



ENTO'21

23rd - 27th August 2021

PROGRAMME AND ABSTRACTS

All times are BST

L = live

R = recorded

Organisers

Dr Richard Harrington (Chair, Royal Entomological Society Meetings Committee, UK)

Prof. Stuart Reynolds (University of Bath, UK)

Francisca Sconce (Royal Entomological Society, UK)

Dr Luke Tilley (Royal Entomological Society, UK)

Monday 23rd August

Session 1

Chair

Introduction and posters

Dr Richard Harrington (Chair, Royal Entomological Society Meetings Committee, UK)

11.00 – 11.10

Introductory announcements and welcome from the President

11.10 – 12.20

Brief introductions to posters

12.20 – 12.30

Break

12.30 – 13.15 R

THE PRESIDENT'S INVITED KEYNOTE LECTURE:

Prof. Claire Kremen (University of British Columbia, Canada)

Mainstreaming insect conservation: are we nearly there yet???

This is a singular moment for insect conservation. While insect biodiversity faces tremendous threats at present, and increasing evidence accumulates of serious declines (1,2), a great opportunity exists to influence public opinion for insect conservation. Gone are the days when insect conservation had to be 'piggy-backed' onto conservation efforts of more charismatic species (3) – now suggestion of an "Insect Armageddon" garners international attention on the pages of the foremost newspapers. As cautious scientists, we rightly understand and must communicate the tremendous uncertainties involved in assessing both insect diversity around the globe and how it is changing over time (4). Yet, we can also seize this moment to capitalize on the glimmering of public understanding of the seriousness of decline of 'the little things that run the world' (5), as well as biodiversity loss more generally. My talk will focus on pollinators as a gateway to the minds and hearts of farmers, land managers and the general public, as we seek to manage large tracts of land (i.e., farmlands, which make up circa 40% of terrestrial Earth's surface) sustainably and compatibly with biodiversity conservation. *Pollinators – what's not to love?* Yes, some of them sting, but.... they are critical for the reproduction of ~88% of the world's flowering plants (6) and the enhanced production of 85% of crop species (7), including many crops that provide essential micronutrients (8), or that we particularly enjoy for their aromatics. Work from my lab and many colleagues around the world shows that native (unmanaged) pollinators are essential for promoting crop pollination, even when managed honey bees are abundant (9,10). But native pollinator populations tend to decline in abundance and diversity most severely in the most intensively farmed landscapes, where huge tracts of pollinator-dependent monocultures (like canola, sunflower and even soy) provide a far greater demand for pollination services than native populations can supply (11,12). Our work shows that re-diversifying these farm landscapes at three scales is essential for promoting pollinator abundance, diversity and functionality (i.e., pollination services) (13). Within fields, polycultures had greater abundance of both generalist and specialist wild bees than monoculture fields, although only a few studies yet examine how pollinator communities respond to in-field crop diversity (14). Around the perimeter of crop fields, non-crop plantings like hedgerows and floral strips promote diverse, abundant and persistent pollinator populations, increasing regional species richness and enhancing metapopulation persistence (15–17). In the surrounding landscape, patches of natural habitat are essential for supporting pollinator diversity, abundance and services (18–21). These techniques work together additively across scales (22) – that is, all are important. Critically, these techniques also promote other ecosystem services important to farmers, such as improved pest control and soil fertility (23), while reducing needs for synthetic inputs that are costly for farmers and the environment (24). Since the acreage of pollinator-dependent crops is not only vast, but also growing (12), re-diversifying landscapes to promote pollinators and reduce yield gaps (25) could

affect a huge land area (26). Thus, using pollinators as ‘ambassadors’ for the concept of diversified farming systems (*sensu* 27) both generalises to other ecosystem services and scales from farms to large regions of the globe.

Cited works

1. van Klink, R. *et al.* Meta-analysis reveals declines in terrestrial but increases in freshwater insect abundances. *Science*. **368**, 417–420 (2020).
2. Wagner, D. L. Insect Declines in the Anthropocene. *Annu. Rev. Entomol.* **65**, 1–24 (2020).
3. Kremen, C. Piggyback Conservation. *Wings, The Xerces Society for Invertebrate Conservation* 4–8 (2009).
4. Simmons, B. I. *et al.* Worldwide insect declines: An important message, but interpret with caution. *Ecol. Evol.* **9**, 3678–3680 (2019).
5. Wilson, E. O. The little things that run the world (the importance and conservation of invertebrates). *Conserv. Biol.* **1**, 344–346 (1987).
6. Ollerton, J., Winfree, R. & Tarrant, S. How many flowering plants are pollinated by animals? *Oikos* **120**, 321–326 (2011).
7. Klein, A. M. *et al.* Importance of pollinators in changing landscapes for world crops. *Proc. R. Soc. B* **274**, 303–313 (2007).
8. Eilers, E. J., Kremen, C., Greenleaf, S. S., Garber, A. K. & Klein, A. M. Contribution of pollinator-mediated crops to nutrients in the human food supply. *PLoS One* **6**, e21363 (2011).
9. Garibaldi, L. A. *et al.* Wild pollinators enhance fruit set of crops regardless of honey bee abundance. *Science*. **339**, 1608–11 (2013).
10. Rader, R. *et al.* Non-bee insects are important contributors to global crop pollination. *Proc. Natl. Acad. Sci.* **113**, 146–151 (2015).
11. Koh, I. *et al.* Modeling the status, trends, and impacts of wild bee abundance in the United States. *Proc. Natl. Acad. Sci.* **113**, 140–145 (2016).
12. Aizen, M. A. *et al.* Global agricultural productivity is threatened by increasing pollinator dependence without a parallel increase in crop diversification. *Glob. Chang. Biol.* **25**, 3516–3527 (2019).
13. Gemmill-Herren, B., Garibaldi, L. A., Kremen, C. & Ngo, H. T. Building effective policies to conserve pollinators: translating knowledge into policy. *Curr. Opin. Insect Sci.* **46**, 1–8 (2021).
14. Guzman, A., Chase, M. & Kremen, C. On-farm diversification in an agriculturally-dominated landscape positively influences specialist pollinators. *Front. Sustain. Food Syst.* **3**, 87 (2019).
15. Albrecht, M. *et al.* The effectiveness of flower strips and hedgerows on pest control, pollination services and crop yield: a quantitative synthesis. *Ecol. Lett.* **23**, 1488–1498 (2020).
16. Kremen, C., Albrecht, M. & Ponisio, L. Restoring pollinator communities and pollination services in hedgerows in intensively managed agricultural landscapes. in *The Ecology of Hedgerows and Field Margins* (ed. Dover, J. W.) 163–185 (Routledge, 2019).
17. Ponisio, L. C., de Valpine, P., M’Gonigle, L. K. & Kremen, C. Proximity of restored hedgerows interacts with local floral diversity and species’ traits to shape long-term pollinator metacommunity dynamics. *Ecol. Lett.* **22**, 1048–1060 (2019).
18. Kremen, C., Williams, N. M. & Thorp, R. W. Crop pollination from native bees at risk from agricultural intensification. *Proc. Natl. Acad. Sci.* **99**, 16812–16816 (2002).
19. Klein, A. M. *et al.* Wild pollination services to California almond rely on semi-natural habitat. *J. Appl. Ecol.* **49**, 723–732 (2012).
20. Garibaldi, L. A. *et al.* Stability of pollination services decreases with isolation from natural areas despite honey bee visits. *Ecol. Lett.* **14**, 1062–1072 (2011).
21. Dainese, M. *et al.* A global synthesis reveals biodiversity-mediated benefits for crop production. *Sci. Adv.* **5**, eaax0121 (2019).

22. Kennedy, C. M. *et al.* A global quantitative synthesis of local and landscape effects on wild bee pollinators in agroecosystems. *Ecol. Lett.* **16**, 584–599 (2013).
23. Tamburini, G. *et al.* Agricultural diversification promotes biodiversity and multiple ecosystem services without compromising yield. *Sci. Adv.* **6**, eaba1715 (2020).
24. Rosa-Schleich, J., Loos, J., Mußhoff, O. & Tschardtke, T. Ecological-economic trade-offs of diversified farming systems – A review. *Ecol. Econ.* **160**, 251–263 (2019).
25. Garibaldi, L. A. *et al.* Mutually beneficial pollinator diversity and crop yield outcomes in small and large farms. *Science* **351**, 388–391 (2016).
26. Garibaldi, L. A., Schulte, L. A., Nabaes Jordar, D. N., Gomez Carella, D. S. & Kremen, C. Time to integrate pollinator science into soybean production. *Trends Ecol. Evol.* **xx**, 1–3 (2021).
27. Kremen, C. & Miles, A. Ecosystem services in biologically diversified versus conventional farming systems: benefits, externalities, and trade-offs. *Ecol. Soc.* **17**, 40 (2012).

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13.15 – 13.50

Break

Session 2 **Grand challenges in entomology**
Convenor and Chair **Dr Luke Tilley (Royal Entomological Society, UK)**

13.50 – 14.35 L KEYNOTE: Dr Sarah Luke (University of Cambridge, UK)
Grand challenges in entomology

Insects are highly biodiverse and play key roles in many ecosystems. For humans, they provide crucial ecosystem services, but also pose serious dangers through disease and as pests. Given their importance, it is critical that we develop a good understanding of insect diversity, physiology and ecology, and learn how best to harness the benefits and mitigate the negative impacts that insects can have. The 'Grand Challenges in Entomology' initiative is a collaborative effort by entomological societies from around the world to develop a series of priority topics and questions on which we should focus our research efforts and activities. As part of the global initiative, the Royal Entomological Society (RES) has conducted a multi-stage prioritisation exercise to gather together topic suggestions from all of its members and associates, and to distil them into a shortlisted set of priorities. This has been done through a multi-stage process comprising the following main steps: (1) an initial online survey of all members to gather topic suggestions; (2) processing of suggestions into themes with cross-checking of decisions across multiple scorers; (3) a second online survey of members to start prioritising suggestions; and (4) a two-day-long online workshop to discuss longlisted suggestions and produce a shortlist. Over 700 suggestions were submitted by 189 RES members and associates. 118 members and associates contributed at the online prioritisation stage, whilst 54 people were involved in workshop discussions. The final list of 'Grand Challenge' priorities comprises 61 suggestions, within 11 diverse themes, across which there is a range of cross-linking ideas. The prioritisation process has provided an opportunity for wide-ranging engagement and discussion across the society, and a novel approach for gathering opinions from the society's members and associates. We hope that the final list of priority topics will provide a valuable resource to guide the agenda and activities of the RES over the coming years and decades.

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14.35 – 14.50 L Dr Luke Tilley (Royal Entomological Society, UK)
Next steps: how does the RES address grand challenges?

The Royal Entomological Society (RES) is at an exciting time in its 188-year history. The Grand Challenges in Entomology project sits within a wider framework of ongoing reviews, consultations, and improvements at the RES. There has also been an external governance review and intensive membership consultation, which together with Grand Challenges in Entomology, means that the RES is well-equipped to help improve entomology in the UK and beyond. We will outline some of the proposed next steps which will lead into a panel discussion after the break about "The Future of Entomology", in particular the role entomological societies can play in securing the next generation and helping to improve the sector worldwide.

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14.50 – 15.00 Break

15.00 – 16.00

Panel discussion

The future of entomology

Panellists:

Dr Erin Cadwalader (Director of Strategic Initiatives,
Entomological Society of America)

Dr Lynn Dicks (University of Cambridge, UK)

Dr Sarah Luke (University of Cambridge, UK)

Prof. Helen Roy (UK Centre for Ecology & Hydrology;
President, Royal Entomological Society, UK)

Chris Stelzig (Executive Director, Entomological Society of America)

Prof. Chris Thomas (University of York, UK;
Previous President, Royal Entomological Society, UK)

Tuesday 24th August

Session 3 **Insect declines – the evidence and causes** Convenor and Chair **Prof. William Kunin, University of Leeds**

11.00 – 11.40 L KEYNOTE: Prof. Michael Samways (Stellenbosch University, South Africa)
Solutions for saving South African insects

South Africa has scrubland, savanna, desert, temperate rainforest and swamp forest, a biome variety driven by two major oceanic currents. One is warm, running south down the east coast, and the other cold, running up the west coast. The moisture-laden air currents interact with mountains to create high ecosystem variety, against a background of no glaciations for > 200 my and ongoing El Niño Southern Oscillation events. This geography has led to much insect local adaptation and speciation, and many specialised endemics. Insects move or hide in response to natural recurrent fires, droughts and floods, demonstrating remarkable population resilience to these harsh natural events. However, they are ill-equipped to deal with novel anthropogenic impacts, especially invasive alien plants. In response, conservation measures have involved a massive national programme to remove alien plants, implementation of huge networks of conservation corridors, and widespread adoption of agro-ecological approaches, additive to protected areas and biosphere reserves. These strong and expansive actions have been highly effective in saving insects.

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11.40 – 12.00 L Prof. Chris Thomas (University of York, UK)
Moth biomass has fluctuated over 50 years in Britain but lacks a clear trend

Despite widespread declines of many individual insect species, including Lepidoptera, there have also been some increases. Furthermore, some reports of insect decline have extrapolated beyond the scales and regions for which data have been available. Steep insect biomass declines ('insectageddon') have been widely reported, despite a lack of continuously collected biomass data from replicated long-term monitoring sites. Such severe declines are not supported by the world's longest running insect population database: annual moth biomass estimates from British fixed monitoring sites revealed substantial between-year biomass change but no difference in mean biomass between the first (1967–1976) and last decades (2008–2017) of monitoring. High between-year variability and multi-year periodicity in biomass emphasise the need for long-term data to detect trends and identify their causes robustly.

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12.00 – 12.10 Break

12.10 – 12.30 L Dr Diana Bowler (iDiv, Germany)
Contrasting trends of terrestrial and freshwater insects

While there is clear evidence of declines for some insect taxa, the available data also point to a diversity of insect trends over the last decades. I will especially focus on the contrasting trends of freshwater and terrestrial insects, using results from a large-scale meta-analysis, as well as results from different projects at European and German-scales. Overall, these projects suggest greater declines in terrestrial compared with freshwater insects. The lack of large-scale data on likely threats to insects, such as pesticide use and habitat degradation, reduce the opportunities for direct analysis of the role of different drivers. Instead, analysis of variation in trends among taxon groups and species, which vary in exposure and sensitivity to specific threats, could help indicate the dominant pressures.

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12.30 – 12.50 L

Dr Anuj Jain (Nature Society, Singapore)

Almost half of Singapore's butterfly species extirpated in 160 years, nearly a third discovered in recent decades

Habitat loss and urbanisation in the tropics have been recognised as major drivers of species extinctions. However, few studies have assessed long-term patterns of insect extinctions and discoveries in response to these drivers in the tropics. We studied detected and undetected extirpations among butterflies, in the highly developed and biologically well-surveyed island city-state of Singapore and how these relate to land use change over 160 years in Singapore. Building on existing butterfly species lists, we collated museum and naturalist records over the last two centuries and used statistical models to estimate the total extirpation rate since the first major collections in 1854. In addition, we compiled a set of traits for each butterfly species and explored how they relate to species discovery and extirpation. We found that nearly a third of Singapore's butterfly species have been identified to be extirpated to date. In addition, 104 unknown species were likely extirpated before they were ever discovered, suggesting a total extirpation rate of 46% (41–51%). In the trait analyses, we found that butterfly species that were discovered later were weakly associated with rarer larval host plants and smaller wingspans, while species that persisted for longer were weakly associated with higher larval host plant abundance and lower forest dependence. We also found that over the past 3 decades, over 50 new species were discovered (new country records), while 65 species were rediscovered, suggesting the dynamic nature of Singapore's diverse butterfly fauna. This exercise is one of the first to offer a holistic estimate of extirpations for a group of insects by accounting for undetected extirpations. It suggests that extirpations among insects, specifically in the tropics, maybe higher than naïve estimates based only on known records.

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12.50 – 13.10 L

Dr Charlie Outhwaite (UCL, UK)

Agriculture and climate change interact to drive insect biodiversity declines worldwide

Recent studies suggest that insects have experienced large-scale declines. In general, considerable progress has been made in understanding the global responses of biodiversity to major drivers of change. However, few studies consider the potential synergistic interactions between drivers, and those studies that do tend to focus on vertebrate responses. Here, we show that climate change and land use interact leading to greater insect declines in agricultural land uses compared to

areas of primary vegetation that have also experienced climate warming. The greatest declines in insect abundance were seen in intensive agriculture in areas that experienced the high climate warming. Importantly, the availability of nearby natural habitat buffered against the negative impact of climate warming, but only in areas of low use-intensity. This ability of nearby natural habitat to buffer negative climate responses in agricultural systems suggests a way to conserve biodiversity in human-dominated landscapes.

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13.10 – 13.50

Break

Session 4 **Insect declines – impacts and responses**
Convenor and Chair **Prof. Nick Isaac, UK Centre for Ecology & Hydrology**

13.50 – 14.30 L KEYNOTE: Dr Lynn Dicks (Cambridge University, UK)
Why should we care about insect decline?

Analysis of national and international datasets has shown that arthropods, or at least some species of arthropod, are declining in diversity or overall abundance. Whilst there is still huge uncertainty about how rapid or widespread this phenomenon is, the precautionary principle states that if there is a threat of serious or irreversible damage, scientific certainty isn't needed for action. Scientific evaluation of the potential threats caused by insect decline is urgently required. Using a conceptual framework drawn up by the Intergovernmental Science Policy Platform on Biodiversity and Ecosystem Services (IPBES), I will provide an overview of what is known about how insect decline might affect nature, nature's benefits to people and ultimately human well-being. I will focus on pollinators, including a recently published assessment of the risks to human well-being associated with pollinator decline. The framework can and should be applied to all arthropods, their ecological functions and what we stand to lose if they decline irreversibly.

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14.30 – 14.50 L Prof. Richard Pywell (UK Centre for Ecology & Hydrology)
E-Planner: a web-based decision support tool for planning
environmental enhancement

E-Planner (<https://assist.ceh.ac.uk/e-planner>) is a web-based decision support tool which provides land managers with fine-scale data on the suitability of land for habitat restoration for the whole of Great Britain. Suitability scores are calculated by integrating a range of biophysical data sets and presented as easy-to-interpret maps, at fine-scale (5m) resolutions. E-Planner is designed to streamline decision-making around the type and location of management interventions to provide: a) biodiversity habitats, including flower-rich habitat for insects, and b) environmental protection, such as buffer strips to protect water resources from pollution. The information provided by E-Planner is important for planning both landscape-scale collective actions by practitioners and field-scale spatial targeting of management to maximise the environmental benefits of habitat restoration.

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14.50 – 15.00 Break

15.00 – 15.20 L Dr Martin Dallimer (University of Leeds, UK)
Public perceptions of insects: what people really think

Researchers, practitioners and policymakers have widely documented the multifarious ways that biodiversity, including insects, influences human well-being. However, we still have only a limited understanding of how the public interact with, respond to and talk about attributes of biodiversity. We used image-based Q methodology to explore the shared and contrasting perspectives people hold for insects and other invertebrates. This approach is a powerful way of allowing people to articulate what is, or is not, important to them, free from constraints associated

with statement-based stimuli. Public perspectives varied, and the reasons underpinning those perspectives were rich and diverse. People articulated reasons related to an array of biodiversity attributes (e.g., functions, behaviours, colours, smells, shapes). Many of the perspectives transcended specific species or taxonomic groups. People frequently referenced perceptions and experiences from their everyday lives. Cultural influences and memories linked to particular people and places were also prominent. However, few of the shared perspectives map onto the objective measures and dimensions that researchers use to describe and categorise biodiversity (e.g., rarity, ecosystem service provision). As we consider how best to reverse insect declines, a more complete appreciation of what people really think of the insects around them provides valuable insights to inform conservation efforts.

Other authors: Davies, Z.G., Austen, G.E., Fish, R.D. (all University of Kent), Irvine, K.N. (James Hutton Institute)

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15.20 – 15.40 L

Dr Blaise Martay (British Trust for Ornithology, UK)

How do insect declines affect birds? BTO research

Over 50% of UK birds eat insects or other invertebrates at some point throughout their lifecycle. For many birds, insects are the main food source for chicks while others are invertivores throughout the year. There is currently very little research into how invertebrate population trends and bird population trends are linked. One dietary group with fairly consistent declines was aerial-feeding migrant birds, including swallows, swifts and flycatchers. However, the trends of flying insects in the UK are spatially variable and although swallow chick survival correlates with aerial insect abundance, this has little impact on swallow populations. There are also declines in many soil-invertebrate-feeding birds such as waders and thrushes. Trends in soil invertebrates are largely unknown but increasingly frequent droughts may have caused declines. Earthworm-eating birds were more abundant where earthworm abundances were high, and golden plover productivity correlated with Tipulidae larvae abundance. However, the impact of invertebrate abundance on population trends relative to other drivers such as predation and agricultural practices are unknown. It has also been hypothesised that insectivorous birds may experience combined pressures from insect declines and phenological asynchrony between birds and insects, driven by climate change. Recent BTO research has found that bird declines were greatest among species sensitive to asynchrony but did not support the hypothesis that declines were caused by productivity declines. There is a need for more research into bird diets throughout the year, and monitoring of invertebrates at a scale and resolution that can be linked to outcomes for birds. It is likely that some bird declines are due to invertebrate declines but the evidence is sparse and we hope to continue research into this topic.

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15.40 – 16.00 L

Prof. David Roy (UK Centre for Ecology & Hydrology)

Developments in monitoring butterflies in Europe

Butterfly monitoring enjoys a growing popularity in Europe, encouraged in particular by Butterfly Conservation Europe and its partners. I review the current status of monitoring of butterflies across Europe, including results from the Assessing Butterflies in Europe (ABLE <https://butterfly-monitoring.net/able>)

project, funded by the EU for two years (2019-2020), and wider initiatives to develop a European Pollinator Monitoring Scheme. I will review the main achievements of butterfly monitoring across Europe to date, as an exemplar of a citizen science approach, including development of biodiversity indicators and tools to support monitoring. I will give some perspectives on the future direction of butterfly monitoring and how it can contribute to the urgent need for evidence of the status and trends of insects.

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1630

LGBTQ+ & allies mixer

Wednesday 25th August

Session 5
Convenors
Chair

Genomics in taxonomy and biodiversity
Amy Withers and Dr Philip Donkersley (Lancaster University, UK)
Dr Philip Donkersley

11.10 – 11.40 R

KEYNOTE: Prof. Christine Weirauch (University of California Riverside, USA)
From species discovery to the true bug tree of life: advances in heteropteran systematics (Hemiptera: Heteroptera)

Heteroptera, the true bugs, include >45,000 described species and are part of the largest order of non-holometabolous insects, the Hemiptera. True bugs inhabit a wide range of terrestrial, aquatic and even certain marine habitats, and engage in feeding strategies that include phytophagy, mycetophagy, predation on other arthropods, and hematophagy on vertebrates. This makes Heteroptera one of the ecologically most diverse insect lineages. In addition, true bugs contain medically important disease vectors, nuisance pests and species that impact agriculture as either plant pests or beneficial biological control agents. Despite this undeniable ecological and economic importance, there are large gaps in our understanding of the biodiversity and evolution of Heteroptera. Discovering and documenting species, investigating phylogenetic relationships, and tracing the evolutionary history of Heteroptera are therefore worthwhile research areas. This lecture is composed of two parts. The first part consists of an overview of advances in heteropteran systematics and evolutionary biology of true bugs. The emphasis is on summarising major developments during the 25 years between the first and second editions of "True Bugs of the World (Hemiptera: Heteroptera), a comprehensive review of heteropteran biology, morphology, and classification". The second part highlights some of the original research conducted in my laboratory, focusing on the assassin bugs (Reduviidae) and minute litter bugs (Dipsocoromorpha).

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11.40 – 12.00 L

Dr Gabriela P. Camacho (Museum für Naturkunde, Berlin, Germany)
Diversity and endemism of Malagasy ants: a phylogenomic approach

Two key elements of measuring biodiversity across space and time are species diversity and endemism. In the past, most survey efforts have been focused on using taxonomic species as the units of diversity and endemism, but over the last decade it has become more common practice to assess phylogenetic diversity alongside taxonomic species richness. Measuring arthropod diversity based on either of these units is challenging, given that surveys are often too limited in geographic scope to capture the magnitude of arthropod species distributions and diversity. Arthropods are thus often excluded from conservation planning decisions. Here we outline the goals of our project MAMI (Malagasy ant microendemism), which aims at a synthesis of survey efforts for ants in Madagascar spanning two decades. We use a phylogenomic approach to investigate regional patterns of phylogenetic diversity, endemism, and community structure across ants in Madagascar based on ~2,200 loci of ultraconserved elements. We present first results from our project using a data set of 32 species of Malagasy acrobat ants (genus *Crematogaster*), for which we compiled distribution data from approximately 2,400 collection records across 168 well-sampled communities.

We analysed phylogenetic patterns of community structure, diversity and endemism of these ants in Madagascar across eleven different habitat types and along climatic and primary productivity gradients. Our island-wide community analyses will uncover general patterns of species richness, lineage diversity and endemism across ant communities in Madagascar, allowing us to draw broad, widely applicable conclusions about the importance of these patterns for conservation planning.

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12.00 – 12.10

Break

12.10 – 12.30 L

Prof. Alfried Vogler (Imperial College London and Natural History Museum, UK)

Biodiversity genomics and the phylogeny of Coleoptera

The proverbial species richness of beetles has hampered the synthesis of global diversity patterns, but this is changing with the advent of genomic sequencing techniques. This study combines genome sequencing, metagenomics and DNA barcoding to generate a phylogenetic tree of Coleoptera of high resolution (eventually comprehensive at the species level). Unlike conventional lineage-based approaches to phylogenetics, we are using 'site-based' sampling and metagenomic sequencing and metabarcoding of bulk specimens to generate phylogenetic information from places around the world that are integrated in a combined tree. With each site added the tree becomes ever more complete, while at the same time the explicit collecting information is used to study the biogeographic history of numerous lineages in a single analysis. Applying genomic techniques in the study of biodiversity can now be used to infer the evolutionary history at species-level even in the most species-rich lineages of insects.

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12.30 – 12.50 L

Dr Jennifer Rowntree (Manchester Metropolitan University, UK)

Of microbes and insects: tales of symbiosis in bees and aphids

Symbioses involving microorganisms are ubiquitous and symbionts perform important functions for their hosts including insects. We used a variety of molecular methods to elucidate the bacterial communities present in the guts of the honey bee (*Apis mellifera*) and the banana aphid (*Pentalonia* sp.) and explored some of the many factors influencing diversity and structure of the microbiota. Using data collected from honey bee hives across North West England, we found a strong influence of hive on bee gut bacterial community, but no influence of hive location and only weak relationships with the surrounding landscape composition. While more genetically similar colonies did not have more similar bacterial communities, in colonies where the individual bees shared a higher proportion of alleles determined by microsatellites, we found a lower bacterial diversity in the bee guts, suggesting that more genetically diverse colonies support a greater diversity of gut bacteria. In the Philippines, examining banana aphids collected from the fibre crop *Abaca*, we found four facultative bacterial symbionts alongside the obligate *Buchnera*. These symbionts were present across two species of banana aphid. Multiple infections were common, but single infections and aphids without any detectable facultative endosymbionts were also detected. Collection location strongly influenced aphid symbiont community composition and the presence of *Wolbachia* was linked to increased detection of the highly destructive bunchy top

virus in one location. These two studies suggest that local context has a significant influence of the pattern and dynamics of insect symbioses.

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12.50 – 13.10 L

Dr Philip Donkersley (Lancaster University, UK)
Insect biodiversity monitoring: landscape scale pollinator ecology through metabarcoding

We stand at the precipice of a global crisis for insect biodiversity: anthropogenic pressures are growing and space for insects is shrinking. Insects are vital for ecosystem sustainability; pollinators in particular are key to global food security, with 35% of global crop production dependent on insect pollinators. The proportion of insect species in decline in Europe (41%) is twice as high as vertebrates; specifically, the UK has largest documented declines across taxa (60% of species). The primary factors causing declines in insect diversity and abundance are: climate change, pollution, invasive species and, most importantly, habitat destruction. Methods to mitigate the impact of habitat loss have not been rigorously addressed; the focus has been on eliminating pesticide use. Monitoring schemes are ongoing, using classic microscope-based identification that is time consuming and resource intensive. The affordability of metabarcoding approaches has substantially improved over the past decade, as has the robustness of reference databases and data-processing pipelines. Consequently, we are at a fortunate paradigm shift in insect monitoring towards meta-barcoding approaches. This talk presents:

- the insect biodiversity and conservation crisis;
- the questions meta-barcoding data can be used to answer;
- fundamental axioms of meta-barcoding and how to address these when designing monitoring studies;
- the "pipeline" of samples to data;
- available barcode sequences;
- complementarity between taxonomic identification and meta-barcoding.

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13.10 – 13.50

Break

Session 6
Convenor
Chair

“Blue skies” entomology
Prof. Stuart Reynolds (University of Bath, UK)
Dr Richard Harrington (Chair, Royal Entomological Society Meetings Committee)

13.50 – 14.10 L

Prof. Nina Wedell (University of Exeter, UK)
Do endosymbionts affect sexual ornament expression in butterflies?

Endosymbionts are prevalent in insects and almost exclusively transmitted in the cytoplasm of eggs from mother to offspring. To increase their transmission, maternal endosymbionts frequently enhance female fitness as they cannot be transmitted through males. Some endosymbionts bias the sex-ratio by male-killing or feminising genetic males to increase their transmission success. The possibility that endosymbionts with sex-specific effects can impact on sexual selection has recently been considered. However, the potential that sex-ratio biasing endosymbionts can affect the expression of sexually selected male traits is largely overlooked. Here we explore whether the presence of a naturally occurring maternally inherited bacterium that causes a female-biased sex ratio, is associated with reduced trait value of a sexually selected signal. Males of the pierid butterfly *Eurema hecabe* express a visual sexually dimorphic signal – a bright, exaggerated ultraviolet (UV) iridescence across most of their dorsal wing surface. This signal is sexually selected, with females preferring males with bright UV reflectance in the lab and in the field. We quantified whether a naturally occurring sex-ratio distorter contributes to generating variation in UV trait expression. Long-term field data of naturally occurring variation in trait expression were combined with experimental manipulations through exposing male genotypes to both short-term and long-term feminising selection and the resulting changes in UV reflectance quantified. Our findings indicate that endosymbionts can cause substantial erosion of the UV trait value, and therefore may potentially contribute towards the maintenance of variation in this sexually selected trait.

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14.10 – 14.30 L

Prof. Judith Korb (University of Freiburg, Germany)
Evolution of ageing in social insects

Social insects such as termites, ants or honey bees are nascent models for studying ageing. They promise new insights into proximate ageing mechanisms because within colonies individuals occur that share the same genetic background but have vastly different lifespans. Queens can live for decades, while nestmate workers often only have a lifespan of a few months. This offers opportunities to unravel mechanisms underlying longevity. Additionally, variations in longevity across species exist that differ in social complexity, with more social species generally having longer lived queens. This allows us to gain insights into ultimate causes selecting for increased longevity. I will present recent results from termites, providing answers to the question why queens can live so long, addressing both proximate and ultimate causes. I will discuss the importance of transposable elements and potential re-wiring of ageing pathways to explain differences in caste-specific ageing. Furthermore, experimental manipulations suggest that queens can live so long, at least partly because workers take over the burden of reproduction and other costs, supporting the superorganism concept. Accordingly, queens can be regarded as the germline of a colony and workers as disposable soma. The degree to which this germline/soma separation applies within a colony depends on the degree of

sociality of a species. Finally, I will briefly compare our results for termites with those obtained for some ants and bees.

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14.30 – 14.50 L

Prof. James Mallet (Harvard University, USA)
The evolution of mimicry in butterflies

The understanding of natural selection for butterfly mimicry goes back to the beginnings of Darwinian evolutionary theory. Studies of the genetics of mimicry began early in the 20th Century, soon after the rediscovery of Mendel, and became one of the sources of disagreement between the mutationists Punnett and Bateson and gradualists led by R.A. Fisher. It is now clear from field and laboratory studies with predators that mimicry is under very strong natural selection. It does seem somewhat surprising that alleles that switch among mimicry colour patterns often have such major effects. We still don't know why mimicry is often not polygenic, with each gene having a very small overall effect on pattern, as is common in other sorts of adaptation. The latest genomics work on these mimicry genes is uncovering some of the reasons, but there are still more things to be explained.

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14.50 – 15.00

Break

15.00 – 15.20 L

Prof. H. Frederik Nijhout (Duke University, USA)
The regulation of body size in insects

Size and shape are the most characteristic attributes by which we recognise species. Yet, the developmental mechanisms that regulate the final sizes and shapes of a body and its parts are largely unknown. A mechanism that determines body size must somehow receive feedback from the body, so that growth is caused to stop when the “correct” size is reached. In insects there are two size checkpoints in development. These are the Critical Weight, which determines the size within each instar at which a moult will occur, and the Threshold Size, which determines which instar will be the last one. In the tobacco hornworm, *Manduca sexta*, we now know the physiological mechanisms that sense size for both these checkpoints. I will outline both these size-sensing mechanisms and suggest they are probably general mechanisms that determine adult body size in insects.

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15.20 – 16.00 L

KEYNOTE: Prof. James W. Truman and Lynn M. Riddiford (University of Washington, USA)
Insights into the molecular trinity underlying the evolution and control of insect metamorphosis

The fundamental change essential for the evolution of complete metamorphosis occurred during embryogenesis. In the ancestral condition, embryogenesis produced a miniature version of the adult body plan, but in the Holometabola this ancestral program has been redirected to making a novel, larval body plan. The larva bears no resemblance to the adult and is able to acquire specialisations for feeding and growth without compromising the eventual adult form. The end of

larval growth is then punctuated by the formation of the adult via a pupal intermediate. Molecular genetic approaches have shown that the two metamorphic stages, the pupa and the adult, are specified by two master control genes, the transcription factors *broad* and *E93*, respectively. The genetic control over the larval form has been much more enigmatic, though. *Krüppel-homolog1 (Kr-h1)* has been a major candidate but its role in specifying the larval form is complicated because it mediates the *status quo* function of juvenile hormone and appears in whichever stage JH is acting. Our work on *Drosophila* metamorphosis has focused on the gene *chinmo* (chronologically inappropriate morphogenesis), which was first identified by its action in controlling temporal identity in the neuroblasts (Zhu *et al.*, *Cell*, 2006). Our interest in *chinmo* was sparked by Syed *et al.* (*eLife*, 2017) who showed that the temporal expression of *chinmo*, then *broad*, then *E93* established early, intermediate, and late neuronal phenotypes in fly neuroblasts. We find that *chinmo* has a broader role, though, and serves as the third member of the transcription factor trinity, *chinmo*, *broad*, and *E93*, that specifies the larval, pupal and adult stages, respectively. *Chinmo* expression begins in late embryogenesis in anticipation of larval differentiation and is maintained through the first two larval instars, but then decreases in the last instar as it prepares for metamorphosis. Removal of *chinmo* function either through mutation or RNA interference results in the precocious expression of the metamorphic members of the trinity in the first instar, with *broad* appearing in the imaginal discs and *E93* in the larval cells. These larvae are incapable of moulting and die at the end of the first larval stage. The loss of *chinmo* function in the embryo is an embryonic lethal, with embryonic development being affected at a time when larval specialisations normally appear and the embryos retaining some features characteristic of their hemimetabolous ancestors. Insights into the ancestral role of *chinmo* have come from examination of its expression in the ametabolous *Thermobia domestica*. It appears very early in embryogenesis during the phase of intense proliferation and cellular determination that establishes the extended germ band. It then begins to decline as differentiation begins and embryonic expression of *broad* becomes prominent. This relationship of *chinmo* and *broad* to proliferation versus differentiation is the same as seen in *Drosophila* imaginal discs (Narbonne-Reveau & Maurange, *PLoS Biol.*, 2019). It suggests that modification in the expression and function of *chinmo* may have been the key molecular event that supported the evolution of the larval stage and complete metamorphosis.

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17.00

Royal Entomological Society Annual General Meeting

Members and fellows can register for this event:

<https://us02web.zoom.us/meeting/register/tZUdOCvpzkvGNAnveqbEsfBIBCFjPJICemW>

Thursday 26th August

Session 7 **Vectors of human and animal pathogens**
Convenor and Chair **Dr Marion England (The Pirbright Institute, UK)**

11.00 – 11.20 L Priscilla Ankamaa Opare (University of Cape Coast, Ghana)
Incriminating *Culicoides* as vectors of *Leishmania* in Ghana and validation of standard light-traps against explicit human biting rates

Human cutaneous leishmaniasis (CL) has been endemic in communities in south-eastern Ghana since 1999 and is caused by a newly identified species of *Leishmania* ("*Leishmania* GH"), belonging to the *Leishmania* (*Mundinia*) subgenus. The vector(s) responsible for transmitting this *Leishmania* species in Ghana remain unknown as very few sandflies have been collected in endemic regions. Previous laboratory studies have shown that *Leishmania* GH colonises and replicates successfully within the gut of *Culicoides sonorensis*. In this study, CO₂-baited CDC light-traps were validated against human landing catches (HLC) for *Culicoides* caught in the *Leishmania*-endemic Ho district, Ghana.

The *Culicoides* fauna was characterised to incriminate species of *Culicoides* as vector candidates responsible for CL. Collections took place from May to August 2020 using CO₂-baited CDC light-traps and filtered mechanical aspirators for HLCs. Light-traps and human volunteers were rotated around four collection locations using a Latin square design. A morphological key was developed for the identification of *Culicoides* collected and collection data were analysed in R. Significantly more *Culicoides* were collected by HLCs than by the CO₂-baited light-traps ($p < 0.001$). This indicates that CO₂-baited CDC traps do not accurately reflect the biting rates of *Culicoides* on humans. *Culicoides grahami* was the predominant species identified from both CDC traps and HLCs (98.5%). Other species identified in small numbers (1.5%) included *C. imicola*, *C. inornatipennis* and *C. leucostictus*. Therefore, *C. grahami* is proposed as the putative vector of *Leishmania* GH in the Ho District of Ghana.

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11.20 – 11.40 L Dr Eva Veronesi (University of Zürich, Switzerland)
Insights on the mechanical transmission of lumpy skin disease virus (LSDV) by the stable fly *Stomoxys calcitrans*

Introduction Lumpy skin disease (LSD) is a viral disorder of cattle caused by the lumpy skin disease virus (LSDV), which can induce severe infections leading to high economic losses. Being of African origin, the first LSD outbreaks in Europe occurred in Greece and later in the Balkan region. Little is known about the mode of transmission, especially concerning the potential role of arthropod vectors. The purpose of our study was to investigate the role of *Stomoxys calcitrans* in the transmission of LSDV and their presence at different farms in Switzerland.

Methods Laboratory-reared flies were exposed to LSDV-spiked blood and incubated under a realistic fluctuating temperature regime. Body parts, regurgitated blood, and faecal samples were analysed by qPCR for the presence of viral DNA and infectious virus at different time points post-feeding (p.f.).

Results LSDV DNA was detected in heads, bodies, and regurgitated blood up to three days p.f. and up to two days p.f. in the faeces. Infectious virus was

isolated from bodies and faeces up to two days and in the regurgitated blood up to 12 h p.f. There was no increase in viral load, consolidating the role of *S. calcitrans* as mechanical vectors for LSDV. *Stomoxys* flies were present at all eight farms investigated, including a farm located at 2128 m asl.

Conclusions The persistence of LSDV in *S. calcitrans* in combination with the long flight ranges of this abundant and widespread fly might have implications on LSD epidemiology and on implementing control measures during disease outbreaks.

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11.40 – 12.00 L

Dr Simon Carpenter (The Pirbright Institute, UK)

Epidemic within a pandemic: combating African horse sickness virus in Thailand from a distance

African horse sickness virus (AHSV) is one of the most lethal known viruses of equids and is transmitted primarily by biting midges of the genus *Culicoides* (Diptera: Ceratopogonidae). In this talk, I will give an account of the emergence of AHSV in Thailand during March 2020 from an entomological perspective. This AHSV outbreak was notable both for being the first occurrence of the virus in this region in recorded history and for arising during a time when global lockdown of travel was already being implemented due to the emergence of SARS-CoV-2. Firstly, I will outline The Pirbright Institute's role as an OIE Reference Laboratory for AHSV and discuss the suite of frontline assays we use in diagnostic procedures. I will then examine the difficulties that we experienced in continuing to function as a frontline diagnostic service during the SARS-CoV-2 pandemic including management of a high containment site. Then, I will place the AHSV outbreak in context with what is known about *Culicoides* populations in the affected region and how an international group of entomologists assisted in the response to the incursion. Lastly, I will discuss the advantages and disadvantages of remote working within this subject area and what lessons might be learned for the future.

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12.00 – 12.10

Break

12.10 – 12.30 L

Dr Stefanie Schäfer (UK Centre for Ecology & Hydrology)

MonkeyFeverRisk – a OneHealth collaboration to identify drivers of a tick-transmitted viral zoonosis in Southern India

Kyasanur Forest Disease (KFD) or Monkey Fever, is a tick-transmitted haemorrhagic viral infection that can be fatal to humans. Endemic to the Western Ghat mountain region in southern India, the disease has undergone considerable range expansion since 2012. Like many other neglected zoonoses, KFD disproportionately affects resource-poor communities that rely on the increasingly degraded local forest ecosystems for their livelihoods. Kyasanur Forest Disease is currently managed through vaccination campaigns but a lack of awareness about exposure risk and

poor vaccine uptake can exacerbate epidemics. An average of over 500 cases are reported each year, with mortality ranging between 3 and 10%. The KFD disease system is highly complex, with numerous tick, small mammal, avian and primate species suspected of playing a role in the virus transmission cycle. How these contribute to zoonotic disease risk is, as yet, poorly understood. We will present how our Indo-UK collaboration took an interdisciplinary One Health approach to identify critical knowledge gaps and needs of local communities and disease managers. Our team, with expertise in public and animal health, forest and wildlife ecology, Earth observation and social science, gathered empirical data both on the habitat associations and seasonal abundance of potential vectors and hosts, and how and when these habitats are frequented and used by the local communities. Disentangling the socio-ecological mechanisms driving disease exposure was vital to co-produce guidance and decision support tools with stakeholders from the public health, animal health and forestry sectors, enabling them to design improved disease intervention strategies and help communities avoid exposure to the KFD virus.

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12.30 – 13.10 L

**KEYNOTE: Dr Lee Cohnstaedt (Agricultural Research Service, USDA)
Benefits and Issues of funding research based on the latest outbreak**

Vector-borne disease outbreaks of medical or veterinary importance typically result in rapid and comprehensive responses by government organisations. The response is typically a shift of personnel and resources to address the immediate concern as well as a large tranche of monetary resources to focus research programs on the current outbreak. Although the money rapidly vanishes after the initial investment, the output of this resource boom results in increased innovation, publications and training. This was seen in 1999 during the West Nile virus introduction to the United States, the bluetongue virus outbreak in England (2008), Schmallenberg in northern Europe (2011), Chikungunya and Zika in 2013 and 2014 and planning for the next outbreak. This presentation will address some of the innovations resulting from the outbreaks (citizen science, surveillance methods, and population management tools), problems of boom-and-bust funding cycles from outbreaks, and how to take advantage of the cycles.

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13.10 – 13.50

Break

Session 8

Convenor and Chair

Insects as inspiration for technology

Prof. Andreas Vilcinskas (Institut für Insektenbiotechnologie, JLU Gießen, Germany)

13.50 – 14.30 L

KEYNOTE: Dr Tim Lüddecke (Fraunhofer IME, Giessen, Germany)

Many-legged assassins and master chemists: understanding arthropod venoms as a source for biomolecular innovation

Animal venoms are tremendously complex chemical systems that are composed of powerful biomolecules. These acquired their lethal properties through an evolutionary fine-tuning process over millions of years. The resulting toxic molecules represent outstandingly potent weapons that, on one hand, enable their inventor to subdue much larger opponents and prey items and are thus instrumental for their survival. On the other hand, these evolutionary innovations can also be exploited for human benefit, for instance as innovative drug leads or biodegradable insecticides. Facing this great potential, it is remarkable that rather little is known about the venoms of many animal lineages. This is mostly a result of methodological limitations, especially for small species with limited venom yields. In particular, therefore, the venoms of arthropods are tremendously understudied, facing the sheer diversity of venomous species within the phylum plus the unprecedented biomolecular complexity displayed within their venoms. However, the recent rise of combinatorial -omics technologies and their application to venom systems, in a novel field coined as “venomics”, recently allowed us to explore also the venom systems of smaller arthropods on a regular basis. These powerful technologies enable us now to ask pivotal questions e.g., how are arthropod venoms composed? How do they evolve and how do they work mechanistically? Moreover, in tandem with synthetic biology approaches, it is now possible to investigate the biomolecular inventory of arthropod venoms in regard to their translational potential, either on the level of native toxins or by designing artificial isoforms that are specifically engineered towards a desired function. While the plethora of available methods has already yielded several new insights into arthropod venom biology, alongside some promising bioresources that may be developed in future therapeutics and agrochemicals, it becomes increasingly clear that venom biodiscovery needs to be optimised in arthropods and beyond. As global extinction rates are rising, we are currently facing a real threat of losing valuable bioresources hidden in venoms before having opportunities to even study these. It will require stringent economisation and strategic planning of biodiscovery strategies, development of non-invasive sampling approaches and inclusion of collaborators and stakeholders local to critical regions in order to provide a sufficient coverage throughout the taxonomic space of venomous organisms in due time to prevent the loss of millions of biomolecules prior to their discovery.

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14.30 – 14.50 L

Prof. Stanislav Gorb (University of Kiel, Germany)

Insect-inspired technology: an endless diversity of biomimetic solutions

Why does not a fly fall from the wall? Insects possess attachment devices of remarkable quality. Their secret is based on the structure and material properties of adhesive surfaces. Modern high-resolution techniques aided in both the precise structural analysis of these surfaces down to the nanometre scale and precise

characterisation of their micromechanical properties. Recently-obtained results are of strong interest for technological applications. Basic-oriented research on insects may provide essential information for industrial developments of bio-inspired material surfaces with enhanced adhesive properties, which enable robots to climb up the wall. A few other examples on insect-inspired technology are additionally reported.

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14.50 – 15.00

Break

15.00 – 15.20 L

Dr Clemens Schaber (University of Kiel, Germany)

Adhesive setae of a spider: morphology, performance and biomimetic approaches

As with many biological structures, the adhesive system of wandering spiders can be the source for bioinspired and biomimetic solutions in technology. Wandering spiders such as the large Central American species, *Cupiennius salei*, easily climb vertically and walk upside down on many surfaces. Different from insects with fibrous attachment systems, which use a gluey secretion between their feet and the substrate, the spiders rely on dry adhesion of their nanostructured cuticular attachment setae without any sticky fluid involved. Responsible for this remarkable ability are the approximately 2,400 attachment setae arranged as the so-called claw tuft located on the pretarsi of each of the spider's legs. In the tip 50 μm of each seta, up to 1,000 microtrichia branch off its backbone. These microtrichia are equipped with approximately 1 μm wide and 20 nm thin spatula-shaped adhesive contact elements. During locomotion, the alignment of these structures with the surface of a substrate leads to intimate contact and thus adhesion. Morphological studies including scanning X-ray diffraction techniques revealed the specific structural arrangement and distribution of the reinforcing chitin fibres within the seta's cuticle to prevent material failure by tensile reinforcement and proper distribution of stresses that arise upon attachment and detachment.

Micromechanical measurements showed that the adhesive force of a single seta preloaded in shear amounts up to 25 μN , which suffices for an adult female spider (weight 3.6 g) to adhere on smooth glass with less than two thirds of the setae of a single leg in contact. Regarding their dimensions, vertically aligned carbon nanotubes (VACNTs) and freestanding anchored cellulose nanofibrils (CNFs) from plant seed mucilage are candidate materials for the design of structures with adhesive and frictional properties similar to the spider's biological model attachment system. Whereas the VACNTs are synthesised at high temperatures in a chemical reactor, the CNFs can be produced in a more environmentally-friendly way by hydration of plant seeds followed by critical point drying. The coefficients of friction of up to 6 on the surface of VACNT arrays are among the highest values of friction ever reported. With friction coefficients up to 3, friction is also remarkable on CNF arrays. These high values can be explained by the same mechanism of alignment of the fibres with the counterpart as in the biological model. However, adhesive forces at perpendicular pulling-off were never observed. Both materials have the potential as biomimetic solutions where high contact forces to surfaces are desired, especially in dry environments. To reach a performance similar to that of the biological model, e.g., in climbing robots, more research is needed in both dynamic spider adhesion and fabrication of the artificial structures to transfer the biological building principles to materials for specific applications.

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15.20 – 15.40 L

Dr Heiko Vogel (Max-Planck Institute for Chemical Ecology, Jena, Germany)

Combining host biology with potential applications of insect-associated microbes: the burying beetle example

The tremendous evolutionary success of insects is at least in part due to microbial symbionts which help them to explore novel ecological niches such as the ability to utilise unusual diets. Selective pressures from xenobiotics, nutrient limitations and natural pathogens may contribute to driving insects to adapt towards and enable exploitation of these diets. A highly efficient digestive mechanism is required by such insects to support rapid nutrient assimilation and biomass conversion during development. Furthermore, an effective immune system is required to cope with elevated levels of pathogenic microorganisms. An intriguing example of food preservation and controlling food-associated microbiomes is the burying beetle (*Nicrophorus* spp) that has evolved to occupy a unique ecological niche by reproducing on small vertebrate cadavers buried in the soil. Carrion-feeding insects that breed on decaying carcasses must overcome the challenges arising from competing microbes, which decrease its nutritional value and render it unpalatable or even toxic to animals. We show that the burying beetle modifies the microbial communities of carrion, since beetle-tended carcasses showed no signs of degradation and supported the growth of the beetles' gut microbiota, including the yeast *Yarrowia*, in a biofilm-like matrix. In contrast, untended carcasses showed visual and olfactory signs of putrefaction and supported the growth of endogenous and soil-originating microbial decomposers. The beetles and their microbiome thus coordinate a specialised adaptive strategy of carrion management, enabling them to preserve carrion quality and support larval growth on a challenging resource such as carrion. The symbiotic yeasts associated with the burying beetle are being tested for their impact on the host as well as their biotechnological potential for enzyme production, compound and biomass transformation.

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15.40 – 16.00 L

Prof. Andreas Vilcinskis (Institut für Insektenbiotechnologie, JLU Gießen, Germany)

Molecular basis of explosive defensive secretions in the Bombardier beetle

Bombardier beetles (Insecta: Carabidae) have evolved one of the most sophisticated chemical defence mechanisms in the animal kingdom. Paired pygidial glands in their abdomen produce secretions that can generate controlled explosions associated with the ejection of a boiling, noxious chemical spray to fend off attackers. The beetles store hydroquinones and hydrogen peroxide in their reservoir chamber, but when attacked they contract the surrounding muscles, forcing the chemicals through a one-way valve into the rigid-walled and highly-sclerotised reaction chamber. This contains catalases and peroxidases, triggering an exothermic reaction that produces benzoquinones, free oxygen and water at high pressure and at temperatures of up to 100°C in what is termed an explosive secretory discharge.

Here we report the first combined transcriptomic and proteomic analysis of the defensive glands and defensive secretions of the bombardier beetle *Brachinus crepitans*. Illumina Hi-Seq analysis of gene expression was combined with protein analysis by SDS-PAGE, LC-MS/MS and high-resolution MS imaging. We combined precise dissections of the different compartments of the defensive glands with protein sequence analysis to determine the origin of the different proteins found in the explosive secretions. Our data provide insight into the molecular basis of the Bombardier beetle's secretions and the complex morphological and physiological adaptations required for such a sophisticated chemical defence mechanism.

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16.30

ENTOlympics: A fun quiz for students and early career entomologists

Students and early career entomologists can register for this event:

<https://us02web.zoom.us/meeting/register/tZYvdeytrTkVg92JuQdfWcYcEJ90mYic2TMG>

Friday 27th August

Session 9
Convenors
Chair

Engaging diversely
The Royal Entomological Society Outreach Committee
Prof. Helen Roy (UK Centre for Ecology & Hydrology; RES President)

11.00 – 11.40 L

KEYNOTE: Kevin Coutinho (Linnean Society of London; Windsor Fellowship, UK)
Fixing the leaky pipeline

Ensuring the diversity of the academic community is good for society but also critical for research. This presentation outlines the challenges and opportunities to explore options for organisations to redress inequalities through positive action to ensure that tomorrow's academic community better reflects society and its research needs.

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11.40 – 12.00 L

Dr Julie Moote (UCL, UK)
Understanding STEM aspirations and participation: key factors related to aspirations and attitudes between the ages of 10 and 19

This talk draws on data from ASPIRES – a large, national, mixed-methods project, which sought to understand the subject choices and career aspirations of young people aged 10–19. A cohort of students was tracked from primary through secondary school, via five surveys with approximately 40,000 students and in-depth longitudinal interviews with 60 students (and their parents). Focusing in particular on students' science trajectories and aspirations, the talk explores several key factors that shape students' "choices" and produce persistent patterns in post-16 participation. The talk concludes with recommendations for policy and practice, including strategies to encourage uptake into specialist areas of STEM.

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12.00 – 12.10

Break

12.10 – 12.30 L

Dr Alex Ball (Natural History Museum, UK)
Design considerations for 3D-printed models targeting blind and visually impaired participants

3D printing has opened huge opportunities for reproduction of replica objects. However, there are very few studies which have looked at the design considerations required for interaction with blind and visually impaired audiences. Robust and well-defined standards exist for print media, tactile diagrams and drawings and even signposting, but similar design guides for 3D objects do not appear to have been prepared. Studies into the design of 3D objects from Museum collections for engagement with visually-impaired audiences have typically focused on the reproduction of large-scale objects such as statuary or fossils. Feedback from the participants often includes questions on why they are not allowed to handle the original objects. This lack of authenticity is thus cited as a negative part of the

experience. Our study uses electron microscopy and photogrammetry or micro-CT scanning and makes specimens accessible to participants through the medium of 3D printing or casting from 3D prints. However, by choosing to focus on natural history objects which are too small to be handled and by enlarging them considerably, the practice of accessibility is thus, in part, a shared experience made possible through the technology involved. We also avoid the controversy of using original objects which the participants might otherwise have been able to handle. Our initial test samples focus on the heads of three types of insect: blowfly; butterfly and damselfly as well as domestic items used to teach participants the principles of microscopy and magnification. In our future research we aim to explore the role of colour, contrast, texture and physical properties in the objects we develop in conjunction with focus groups. Our long-term goals are to develop robust, tested standards which can be used as a basis for the design of 3D printed objects for education and outreach in the future.

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12.30 – 12.50 L

Dr Sarah Bearchell (STEM; Lightyear Foundation, UK)
Making your activities work for EVERYONE!

Dr Sarah Bearchell has a particular passion for making science activities work for audiences with diverse needs. She will cover the value of making your activity accessible from the outset and give you ideas for improving your existing outreach.

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12.50 – 13.10 L

Prof. Rebecca Kilner (University of Cambridge, UK)
Public engagement in museums: opening laboratories of the imagination for everyone

Museums are community centres with a difference. The collections they house can bring people together: in shared delight and wonder, in the thrill of discovery, and in being exposed to the big ideas that bind societies together. Public engagement in museums is about giving everyone the opportunity to explore these laboratories of the imagination. In the University Museum of Zoology at Cambridge, our public engagement team has used the Covid pandemic to experiment with new forms of engagement targeted to diverse new audiences. Much of this work has involved our insect collections. I will describe approaches we have taken using interactive digital resources in events and programming, and in engaging the public in conservation efforts. One surprising advantage of the pandemic ways is that it has shown us that we can target specific community groups, including ones that have suffered more than most during the last 18 months. Best of all, there are signs that this has measurable positive effects on the wellbeing of those taking part.

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13.10 – 13.50

Break

Session 10
Convenor and Chair **Insecticide issues**
Dr Ralf Nauen (Bayer, Germany)

13.50 – 14.10 L Prof. Chris Bass (University of Exeter, UK)
The molecular innovations underlying resistance to natural and synthetic xenobiotics in the aphid *Myzus persicae*

The aphid *Myzus persicae* is a destructive agricultural pest that displays an exceptional ability to develop resistance to both natural and synthetic insecticides. In this talk we will describe new genomic and biological resources created for *M. persicae* comprising a chromosome-scale genome assembly and living panel of >110 fully sequenced globally sampled clonal lines. We demonstrate the utility of these resources in an investigation of the molecular and ecological processes underpinning the evolution of insecticide resistance in *M. persicae*. Our analyses reveal a remarkable diversity of resistance mutations segregating in global populations of this species. We show that the emergence and spread of these mechanisms is influenced by host-plant associations, uncovering the widespread co-option of a host-plant adaptation that also offers resistance against synthetic insecticides. We identify both the repeated evolution of independent resistance mutations at the same locus, and multiple instances of the evolution of novel resistance mechanisms against key insecticides. Our findings provide fundamental insights into the genomic responses of global insect populations to strong selective forces. The chromosome-scale assembly, resequenced genomes, and living library of *M. persicae* clones generated in this study represent a powerful resource for further research on aphids.

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14.10 – 14.30 L Prof. Guy Smagghe (Ghent University, Belgium)
RNAi as a novel technology to overcome insecticide resistance

In recent years, RNAi has been established as a promising novel control approaches against important pest insects. The strategy aims to control pest insects by exploiting the natural RNAi gene silencing mechanism to knock down genes that are essential for the insect's survival. The most practical approach to achieve this is by orally administering dsRNA, specific for the target gene. However, the sensitivity of insects to RNAi triggered by exogenous dsRNA is highly variable. Here, we present our data on dsRNA delivery strategies that are being developed to improve RNAi efficacy. Interestingly, RNAi can be employed as a novel technology to overcome insecticide resistance and some examples are presented.

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14.30 – 14.50 L Prof. Lin Field (Rothamsted Research, UK)
Neonicotinoids: issues with both resistance and legislation

Since their introduction onto the market around 30 years ago, the neonicotinoids fast became the most widely used insecticide chemistry worldwide. They held on to this position partly because of their success as seed dressings and partly because it took a long time for resistance to develop in the target pests. However, their use has more recently been severely restricted by legislation banning them as seed

dressings, which pose potential threats to non-target insects including pollinators. These aspects affecting the history of neonicotinoid use will be discussed.

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14.50 – 15.00

Break

15.00 – 15.20 L

Prof. Emmanouil Roditakis (Hellenic Mediterranean University, Greece) and Dr Ralf Nauen (Bayer, Germany)
Diamide insecticides as pest management tools: current status, problems and perspective

Diamides are a novel and extremely potent class of insecticides acting as activators of insect ryanodine receptors (RyR) which are tetrameric calcium release channels important for insect muscle function. Due to their unique mode of action, the extremely high efficacy and the favourable ecotoxicological profile, diamides were rapidly adopted in management schemes for a range of pests in diverse cropping systems and environments. However, extensive adoption and use rapidly resulted in resistance development with striking phenotypes significantly compromising pest control levels at recommended label rates. First diamide resistance reports involved the diamondback moth *Plutella xylostella*. To date at least nine lepidopteran species have been reported exhibiting resistance to diamides including globally important invasive pests such as tomato leafminer, *Tuta absoluta* and fall armyworm, *Spodoptera frugiperda*. The resistance phenomenon against diamides has been extensively investigated. It was demonstrated that target-site mutations located within the RyR transmembrane domain play a key role in resistance phenotypes, whereas possible metabolic resistance is less well investigated. Recently, diamide resistance has been documented in dipteran pests (oriental fruit fly and house flies) and thrips (*Frankliniella occidentalis*). Despite the major resistance issues in lepidopteran pests, the wide target range of diamides is providing novel solutions for key pests with currently problematic implementation of pest management tactics. Such key pests include the cotton whitefly *Bemisia tabaci* and the olive fruit fly *Bactrocera olea*. As current pest control schemes are challenged by rapid resistance development along with continuous withdrawal of active substances from the officially registered products, diamide insecticides gradually re-enhance their role in future crop protection.

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15.20 – 16.00 L

KEYNOTE: Prof. Bruce Tabashnik (University of Arizona, USA)
Global patterns of resistance to Bt crops: what went right and wrong?

Crops genetically engineered to produce insecticidal proteins from the bacterium *Bacillus thuringiensis* (Bt) can suppress some key pests, reduce insecticide sprays, and enhance biological control. However, these benefits have been reduced by evolution of resistance to Bt proteins in pests. The global monitoring data reviewed here reveal 22 cases of practical resistance to Bt crops, which is genetically based, field-evolved resistance that reduces Bt crop efficacy and has practical consequences for pest control. Each case represents the responses of one pest species in one country to one Bt toxin. The global data also reveal a roughly equal number of cases where pests have remained susceptible to Bt crops, sometimes for 20 years or more. Analysing the responses of one pest exposed to the same Bt crop in three countries provides some compelling insights. The field outcomes with the

pink bollworm (*Pectinophora gossypiella*) and Bt cotton differ strikingly among the world's three leading cotton-producing nations: India, the United States and China. In India, where non-Bt cotton refuges have been scarce, pink bollworm rapidly evolved widespread resistance to transgenic cotton producing Bt proteins Cry1Ac and Cry2Ab. In the southwestern United States, farmers delayed resistance by planting non-Bt cotton refuges from 1996 to 2005. From 2006 to 2018, farmers in the United States and Mexico cooperated in a program that used Bt cotton, mass releases of sterile moths, and other tactics to eradicate this pest from the region. In China, farmers reversed low levels of pink bollworm resistance to Bt cotton by planting second-generation hybrid seeds from crosses between Bt and non-Bt cotton. This approach yields a refuge of 25% non-Bt cotton plants randomly interspersed within fields of Bt cotton. Farmers adopted this tactic voluntarily and unknowingly, not to manage resistance, but apparently because of its perceived short-term agronomic and economic benefits. Consistent with global trends, the results with pink bollworm imply that refuges of non-Bt host plants can delay or even reverse evolution of resistance to Bt crops in pests.

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16.00 – 16.10

Closing words