inadvertently harvest. Across foraging landscapes in North America, some flower species have shown the potential to act as transmission hubs disproportionately to others. However, gaps remain in our knowledge about how this relates to the type of pathogen considered, how this fits in the broader context of the foraging network, and how it links to the morphology of the flowers and pollinators. Here, I will present data on previously untested European wildflower species on their likelihood to become transmission hubs for various bee pathogens and discuss how the patterns observed can have broader implications on managing wild pollinator health.

Other authors: Ellen Marandola- Imperial College London, Yeah Ji Jeong - Queen Marry University of London, Peter Graystock - Imperial College London

Ciaran Harris – University of Sussex, UK

Phenological imbalance in the supply and demand of floral resources

Declines in floral resources, pollen and nectar, are considered one cause of pollinator decline. However, the supply and demand of floral resources can vary temporally. In Britain, autumn has been suggested as a period of high floral resource availability due to the flowering of ivy (Hedera helix), a common native plant, combined with fewer insects active during this season. However, previous work examining supply and demand of floral resources have only used indirect indicators of foraging conditions, such as by using honeybee foraging distances communicated by waggle dances. No study has yet directly quantified production and use of floral resources in an ecosystem.

As ivy is the main source of floral resources in autumn, comprising c.90% of the pollen collected by honeybees, by using ivy as a study species we are able to directly quantify overall floral resource production and utilisation across the entirety of Autumn, a whole season, by studying a single plant species. Here, we directly quantified the proportion of pollen and nectar produced by ivy which is uncollected by the flower-visiting insect community.

We quantified the proportion of nectar produced but uncollected by comparing the mass of nectar sugar accumulated in insect-accessible versus inaccessible ivy flowers and by surveying the presence of wasted, crystalised, nectar on flowers. Pollen wastage was quantified by comparing pollen counts on anthers at the start of anthesis versus anthers dropped from ivy flowers.

Approximately, half the floral resources, 59% nectar and 44% pollen, were uncollected by the flower-visiting insect community in autumn. As ivy flowers supply most of the available nectar and pollen in autumn, our results show that a large proportion of all floral resources are uncollected in

autumn. Importantly, the ivy bee (Colletes hederae) was the most frequent insect recorded foraging on ivy (27% of recorded visits). This species first colonised Britain in 2001 and is now widespread throughout Britain and has recently colonised Ireland. Although colonising species can be major competitors for native species which forage on the same plants, our results suggest that at present numbers ivy bees are unlikely to harm native species through exploitative competition. However, further work is needed to confirm this.

Our results are the first to show that a season can be characterised by a large surplus of floral resources relative to collection by flower-visiting insects. These results demonstrate the importance of considering seasonal variation in floral resources in the conservation of bees and other flower-visiting insects. Conservation strategies aiming to improve floral resource supply will likely be more effective if targeted at seasons with shortages of floral resources such as late summer (July – August).

Other authors: Hannah Ferguson, Ethan Millward, Phoebe Ney, Nadia Sheikh, Francis L. W. Ratnieks

Invited workshop Emilie Aimé

Royal Entomology Society

How to get published in entomology

Publishing in academic journals is important to disseminate your work to your peers and to progress your career, but have you ever wondered how the process works, and what editors look for in papers they accept for publication? Join the RES Head of Publishing and several journal editors for this workshop to find out.

Invited speaker Dr. Nathalie Stroeymeyt

University of Bristol

Social network plasticity decreases disease transmission in the ant *Lasius niger*

Animal and human social networks are shaped by multiple selection pressures, including the need to ensure efficient group functioning and communication while simultaneously limiting the spread of infectious diseases. It has been hypothesised that social animals could further reduce epidemic risk in the presence of pathogens by altering the transmission properties of their social networks, yet there is little evidence for such pathogen-triggered network changes. We tested this hypothesis experimentally in colonies of the ant Lasius niger using a combination of automated behavioural tracking, controlled exposure to an infectious pathogen, precise quantification of individual pathogen load, and temporally-explicit transmission simulations. We first describe important constitutive properties of the ant social network that simultaneously inhibit overall transmission and isolate valuable individuals (queen, brood and young workers) from disease sources. We then show that the ants adaptively respond to the presence of an

infectious pathogen by reinforcing key disease-inhibitory properties of their social network, conferring additional disease defence to the colony. Finally, we show that these network changes result from early behavioural changes in both pathogen-exposed workers and their untreated nestmates, increasing the spatial and social segregation between individuals. Our results indicate that the alteration of social organisation in response to pathogen entry is an effective strategy to mitigate the effects of disease in social groups.

Laura Campbell – **Durham University, UK**
The evolution of plant cultivation by ants
Outside humans, true agriculture was previously thought to be restricted to social insects farming fungus. However, obligate farming of plants by ants was recently discovered in Fiji, prompting a re-examination of plant cultivation by ants. Here, we generate a database of plant cultivation by ants, identify three main types, and show that these interactions evolved primarily for shelter rather than food. We find that plant cultivation evolved at least 65 times independently for crops (~200 plant species), and 15 times in farmer lineages (~37 ant taxa) in the Neotropics and Asia/Australasia. Because of their high evolutionary replication, and variation in partner dependence, these systems are powerful models to unveil the steps in the evolution and ecology of insect agriculture.

Other authors: Guillaume Chomicki (as of 1/3/23 Durham University) E. Toby Kiers (Vrije Universiteit Amsterdam)

Adeyemi Daniel Adetimehin (Online Talk) – **University of Cape Town, South Africa**
Flowing with the stream: unidirectional dispersal of blow fly larvae following decomposition fluids from an adult pig carrion
After death, vertebrate carrion undergoes a series of complex chemical, biological and physical processes/changes known as decomposition. As these changes progress, insects belonging to the family Calliphoridae (blow flies), become attracted to the carrion – as first responders and colonisers – by the volatile organic compounds associated with the gaseous and liquid discharges emanating from the remains. Following their arrival, gravid female individuals oviposit in or close to natural body openings (e.g., ocular, nasal and/or oral cavities), between the limbs and/or underneath the carrion after which the emerging larvae start feeding on the soft tissues of the carrion. At late stages of decomposition, the blow fly larvae begin to migrate away from the body, typically in random directions searching for favourable conditions for pupation. Here we report on a rarely described phenomenon of unidirectional mass migration of blow fly larvae in contrast to the normal random dispersal and postulate on external factors which may drive this process. A decomposition trial utilizing a 60 kg pig carcass, deployed in the summer months in Table Mountain National Park, Cape Town, South Africa was conducted in 2022. On the 5th day of the trial, simultaneous unidirectional dispersal of blow fly larvae was noted. Larvae were moving downhill in a southwestern direction, following the flow of decomposition fluids emanating from the carrion. The "larval migration stream" had a length of approximately 1.5m with a width of 40cm, tapering to 17cm at the terminal point. At the terminal point of the stream, larvae resumed random dispersal. The

"larval migration stream" predominantly consisted of Chrysomya albiceps Weidemann (Diptera: Calliphoridae) and, to a lesser extent, Chrysomya chloropyga Weidemann (Diptera: Calliphoridae), consistent with the previously documented seasonal carrion entomofaunal assemblage in this region. The downhill dispersal pattern of blow fly larvae together with the decomposition fluids may be attributed to both the topography of the study site and associated force of gravity, along with the protection from desiccation conferred upon the blow larvae by the decomposition fluids during the migratory process. In conclusion, this study demonstrates the importance of observing patterning of decomposition fluids and possible utility in the location and collection of post-migration larvae from decomposing vertebrate remains during crime scene investigations.

Other authors: Calvin Gerald Mole: University of Cape Town, South Africa; Devin Alexander Finaughty; University of Kent, United Kingdom; Marise Heyns: Ulster University, United Kingdom.

Laura Martinez-Chavez – Harper Adams University, UK

Potato aphid (Macrosiphum euphorbiae) clonal variation determine its susceptibility to Aphidius ervi

The potato aphid (Macrosiphum euphorbiae) is an economically important pest of strawberry crops. There is increased reliance on aphid parasitioids and predators to control this species due to withdrawal of some insecticides and indirect insecticide effects on pollinators and other beneficial insects in strawberry crops. However, the recent description of innate resistance to a parasitic wasp (Aphidius ervi) in some populations of M. euphorbiae feeding on potato could indicate reduced effectiveness of biological control of aphids in strawberry crops using parasitoids. As it is not yet known if the parasitoid-resistant genotypes of M. euphorbiae also infest strawberry crops, experiments have been completed to characterize different clones of M. euphorbiae collected from strawberry crops. This study will use aphids sampled from different geographical locations in the UK, microsatellite information to genotype these aphid populations, and diagnostic PCRs to identify the presence of 'protective' facultative endosymbionts. Also, the susceptibility of these aphid clonal lines to parasitism by A. ervi will be also recorded. The present study included 14 different clonal lines of potato aphid, from which we found genotypes with different combination of facultative endosymbionts, including the presence of Hamiltonella defensa, Serratia symbiotica, Regiella insecticola and Rickettsia. Preliminary parasitism assays showed great variation on the levels of parasitism rates of the parasitoid A. ervi on different clonal lines, ranging from 4-55%. In addition, parasitoid acceptance of A. ervi to a subset of M. euphorbiae genotypes will be characterized in laboratory bioassays to understand the role of aphid intrinsic genetic variation in aphid-parasitoid interactions. Together this information will inform on the likely effectiveness of biological control programmes based on releases of A. ervi for control of M. euphorbiae in strawberry crops.

Other authors: A.J Karley (The James Hutton Institute), T.W Pope (Harper Adams University), J. Roberts (Harper Adams University) and M. Fountain (NIAB-EMR)

Invited speaker Dr. Jordan Cuff
University of Newcastle
PhD to postdoc in a pandemic: COVID, conflict and other conundrums

PhDs are often cited as being among the career highlights of academic scientists and leave many eager to pursue careers in academia. Transitioning from a PhD to a postdoctoral position can be a precarious path at the best of times, and the COVID-19 pandemic has made that all the more complicated for many people. Whilst everyone's journey of this is unique, and my experience was far from representative of most, I will detail the trials and tribulations of my attempts to secure a postdoctoral position at the height of the pandemic. From Zoom vivas through repeated job applications to moving across the country (and nearly the world), I will share the ups and downs of my journey. Framed by my failures and successes, I will also impart my personal insights and advice for searching the academic job market and securing a postdoc.

Throughout this, I will also describe my research which uses molecular methods to detect and identify interactions between invertebrates, but also tangents I explored along the way which have ultimately been enriching. From designing protocols for the molecular diagnostics and sequencing of wastewater to attempting to launch a compost-related independent business venture, I will discuss how all of these experiences have helped me through my career so far, often in unexpected ways. I hope that this talk will provide background on my research, a compelling story, and some tangible advice for seeking further employment within academia.

Poster Abstracts

In-Person Posters

Fiona Tainsh - University of Warwick, UK
Red Mason Bees for Commercial Pollination
The cultivation of commercial horticultural edible crops is reliant on insect pollinators to produce fruits and seed, most of which is done by bees, including wild bees (solitary species, as well as social bumblebees) and managed bees, primarily honeybees (Apis mellifera) and bumblebees. Increasing pressures on production – associated with increased demand for fresh produce from consumers, concerns about food security, and the challenges of climate change – mean that growers are having to pay more attention to pollination.

This project concerns the red mason bee (RMB), Osmia bicornis, which is important as a wild pollinator of horticultural crops and is used on a commercial basis throughout Europe. For commercial use, cocoons are placed in the crop in the spring, alongside a series of nest tubes spaced throughout the crop in which the bees can make cells. The tubes are collected back in

the summer and cocoons are extracted in the autumn and overwintered. The system allows larger populations of mason bees to be maintained in the crop than would otherwise be the case with no intervention, and this translates into better crop pollination.

Relatively little is known about red mason bee basic biology and therefore keeping large, dense populations in the field has the potential to negatively impact wild bees, with the risk that an unknown infectious disease could spread through a dense commercial population and into wild bees. This project will therefore identify RMB immune associated genes as well as using traditional pathology to identify common diseases and their symptoms. There is also a lack of information regarding RMB population genetics, including the structure of metapopulations and levels of gene flow between them. To better understand the relatedness of different populations of RMB, we will monitor how artificially added red mason bee populations spread within an orchard where the species was not previously present as well as identifying microsatellites within the RMB genome to compare the relatedness of different populations across the UK.

Other authors: David Chandler, University of Warwick

Ben Hawthorne - Newcastle University, UK

Applying eDNA/metabarcoding for the biomonitoring and assessment of Environmental Land Management schemes (ELMs)

Agricultural intensification in the UK has been detrimental to biodiversity, threatening ecosystem services such as pollination and natural pest control; this is a great challenge for meeting targets on food security and biodiversity recovery. Environmental Land Management schemes (ELMs) were developed by the UK Government to improve biodiversity, as well as carbon sequestration and water quality. Within ELMs, farmers and land managers will be financially incentivised to implement measures that safeguard these properties. To ascertain whether ongoing ELMs trials are successful, it is important to evaluate if the schemes produce the desired outcomes. Assessing the impact of these schemes on biodiversity using traditional surveys can, however, be laborious and inaccurate given the sampling effort required and the difficulty involved in identifying many taxa. Molecular methods such as DNA metabarcoding may provide a potentially rapid and highly accurate method for environmental monitoring of bulk samples of invertebrates collected in the field.

This project will assess the impact of ELMs on biodiversity using DNA metabarcoding. Partnering with Fera Science and Syngenta, samples will be collected with water pan traps from established ELMs trial sites. Following metabarcoding, DNA will be sequenced using both Oxford Nanopore Technology and Illumina platforms, and the species present identified. An ecological network approach will be used to assess ecosystem function, with a particular focus on pollinators, natural pest predators and crop pests (i.e., ecosystem service and disservice providers). This project will develop methods and data to inform decision making when selecting ELMs to benefit different taxa within ecological networks, with implications for policy and industry. This will, in turn, exemplify the suitability of metabarcoding for broad-scale biodiversity assessments, such as for the Natural Capital and Ecosystems Assessment (NCEA) programme by the UK Government.

Simeon Wilton - UK Centre of Ecology and Hydrology, UK

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

The Asian hornet, Vespa velutina, was first observed in France in 2005 and has spread rapidly within Europe. There have been observations from the UK but all confirmed sightings have led to successful eradication. Models have demonstrated the environmental suitability of the UK for the Asian hornet but it is currently absent. In invaded regions it is well-documented as a predator of the European Honeybee, Apis mellifera. Less is known about the impact of Asian hornets on other prey, which include wild pollinating insects. Risk maps provide a useful tool for contingency planning in the event of an incursion. Here I will present models investigating potential co-occurrence of wild pollinators and the Asian hornet and consider the effects of body size and seasonality of the potential prey to inform risk maps.

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Louise Hutchinson - University of Reading, UK

Characterizing the pollinator communities & pollination sustainability of four economically important crops in Great Britain.

Bees provide vital pollination services to crops in Great Britain, yet little is known about which species provide this service, how best to monitor their populations in agricultural areas, and how increased species richness may affect the resilience of pollination services in the future. Using four crops - apples, field beans, oilseed and strawberries -we used a combination of ecological traits databases, crop field studies and data from occupancy models to answer these questions. We produced national lists of bee flower visitors for all four crops, and found that a diverse set of species could contribute to the pollination of our focal crops. We also assessed the ability of different sampling methods - observation plots, pan traps and transect walks - to measure the abundance and species richness of bee crop pollinator communities, and found that and the efficacy of different survey methods to sample bee crop pollinators may be contingent upon the guild and crop being targeted. Additionally, we used data outputs from occupancy models to test how the stability of crop pollinator occurrence is influenced by crop pollinator community composition and species richness. We found that bee crop pollinator communities composed of a small number of closely related species are likely to exhibit more synchronized inter-annual occupancy dynamics, and show a greater variance in mean occupancy, compared to crop pollinator communities comprised of a more diverse set of bee species. Additional analyses also indicate that more species rich pollinator communities may result in greater stability of crop pollinator occurrence over time, which could have positive benefits for the resilience of crop pollination services under future environmental changes. We use our finding to provide recommendations on how species-rich and stable bee crop pollinator populations could be protected and promoted in agricultural landscapes in order to safeguard production of insect pollinated crops in Great Britain.

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Jack Perry - Teagasc and Harper Adams University, UK & Ireland

Improving aphid and BYDV Management

Cereals are the leading crop produced worldwide, forming the basis of human nutrition. The demand for cereal crop production is continuously increasing, owing to an ever expanding human population. Thus it is critical to increase cereal yields, a considerable barrier is yield losses caused by insect pests. Aphids are a major insect pest, reducing both grain yield and quality via direct feeding or vectoring plant viruses. The most economically important aphid vectored virus in cereals is Barely Yellow Dwarf Virus (BYDV), causing up to 80% yield losses. Managing aphids is becoming increasingly difficult due to; reduced insecticide availability, insecticide resistance, lack of robust thresholds and climate change. To navigate these challenges it is critical to implement robust monitoring techniques that account for the spatial and temporal distribution of aphids. Monitoring aphids is a highly valuable management tool, enabling informed insecticide applications. Different Monitoring tools are applied to monitor aphids at varying scales; Visual assessments at plant level, Water traps at field level and suction towers at region levels. One caveat to employing monitoring tools to manage BYDV is the viral risk of a signal aphid is currently unknown. The presence of an aphid is not a clear indicator of BYDV presence, the severity of BYDV infection is linked to both the number of aphids and the proportion of which are viruliferous. This project has established a national aphid trapping programme in Ireland, to assess if aphid monitoring tools provide a good indication of aphid populations and BYDV outbreaks. The nationwide programme has ran throughout 2022 in spring barley and winter barley, with aphids collected being tested for BYDV.

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Faye Hindley - Edge Hill University, UK

The impact of lowland raised peatbog fragment size and micro-habitats on Coleoptera (Beetle) communities.

Lowland raised peatbogs are one of the rarest habitats on earth and provide one of the most unique ecosystem services by sequestering large amounts of carbon. As the importance of peatlands has become increasingly obvious as a possible mitigation of climate change, many damaged peatlands have been restored by wildlife charities in the UK, such as the Wildlife trust, with the aim to restore the diversity and provide for the rare species that can be found in these habitats. Due to anthropogenic disturbance, peatlands have become fragments in the habitat matrix found in modern day countryside. This fragmentation has a huge impact on diversity of the species found affecting distribution, especially with specialist species. In this study, Coleoptera Beetles will be collected using pitfall traps in three micro-habitats found in the restoration peatlands: Edge, bund, and centre in the North-west of England. Each micro-habitat differing plant species will be measured. Coleoptera are the largest order of invertebrates and play an extremely important role in the cycling of nutrients globally, but like many species have rapidly

declined. The diversity of species found in the micro-habitats will be compared within each site. This data will be used to compare Coleoptera communities in Large (>20ha) (Astley moss 40ha, Little Woolden moss 107ha, and Winmarleigh 120ha) and small (<20ha) sites (Cadished 7ha, Highfield 8ha, and Holiday moss 3.2ha).

The aim of this study is to find how the size of fragments and micro-habitats influences the Coleoptera communities in lowland raised peat bogs, which will hopefully provide an insight in the ability for restoration sites to provide for specialist Coleoptera species and ways in which to improve restoration techniques to better provide for Coleoptera communities.

Rebecca Sanders - Warwick University, UK

A holistic approach to Integrated Pest Management: investigating a new strategy for aphid management combining durable host plant resistance with fungal bioprotectants

Insect pests of horticultural crops lead to loss of marketable yield through direct damage to the crop, transmission of diseases and through their physical presence on the harvested material. The historical reliance on chemical pesticides for their control has paradoxically engendered the twinned crises of the emergence of pesticides resistance in pest species in synchrony with alarming collateral-damage to non-target invertebrate species. Integrated Pest Management (IPM) offers a holistic, sustainable approach to crop health management that reduces reliance on synthetic pesticides and thus the impact these have on the wider environment. Previous work has identified a possible synergistic effect between partial host-plant resistance to aphids in Brassica crops and entomopathogenic fungi (EPF) biocontrol agents. We hypothesise that partial host-plant resistance slows the progression of aphid-nymph development, and thereby delays exuvium-shedding between larval-instars, leaving nymphs more vulnerable to transcutaneous infection by germinating fungal spores. In-silico modelling of aphid population-growth dynamics will help to optimise strategies for aphid biocontrol protocols. Elucidating the mechanisms by which synergistic forms of pest management interact contributes to the increasingly important IPM discipline, providing the means to continue to grow horticultural crops as we transition to a post-pesticide era in agriculture.

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Adam Cutts - Cardiff University, UK

Interactions of Insecticidal Proteins with Target Membranes

Members of the order Lepidoptera, including several polyphagous pests, pose significant risks to agriculture and, as such, require decisive strategies to contain these risks. Bacillus thuringiensis (Bt) is a bacterium that produces a broad range of insect-killing proteins and represents a candidate to fulfil this need. Vegetative insecticidal proteins (Vips) comprise a family of pesticidal proteins, known to target lepidopteran organisms. Vips expressed by Bt have been used as natural insecticides in various crops, such as corn across the US; however, their exact mechanism of action is poorly understood. This project aims to elucidate these mechanisms through three main threads of enquiry; biochemical characterisation, biophysical analysis, and molecular

modelling. Biochemical characterisation will establish details on structure and activity through binding assays of lipids and sugars, particularly those associated with insect midgut environments, and activity assays on known-target insect cell lines, such as Spodoptera frugiperda, a major lepidopteran pest. Artificial lipid membranes will act as the model system for biophysical analysis of toxin-membrane interactions as a parallel system to insect cells. Supported by the use of novel microscopy techniques to image these interactions, we will characterise quantitative changes in the membranes upon protein insertion. Microscopy in conjunction with electrophysiology studies will be conducted on insect cell lines to complete this thread. Powerful tools within the molecular modelling space, such as AlphaFold and Molecular Dynamics (GROMACS) will be used to establish predicted assemblies of toxin structures and insertion into target membranes, to support and extend experimentally-determined results. In developing our understanding of these pesticidal proteins, we can expand our suite of pest resistant crops and help achieve food security in the future.

Clare Boyes - Manchester Metropolitan University, UK

A bee's eye view of landscape change

Pollinator declines are linked to landscape change affecting 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 (Chambers, 1968), 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 work, pollen was collected and identified using the methods described by Chambers (1946). The 1940s data was collated from Chambers' notebooks. Landscape change was analysed using QGIS. Statistical analyses were conducted using 'R': Wilcoxon rank-sum was used to test for differences in pollen use between the periods; and iNEXT to calculate Chao species richness for the total pollens used.

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 reduced species richness. Other notable findings were that in 2021, there were significantly more types of pollen per load for A. flavipes; and 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, but Aspley Heath showed little apparent change.

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 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.

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Emily Heath - Cardiff University, Wales, UK

Establishing the role of glycans and lipids in the mechanisms of Tpp1/Tpp2 (Bin) toxin in target insect and cancer cells.

Tpp1/Tpp2 (formerly BinA/BinB) toxin is a two-part (binary) toxin of the toxin_10 family composed of Tpp1 and Tpp2 which, combined, target the larvae of Culex and Anopheles mosquitoes. In addition to toxicity against target insect larvae and cells, Tpp1/Tpp2 toxicity against a range of cancer cells has also been reported even in the absence of the putative Bin receptor (Cqm1). Previous studies, with invertebrate-active pore forming toxins (Cry5B and Cry14A), have identified that glycan moieties can mediate toxicity through facilitating toxin/receptor binding, and indeed some work suggests Tpp1 may also have the ability to interact with L-fucose, L-arabinose, and glycoproteins.

We have investigated the roles of lipids and glycans in Tpp1 and Tpp2 toxin binding and efficacy in various insect and cancer cell lines – with a focus on its known target species, Culex quinquefasciatus and HepG2 cancer cells against which toxicity has previously been reported. Preliminary findings indicate Tpp1/Tpp2 does not interact with sugars previously associated with toxicity in other insecticidal proteins (e.g GalNAc, GlcNAc). Initial studies using total lipid extracts from C. quinquefasciatus cells and multiple cancer cell lines suggest Tpp1 and Tpp2 bind several lower phase lipids (simple glyco and other non-polar lipids). Early work has shown that there are differences in the lipid profiles between the target insect cells and across multiple cancer cell lines tested. Differences in the lipid profiles in cells may be an important determinant of Tpp1 and Tpp2 binding. Future work will focus on identifying the profile of these bound lipids and establishing their role in toxicity.

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Joshua M. Sammy - University of York, UK

Invertebrate increases 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. Ongoing and future responses of species to these different levels of modification will determine the capacity of biodiversity to adjust to human associated ecosystem change. Analysing 38,265,792 site-specific records of 2,106 invertebrate species from 14 taxonomic groups between 1981-2000 and 2001-2020, we find here that 'human-associated' species in Great Britain have been increasing relative to 'human-avoiding' species. 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. Contrary to previous hypotheses, we also find no evidence that human associated species are more likely to be habitat generalists. 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.

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Rose Lownds - University of Reading, UK

The impact of elevated aestivation temperatures on the behaviour of Bogong Moths (Agrotis infusa)

Bogong moths are an iconic Australian insect that migrates annually in spring from low elevation locations in southern and eastern Australia to the Australian Alps where they aestivate during summer. As summer ends they make their return journey to the breeding grounds where they mate, lay eggs and die. Given the moth's extreme behaviour in seeking out cool alpine habitat and with the knowledge that average temperatures at their aestivation sites are rising because of climate change, we assessed whether increased temperatures affect bogong moth activity during aestivation. Our first hypothesis was that moth activity would be affected by temperature, and we found that moths were more active at higher temperatures, especially during the day, with near-constant activity at 15˚C at all times of day. Our second hypothesis was that moth mass would be different after aestivating at different temperatures for a week due to dehydration or consumption of body energy reserves. We found that moth wet mass loss increased with increasing temperature, but found no difference in dry mass among temperature treatments. Overall, our results suggest that bogong moth activity will increase with increasing temperatures at their aestivation sites. The impact of warming on the success of individuals to complete their aestivation and journey back to their lowlands to breed should be investigated as a matter of

priority to better understand the impact of changes in aestivation behaviour on population dynamics.

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Zann Teo - Nanyang Technological University, Singapore

Checklist of the Dung Beetles of Singapore (Coleoptera: Scarabaeidae: Scarabaeinae)

Dung beetles provide a variety of ecosystem services and are functionally important in tropical ecosystems. They are an excellent proxy for monitoring ecosystem health and can act as surrogate indicators for elusive mammals. However, information on the distribution of dung beetles across Singapore, particularly ion in urban parks and green spaces is currently lacking as sampling efforts were previously concentrated in the Central Catchment and Pulau Ubin.
This study aims to create a species checklist to better understand present diversity, add value to taxonomic records, and support implementation of meaningful biodiversity conservation strategies. A dichotomous morphological key of local species was also created to support future dung beetle studies in Singapore and encourage citizen science. Increased sampling effort at green spaces was carried out in 2021 to supplement distributional records in previous studies focused on the Central Catchment.

In our recent sampling, 15 species across 4 genera were identified, and 9 morphospecies have yet to be identified. 12 species found in previous studies were not sampled in our direct collection. In total, we have identified 27 valid species and 9 morphospecies. Species which were not recollected in recent sampling may have become locally extinct, or the trap types or baits used are not suitable in collecting these species (e.g. arboreal species, specialist feeders). Identification of most specimens, both historical and recently collected, are done via morphological traits. Future work may utilize integrated taxonomist approaches, such as DNA barcoding to confirm species identity, to increase accuracy of identification.

Michael O'Shea - University of Plymouth, UK

The contrasting copulatory behaviours exhibited by Orthetrum coerulescens and Sympetrum striolatum and how the headbutt prompt and oviposition in tandem impact female oviposition.

Odonata are an ancient clade of winged Insecta with a wide range of behavioural traits which have evolved for the purpose of reproduction. These adaptations vary greatly between species, such as post-copulatory resting (PCR) and the headbutt prompt exhibited by Orthetrum coerulescens, and oviposition in tandem exhibited by Sympetrum striolatum. This field-study investigates the contrasting copulatory behaviours of both species highlighting the importance of male behavioural traits on oviposition. Both species were subject to tests to determine the mechanisms of oviposition; eggs are released from the abdominal tip through water dispersal when performing the dipping action. Sympetrum striolatum released more eggs than Orthetrum coerulescens due to the increased number of successful dipping actions. However, there was a clear contrast in the amount of time males invested in oviposition in tandem. Male Sympetrum

striolatum dip females on average 130 times, in contrast to the average of 30 times eggs were released when subject to the oviposition dip test. Furthermore, we found the headbutt prompt was commonly used by Orthetrum coerulescens. 70% of the males used this behaviour to end PCR and coax oviposition. Significant corelation was observed in the amount of oviposition dips exhibited in relation to increased headbutt prompts.

Mireia Larrosa - The Pirbright Institute, UK

Optimization of assays to determine the fitness competence of Anopheles stephensi mosquitoes

Anopheles stephensi is the primary urban malaria vector in parts of southern Asia. In 2012 it invaded the Horn of Africa and has since established in several African countries being an emerging risk for malaria outbreaks, especially in cities. The continuous propagation of insecticide resistance has encouraged research into alternative vector control strategies such as the release of genetically engineered mosquitoes into the wild to reduce or replace mosquito populations disrupting disease transmission. However, the efficiency and economic feasibility of these systems depend heavily on the mating competitiveness of these transgenic strains.

Mating success can be compromised due to the genetic modification itself as well as laboratory mass-rearing. Thus, assessing the fitness of any lab-reared insect species prior to their release is key. Unfortunately, different insects have significant behavioural differences. Therefore, these methods need to be adapted to each one of them. Most of the published methods to determine vector competence of lab-reared mosquitoes are based on Aedes species. However, the growing interest in genetic modification has generated new methods in Anopheles and Culex mosquitoes. The increase in the number of laboratories that are focusing on vector biocontrol and the discovery of new target sites have diversified the methods to determine fitness of lab-reared mosquitoes. Here, we reviewed fitness assays from the published literature and optimized three main assays to determine the fitness of An. stephensi lab-reared strains. These methods will unable researchers to gather enough information prior to semi-field trials, an extremely time-consuming and costly procedure.

Mating in Aedes, Culex and Anopheles occurs in swarms, but when, where and how these occur vary among species. Mosquitoes' mating rituals require a male to locate and pursue a female within a swarm until it is accepted, then the precopulatory interaction occurs mid-air, requiring males and females to be able to fly. Consequently, the three established assays are: (1) fecundity and fertility assays to determine the reproductive ability of both males and females; (2) a male competitiveness assay to determine if the altered mosquitoes can detect and compete against WT mosquitoes for a determinate female; and, (3) a flight assay where we determine if the transgenic mosquitoes have the same ability to fly as WT mosquitoes.

In summary, we established three different methods to assess An. stephensi lab-reared mosquitoes' reproductive fitness, serving as a first step to determine their mating competitiveness in the field. However, the increasing interest in the fitness of these strains has opened new questions regarding males' fitness involvement in mating success, which have yet to

be answered. Although the presented methods are species specific, these could easily be adapted to different lab-reared insect species, being of great interest for the entomological field."

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Aditi Rawal - University of Zurich, Switzerland

Impact of toxic substance exposure on life history and reproduction of Black Scavenger flies (Diptera: Sepsidae)

Neonicotinoids are widely used insecticides which have been highly toxic to non-target organisms and reported to have both sub-lethal and lethal effects on the development, survival, or physiology. We experimentally quantified the effects of juvenile (larval) exposure to the neonicotinoid imidacloprid on the life history of four non-target species of Black Scavenger flies which are beneficial as decomposers of vertebrate dung. We hypothesized that with increase in imidacloprid concentration in dung, it will gradually lower larval survival and adult emergence due to high mortality. Also result in lower fecundity of the surviving adults.

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Becca McGowan - University of Warwick, UK

The Biology & Integrated Management of the Bean Seed Fly

The Bean Seed Fly (BSF) (Delia platura & Delia florilega) is a pest of over 40 crop species, causing the greatest problems in legumes and alliums. It usually causes the most crop damage early in the year. Crop yields are reduced when BSF larvae feed on developing seedlings, often killing them. Discussions with growers indicated that they would like to know when BSF are going to lay eggs in susceptible crops and to find methods of reducing colonisation by the pest. A key aim of the project is to better understand the life-cycle of the BSF, including the effects of temperature on development and on the overwintering stage (diapause). This information will be used to develop a forecasting system to estimate times of peak activity. A second aim is to examine different approaches to monitoring BSF activity using traps, to validate the forecasting system and work out how such information can be used by growers. A third aim will be to investigate cultural and biological methods of managing the pest. All of these approaches will contribute to an Integrated Pest Management (IPM) strategy that will help growers to manage BSF without relying so heavily on insecticides.

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Poster Abstracts

Online Posters

Jasvinder Kumar - Panjab University, Chandigarh, India

Microhabitat characteristics determine the succession of Histeridae on carcass

The succession of insects on the carcass assists in determining the post-mortem interval (PMI). Experts estimate PMI using blowfly maggots. In terrestrial ecosystems, decomposing cadavers act as ephemeral resources. However, numerous other insects are particular to carcass decomposition stages, such as Histeridae, Dermestidae, Cleridae, Scarabaeidae, Silphidae, and Staphylinidae. Throughout our study, we found that the coleopterans that accompany the blowflies are Histeridae beetles. They feed on dipteran eggs, maggots, and decaying or rotting carcasses. Their populations are entirely dependent on the stages of decomposition of carcasses and the populations of maggots in carcasses.

In the early phases of decomposition, a few countable Histeridae can be found on carcasses. However, after the bloated stage, their populations increased exponentially in the active decay stage but progressively declined. There were fewer Histeridae found on the remains; however, because maggots pupate in damp environments, certain Histeridae are also found under the soil to feed and reproduce.

Instead, the temperature of the corpse, the temperature beneath the carcass, and the ambient temperature all significantly change during the stages. In contrast to all of this, identifying forensically significant Histeridae beetles has a greater impact on the study and helps in comprehending the diversity of species and distribution. For this study, we collected around 5290 Histeridae beetles from the genera Saprinus, Hister, Pachylister, Atholus, Merohister, etc.

Keywords. Forensic entomology, Histeridae, Ecology, Succession, Post-mortem interval (PMI)

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Identification of predatory mosquitoes and associated vector mosquito larvae in Matra district, Sri Lanka

Mosquitoes are medically important insects, not just as nuisance biters but also as carriers of deadly diseases such as dengue, malaria, Japanese encephalitis etc., particularly in tropical countries. The larval and pupal stages of their life cycle are frequent in most tropical and temperate water bodies. Control strategies for pestiferous mosquitoes have been developed due to their very high medical importance. The main control measures utilized are source reduction (environmental alteration to minimize ideal habitats), larvicides, and adulticides. With growing concern about chemical control due to its adverse impacts on the environment and biodiversity, the search for better alternatives become a necessity. The use of insect predators in mosquito

control has been explored to a limited extent, especially the use of predatory mosquito species to control the population of other mosquitoes. Despite the fact that capability can be influenced by biological and physical conditions, they have the potential to play a significant role in vector mosquito control. To collect predatory mosquitoes, we selected 11 different sites in Matara district, Sri Lanka, and collected mosquito larvae in various water bodies and water collecting containers (coconut shells, refrigerators, plastic cups, etc.). In each site collected larvae were reared in separate containers (15 mL) to observe their feeding behaviour. For species identification (using a Sri Lankan mosquito identification key) 4th instar larvae were used. With the assistance of entomologists in the dengue control unit in Matara, Sri Lanka, the feeding behaviour of predatory mosquito larvae was confirmed. There were four different species identified and among them Toxorynchities sp., Lutzia. vorex and L. tigeripes were found in small water containers and shallow permanent rock pools, and L. fascanus was found in a drainage channel. Other mosquitoes live associated with Toxorynchities sp. were Aedes vitataes, Culex lophoseromia, and C. demissus. L. vorex and L. tigeripes have been identified in the same locality associated with Anophillus Karwari, A. japonicas, A. lindesayi japonicas, C. parioji, C. barraudu, C. infantilus, and C. edwardsi. Nevertheless, C. quinquefasciatus, the main vector of filariasis (filarial nematodes), was associated with L. fuscanus in the highly polluted larger water body in the Matara urban area. Temperature, pH, salinity, and nitrate concentration were all positively correlated with mosquito abundance in each water body. Even though predatory mosquito abundance is very low, their population could control certain vector mosquito species satisfactorily. The use of these mosquito predators in mosquito vector control programs needed further investigations, especially in their natural habitats.

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Identification of the taxonomic status of fruit flies (Diptera: Tephritidae) in Sri Lanka; An initiation to establish a tephritid barcoding library

Fruit flies (Diptera: Tephritidae) are important insect pests in the commercial fruit and vegetable industry worldwide. In the Sri Lankan scenario, the majority of tephritid taxonomic studies relied on morphological features and that modus faces some phenotypic confusions and limitations over the presence of closely related species having cryptic or hybrid speciation. As a long-felt need, the rapid and accurate species identification approaches such as DNA barcoding for fruit flies in Sri Lanka are vital for their population regulation, biodiversity management and quarantine. Due to the efficiency of mitochondrial cytochrome c oxidase I (COI) barcoding gene analysis, the barcoding library concept was introduced. This study aims to establish the first Sri Lankan barcode library of tephritid fruit flies as an informative platform to facilitate reference data acquisition, storage and analysis. As an initiation of the barcoding project, two phenotypically related Bactrocera species, B. dorsalis (oriental fruit fly) and B. kandiensis (endemic fruit fly) were considered. Male individuals were collected from geographically isolated sites using pheromone traps (methyl eugenol) (5 cm diameter, 10 cm height) from March to May 2022. Captured fruit

flies were first identified based on their morphological features using standard taxonomic keys. Randomly selected samples of each selected fruit fly species were amplified for the itochondrial DNA barcoding gene region (~710bp) using the metazoan universal primer pair HCO2198/LCO1490. The consensus sequences' maximum compatibility was compared with the previously published reference sequences under the blastn algorithm available in the National Center for Biotechnology Information (NCBI) (https://www.ncbi.nlm.nih.gov/). The utility of the COI barcoding in the species delimitation was assessed by the Pairwise P-distance method and simultaneous phylogenetic tree analysis. The corresponding consensus sequences and taxonomic data were then submitted to the Barcode of Life Database (BOLD) (https://www.boldsystems.org/) to establish the barcode library under the project, TEPSL: Taxonomic Identification of Fruit flies (Diptera: Tephritidae) in Sri Lanka. Blastn algorithm showed all the consensus sequences were compatible (more than 99 %) with the initial phenotypic identification of species. The pairwise genetic divergence within species (intraspecific) ranged from 0.00 % to 1.80 % and between species (interspecific) ranged from 6.10 % to 7.60 %. The average interspecific divergence is greater than the intraspecific divergence and follows the 2 % conceptual divergence of discriminating two individuals as two species. Further, the resulting divergence levels were consistent with the reported values for Bactrocera fruit fly species and revealed that the COI barcoding gene region was successful in discriminating the selected fruit fly species. BIN clustering led to the recognition of two distant BIN clusters: B. dorsalis (BOLD: AEV8480), B. kandiensis (BOLD: AAA2296) and those were taxonomically concordant with the other barcode data and maximum likelihood isolations. Study results provide an excellent initiative for the Tephritids barcoding library in Sri Lanka and further studies will be expanded to place the remaining fruit fly species in this library.

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Effect of species composition and stand age on spider (Araneae) and harvestmen (Opiliones) communities in Scottish managed plantations

Plantation systems for commercial timber production can provide refuge for native biodiversity in fragmented and urbanised landscapes. However, species composition and stand age can result in homogenous conditions reducing plant architecture in dense stands, particularly in mature Norway (Picea abies) and Sitka spruce (Picea sitchensis), thus reducing arthropod diversity. There is a lack of consensus in literature regarding spruce plantation effects on spiders (Araneae) and harvestmen (Opiliones) and determining which environmental variables drive variation in forestry systems. Ground and litter dwelling arachnids were sampled using pitfall traps and litter sieving over five weeks between May-July in Falkland Estate Scots pine (Pinus sylvestris) and spruce mixture plantations of different ages, accounting for environmental variables including canopy openness, litter depth, soil pH and Collembola abundance. Results revealed a significantly higher

spider richness and diversity in Scots pine and young spruce stands compared to mature spruce, possibly explained by higher vegetation structure and complexity positively impacting assemblages. Regarding harvestmen, although no differences in family-level richness were found between stands, the PCA revealed stronger association with high tree cover and low understory vegetation. Overall, 10 species of high conservation importance were collected, highlighting the need to maintain a habitat mosaic during all forest cycle stages, to ensure habitat specialist conditions are achieved. These findings directly contribute to practical management of spruce plantations to maximise habitat heterogeneity and enhance natural enemy diversity at a local scale, compatible with conservation goals.

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Lavandula angustifolia Mill. essential oil exhibits distinct insecticidal activities against pea leaf weevil adults on faba bean under laboratory and greenhouse conditions.

The pea leaf weevil, Sitona lineatus L., (Coleoptera: Curculionidae, PLW) is an oligophagous legume pest that causes huge losses in yield and quality of pea and faba bean crops worldwide (Vankosky et al., 2009). Chemical pesticides are the most used practices to control this pest; however, they are associated with several health disorders (Cárcamo et al., 2018). Botanical-based insecticides, among them essential oils, furnished promising protective effects and gained a considerable attention as an alternative solution to control insect pests (Shrestha et al., 2020). In this context, the present study aims to evaluate the insecticidal activities of seven essential oils (Lavandula angustifolia Mill., Artemisia herba alba Asso., Mentha arvensis L., Pelargonium graveolens L'Hér, Eugenia caryophyllata Thunberg, Eucalyptus globulus Labill, and Myrtus communis L., under laboratory and greenhouse conditions against S. lineatus adults.

Under laboratory conditions, the toxicity of seven EOs was performed by direct contact and ingestion application, using five concentrations (0.25, 0.5, 1, 1.5, 2% (v/v)) prepared by dispersing the concentrated EO in distilled water containing 0.1% Triton X-100. The mortality was recorded after 1, 2, 3, 24, 48, 72, and 96 h. The most active ones under laboratory conditions were tested at a concentration of 1.5% under growth chamber conditions. The volatile compounds profile of the most effective EO was carried out using gas chromatography coupled to mass spectrometry. The mortality rates of pea leaf weevil adults using contact toxicity after exposure to EOs reached 100% at different concentrations and exposure times. These include A. herba alba at 2%, L. angustifolia at 1.5 and 2% and M. arvensis EOs at 1.5% after 3h. The probit analysis indicated that M. arvensis was the most effective EO against the pea leaf weevil and its LC50 and LC90 values were 0.02% and 1.29% at 48h after application respectively, followed by L. angustifolia with LC50 and LC90 of 0.27% and 1.11% at 96 h after treatment.

L. angustifolia at 1.5 and 2% by ingestion furnished mortality rates of 40 and 50% after 24 h, respectively, and reached 70% mortality for both concentrations after 48h with LC50 and LC90 of 1.38% and 2.23% respectively. M. arvensis EO as well, at 2%, displayed a mortality rate of 30% at 48h with LC50 and LC90 of 3.29 and 5.94 %, at 96 h after treatment. However, the other tested EOs did

not show any ingestion activity at any tested concentration. L. angustifolia at a concentration of 1.5% displayed the highest activities among the tested EOs at all time points and reached a 70% mortality rate at 96h. Noteworthy, L. angustifolia exhibited better activities than the bioinsecticide, while lower activities than the chemical insecticide (Lambda-cyhalothrin). GC-MS analysis showed that linalool acetate (32.91%) and linalool (26.69%) were the major compounds of L. angustifolia.

L. angustifolia essential oil is a promising bioinsecticide; however, more research is needed to develop biopesticides using its major compounds for field use as a safe and sustainable alternative to chemical insecticides and studying its safety against non-target organisms.

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Nocturnal orientation of individually identified Apis dorsata foragers

Apis dorsata is unique among honey bees in that it evolved the capability to fly at low light intensity, which allows them to forage during moon-lit nights. However, it is still not known how they navigate and communicate the location of food sources when they can't use their sun-compass system. We studied changes in dance orientation of individually marked A. dorsata foragers visiting an artificial feeder during moon-lit nights. Most foragers showed a 180° shift of the dance orientation during the evening twilight and kept this orientation till morning. This finding indicates that the bees reset their compass system to the morning position of the sun during evening twilight. Some bees showed a bimodal distribution of dance orientations, with some waggle runs indicating the position of the sun at sunset and some indicating the 180° opposite direction. Other foragers even showed dance orientation in between. This variability in the behavior suggests an interaction between an innate mechanism to reset the orientation by 180° and the individual's experience of the sun's position at sunset.

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Discovering the undiscovered: the story of Sericini

Insects are the most diverse group of organisms consisting of 8 to 10 million species in the world which covers almost 80% of the world's species. But as per scientists only around 1 million species of insects, and new species are constantly being discovered, which leaves 60 -70 % of entomofauna undescribed. For the taxonomist and conservational scientist museum specimens play a pivotal role because of their importance in systematic and taxonomic research as well as for biodiversity and conservation initiatives. The major goals of the museum are collection, curation, identification and conservation. Still, interestingly they also play a huge role to unveil some taxas which were unexplored due to a lack of entomological experts.

Most of the time new taxas are emerging from those valuable museum specimens which were collected many years back and were kept in the insect cabinets of the museums like an unpolished and unrecognised diamonds. Here we are going to talk about such as case of Tribe Sericini (Coleopters: Scarabaeidae: Melolonthinae), which was in the National Zoological Collection of Zoological Survey of India, Kolkata. Sericini chafer beetles (Coleoptera: Scarabaeidae: Melolonthinae) are herbivores, with a worldwide distribution of nearly 4,600 described species globally but are poorly explored in taxonomy for many regions in the world. Approximately 682 species of Sericini are known from India, which accounts for 16 % of the global diversity of the tribe. The majority of the species are reported from the Himalayas and southern areas of the country, while many regions remained poorly sampled or represented only by old collection records which had too inaccurate data to be geo-localized. Despite their great diversity, almost nothing is known about the ecology of Sericini.

Our study aims to exemplify the importance of preserving and maintaining museum specimens as they provide baseline information for many unexplored taxa like Sericini, and we will also fill the spatial and temporal gap in the sampling effort of this tribe by proper identification and distributional mapping. During this Anthropocene a large fraction of insects are threatened, and there are many species that are well preserved in the museum that might actually be extinct in the wild. However, in the case of Sericini, the scenario is quite different, in the past few years we have described a total of 9 new species and redescribed one lectotype, all are from museum specimens.

Surprisingly most of them being nearly 100 years old and were intact with its all morphological characteristics. This means they somehow escaped from anthropogenic threats, in in-situ as well as ex-situ conditions. Every year the number of undescribed and unidentified species is increasing due to the recent shift of the modern systematics approach, which led the young science enthusiast to lean opposite the classical way of doing taxonomy, using taxonomic keys with morphological characters. And it is estimated that more new species are hidden in the museum, hence there is an urgent need to develop expertise to explore more diversity of the species that will help to get insights into the systematics and biodiversity of Indian Sercini.

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