



# ENTO'21

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## POSTERS

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**The Pollinators Monitoring Scheme of Kýpros**

The Akrotiri wetland is a biodiversity “hotspot” area which hosts endemic species and sub-species of the Cypriot flora and fauna. However, to date the insect fauna of Akrotiri is not well documented thus, establishing monitoring schemes and recording insects is very important. Through the Darwin Plus Initiative we developed a scheme for monitoring pollinating insects in Cyprus – **PoMS-Ký** (<http://www.ris-ky.info/poms-ky>). PoMS-Ký adopts citizen science approaches to record insects visiting flowers (**FIT count**) and provides an opportunity to address current data gaps for species populations and distributions across Cyprus, while it also aims to improve the knowledge of the general public regarding the pollinating insects. From November 2018 till June 2019, we performed 194 FIT counts and recorded 272 bees (107 solitary bees, 141 honeybees, 5 bumblebees and 19 wasps), 329 flies (67 hoverflies and 262 other flies) and 74 butterflies and moths. Furthermore, we undertook awareness-raising activities regarding the importance of insects of the Akrotiri Peninsula. A second scheme was developed for elementary and high school children, mini PoMS-Ký.

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**2) Katrina Athanasiou (Joint Services Health Unit, British Forces Cyprus / Cyprus University of Technology)**

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**Assessing the efficacy of mosquito traps and different types of land use at the Sovereign Base Area (SBA) of Akrotiri in Cyprus**

Historically, the wetland of Akrotiri was a malaria endemic site till the 1960s. The mosquitoes at present are mainly a nuisance problem, however anthropogenic activities such as land use change and urbanisation could lead to the re-introduction of malaria and the proliferation of diseases, such as West Nile Virus, by altering the current mosquito community composition. We assessed the abundance of mosquito populations at Akrotiri SBA by using mosquito traps. In total, 20 traps were placed at each site, i.e., 10 ovitraps containing tap water and 10 hovitraps containing hay-infused water. In addition, one BG sentinel trap with BG lure was placed at each site. Five sites were selected: the Royal Air Force (RAF) Airport in Akrotiri, the Limassol Port near the RAF, the Akrotiri freshwater

marsh, the Akrotiri Forest and the stables in RAF. Traps were checked every 2 days between 29/06/2020 and 28/08/2020. Mosquitoes collected were morphologically identified at the laboratory. Only specimens of *Culex pipiens* s.l. were found in the ovitraps and the hovitraps. *Culex pipiens* was recorded at all sites except the forest habitat. By applying a two-way Anova, the analysis showed that the effect of site was significantly important (p-value < 0.001). More research is currently being undertaken to characterise the land use at different breeding sites and their effect on mosquito abundance. We aim at guided mosquito control actions using a science-based approach to inform experts and the general public regarding the risk of mosquito borne diseases.

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**Genetic diversity of *Phlebotomus perniciosus* around the Mediterranean Basin**

Introduction: *Leishmania* parasites are mainly transmitted by hematophagous insects belonging to the genus *Phlebotomus*. *Phlebotomus perniciosus* is a major vector of visceral leishmaniasis in the western part of the Mediterranean basin, reported from North Africa (Morocco, Algeria, Tunisia and Libya) and Europe (Portugal, Spain, France, Italy, Slovenia and Croatia). Due to its proven role in the transmission of *L. infantum* and large distribution, its genetic structure requires more interest.

Material and methods: Specimens of *Phlebotomus perniciosus* were trapped in Kherrata and Bougaa, two districts located East of the capital city of Algeria. 40 sequences (700bp of mitochondrial DNA, COI gene) were amplified and sequenced. In addition, 85 sequences of *Ph. perniciosus* from different countries of the Mediterranean basin were downloaded from NCBI and BOLD databases and included in the analysis.

Results and discussion: The phylogenetic tree using neighbour-joining (1000 bootstraps) revealed three distinct clades: one included only the Moroccan specimens, the second included specimens from Portugal and Spain, and the last one included specimens from Algeria, Tunisia, Italy and Slovenia. On the other hand, the median-joining network showed that the common ancestral was either lost or mis-sampled between the three clades. The statistical analysis revealed the presence of 24 haplotypes. The Fst value showed a significant difference between samples from Morocco, Portugal and Spain and the rest of the countries. No positive correlation between the distance of sampling and their location was shown, suggesting that the observed differences could be linked to the environmental factors rather than distance.

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**4) David Bennett (Christian Albrechts Universitat zu Kiel, Germany)**  
**Effect of wildflower species richness, semi-natural habitats and habitat fragmentation on invertebrates in northern Germany**

Nature compensation measures are an increasingly common tool used by local and national governments to arrest the decline in insect biodiversity. Wildflower meadows, especially in agricultural areas, are a prominent example of these measures. Wildflower meadows are especially intended to support invertebrate populations, with particular focus on pollinating insects. However, controversy remains regarding the effectiveness of these measures, and how they might be optimised for conservation goals – concerns have been raised about the seed mixes used, the timescales involved and their placement in the landscape. To help answer these questions, we have deployed

yellow pan traps, nest traps and pitfall traps at 37 wildflower meadow compensation sites across Schleswig Holstein, northern Germany. These sites cover a wide range of different landscape factors - including different percentages of semi-natural habitat within a 3km radius and habitat fragmentation (as indicated by Mesh Index). The main target invertebrates for the study are Syrphidae, Carabidae, Apidae, Lepidoptera and Orthoptera. Half of all samples will be analysed by DNA metabarcoding, allowing for a comparison of conventional hand-analysed traps with those analysed by high-throughput genetic sequencing. We aim to identify if soil factors, habitat fragmentation and the provision of semi-natural habitats in the landscape affect invertebrate communities at wildflower compensation sites. We will compare wildflower richness and species composition with invertebrate community composition. Further analyses will indicate which specific types of semi-natural habitat have the greatest influence on invertebrate diversity.

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**Morphological change in a threatened butterfly suggests altered flight capacity in fragmented landscapes**

Species' dispersal capacity and responses to site isolation are important considerations in management strategies, particularly in the face of habitat fragmentation and environmental change. In butterflies, where morphology is often indicative of dispersal ability, flight-related morphological traits can be used to understand selection on dispersal in response to factors such as habitat structure and isolation. We used non-lethal methods of collecting morphological data under field conditions to investigate spatial and temporal variation in flight-related morphological traits in a threatened butterfly in the UK. Morphology was compared between extant populations of the pearl-bordered fritillary, *Boloria euphrosyne*, in north-west England and museum specimens collected from the area historically. There were no significant morphological differences between sites in the current populations. However, morphometric analysis revealed that strong population declines in the region from the 1970s onwards have been accompanied by phenotypic changes. There was significant variation between the museum specimens and current populations, with individuals in extant populations showing increased forewing size, smaller thoraxes and lower wing loading. The observed changes in morphology, which are indicative of gliding rather than rapid, powered flight, are associated with improved energy efficiency and are therefore consistent with the hypothesis that current populations are better suited to make sustained, long-distance movements. Although such long-distance movements could be adaptive in fragmented habitats, at low population densities, where colonisation success may be limited, elevated emigration could have detrimental effects for population persistence.

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**Bumblebees strategically use paths and roads to navigate**

Extended ground-level structures like roads or field edges can be important cues for navigating animals, seen for example in road-following pigeons. In a landscape devoid of skyline cues but with a rectangular grid of pathways and roads, we used harmonic radar to track free-flying bumble bees, *Bombus terrestris*. Individual bees consistently used ground-level linear features for navigation in a wide range of behavioural contexts. Bee exploration flights, search behaviour and foraging routes were shaped by linear features, with bees frequently flying along and parallel to pathways and roads. Comparisons of flight trajectories across these behavioural contexts show that individuals modulated their use of linear features strategically with respect to their individual goals and experience. Bees

searching for a feeder used linear features to target their search, while foragers often followed pathways to return to their hive without overshooting. These findings on a major pollinator have important implications for the placements of bee colonies for agriculture and floral resources for conservation.

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**7) Victoria Burton (Natural History Museum, London, UK)  
Soil biodiversity in horticultural agriculture – call for data**

Conventional intensive agricultural methods increase crop yield but reduce biodiversity, potentially reducing the long-term provision of other ecosystem services such as pollination, biological pest control, and nutrient cycling. Soils are often rich in biodiversity, and the soil microbiome (bacteria, archaea, fungi and protists) together with soil invertebrates such as insects, collembola, arachnids and earthworms, and their interaction with plants, is key to healthy agricultural systems. Adding certain microorganisms, known as bioinoculants, to agricultural systems may be able to increase plant growth and health with less environmental degradation than synthetic chemicals, but there are knowledge gaps around their effectiveness, persistence, and impacts on native soil biodiversity. The Excalibur project brings together 16 partners across Europe, aiming to improve understanding of the links between management practices, underground soil biodiversity and crop dynamics – looking at broad indicators of plant health, soil biodiversity, fertility, productivity and costs. As well as field trials of how bioinoculants affect three crops (strawberries, tomatoes and apples) and native soil biodiversity, we are developing statistical models to estimate how contrasting agricultural management practices and bioinoculants affect soil biodiversity, and test whether these effects are consistent among taxonomic groups. Our poster presents existing data on soil biodiversity in agricultural systems collated as part of the PREDICTS (Projecting Responses of Ecological Diversity In Changing Terrestrial Systems) project. We highlight gaps in our data and invite any holders of relevant data to contribute them. Contributors will be acknowledged appropriately in all outputs and invited to co-author the dataset.

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**Biological control of the fruit pest *Drosophila suzukii*: a laboratory investigation with bioinsecticides**

*Drosophila suzukii* Matsumura (Diptera: Drosophilidae), also named Spotted Wing Drosophila (SWD), is an invasive polyphagous pest, endemic to eastern areas which has recently invaded Europe and the Americas, becoming a serious threat to the cultivation and marketing of thin-skinned fruits, such as berries, peaches and apricots. Control of spread of SWD is done by various methods, based on different strategies, but chemical insecticides are still commonly used today. Alternatives to chemical control could be biological control methods based on bioinsecticides, such as nematodes or bacteria. Mainly, biological control assays on this dipteran are carried out at lab-scale by the application of single or combined bioinsecticides; *Bacillus thuringiensis*, *Steinernema carpocapsae* or other entomopathogens could, once experimentally validated, be promising for potential use in the field. Since development of SWD within the fruit is rapid and the larvae feed on the pulp, damaging the crop, biological control treatments should be optimised in order to reduce the treatment time, so we performed a series of susceptibility tests on early-stage SWD larvae (L1/L2), comparing the effects of single administrations of *B. thuringiensis*, *S. carpocapsae*, *Xenorhabdus nematophila*, and its

secondary metabolites, with different combined formulations of these bioinsecticides. Our data show that administration of combined bioinsecticides improves the efficacy of biological control of SWD larvae and reduces treatment time when compared with single administrations. This knowledge could be a good starting point for the development of bioinsecticide formulations potentially applicable in-field.

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**9) Thomas Chen (Academy for Mathematics, Science, and Engineering, USA)  
Butterfly species recognition in imagery enabled by deep learning technology**

Machine learning has enabled numerous advances in entomology in recent years, particularly in the area of recognition and classification of insects in imagery. These technologies aid in the tracking of population trends and interspecies relationships within ecosystems. Such automated mechanisms are primarily driven by deep learning and artificial neural networks. In this work, we focus on classifying 6 different butterfly species in imagery: *Danaus plexippus*, *Limenitis archippus*, *Vanessa atalanta*, *Vanessa cardui*, *Danaus gilippus*, and *Danaus eresimus*. We harness a convolutional neural network trained on a data web scraped from Google Images. The goal is for the deployment of this technology in the future to allow conservation biologists to effectively understand butterfly populations. Further work includes expanding the model to a larger range of species.

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**Investigating the environmental influence on mosquito population dynamics in Akrotiri wetland, Cyprus**

Urbanisation around wetlands in combination with climate change are expected to exacerbate the exposure of humans to the natural breeding sites of mosquitoes. In order to minimise the risk of disease, reduce nuisance, and protect the biodiversity in natural areas, efficient and targeted mosquito management strategies are needed, under the One Health approach. In turn, a better understanding of the environmental influence on the relevant mosquito species is needed. In this study, we monitored the abundance and diversity of mosquito populations in the Akrotiri wetland in Cyprus, by sampling the aquatic stages from 15 natural mosquito breeding sites located around the wetland. Sampling was carried out twice a week between 11/11/2020 and 27/04/2021. The physicochemical properties of the water, depth, perimeter, air temperature, humidity and wind velocity were recorded during each visit. Mosquito specimens were counted and sorted according to the development stage and morphologically identified. In total, 4328 specimens were collected across the area and six species were identified (*Aedes mariae*, *Ae. caspius*, *Ae. detritus*, *Culex pipiens*, *Cx. perexigus*, *Culiseta longiareolata*) of which *Ae. detritus* was the most abundant species. The application of Bayesian linear mixed models suggested that temperature and salinity are the main factors influencing the abundance of mosquitoes at different development stages, while this largely varied depending on the sampling station. Further research is needed to improve understanding of the environmental drivers of mosquito population dynamics, by applying comprehensive climate- and environment-driven mathematical models to assess the mosquito-borne disease risk in wetland protected areas.

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**How citizen science, big data and open-source hardware could help us understand insect declines.**

With recent research indicating terrestrial insect declines of up to 9% per decade, monitoring the rise and decline of insect populations has never been as critical. However, most conventional methods are time-consuming, laborious and inefficient. Recent advances in computer vision and machine learning algorithms provide valuable opportunities for rapid, real-time insect monitoring. The efficacy of these algorithms is greatly affected by the quality and quantity of data used to train them. We aim to develop a range of open-source insect monitors that will capture data from an array of sensors (climatic, spectral and acoustic). The devices link to an online platform accessible to professional, academic and citizen science researchers. The platform can manage, classify and share standardised data globally. This system could answer fundamental questions about changes in insect abundance and diversity and how we affect them. More importantly, perhaps, we believe that by engaging the global community in meaningful research, it is possible to shift society's attitude towards insects.

Use cases include:

*Insect conservation and identification:* Monitors are a non-destructive and non-invasive insect sampling device, where insect identification through deep learning could save hours of lab work;

*Agriculture:* Applications include early pest detection, measuring the efficacy of pest management and monitoring the health of beneficial insects;

*Education:* Devices and data packaged as educational modules for use in schools from pre-primary to tertiary levels.

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**Non-native insect species associated with eucalypts in Cyprus**

The trade of eucalypts around the world for ornamental purposes, the drying of marshes as well as for the production of pulp and timber has resulted in the unintentional introduction and establishment of some non-native insects associated with this plant. In Cyprus, eucalypts were first introduced in the late 1800s and are nowadays widely distributed in the island. Surveys from February to June 2021 and a review of literature have provided information on 19 non-native insects, collected from *Eucalyptus* spp. in Cyprus. The vast majority of species originate from the plant's native range and are specialists, exclusively reproducing and feeding on eucalypts' wood, leaves or flowers. Order representation and trophic preferences of species are depicted. These surveys are ongoing and constitute the first holistic survey regarding alien insects of *Eucalyptus* spp. in the island. We hope not only to unravel the non-native entomofauna of eucalypts present on Cyprus, but also catalogue and manage their adverse socioeconomic and environmental impacts.

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**Management of whitefly, *Aleurocanthus arecae*, and wax scale, *Chrysomphalus aonidum*, in arecanut**

Arecanut is one of the major commercial plantation crops grown in India. Arecanut is mainly cultivated in the plains as well as in the hills of Western Ghats and the North Eastern part of India. It is extensively grown in states like Karnataka, Kerala, Assam and West Bengal. A field experiment was conducted to evaluate the efficacy of different insecticides against whitefly, *Aleurocanthus arecae* and wax scale, *Chrysomphalus aonidum* in arecanut in 2019 and 2020 at two locations under the jurisdiction of the University of Agricultural and Horticultural Sciences, Shivamogga, Karnataka. Observations were taken on the number of whiteflies and wax scales a day before spraying, and seven days, 14 days and 21 days after treatment on selected plants of 5×1cm<sup>2</sup> leaf area. The leaf samples were brought to the laboratory and examined for live whitefly and wax scale populations using a stereo binocular microscope. Among the different insecticides evaluated for the management of *A. arecae* and *C. aonidum*, neem oil 1% @ 2ml/l showed maximum per cent reduction against the whiteflies (72.92) and wax scales (81.60). This treatment was followed by chlorpyrifos 20 EC @ 2ml/l (62.09 %) for *A. arecae* and dimethoate 30 EC (66.51 %) for *C. aonidum*.

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**Insect fauna diversity and abundance in abattoirs in Enugu North senatorial zone, Eastern Nigeria**

Insects are vectors for various microorganisms. They have the potential for spreading diseases in the environment where they are found. Many insects are associated with animal faeces and manure, and abattoirs are one of the important sources for such contacts and disease dissemination. We believe that understanding the diversity of insect fauna might help to shed light on vector insect-borne diseases, prevalence, and transmission rates in abattoir communities. Here we randomly selected three (Orba, Ikpa and Obollo-afor) abattoirs in Enugu senatorial zone and surveyed for insect fauna abundance, diversity and distribution. The sampling was carried out over a period of eight weeks, using a sweep net and handpicking as the collection methods. Overall, 12 species were recorded. Orba had the lowest species diversity with 7 species while Obollo-afor and Ikpa recorded 10 and 9 species respectively. Diptera and Coleoptera were the most diverse and abundant orders observed with *Musca domestica* being the most abundant species encountered. Equitability index of evenness revealed that *Calliphora vomitoria*, *Blattella Orientalis*, *Monomorium minimum*, *Dermestes lardaceous*, *Lucilia caesar*, *Musca domestica* and *Calosoma scrutator* were evenly distributed. While the lowest evenness was recorded in Ikpa. The information generated from this study will provide much-needed assistance in disease monitoring and guideline in health policy decision-making in the study area.

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## **Journey of world drosophilid taxonomy**

The science of identifying, naming and characterising species, making it known to the world is Taxonomy. All credit goes to the taxonomists who had/helped in distinguishing similar-looking but different species or letting us see difference between sibling species. Major work on taxonomy of drosophilids was done by many taxonomists including J.W. Meigen, O. Duda, T. Dobzhansky, H. Burla, Francis Walker, C.R. (Baron) Osten Sacken, Prof. M.R. Wheeler, Prof. Dr. M. Bezzi, Prof. L. Tsacas, T. Okada, Dr I.R. Bock, Prof. D.A. Grimaldi, H. Takada, Prof. M.J. Toda, Dr G. Bächli, Prof. H.A. Watabe, Prof. P.M O'Grady, Prof. T.A. Markow, Prof. S.P.Ray-Chaudhuri, Dr D.P. Mukherjee, Prof. J.P. Gupta, Prof. B.K. Singh, Prof. J.J. Gao and many more. Like many species of drosophilid, the taxonomy of drosophilids has migrated to different countries like USA, France, Switzerland, Germany, Australia, Japan, India, Indonesia, China and many more. Here, the taxonomic work related to drosophilids was further taken to new depths. At present there is only a handful of drosophilid taxonomists with no or very few successors. In current scenario, the taxonomy itself is on the verge of going extinct and thus needs revivalist steps. To make the taxonomy relevant, it must be integrated with ecological, behavioural, host plant interaction, pest and molecular and evolutionary biology of drosophilids.

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### **16) Magdaléna Fialová (Charles University, Czech Republic)**

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#### **Complete life cycle of *Trypanosoma thomasbancrofti*, an avian trypanosome transmitted by culicine mosquitoes**

Trypanosomes are blood parasites transmitted by bloodsucking invertebrates, notoriously known for illnesses they cause in humans and animals (Chagas disease, sleeping sickness, nagana, etc.) They were found in birds more than 120 years ago by Danilewsky. Even though avian trypanosomes are widespread and their prevalence can be high, knowledge about their life cycles and vectors remains incomplete. Mosquitoes have been confirmed as vectors of *T. culicavium* and suggested as vectors of *Trypanosoma thomasbancrofti*; however, transmission has been experimentally confirmed only for the former species. This study aims to confirm experimental transmission of *T. thomasbancrofti* to birds as well as localisation in vectors. *Culex pipiens* were fed on blood using four strains of *T. thomasbancrofti*, isolated from vectors and avian hosts; all strains established infections, and three of them were able to develop high infection rates reaching 92% in fed females with heavy infections in 90% of positive females. Contrary to *T. culicavium*, trypanosomes were localised in the hindgut as rosettes with occurrence of free epimastigotes in the hindgut and midgut during late infections. Transmission to birds was achieved by ingestion of positive mosquito guts and via conjunctiva. Prevalence of *T. thomasbancrofti* in wild-caught mosquitoes is lower (0.1%) than prevalence of *T. culicavium* (3.6%). In avian hosts, the prevalence of *T. thomasbancrofti* is low as well: only 0.4 % of screened passerines were positive. This study confirms the vectorial capacity of culicine mosquitoes for *T. thomasbancrofti*, a worldwide occurring trypanosome related to *T. avium*.

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### **17) Dipsikha Ghosh (University of Calcutta, India)**

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#### **Feeding response in four tropical grasshopper pests: a nutritional ecology comparison with paddy and weed**

Quantitative nutritional indices were measured in all nymphal stages and adults (males and females) of four grasshopper paddy pests (Acridoidea: Orthoptera) from tropical agro-lands. The species of interest were *Atractomorpha crenulata* Fabricius, *Oxya hyla hyla* Serville, *Oxya japonica japonica* Thunberg, and *Phalaeoba infumata* Brunner. The tested two host plants were the affected crop, paddy (*Oryza sativa* L, Poaceae), and the grass-weed that was commonly found in paddy field



bundhs (*Eleusine indica* L, Cyperaceae). The interactive effects of consumed host plants (paddy and weed), foliar nutritional quality (chemical constituents in plants) and nymphal dietary phase (instar stage) indicate that food consumption index, approximate digestibility of food, efficiency of conversion of ingested food, efficiency of conversion of digested food, relative growth rate and survivability varied significantly among the insects. However, both strong and weak significances in relation to the larval stage were observed. Several nutritional qualities of plant foliage were investigated, and it was observed that they differed and had an impact on the growth and survivability of the insects.

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**18) Thibaud Glinez (National Museum of Natural History, Paris, France)  
New insight into the Acratini tribe (Brentidae, Coleoptera); an example of an Andean vicariance?**

The Curculionoidea beetles or vernacularly "weevils", form one of the largest current zoological groups with nearly 70,000 described species, most of which are particularly diverse in tropical regions. The exclusively Neotropical tribe Brentidae Acratini (Alonso-Zarazaga, Lyal, Bartolozzi and Sforzi, 1999) currently comprises 107 species in 14 genera. Despite several works published in recent years concerning the systematics of this group, many taxa belonging to this tribe are of enigmatic affinities and do not seem to relate to any of the genera currently defined. This is the case of an unpublished species from Ecuador, recently received from the Museum of Florence and currently on loan to the Muséum national d'Histoire naturelle in Paris. This Brentidae presents a mosaic of characters making it difficult to place it in one or other of the established generic sections. In this respect, it could constitute an evolutionary lineage that is significantly distinct from the others and could thus justify the description of a new genus within the tribe, especially since its geographical position is unprecedented since it is the only species present west of the Andes. This presentation aims to share an example of progress on this little-known beetle group, as well as the kind of research that a Masters student can conduct.

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**19) Gabriele Gloder (KU Leuven, Belgium)  
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Parasitoid wasps shape the microbiome of a caterpillar host**

In recent years studies on the effects of parasitoids on their hosts have been many, but little is known on how parasitism affects the microbiome of the host. The microbiome of insects consists of a diverse community of microorganisms that play a critical role in the development and overall health of their hosts. A variation in such a community, induced by parasitism, can therefore deeply influence host functioning. To assess if parasitism influences the microbial community of hosts, the microbiome of healthy and parasitised caterpillars have been compared. In this study, we used high-throughput amplicon sequencing targeting both bacteria and fungi to test the hypothesis that parasitism by the endoparasitoid wasp *Cotesia glomerata* affects the microbiome of its host caterpillar *Pieris brassicae*. Microbiomes of healthy and parasitised caterpillars from natural populations and a laboratory-reared population have been collected. Significant differences between the microbiome of field-collected and laboratory-reared caterpillars, and between the external and internal microbiome of the caterpillars have been found. Parasitism significantly altered the internal microbiome of caterpillars while it was not affecting the external microbiome. The internal microbiome of parasitised caterpillars was dominated by one bacterial species (*Wolbachia*), which was completely absent in healthy caterpillars, suggesting that this bacterium was transferred to the caterpillars during oviposition by

the parasitoids. We conclude that parasitism has pronounced effects on the microbiome of a caterpillar host and could possibly affect interactions with higher trophic levels.

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**Are Nature Ways in the way of nature?**

Nature Ways (NWs) are green corridors in Singapore that connect isolated nature spaces, and aim to facilitate wildlife movement by mimicking the natural forest canopy. This study investigates how individual NW characteristics (connectivity, urban disturbance, proportion of surrounding natural area, and floral diversity) influence species richness, abundance, diversity, and plant–pollinator interactions of butterflies and bees. Fifty-five 500-metre transects along nineteen NWs were identified and surveyed for butterflies. The last 100 metres of each transect were surveyed for flora diversity and plant–pollinator interactions. Overall, NWs with the highest pollinator diversity, abundance, and most complex interaction networks were characterised by low urban disturbance and a high proportion of surrounding natural areas. Connectivity (the number of connections the NW had to natural areas) had little effect on biodiversity, but NWs that overlapped with parks and reserves harboured a distinctly higher diversity of butterflies. These results support the importance of protecting natural areas in tandem with NWs. Plant–pollinator interactions showed that pollinator community structure in NWs was affected by its floral diversity. Butterflies and bees had different nectaring preferences, with bees tending to be more specialised. Several wildflowers that are commonly removed as “weeds” were actually highly attractive to both groups of pollinators. The biodiversity value of highly urban sites can therefore be boosted by planting a selected variety of flora attractive to different pollinators, and adjusting weeding regimes. NWs are still a fairly new conservation strategy in Singapore and this study’s findings will help to improve current and future NW design to enhance Singapore’s biodiversity.

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**Evidence for female resistance traits in traumatically-mating Strepsiptera (Insecta)**

Traumatic insemination is an example of sexual conflict. It is characterised by males penetrating the body wall of the female partner to inject sperm. Females unable to avoid unnecessary mating have been predicted to tolerate or resist by developing defence traits reducing damage caused by mating. Evolution of tolerance traits has so far only been demonstrated in the bed bug, where the male's penis penetrates the cuticle of the female's paragenital organ. However, tolerance was also suggested for Strepsiptera. Here we show the example of *Stylops ovinae* (with paragenital organ) and *Xenos vesparum* (without paragenital organ) that female defence against traumatic penetration is also realised via resistance in this insect order. Using confocal laser scanning microscopy, we show that areas where traumatic insemination takes place do not differ from control sites in the material composition of the cuticle and that both contain large proportions of resilin. Micro-indentation experiments revealed that the force required to penetrate the cuticle at the wounding sites is significantly higher than at control sites. Our results demonstrate that resistance of Strepsiptera females is a direct result of an increased thickness of their cuticle at the wounding site, rather than changes in material composition. A comparison of the shape of the penises of different species of the genera *Stylops* and *Xenos* suggests that antagonistic co-evolution resulting from female resistance is

restricted to *Stylops*, where allospecific males were unable to penetrate the female's paragenital organ. Our results suggest that resistance can be a driver of trait diversity.

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**Mitochondrial genetic homogeneity of South American leafminer, *Tuta absoluta* (Lepidoptera : Gelechiidae) in Tamil Nadu, India**

South American leafminer, *Tuta absoluta* (Meyrick) (Lepidoptera: Gelechiidae), an invasive species to India, is one of the most destructive pests of tomato causing 100% yield loss. It was initially discovered outside of its original habitats in Spain in 2006, and it quickly expanded to most tomato-growing countries in Central America, Europe, Africa and Asia, where it has become a significant hazard to tomato production. Molecular markers help to compare the genetic structure and diversification of an invading species population to indigenous populations and also aid in understanding its gene flow, migratory rates and genetic diversity. In the present study, *T. absoluta* samples collected from three districts of Tamil Nadu, India were utilised for the investigation of genetic diversity of *T. absoluta* by employing a fragment in the mtDNA gene-encoding cytochrome oxidase I (COI). The results revealed that the phylogenetic tree based on all NCBI and BOLD database retrieved sequences of *T. absoluta* showed 99% similarity and clustered together in a single clade. Based on the partial COI gene, high genetic homogeneity was detected in *T. absoluta* populations of India and with rest of the world which is evident by less nucleotide variation. This startling discovery could be the result of multiple other factors and phenomena, including widespread gene flow, severe bottlenecks, the reproductive system and anthropogenic impacts and this will be examined in the context of biological invasion and pest management.

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**The Pest Genomics Initiative**

As the world population grows – along with demands for high-quality, nutritious food, produced with less impact on the environment – there is a need for new pest-control strategies that can both reduce crop losses and conserve biodiversity and ecosystems. These goals can benefit greatly from the availability of high-quality genomic resources. With this in mind, research leaders from Rothamsted Research Ltd., Bayer Crop Science and Syngenta Crop Protection are working together on a Pest Genomics Initiative (PGI) which will sequence and annotate the genomes of key global pests and beneficial insects. The results from this pre-competitive, early-stage research collaboration will be put into the public domain for the benefit of all. There are many opportunities for using high quality insect genomic data to aid the design of better, more selective crop protection compounds, for better mitigation of the effects of resistance, and for the development of biologicals and improved traits for insect control. Such genomic resources will also open up exciting new areas that are not being widely exploited at present. What is needed is high quality genome data from insect strains that are well characterised, and that are well assembled and annotated for biological function. As well as industrial research labs needing high quality information for developing novel pest control technologies, the resources will benefit academic research in many areas of entomology.

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**Conferring the Midas touch on integrative taxonomy: a nanogold-oligonucleotide conjugate-based quick species identification tool**

Nanogold or Gold nanoparticles (GNPs) have myriad applications in medical sciences. GNPs are widely used in the area of nanodiagnosics and nanotherapeutics. Non-medical applications of GNPs in biology have not been studied vis-à-vis its extensive medical applications. GNPs have great potential in the area of integrative taxonomy. We have realised that GNPs can be used to visually detect animal species based on molecular signatures. In this regard, we have synthesised ultra-small gold nanoparticles (<20 nm) and have developed a method based on interactions between DNA oligonucleotide probe molecules and small-sized GNPs, interactions between DNA oligonucleotide probe molecules and host DNA molecules, and self-aggregating properties of small-sized GNPs under high salt concentrations. Exploiting these intermolecular and interparticle interactions under aqueous conditions in the present work, we have also demonstrated the application of our procedure by using a DNA probe designed against a portion of the mitochondrial genome of the codling moth *Cydia pomonella*. This method is accurate, quick and easy to use, and can be used as an add-on tool with DNA barcoding in molecular taxonomy. We suggest design and selection of a highly specific DNA probe as a crucial step in increasing specificity and sensitivity of the procedure. Hereby, through use of gold nanoparticles, we have tried to introduce nanotechnology as a new discipline to the extensive field of integrative taxonomy where disciplines like palaeontology, embryology, anatomy and molecular biology have been in use for a long time.

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**Toxicological studies of essential oils against *Sitophilus oryzae* (L.) and *Rhyzopertha dominica* (F.), in wheat and their effect**

Experiments were conducted for toxicological studies of essential oils against *Sitophilus oryzae* (L.) and *Rhyzopertha dominica* (F.) in stored wheat. Essential oils of *Curcuma longa*, *Pinus roxburghii*, *Callistemon citrinus*, *Citrus reticulata* and *Lantana camara* were evaluated against *S. oryzae* and *R. dominica*, for fumigant toxicity, mortality and repellent activity. The fumigant toxicological study of *C. longa*, *P. roxburghii*, *C. citrinus*, *C. reticulata* and *L. camara* essential oils at 0.4% or combination of *C. longa* + *P. roxburghii*, *C. longa* + *C. citrinus*, *C. longa* + *C. reticulata*, *C. longa* + *L. camara*, *P. roxburghii* + *C. citrinus*, *P. roxburghii* + *C. reticulata*, *P. roxburghii* + *L. camara*, *C. citrinus* + *C. reticulata*, *C. citrinus* + *L. camara*, and *C. reticulata* + *L. camara* essential oils at 0.2 % concentration caused full inhibition in progeny development of *S. oryzae*, and *R. dominica*, in stored wheat. The essential oils of *C. longa*, *P. roxburghii*, *C. citrinus*, *C. reticulata* and *L. camara* at 0.4 % concentration resulted 100% mortality of *S. oryzae*, and *R. dominica* after twenty-four hours of treatment. The tested essential oils had highly repellent activity against *S. oryzae*, and *R. dominica*. All tested essential oils were highly effective as fumigant toxicity, mortality and repellent activity against *S. oryzae*, and *R. dominica*. The tested essential oils at 0.2 and 0.4 % concentration do not affect percent germination, vigour index and significance of viability after one year of stored wheat.

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**Identification of a gut-specific antimicrobial peptide in *Phlebotomus papatasi* induced by *Leishmania major* infection**

*Phlebotomus papatasi* is a vector of *Leishmania major* parasites causing cutaneous leishmaniasis in the Old World. In the vector, parasites develop in the gut within a diverse microbial environment, and the sand fly immunity responds to this complex system to maintain a balance. We focused on molecules involved in innate immunity such as transcription factors *dorsal* and *relish*, belonging to Toll and IMD pathways respectively, and antimicrobial peptides attacin and defensin. We investigated the expression of these genes in response to different bacteria loads or *Leishmania* infection using qPCR. First, we compared the gene expression in larvae at different developmental stages fed on microbe-rich food compared to autoclaved food. We observed an increase in both transcription factor expression in the early L4 stage. Attacin expression increased in all stages, while defensin was increased in L2 and L3 stages. Our results show that an increased gut microbial load can upregulate these genes depending on the larval stage. Second, we used sand flies treated with antibiotics to deplete the commensal bacteria, and infected with *L. major*. The gene expression was analysed in samples collected at several times post-infection in comparison to non-infected females. We identified a *P. papatasi* gut-specific defensin gene upregulated in the late phase of *L. major* infection, while in sand flies with recovered gut bacteria it occurs at earlier times. Identifying a tissue-specific gene involved in the sand fly immune response upregulated by *L. major* infection is important for future genetic-based strategies to control the parasite transmission.

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**Common resistance mechanisms are deployed by plants against sap-feeding herbivorous insects**

Sap-feeding herbivorous insects are important agricultural and horticultural pests that cause significant plant damage with economic consequences for food producers. A key avenue being explored to improve crop protection against herbivorous insects is the development of crop varieties that are more resistant to, or tolerant of, insect damage. The Electrical Penetration Graph (EPG) technique is a unique method that is used to monitor the feeding behaviour of sap-feeding herbivorous insects. A key application of the EPG method in crop protection research is to identify the resistance mechanisms present in resistant plant types. As a result of extensive examination of the feeding behaviour of sap-feeding insects on susceptible vs. resistant plant types, there is a comprehensive and robust archive of scientific literature available that can be screened to identify whether resistance mechanisms are common across multiple plant families and to highlight any common traits associated with plant resistance against different insect groups. Here we report the preliminary results of a meta-analysis and literature synthesis where the feeding behaviour of economically important sap-feeding herbivorous insect groups (aphids, leafhoppers, planthoppers, psyllids, whiteflies) on resistant vs. susceptible plant types was examined. Our results suggest that the resistance mechanisms deployed against sap-feeding herbivorous insects are widely conserved across multiple plant families and that similar mechanisms are active against multiple insect groups. We identify common resistance mechanisms and our results indicate that the main resistance mechanisms are located in the vascular tissue, with decreases in plant-sap ingestion representing the main resistance mechanism identified.

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**Characterisation of larval habitats and target site *kdr* mutations in *Aedes aegypti* in Saudi Arabia**

*Aedes aegypti* (Diptera: Culicidae) is the main vector of dengue, chikungunya, Zika, and yellow fever viruses worldwide. In Saudi Arabia, many outbreaks and cases of dengue fever have been reported since 1994 and have increased in recent years. Vector control mainly uses pyrethroids in outdoor and indoor space spraying. Still, there are no reliable reference data on common larval ecological habitats in Saudi Arabia. Here, we surveyed the southwestern region of the country during the peak season (December and January) for *Aedes aegypti* larvae. The collected samples were assayed for resistance mutations in the target-site mechanism using PCR amplification, sequencing and genotyping. Thirty-three provinces were visited in Jazan, Sahil and Makkah regions. Larvae of *Aedes aegypti* were reported positive in 88 sites. The most positive sites were revealed to be air conditioning water containers, followed by animals' water sources, then water coolers in mosques and neighbourhoods. Additionally, three *kdr* mutations were identified: domain II S989P (TCC → CCC), V1016G (GTA → GGA) and domain III F1534C (TTC → TGC). The allele frequency of mutations varied between regions. Community awareness and engagement to eliminate these sites is critical to minimise the intensive spread of insecticide resistance and to develop effective management strategies.

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**The biology and 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 and daylength 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 is 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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**The effects of heat on the behaviour and life-history traits of sedentary antlions**

One of the key features of climatic changes in the Anthropocene is an increase in the frequency and intensity of heat-related weather events, such as heatwaves. Here, we present a series of results on

the effects of exposure to heat in antlions (Neuroptera: Myrmeleontidae). These peculiar insects spend the majority of their lives as larvae and live in sandy habitats where they create aggregations of pit-traps to hunt small arthropods. We demonstrate that, when exposed to heat, antlion larvae show increased mortality and a reduction in hunting activity. Furthermore, following heat exposure, they show prolonged developmental time, establish smaller pit-traps and display a decrease in neighbouring distance. In addition, they display higher responsiveness to prey cues. While some of the listed effects clearly decrease individual fitness, others might indicate larval attempts to compensate past experiences. The severity of these effects, on the other hand, depends on the species, with little effect in those inhabiting sunny, open areas and pronounced effect in those inhabiting shaded, sheltered areas. Our results help to consider the potential effects of heat on various aspects of the biology of insects in general and other sit-and-wait predatory insects in particular.

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**Evaluation of the colour and height of sticky traps in the attraction of onion thrips, *thrips tabaci* (L.)**

The results of the current study indicated that yellow-coloured traps which were installed at 75 cm above the ground were the suitable choice for monitoring onion thrips. Use of yellow-coloured sticky traps may not be solely able to restrict the build-up of thrips population during the entire crop growing period. However, they can be integrated with other components of IPM where detection and monitoring of thrips population is an integral part to decide upon commencement of pesticide application.

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**A comparative analysis of indoor insect pests and illnesses of inhabitants in Malappuram, Kerala, India.**

Indoor insect pests have a direct and negative impact on human health by causing annoyance, inflicting bites and stings, causing allergic reactions and transmitting diseases. The increased amount of time spent indoors by an individual, particularly during the current pandemic, and its long-term effects, makes it especially urgent to establish health-based goals for indoor air pollutants. Factors that impact indoor air quality include chemical contaminants such as pesticides, disinfectants, combustion gases and biological contaminants such as animal dander, mould, pollen and dust mites. Certain volatile and non-volatile organic compounds, i.e., semiochemicals and pheromones, secreted by indoor insect pests (ants, bugs, beetles, weevils, cockroaches, houseflies, mosquitoes, etc.) are an important component of indoor air quality. Volatile compounds have been associated with health disorders such as eye irritation, vascular nervous dysfunction, acute chronic health pathologies and even cancer. The indoor insect population was quantified from 404 indoor spaces in different villages and municipalities from the most populated district of Kerala in India, focussing on the features of the indoor systems and the symptoms observed by the inhabitants. Information was collected regarding the number of inhabitants, age, structural components and ventilation status of the indoor spaces. The surrounding environment, biological contaminants and possible reasons that the inhabitants thought was behind the increase in the number of certain pests were recorded. The number of increasing allergic patients in the past few years and increasing health issues reported from indoor spaces with a higher number of indoor pest populations signifies their impact on humans.

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**Investigating the tarsonemid (Acari: Heterostigmata) mites of Himalayan forests In eastern India**

The family Tarsonemidae Canestrini and Fanzago, 1877 includes a group of tropical and subtropical mites consisting of more than 600 species which include phytophagous, fungivorous, algivorous and insect parasitic species living in various terrestrial, arboreal, subcortical or nidicolous habitats. India, being one of the 17 megadiverse countries supports a rich biodiversity of animal fauna accounting for 6.4% of species worldwide while constituting only 2.4% of the total geographical land surface. Among the four major biodiversity hotspots of India, the Indian Himalaya has the highest land coverage which potentially harbours a rich diversity of arthropod taxa due to extreme altitudinal variation, environmental variation and huge assemblage of different flora and fauna. Among the total arthropod fauna documented from India until 2017, 35% (mostly insects, spiders, crustaceans and myriapods) were recorded from Himalayan Mountains which accounts for 88% of all animal biodiversity of this region. Till the year 2020, only two species of *Tarsonemus* and three species of *Steneotarsonemus* were described from India of which three were from south India and two from the Indo-Gangetic plains but Indian Himalayan forests remained unexplored. Our recent exploratory surveys in this region registered several new species of *Floridotarsonemus*, *Metatarsonemus*, *Fungitarsonemus* and *Steneotarsonemus* associated with both cultivated crops and wild vegetations such as Rhodendron, Cinchona, Tea, Coffee, Alstonia, Annona, Cadamba, Citrus, Prunus, Jasminum, Tiger grass and Bamboo.

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***Aedes aegypti* borne viruses and insecticide resistance in Colombia**

Arboviruses including dengue, Zika and chikungunya are amongst the most significant public health concerns worldwide. Their control relies heavily on the use of insecticides to control the vector mosquito *Aedes aegypti*, the success of which is now threatened by widespread insecticide resistance. This study investigated arbovirus incidence and *Ae. aegypti* insecticide resistance in Colombia, one of the most heavily burdened countries, using a holistic and multifactorial approach. Arbovirus incidence and factors influencing it in three distinct Colombian regions, Bello, Cúcuta and Moniquirá, were investigated using epidemiological data. Temephos susceptibility was profiled in *Ae. aegypti* larvae from Bello and Cúcuta and resistance-associated differential gene expression (DGE) characterised using RNA-Seq. Finally, rapid evaporative ionisation mass spectrometry (REIMS) was trialled as a novel tool for the rapid identification of insecticide resistance in *Ae. aegypti* larvae. The results show differences in the burden of arboviruses in the three Colombian regions over the study period of 2007–2017 and identify climatic and socioeconomic factors associated with disease burden. Cuticle biosynthesis, ion exchange homeostasis, an extensive number of long non-coding RNAs, and chromatin modelling were among the differentially expressed genes in field resistant *Ae. aegypti* larvae. The results also demonstrate the over estimation of DGE that occurs when only a field-to-lab comparison is used. Classification models built using REIMS mass spectra were able to distinguish between temephos-resistant and temephos-susceptible larvae, demonstrating the potential use of REIMS as a novel and rapid approach to identifying insecticide resistance in *Ae. aegypti*.

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**First data of the presence of *Aedes albopictus* (tiger mosquito) in Kosova**

The tiger mosquito, *Aedes albopictus*, is an invasive mosquito species that is considered an important vector of about 22 arboviruses, among which are dengue, chikungunya and Zika. Despite the investigations carried out for the presence of this specie in Kosovo since 2017 under the framework of the VectorNet project, there has been no record of *Ae. albopictus* in the country until now. Here we report the first detection of the tiger mosquito *Ae. albopictus* in the territory of the Republic of Kosovo. A field investigation in July 2020 confirmed the presence of males, females, by HLC and eggs in the ovitraps at the village of Zhur. Ovitrap with seed germination paper have been deployed at point of entry Morina, in Prizren, Pand and several villages near the border with Albania. Monitoring was made in 10 stations, 36 sampling stations in the northern part of Kosovo, for 7 weeks with ovitraps and BG sentinel. Fifty-two out 81 ovitraps were positive for the presence of *Ae. albopictus* eggs. In total 48 eggs were collected and transported to the laboratory of Entomology, University of Prishtina. The eggs were successfully hatched and larvae were reared to adults (18 male/30 female). The adult identification is done morphologically. The citizen science platform Mosquito Alert (AIM Cost action) was presented to the local community to raise local participation and to have more evidence from the other areas. The evidence of the first presence of the tiger mosquito is very important for the health authorities in Kosovo. Starting a surveillance program and implementation of control measures is necessary in order to prevent risk to public health and to mitigate the nuisance problems that *Ae. albopictus* creates during the daytime.

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**36) Jason Newton (Scottish Universities Environmental Research Centre, UK)**

**Using stable isotopes to identify migrant insects**

Insect migration and dispersal are widespread. Much has been learned from radar studies, mark-recapture and tagging. Stable isotopes offer an alternative approach since they are intrinsic markers and thus every insect captured and measured reveals information about that individual's location. Isoscapes (=isotope landscapes) are maps which plot the spatial distribution of stable isotopes in a given sample, but there is no UK-wide isoscape to interrogate. Measuring isotope ratios in a resident insect is an essential precursor to identifying migrant individuals from elsewhere. Thus, I have measured H, C, N and S isotopes in 299 individuals of the non-migratory oligophagous Brimstone Moth (*Opisthograptis luteolata*) collected from 93 locations around the UK and Ireland by members of the National Moth Recording Scheme. In the poster I present the isoscape maps for the four elements and discuss how the resulting patterns relate to what we know about moth diet, climatic isotope variation and geology. An insect of a different isotopic composition outwith the British or Irish range might be taken at face value as suggesting that it is a migrant. Alternatively (since we have no continental insect isoscapes to compare), one might want to focus on areas that are isotopically unique; in this sense, sulphur isotopes may be of particular use for distinguishing individuals from areas of unique geology. Isoscape patterns may (with care) predict isotope compositions of other, herbivorous, non-aquatic, chitinous taxa. Such isoscapes, when extended beyond the UK and Ireland, would provide a useful tool to elucidate insect migration.

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## **Creating bare ground attracts ground-nesting solitary bees**

Solitary bees have experienced a decline in both diversity and abundance over the past decade. Although their foraging requirements have been the subject of some recent studies, their nesting requirements have received little attention. Some species of ground-nesting solitary bees have shown an affinity for hard, bare ground as preferred locations for nests. Here we assessed two different methods for creating bare ground plots on farmland, and observed the different rates at which these plots recruited ground-nesting bees. At 19 locations, three ~ 6 meter-squared plots were created. One was scraped bare using machinery, a second was sprayed-off with herbicide, and the third was left undisturbed as a control plot. The results showed a significantly greater number of nests in the scraped plots compared to the sprayed or control plots, with the majority of these nests being created in April. This trial shows that an agri-environment scheme could be introduced to support the creation of nesting areas for solitary bees on farmland.

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#### **Low species diversification among pigmented dragonflies inhabiting lotic environments**

In dragonflies, species richness shows a marked variation between lineages. Species diversification in this lineage has been linked with habitat but the role of other factors has not been explored. Wing pigmentation, one of the most conspicuous and variable traits in dragonflies, has been associated with speciation in other taxa. Using models that take into account unknown factors, here we investigate the role of wing pigmentation (present/absent) and retest the role of habitat (lentic/lotic) in species diversification in dragonflies. We find that wing pigmentation is associated with slightly slower diversification compared to unpigmented lineages. Inhabiting a lentic habitat is associated with faster diversification. Considering both factors in a single model, lentic environments are associated with faster diversification compared to lotic habitats regardless of pigmentation status. In contrast with results across the whole tree, in lotic environments, wing pigmentation is associated with slightly faster diversification rates compared to non-pigmented species. Ancestral state reconstruction revealed that the last common ancestor of dragonflies was most likely non-pigmented and lived in lotic habitats. Our study provides evidence that wing pigmentation and habitat in conjunction have an important influence in dragonfly species diversification with habitat being a better differentiator than pigmented status.

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#### **Study on population dynamic of fruit fly, *Bactrocera* spp. (Tephritidae: Diptera) and species diversity**

**ABSTRACT AWAITED**

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## **Phytochemical assemblage in insect-induced foliar galls and its correlation to gall development: a case study of three model plants**

In the domain of insect–plant interactions, indirect defence in plants against insect herbivory establishes several hypotheses. Plants defend themselves against insect attacks by attracting natural enemies that kill feeding herbivores and prevent them from causing damage. Insects feeding on different plant tissues can initiate such indirect defence, and the plant gall represents an ideal example of it. Galls exhibit such indirect defence by delivering both nutritive and protective substances to the injured tissues in significant amounts. In response to herbivore attacks, plants manipulate a blend of phytochemicals and develop complex gradients of several chemical candidates in the galling tissue for tissue growth and differentiation, as well as refurbishing defence-related molecules. In this context, we aimed to investigate the extent of growth-promoting and defence-supporting phytochemicals displayed in galling tissue compared to non-infected tissues. Our study also aims to show how the chemical gradients change as gall maturity progresses. After analysing eighteen foliar phytochemicals from three model plants at various galling stages, we conclude that the majority of gall-inducing phytochemicals accumulate gradually with the progression of gall-tissue proliferation, which appears to be co-evolved by modifying chemical gradients in host tissue. Explaining a complex phenomenon such as insect infestation on plants and the resistance to additional insect attacks by the assemblage of chemicals in affected plant tissue induced from invasive insects is largely unknown. This study provides essential knowledge in gall biology, highlighting an unresolved phenomenon of the adoption of a unique strategy by the gall-maker and the host-plant.

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#### **Double the trouble? Impacts of Acute bee paralysis virus and a neonicotinoid insecticide on black garden ants, *Lasius niger***

Pesticides and pathogens are amongst the most important drivers of current insect declines. It is known that simultaneous exposure to multiple stressors results in complex interactive effects, ranging from antagonistic, over additive to synergistic. However, the interaction between pesticides and pathogens remains poorly understood in ants. In this study, we investigated the impacts of single and combine exposure scenarios with two exemplary stressors, i.e., the neonicotinoid thiamethoxam and Acute bee paralysis virus (ABPV). In a fully-crossed laboratory assay we evaluated the interaction between a field-realistic concentration of thiamethoxam and ABPV in *Lasius niger*. Colony development was monitored over 64 weeks before assessing body mass, neonicotinoid residues and virus titres of workers and queens, as well as worker behavioural activity. The data show that the effects of pesticide and virus stressors in social insects can vary depending on the effect level under investigation (individual-, caste-, colony-level). Activity and locomotion of workers were impaired by ABPV but not by thiamethoxam. Body mass of workers but not of queens was reduced by neonicotinoid exposure. ABPV infections were facilitated by thiamethoxam, but only in queens. The data further indicate that virus exposure had no effect on body mass and did not compromise detoxification. Overall, our data suggest additive effects at the level of individuals and castes. However, at the colony level co-exposure with both stressors elicited an antagonistic decrease in colony size. This study highlights the need for long-term holistic risk assessment of stressors and their interactions to protect social insects.

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### **First record of *Phlebotomus perniciosus* in a dog shelter in Lugo province (Galicia, Northwest Spain)**

**Introduction** Phlebotomine sand flies of genus *Phlebotomus* are proven vectors of the zoonotic parasite *Leishmania infantum*, responsible for human and canine leishmaniasis in the Old World. Eleven species have been described in Spain, but two of them, *P. perniciosus* and *P. ariasi*, are of medical and veterinary concern. Regarding the Galician Autonomous Community, previous studies have revealed their presence in Ourense and Pontevedra provinces, and only *P. ariasi* in Lugo. With the aim of deepening the knowledge of vectors, the Galician Entomology Surveillance Network (ReGaViVec) was created in 2017.

**Material and methods** Taking into account phlebotomine biology, a research plan was designed in a dog shelter located in Quiroga County (Lugo, Galicia) from May to October of 2019. In order to capture these arthropods, a CDC UV light trap was hung 1.5-2 m above the ground and connected bimonthly during one night. Once the device was disconnected, the trap container was carefully transported to the laboratory for taxonomic classification.

**Results** A total of 53 *Phlebotomus* spp. specimens were captured and the *P. perniciosus* species represented 60% of the total. This is the first identification of the mentioned species in the province of Lugo.

**Conclusion** The first detection of *P. perniciosus* in the Galician province of Lugo once again demonstrates the importance of entomological surveillance in the territory and alerts veterinarians and doctors to the risk of transmission of *L. infantum*.

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### **Mid-field woodlots: are they attractive habitats for wild bees (Apiformes) in the agricultural landscape?**

It is important to maintain refuge habitats in agricultural landscapes that provide suitable nesting sites for wild bees and a rich food resource. This study aimed to: (1) characterise wild bee communities in three habitat types in the agricultural landscape, i.e., non-linear and linear woodlots (refuge habitats), compared to thermophilous oat-grass meadows (control plots); (2) identify indicator species of the Apiformes for non-linear woodlots, linear woodlots, and oat-grass meadows. The values of species richness and abundance of wild bees were significantly higher in linear woodlots compared to non-linear woodlots. Simultaneously, species richness of wild bees within oat-grass meadows was significantly higher compared to linear and non-linear woodlots. On the other hand, abundance of the Apiformes was significantly higher in oat-grass meadows than in non-linear woodlots. The Shannon index of diversity was significantly higher in meadows than in both non-linear and linear woodlots. In order to focus on indicator species, IndVal analysis was performed on individual habitats. In total, 28 indicator species were recorded: 1 for linear woodlots (*Lasioglossum parvulum*) and 27 for meadows. Results of this study provide valuable tips for property managers, farmers, and various charitable organisations for protection of existing mid-field woodlots and shaping new ones. The findings will make it possible to preserve and/or increase the protection of wild bees in the agricultural landscape. The protection of existing woodlots and establishment of new

linear woodlots in agricultural landscapes that are farmed intensively seem to be the least problematic from the point of view of property owners.

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**44) Zsófia Varga-Szilay (Institute of Biology, Eötvös Loránd University, Budapest, Hungary)**

**Safe heavens or poisonous traps: pesticide use in bee-friendly gardens**

The importance of urban gardens as refuges for pollinators is increasingly acknowledged. However, what risks garden pesticide use may pose to pollinators in these urban green islands is little-known.

Thus, we conducted an online survey to measure plant growers' dependence on pesticide use in Hungary, particularly to investigate smallholders' use and their attitude to wild pollinators. Of the 445 people who completed the questionnaire, 286 had less than 1 hectare of land and only these were included in our analysis. We used machine learning decision trees to investigate socio-economic factors influencing whether pesticide was used in the gardens. Although 81% supported wild pollinators, primarily by pollinator-friendly flowers and bee-hotels, 58% still used pesticides in their immediate environment. Pesticide use was more widespread among gardeners than we expected, and almost all respondents who considered pesticides harming wild pollinators as an unimportant issue used pesticides. Yet, even of those smallholders who acknowledged pesticide use as a serious problem for pollinators, 53% applied them, which can pose a high risk for pollinator communities in allotments and urban gardens. Our questionnaire highlights that pollinator-friendly gardens could become ecological traps for pollinators because pollinators are attracted to bee-friendly gardens, where general pesticide use can stress them in large numbers if gardeners use these chemicals. To fully support pollinators in urban areas plant growers should curb their pesticide use. More research should focus on understanding plant growers' motivations and practices in their gardens and allotments and the trade-offs between pesticides use and pollinator support in urban areas.

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**Infravec2: Expanding access to tools and resources for insect vector research**

The overall objective of the Infravec2 project is to integrate key specialised research facilities necessary for European excellence in insect vector biology, open them for European access, and develop new vector control measures targeting the greatest threats to human health and animal industries. The 24 partners include Institute Pasteur and IRD (France), Imperial College and Pirbright Institute (UK), IRTA (Spain), FORTH (Greece), Radboud University and Wageningen University (Netherlands), Max Planck Institute (Germany), and the European Bioinformatics Institute-EMBL. The partners, including 4 commercial companies, hold the major European biosecure insectaries for experimental infection and containment of insect vectors under Containment Level 2 and 3 (CL2/CL3) conditions, genetic editing of mosquito genomes using CRISPR/Cas9, facilities for the study of insect vector behaviour, facilities for the testing and evaluation of insecticides, facilities for genetic and data analysis of insect vectors, and front-line field sites in Africa, the Pacific, and the Americas. Lack of access to these key infrastructures limits European vector research and vector control development. The resource is open and publicised to European researchers, with the realistic expectation to consolidate European global leadership in insect vector biology. Deployment of common standards is another large goal of this project. Infravec2 will implement comparable standards across the secure insectary facilities as a world first. Networking activities will assure that facility standardisation is

implemented, producing a step change in European vector biology research and the lab-to-rollout vector product pipeline.

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**Preliminary analysis of the main species of ticks affecting people in Galicia (northwest Spain)**

Ticks can transmit a wide variety of pathogens that affect animals and humans, and the infestation behaviour of the different stages in the host body seems very valuable to reduce the risk of infestation. The incidence of tick-borne human diseases is underestimated in Spain due to the small number of studies available. There is an elevated incidence of Lyme disease, transmitted by *Ixodes ricinus*, in Galicia (NW Spain). Within the activities of the Galician Vector Surveillance Network (ReGaViVec), a total of 269 ticks were obtained from 233 humans in Public Health Centres from this region between June 2018 and December 2019. The specimens were identified morphologically to species-level and developmental stages. Data regarding the attachment sites (head, trunk, legs, arms, pelvis, no attachment and unknown), and their age (<13, 14-59 and ≥60 yr) were also recorded. Most bites were caused by *I. ricinus* nymphs (46%) and females (28%), commonly taken from the trunk of the body (31%), legs (29%) and head (10%). Adults (14-60 yr) were most affected (41%), then older people (>60, 24%). Few stages of *I. hexagonus*, *Dermacentor marginatus*, *D. reticulatus*, *Rhipicephalus sanguineus*, *R. bursa* and *Hyalomma marginatum* were also identified. *Ixodes hexagonus* was found in the head (36%), but *R. sanguineus* and *R. bursa* were widely distributed. It is concluded that people should be educated about prophylactic methods against tick infestation and early removal of attached specimens to prevent tick-borne diseases.

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**Importance of surveillance in children's summer camps to prevent the spread of tick-borne diseases**

Summer camps bring many benefits to children because of the possibilities to develop a wide range of outdoor activities, to connect with and enjoy nature, to participate in different sports, and to communicate with other children. To achieve these goals, many summer camps are located in areas surrounded by lush vegetation, forests or even by the sea. Although these are usually fenced facilities, there are often different areas accessible to micro-mammals that can carry ticks. These ectoparasites develop their life cycle in areas with adequate moisture and vegetation. Based on a previous report that several children and monitors had been bitten by ticks in a camp located in Galicia (northwest Spain), six campsites in this Autonomous Community were sampled. As part of the activities designed in the Galician Vector Surveillance Network, these facilities were visited during the summer months (July-September), where a white flannel cloth was dragged over and around the vegetation where ticks might be present. Once in the laboratory, ticks were identified to genus and species according to morphological keys. Six adult ticks were collected in two of the six summer camps and identified as *Rhipicephalus sanguineus* (1 male) and *Dermacentor marginatus* (2 males and 3 females). These results lead us to consider the need to maintain tick surveillance in summer camps, and to implement appropriate measures to prevent the presence of ticks.

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48) **Jamie Weir (University of Edinburgh, UK)**

**Dietary generalism in the winter moth: a buffer in an uncertain environment?**

Winter moth caterpillars are abundant, economically significant early spring defoliators, which serve as a major food source for birds in many temperate woodlands. Recent literature has suggested that precisely timing their hatch date with the appearance of new, nutritionally-rich spring foliage, is extremely important for winter moth caterpillar fitness. However, almost all of this work focuses on a single larval host-plant: oak. Little consideration has been paid to the hugely generalist nature of the winter moth diet and, indeed, that of other functionally related moth species: the oak-winter moth interaction is anything but typical. Here I report the results of an experiment examining fitness (using a variety of metrics) on winter moth larvae from four British populations, fed on nine common host-plants. In contrast to assumptions typically made in the literature, oak appears to be a relatively nutritionally poor host, among the worst for survival to pupation and pupal mass attained. It is clear that host-plant species has a considerable effect on fitness, and that this effect varies geographically between populations. Species wishing to exploit newly available spring foliage must hatch in a narrow, unpredictable time window, and a polyphagous diet may buffer them against a range of environmental uncertainties, including being mistimed with any one host. To understand the impact of global environmental changes (such as climate change), it is important we consider them in light of a fuller picture of the complex ecology of the species involved – in winter moth, oak is only a single facet of that ecology.

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**Fall armyworm (*Spodoptera exempta*) population structure in Africa.**

Understanding the population structure and movements of invasive crop pests is extremely important, it can help to mitigate crop damage, and can help to understand areas most at risk through outbreaks or insecticide resistance. Determining population structure in the fall armyworm (*Spodoptera frugiperda*) in Africa has been a challenge due to genetic mutations affecting the traditionally used markers for strain identification and haplotypes; *mitochondrial cytochrome oxidase I* (COIB) and the Z-chromosome-linked *Triosephosphate isomerase* (Tpi) haplotypes. Here, traditional markers (COIB, TpiE4 and TpiI4) were used alongside highly variable repeat regions called microsatellites to determine what the two approaches can tell us about fall armyworm population structure in Africa. There was very limited genetic diversity using the traditional markers and there was very little evidence of genetic structuring between fall armyworm populations across Africa, with most genetic variation occurring between individual larvae regardless of where they were collected. There was much more genetic diversity identified using the microsatellite approach, enabling a more in-depth analysis of population structure that revealed a largely panmictic population of fall armyworm, however, there was some evidence of genetic structuring between countries. This genetic structuring largely follows known wind patterns, and it is hypothesised here that fall armyworm are using their ability to engage with high-altitude winds to move throughout Africa leading to frequent population mixing. These combined approaches provide important evidence that genetic mixing between fall armyworm populations throughout Africa may be more common than previously reported.

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### **High-throughput Screening of Insect Larvae as Replacement for Mammalian Models of Inflammatory Bowel Disease**

Mammalian models of human disease are expensive and subject to ethical restrictions, encouraging replacement, reduction and refinement. We therefore developed an alternative high-throughput screening approach using larvae of the tobacco hornworm *Manduca sexta*, combining widely-used diagnostic imaging methods for the comprehensive characterisation of aberrant anatomy, tissue structure and metabolism. As proof of principle, we induced gut inflammation using bacterial and chemical stimuli to generate a colitis-like phenotype, revealing highly significant alterations in morphology, tissue properties, and intermediary metabolism. The phenotype became more severe with disease progression but could be rescued by antimicrobial treatment. In independent experiments, the activation of dual oxidase (DUOX), a putative key mediator of inflammatory bowel disease (IBD) and a member of the NADPH oxidase family, led to similar, dose-dependent alterations, which could be attenuated by pharmacological interventions. The close relationship between human and *M. sexta* DUOX ensures that this insect-based model will be suitable to investigate the etiology of human IBD, while improving animal welfare by allowing the replacement of mammals in preclinical studies of drugs and targets relevant to gut inflammation.

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### **AWAITING CONFIRMATION**

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### **Oviposition preferences of an herbivore and its parasitoids are regulated by volatiles, immune status, and enemy-free space**

Oviposition choice is critical for offspring survival but the correlation between preference and performance is still unclear. Here, we report the preference-performance relationship between *Plutella xylostella* and associated parasitoids on two closely related host plants. Mustard was the preferred host for adult moths but larval growth was higher on cabbage. Mustard feeding improved larval immune status and survival against egg parasitoids as well as *Bacillus thuringiensis*. Mustard-fed larvae were attractive to the specialist parasitoid, *Cotesia vestalis* while cabbage-fed larvae were



attractive to generalist, *Bracon brevicornis*. Distinct body odour profiles were recorded for larvae feeding on different host plants and these odours served as short-range cues for parasitoids. Generalist parasitoid fitness was affected by larval diet, whereas specialist parasitoids showed a fitness consequence only when larvae were co-infected. Taken together, our results show that oviposition is context-dependent and can be understood better by studying multiple fitness parameters and interactions with different natural enemies.

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