

# Keynote Address

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## **Making taxonomy and collections-based research relevant in a changing world**

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[Bryan Lessard](#)

*Australian National Insect Collection, CSIRO, Black Mountain, Clunies Ross Street, Acton, ACT, 2601*

In a time of taxonomic decline, insect apocalypses and fake news, it's becoming increasingly more important to conduct and promote our biodiversity research. Recent advances in technology have breathed new life into natural history collections: metabarcoding allows us to identify new insect pollinators in threatened alpine zones; whole genome shotgun sequencing allows us to map mitochondrial genomes from pinned specimens of medically important mosquitoes; and transcriptome sequencing allow us to identify protein-coding genes that cause anaphylactic reactions to horse fly bites. Modern digitisation has also rapidly increased the speed at which we database our collections, opening them to the public and other researchers throughout the world. Taxonomic knowledge and collection data can be useful to inform industry and government policy, as a recent taxonomic revision of the Australian soldier flies led to collaborations with small to medium sized businesses and the opportunity to advise policy makers on the use of insects as livestock feed. Collections can also provide specimen data to support global industry trends, as the United Nations estimate that the emerging edible insect market will be worth \$1.5 billion by 2023. A recent Australian edible insect symposium identified a commercial need for native edible insect species that are currently being identified using entomological collections. New platforms of communication like social media have revolutionised the way we share our science in real time and allow us to reach a wider audience formed of the general public, researchers and industry. By embracing new technologies and ways of communication, we can not only enhance our knowledge of the natural world, but also share our science to a wide audience and foster respect for taxonomy and collection-based science.

*Monday 2 December  
09:45 – 10:45  
Plaza Room 8*

# Keynote Address

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## Fossils, phylogenies and the age of insects

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[Seraina Klopstein](#)

*Naturhistorisches Museum, Basel, Switzerland*

Calibrating molecular trees to reflect absolute time allows us to interpret them in the light of major events in the deep past, be it the movement of continents, a devastating asteroid impact, or the radiation of another group of organisms. The primary source of information for calibrating the molecular clock is the fossil record, which is unfortunately notoriously patchy, especially in terrestrial organisms. There are two major approaches for integrating information from fossils into dating analyses, node dating and total-evidence dating, and they differ strongly in their assumptions.

Node dating relies on the *a priori* placement of a fossil in the tree based on its morphology; if that placement is well supported, it arguably confers a minimum age for the subtending node. Unfortunately, some largely arbitrary probability distribution then has to be chosen, which is supposed to reflect the likelihood of that node being only a little versus much older than the fossil. Total-evidence dating, on the other hand, integrates fossils directly into the analysis via a matrix of morphological characters; both fossil placement and the associated branch lengths are determined by the morphological characters.

After contrasting the assumptions of the two approaches, I propose the concept of the “minimum age tree” as a paradigm shift in node dating. While avoiding arbitrary assumptions, a minimum-age tree still confers a plethora of information and allows for the testing of hypotheses from biogeography and co-evolution. I illustrate the approach with the insect tree of life and show what types of questions can be assessed in this framework.

Moving to total-evidence dating, I discuss recently identified pitfalls related to missing data, taxon sampling and the morphological clock, and suggest future directions for consolidating the approach. Finally, I present the first dated tree of Darwin wasps (Ichneumonidae), the most species-rich family of parasitoids, and discuss it in the context of the dated tree of their insect hosts.

*Tuesday 3 December  
09:00 – 10:00  
Plaza Room 8*

# Keynote Address

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## **Mites on insects: the other other 99%?**

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[Owen Seeman](#)

*Queensland Museum, P.O. Box 3300, QLD, 4101*

Mites are renowned for their dauntingly minuscule size and, partly due to this, have colonised the most extraordinary places and habitats, often in curious symbiotic relationships. One of the most prevalent of these symbioses is their interactions with insects, many of which defy simple definitions. Here, I explore some of these relationships, especially those I have studied over the past twenty-five years of acarology: mites riding on honeybees and moths; in astonishing abundance and diversity on saproxylic beetles; parasitising grasshopper wings; and as sexually-transmitted parasites beneath the wings of carabid and chrysomelid beetles. Mites seem so ubiquitous on insects that ecologists have wondered whether every species of insect could be matched by one species of mite. Such a claim seems extraordinary, and if true, how do we tackle this undiscovered cornucopia of species? If untrue, then why are some groups of mites so diverse on certain groups of insects? In an effort to get some answers, I am surveying the expansive collections of beetles at the Queensland Museum, with a focus on four of the largest families: the Carabidae, Chrysomelidae, Curculionidae and Scarabaeidae. Preliminary results show that the Carabidae are remarkably popular with mites, but the other three families paint a more complex and fascinating picture of mite-insect diversity.

*Tuesday 3 December  
13:15 – 14:15  
Plaza Room 8*

# Keynote Address

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## **Bees are not the only flower visitors to global food crops**

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[Romina Rader](#)<sup>1</sup>, S.A. Cunningham<sup>2</sup>, B.G Howlett<sup>3</sup>, J. Jones<sup>1</sup> & D.W. Inouye<sup>4,5</sup>

<sup>1</sup>*School of Environmental and Rural Science, University of New England, Armidale, New South Wales 2351, Australia*

<sup>2</sup>*Fenner School of Environment and Society, The Australian National University, Canberra ACT 2601, Australia*

<sup>3</sup>*The New Zealand Institute for Plant and Food Research Limited, Christchurch 8140, New Zealand*

<sup>4</sup>*Department of Biology, University of Maryland, College Park, Maryland 20742, USA*

<sup>5</sup>*Rocky Mountain Biological Laboratory, Crested Butte, Colorado 81224, USA*

Insects other than bees (i.e., non-bees) have been acknowledged as important crop pollinators, but our understanding of which crop plants they visit and how effective they are as crop pollinators is limited. To compare visitation and efficiency of crop-pollinating bees and non-bees at a global scale, we reviewed papers published between 1950 and 2018 concerning the visitors and pollinators of 105 global food crops that are known to benefit from animal pollinators. Of the 105 animal-pollinated crops, 77% are visited by both bee and non-bee taxa, with a total gross domestic product (GDP) value of US\$780.8 billion. For crops with a narrower range of visitors, the eight that favour non-bees have a value of US\$1.2 billion, compared to US\$19.0 billion for the 15 that favour bees. Limited pollinator efficiency data were available for one or more taxa in only 58% of the crops. Among the non-bees, some families were recorded visiting a wide range of crops (>12), including six families of flies (Syrphidae, Calliphoridae, Muscidae, Sarcophagidae, Tachinidae, and Bombyliidae), two beetle families (Coccinellidae and Nitidulidae), ants (Formicidae), wasps (Vespidae), and four families of moths and butterflies (Hesperiidae, Lycaenidae, Nymphalidae, and Pieridae). Among the non-bees, taxa within the dipteran families Syrphidae and Calliphoridae were the most common visitors to the most crops, but this may be an artefact of the limited data available. The diversity of species and life histories in these groups of lesser-known pollinators indicates that diet, larval requirements, and other reproductive needs will require alternative habitat management practices to bees.

*Wednesday 4 December*

*09:00 – 10:00*

*Plaza Room 8*

# Invited Presentation

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## **Breaking through the barriers – taxonomy and systematics in the Anthropocene**

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[Kevin Thiele](#)

*Taxonomy Australia, Australian Academy of Science, Ian Potter House, 9 Gordon Street Acton ACT 2601  
Australia*

Taxonomy and systematics have an image problem. We are regarded as a useful but rather fringe discipline, best relegated to the back rooms of our institutions where we will be mostly harmless. We need to understand why this is so, if we are ever to achieve the significantly enhanced investment in taxonomy and systematics that is clearly warranted for such a foundational activity as documenting life on Earth. This talk will explore the reasons why we've failed to break through in the past, and the strategies we need to break through in the future. Along the way we'll explore a key and crucial question: what, if anything, is stopping us from discovering, documenting and naming all the species of plants and animals in Australia and New Zealand, in a time frame commensurate with the urgency of the need to do so.

*Tuesday 3 December  
10:00 – 10:30 (30 min)  
Plaza Room 8*

# Abstract – Orthoptera Symposium

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## Comparative heat and desiccation tolerance in two genera of matchstick grasshopper (Morabidae)

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[Ian Aitkenhead](#)<sup>1</sup>, S. Chown<sup>1</sup> & M.R. Kearney<sup>2</sup>

<sup>1</sup>*School of Biological Sciences, Monash University, Clayton, Vic, 3080*

<sup>2</sup>*School of BioSciences, The University of Melbourne, Parkville Vic, 3010*

To understand distribution limits and how they may be influenced by climate change, we need to characterise the functional traits underlying climatic adaptation. Thermal and hydric adaptations have been little studied in Australian orthoptera with the exception of some pest species. We characterised inter-population and interspecific variation in water loss rate and heat tolerance in two genera of matchstick grasshoppers from a perennial shrub-dwelling genus *Warramaba* from arid Australia (five species) and a terrestrial forb-eating genus from southern Australia *Vandiemenna* (one species and 11 races). We used thermolimit hygrorespirometry whereby the heat tolerance is determined by ramping body temperature by simultaneously measuring activity rate and water loss rate. We also measured water loss and metabolic rates across five constant temperatures. We discuss the similarities and differences between races and species in the context of their local climatic environments and their distinct microhabitats.

*Tuesday 3 December  
12:00 – 12:15  
Plaza Room 10*

# Abstract – Pest Management

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## **Australian *Eadya* (Braconidae) as larval endoparasitoids for classical biocontrol of globally invasive Paropsine leaf beetles**

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[Geoff R. Allen](#)<sup>1</sup>, T.M. Withers<sup>2</sup>, B.J. Sharanowski<sup>3</sup>, R.D. Ridenbaugh<sup>3</sup>, S.R. Quarrell<sup>1</sup> & A.R. Pugh<sup>2</sup>

<sup>1</sup>Tasmanian Institute of Agriculture, University of Tasmania, Private Bag 98, Hobart TAS 7001, Australia

<sup>2</sup>Scion, Private Bag 3020, Rotorua 3046, New Zealand

<sup>3</sup>University of Central Florida, Department of Biology, Orlando, FL, United States of America

A number of countries using *Eucalyptus* in plantations have been the recipient of a number of invasive paropsines (Col.: Chrysomelidae: Chrysomelinae) from Australia. All species are significant defoliating pests. In a departure from the reliance upon egg parasitoids, further investigations into larval endoparasitoids began as a result of interest in locating host specific classical biological control agents. A collaboration between the University of Tasmania and Scion in New Zealand and the University of Central Florida over the last eight years has resulted in the description of four new species discovered in the field and confirmed with molecular identifications, as well as a revised key for the genus of *Eadya*. *Eadya* which are striking black and orange wasps, were found to be larval parasitoids of nine differing paropsine species, and one species studied in most detail suggest all attack any of the four larval instars during spring/early summer when they are feeding either clustered or singly on *Eucalyptus* leaves.

*Paropsis charybdis* is New Zealand's arguably most damaging eucalyptus pest, *Eadya daenerys* which attacks *P. charybdis* has now been approved for release there. The most common field host of this parasitoid in Tasmania is *Paropsisterna agricola*. *Paropsisterna variicollis* is also a pest causing concern in New Zealand and spreading rapidly. Field and laboratory host range data suggest *Eadya annleckieae* specialises on *Pst. variicollis* and *Pst. selmani*. With *Pst. selmani* being a pest of Eucalyptus plantations in Ireland, this species could become a promising biocontrol agent in both New Zealand and Ireland.

*Monday 2 December*

*12:15 – 12:30*

*Plaza Room 8*

# Abstract – Systematics and Evolution

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## Are the evolutionary rates of cockroaches and their *Blattabacterium* symbionts correlated?

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[Daej A. Arab](#)<sup>1</sup>, T. Bourguignon<sup>1,2,3</sup>, Z. Wang<sup>4</sup>, S.Y.W. Ho<sup>1</sup> & N. Lo<sup>1</sup>

<sup>1</sup>*School of Life and Environmental Sciences, University of Sydney, Sydney, Australia*

<sup>2</sup>*Okinawa Institute of Science and Technology Graduate University, Tancha, Onna-son, Okinawa, Japan*

<sup>3</sup>*Faculty of Forestry and Wood Sciences, Czech University of Life Sciences, Prague, Czech Republic*

<sup>4</sup>*College of Plant Protection, Southwest University, Chongqing, China*

Bacterial endosymbionts evolve under strong host-driven selection. Factors influencing host evolution might affect symbionts in similar ways, potentially leading to correlations between the molecular evolutionary rates of hosts and symbionts. Although there is evidence for rate correlations between mitochondrial and nuclear genes in some taxa, similar investigations of hosts and symbionts are lacking. We tested for a correlation in molecular evolutionary rates between the genomes of an endosymbiont (*Blattabacterium cuenoti*) and the mitochondrial genomes of their hosts (cockroaches). We used partial genome data for multiple strains of *B. cuenoti* to compare phylogenetic relationships and evolutionary rates for 55 cockroach/symbiont pairs. The phylogenies inferred for *B. cuenoti* and the mitochondrial genomes of their hosts were largely congruent, as expected from their identical maternal and cytoplasmic mode of inheritance. We found evidence of a correlation between evolutionary rates of the two genomes based on comparisons of root-to-tip distances and sister-pair branch lengths.

*Tuesday 3 December*

*11:00 – 11:15*

*Plaza Room 11*

**STUDENT**

# Abstract – Systematics and Evolution

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## **Phylogeny and systematics of the longhorn beetle genus *Rhytiphora* (Coleoptera: Cerambycidae)**

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[Lauren Ashman](#)<sup>1,2</sup>, A. Ślipiński<sup>2</sup>, A. Zwick<sup>2</sup> & D. Rowell<sup>1</sup>

<sup>1</sup>*Research School of Biology, The Australian National University, Acton, ACT 2601*

<sup>2</sup>*Australian National Insect Collection, CSIRO, GPO Box 1700, Canberra, ACT 2601*

The taxonomy and phylogenetic relationships of longhorn beetles have been debated for decades, with neither morphological nor molecular data reaching a consistent solution. *Rhytiphora*, the largest Australian genus of the subfamily Lamiinae, is no exception. The current concept of the genus encompasses around 200 species (from nearly 40 former genera), united by a putative apomorphy: setose patches on the male abdomen, probably for dispersing pheromones. We sequenced the mitochondrial genome of 24 pinned museum specimens, and estimated the first molecular phylogeny of Australian *Rhytiphora* using maximum likelihood and Bayesian methods. The resulting trees show that the sampled *Rhytiphora* species are divided into two clades, which do not correspond to previous generic divisions or obvious morphological traits such as body size and shape.

*Tuesday 3 December  
16:00 – 16:15  
Plaza Room 11*

# Abstract – Behaviour #2

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## **Come fly with me: searching behaviour of the parasitoid wasp *Goniozus jacintae* in response to susceptible instars of *Epiphyas postvittana***

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[Emma Aspin](#)<sup>1</sup>, M.A. Keller<sup>1</sup> & I.C.W. Hardy<sup>2</sup>

<sup>1</sup>*School of Agriculture, Food and Wine, The University of Adelaide, Adelaide, SA 5005*

<sup>2</sup>*School of Biosciences, The University of Nottingham, Sutton Bonington, Leicestershire LE12 5RD*

*Goniozus jacintae* (Farrugia) (Hymenoptera: Bethylinidae) is a common parasitoid of the light brown apple moth (LBAM), *Epiphyas postvittana* (Walker) (Lepidoptera: Tortricidae), a pest of grapevine and other crops in Australia, yet its behavioural ecology remains unstudied. A novel laboratory study was conducted in order to elucidate searching behaviour exhibited by *G. jacintae* towards susceptible instars of larval LBAM. Observations were made in a wind tunnel to allow for the wasp to express a full range of behaviours. The behaviour of *G. jacintae* and susceptibility of LBAM to parasitism varies significantly amongst instars. The wasp parasitises the third to sixth instars of LBAM, but most readily parasitises the later instars. Later instars are larger and produce more feeding damage, faeces and silk deposits than early instars, so are associated with more volatile cues that may be detected by the parasitoid. Flight duration was shortest when females were exposed to a leaf infested by fifth instars. The profile of behaviours exhibited during pre-flight and post-flight stages of the experiment varied significantly, with the identification of a ‘slow-walk’ behaviour only witnessed in close proximity to a potential host. Analysis of timing, frequency and duration of behaviours indicates that females respond differently to each susceptible instar of LBAM.

*Tuesday 3 December*  
*16:30 – 16:45*  
*Plaza Room 9*  
**STUDENT**

# Abstract – Systematics and Evolution

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## **Hymenopteran predators and parasitoids of spiders: evolutionary transitions and patterns of host switching**

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[Andrew D. Austin](#)

*Australian Centre for Evolutionary Biology & Biodiversity, School of Biological Sciences, The University of Adelaide, AUSTRALIA 5005*

Spiders are a major food resource for the developing larvae of Hymenoptera. Available biological data indicate that most groups exploit the egg or juvenile stages of spiders; it is only the Pompilidae, polysphictine ichneumonids and, to some degree, Crabronidae that have successfully utilised adult spiders as prey. Among other groups it is only the Scelionidae that have radiated as a species-rich lineage that utilise spider eggs. Recent more robust phylogenies for various hymenopteran groups, and additional biological and host data in recent years, has made it possible to track the evolutionary transitions of hymenopterans that exploit spiders as food. In this respect, this presentation will examine several groups and discuss their biology and possible limitations in switching to utilising spiders.

*Wednesday 4 December  
11:30 – 11:45  
Plaza Room 11*

# Abstract – Ticks & Lice Symposium

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## **A new species of *Ixodes* from the short-beaked echidna, *Tachyglossus aculeatus*, in Far North Queensland with a revised key to the male *Ixodes* of Australia**

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[Dayana Barker](#)

*School of Veterinary Sciences, University of Queensland, Gatton, QLD, 4343, Australia*

The new species of *Ixodes* has a distinctive ventrolateral horn-like projection not found in any other species of Australian *Ixodes*, but similar to that of *Ixodes zaglossi* from the long-beaked echidna of Papua New Guinea. I will also present a revised dichotomous key to accommodate the five males of Australian *Ixodes* described or re-described since 1970 when Dr F.H.S. Roberts published the last key to the males of Australian *Ixodes*. Now there are 26 species of *Ixodes* known in Australia.

*Wednesday 4 December*

*12:00 – 12:15*

*Plaza Room 9*

**STUDENT**

# Abstract – Ticks & Lice Symposium

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## **Australasian and other hard ticks: what's new? Three new genera among other things**

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[Stephen C. Barker](#) & T.D. Burger

*School of Chemistry and Molecular Biosciences, Parasitology Section, University of Queensland, Brisbane, QLD4072, Australia*

After years of work by many people, two new genera of hard ticks (Ixodidae) were described in 2018: *Robersticus* named in honour of the late Bob Roberts of Brisbane, and *Archaeocroton* for the tuatara-tick of New Zealand. And moreover, a grand new genus of hard ticks is coming soon to a backyard, vet clinic or research-site near you.

*Wednesday 4 December  
11:45 – 12:00  
Plaza Room 9*

# Abstract – Systematics and Evolution

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## **Investigating the phylogenetic relationships of Tachinidae and Calliphoridae using transcriptomes, with an emphasis on the placement of screw worm flies (Chrysomyinae)**

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[Keith M. Bayless](#)<sup>1</sup>, J.G. Lumbers<sup>1</sup>, G.A. Cardoso<sup>2</sup>, A. Zwick<sup>1</sup>, B.M. Wiegmann<sup>3</sup>, T.T. Torres<sup>2</sup>, J.O. Stireman III<sup>4</sup> & D.K. Yeates<sup>1</sup>

<sup>1</sup>*Australian National Insect Collection, CSIRO National Research Collections Australia (NRCA), Acton, ACT, Canberra, Australia*

<sup>2</sup>*Department of Genetics and Evolutionary Biology, Universidade de São Paulo, São Paulo, Brazil 05508-090*

<sup>3</sup>*Department of Entomology & Plant Pathology, North Carolina State University, Raleigh, NC, USA 27695*

<sup>4</sup>*Department of Biological Sciences, Wright State University, Dayton, OH 45435, USA*

The family Tachinidae is noteworthy within Oestroidea as it is a highly species-rich family that includes only parasitoids. The placement of Tachinidae in relation to other families has also been challenging to resolve. Calliphoridae, in contrast, contains parasitoid and saprophagous lineages, and its monophyly has long been questioned. The subfamily Chrysomyinae contains some carrion feeding species and also screwworms- veterinary pests that feed on live vertebrate flesh. Cluster flies, Polleniidae, are earthworm parasitoids and were a subfamily of Calliphoridae prior to being raised to family status this year. According to recent analyses, Polleniidae are resolved to be the sister group to Tachinidae with strong support. The family level classification and the history of the evolution of parasitoid behavior within this lineage deserve scrutiny. We investigate the relationship of Polleniidae+Tachinidae to the rest of Oestroidea, in particular chrysomyine blow flies, using thousands of genes harvested from de novo transcriptome assemblies of 50 species of flies. This analysis greatly increases the gene coverage and taxon sampling of economically important blow flies and screwworms as compared to previous attempts to decipher the evolutionary relationships of these flies. Subfamily level relationships within Tachinidae conform to the current classification. We continue to find an area of poor support between Polleniidae+Tachinidae, Rhinophoridae, and several subfamilies of Calliphoridae. We explore the high levels of conflict between gene trees, which suggest incomplete lineage sorting or similar population effects that lead to non-bifurcating topologies. We propose that multiple topologies, including one where Chrysomyinae is closer to Tachinidae than to other Calliphoridae, should be considered when reconstructing evolutionary hypotheses for the origin of parasitic behavior in screwworms and other parasitoid oestroids. This study serves as a framework to integrate phylogenetics, functional genomics, and veterinary biology in this diverse group of flies.

*Wednesday 4 December  
12:00 – 12:15  
Plaza Room 11*

# Abstract – Systematics and Evolution

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## Progress in acalyprate fly phylogenomics with an emphasis on Tephritoidea and relatives

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[Keith M. Bayless](#)<sup>1</sup>, A. Norrbom<sup>2</sup>, B.M. Wiegmann<sup>3</sup> & D.K. Yeates<sup>1</sup>

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<sup>3</sup>*Department of Entomology & Plant Pathology, North Carolina State University, Raleigh, USA 27695*

Schizophoran flies constitute a massive radiation of animal life that occurred after the Cretaceous extinction event 66 million years ago. This major fly lineage includes fruit flies such as *Bactrocera* and many other well- and poorly known true flies. With 55,000 described species, a third of fly diversity, rapid diversification has hindered previous attempts to elucidate the phylogenetic relationships among major schizophoran clades. Deciphering the phylogeny of acalyprate flies is a longstanding obstruction to uncovering the Diptera tree of life. We approach this conundrum by analyzing combinations of transcriptome and Anchored Hybrid Enrichment exome data to yield compelling phylogenetic hypotheses of Schizophora. Major findings include Calyptratae being recovered deep within the acalyprates, allied with Ephydroidea, rendering the acalyprates non-monophyletic. A lineage including Sciomyzoidea, Lauxanioidea, and Conopidae is resolved to be the sister group to the rest of Schizophora. All other acalyprate families can be binned into approximately five other major lineages. One of these new lineages of flies contains taxa with variously modified oviscaptus (Tephritoidea, Nerioidea, Psilidae, Tanypezidae, Megamerinidae, Acartophthalmidae, Opomyzidae) and forms the sister group to most other Schizophora. Within Tephritoidea, we find evidence for non-monophyletic Pallopteridae, with Southern Hemisphere taxa forming a clade separate from Holarctic taxa. Tephritidae is non-monophyletic with respect to parasitoid groups, suggesting a major transition from, or multiple origins of, phytophagy. Compelling novel hypotheses based on analyses of large datasets of these flies, examined in light of natural history and functional morphology, yielded a broad and robust view into their evolution through time and morphological space. This approach demonstrates that context is everything in acalyprate flies. A robust understanding of the evolution of the entire group was necessary to form testable hypotheses and discover evolutionary patterns in previously obscure critical lineages.

*Wednesday 4 December*

*11:45 – 12:00*

*Plaza Room 11*

# Abstract – Systematics and Evolution

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## **Digging deeper: parallel genetic evolution in a cockroach symbiont is associated with the repeated acquisition of host burrowing behaviour**

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[Perry G. Beasley-Hall](#)<sup>1</sup>, Y. Kinjo<sup>2</sup>, T. Bourguignon<sup>2</sup>, H.A. Rose<sup>1</sup> & N. Lo<sup>1</sup>

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<sup>2</sup>*Okinawa Institute of Science and Technology Graduate University, Okinawa, Japan*

The genomes of endosymbiotic bacteria are some of the smallest known in nature. Genome shrinkage is largely caused by strong selective pressures associated with living a host-restricted, intracellular lifestyle, as genes previously useful for a free-living existence are discarded. What happens to microbial symbionts when their host undergoes a similarly drastic transition? The Australian soil burrowing cockroaches (Blaberidae: Geoscapheinae) provide a unique natural experiment with which to investigate such a question.

Geoscapheines have experienced a parallel transition to burrowing at least six times from wood-feeding, terrestrial ancestors (Blaberidae: Panesthiinae), a shift likely linked to strong selective pressures stemming from ancient aridification events. Notably, this transition has also involved the acquisition of maternal care from gregarious ancestors. We sequenced 19 whole *Blattabacterium* genomes, an endosymbiont found in almost all cockroach taxa, from a range of geoscapheines and their panesthiine ancestors. Our findings reveal repeated parallel gene loss associated with amino acid synthesis in symbionts of burrowing cockroaches but in none of their wood-feeding sister species. This is potentially due to maternal care facilitating high fidelity transfer of gut microbes to offspring which have supplanted the nutrient-provisioning functions of *Blattabacterium*. These results are the first evidence, to our knowledge, of parallel evolution in a host extending to its endosymbionts and feed into a framework for symbiont genome erosion as a whole.

*Tuesday 3 December*

*11:15 – 11:30*

*Plaza Room 11*

**STUDENT**

# Abstract – Systematics and Evolution

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## **Population genomics of the uniquely eusocial beetle, *Austroplatypus incompertus* (Curculionidae: Platypodinae) – cryptic species complex or diverging populations?**

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[James Bickerstaff](#)<sup>1</sup>, R. Mueller<sup>1</sup>, S. Smith<sup>1,2</sup>, B. Jordal<sup>3</sup> & M. Riegler<sup>1</sup>

<sup>1</sup>Hawkesbury Institute for the Environment, Western Sydney University, Penrith, NSW 2751

<sup>2</sup>Office of the Deputy Vice-Chancellor, Macquarie University, North Ryde, NSW 2113

<sup>3</sup>University Museum of Bergen, University of Bergen, Bergen, Norway 5020

Eusociality has arisen in Hymenoptera (bees, wasps, ants), Blattodea (termites) and Coleoptera (beetles). In Hymenoptera and Blattodea, the evolution of eusociality has led to massive species proliferation. In the hyperdiverse Coleoptera, eusociality only arose once, in the ancient Australian ambrosia beetle *Austroplatypus incompertus* that occurs in mesic eucalypt forests of eastern Australia, from Victoria to northern New South Wales. Originally, this species was moved into a monotypic genus and, based on morphology, synonymised with *Platypus incostatus* described from northern NSW. However, recent mitochondrial data analyses have revealed substantial latitudinal divergence across the distribution of *A. incompertus*. To address this apparent disparity between molecular and morphological data, more extensive and genome-wide data are needed. Using Diversity Array Technology Sequencing, and after stringent locus-filtering, we obtained over 700 nuclear loci from 93 individuals across its distribution. Isolation by distance had a strong confounding effect on genetic distances between pairs of individuals. After accounting for this spatial autocorrelation, we detected three genotypic clusters. The northern populations were more differentiated from the populations of the central and southern clusters which were also distinct from each other. The presence of strong genetic structure between north and southern populations of *Austroplatypus* will require more research as it may warrant the resurrection of the older taxonomy for this genus with implications for the evolution of eusociality in this ancient lineage.

*Tuesday 3 December*

*15:45 – 16:00*

*Plaza Room 11*

**STUDENT**

# Abstract – Pest Management

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## Detection of invertebrate pests using LAMP (loop-mediated isothermal amplification) assays

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[Mark J. Blackett](#)<sup>1</sup>, A. Agarwal<sup>1</sup>, L. Rako<sup>1</sup>, L. Semeraro<sup>1</sup>, I. Valenzuela<sup>1</sup> & J.P. Cunningham<sup>1,2</sup>

<sup>1</sup>*Agriculture Victoria Research, AgriBio, Bundoora, Vic, Australia*

<sup>2</sup>*School of Applied Systems Biology, La Trobe University, Bundoora, Vic, Australia*

Many pest insects intercepted in the field and at state or national borders often appear very similar to non-pests, with immature lifestages being particularly difficult to identify. LAMP (loop-mediated isothermal amplification) assays are rapid, highly specific molecular tests for the detection of target species for use in the laboratory or field, potentially providing portable molecular tools that allow rapid and accurate detection of specific insect pests of biosecurity concern within one hour.

Recently, we have developed LAMP assays for multiple invertebrate pests, including: two tephritid fruit flies (*Bactrocera tryoni* & *Ceratitis capitata*), phylloxera (*Daktulosphaira vitifoliae*), Khapra beetle (*Trogoderma granarium*), brown marmorated stink bug (*Halyomorpha halys*), and Varroa mite (*Varroa destructor*).

These assays have been optimised for simple DNA extraction and amplification in the field using a portable real-time fluorometer (GenieIII). To enable retention of physical voucher specimens for reference and possible morphological confirmation of LAMP results, two non-destructive methods for obtaining DNA suitable for LAMP assays were tested. Each assay was assessed against broad panels of target and non-target species and found to be highly specific, with each test sensitive down to very low levels of target DNA, performing well compared to existing laboratory-based qPCR tests.

Our assays provide new portable molecular tools for the detection of a suite of invertebrates of significant biosecurity and quarantine concern. Applications of these new LAMP assays for insect pest surveillance will be discussed.

*Tuesday 3 December  
11:45 – 12:00  
Plaza Room 8*

# Abstract – Insects and Plants

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## **Does *Paropsis atomaria* larval feeding induce chemical responses in *Corymbia citriodora* subsp. *variegata*?**

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[Flávia S. Bonora](#), H. Nahrung, D. Lee & A. Hayes

*University of the Sunshine Coast, Sunshine Coast, Australia*

The eucalypt tortoise beetle *Paropsis atomaria* Olivier (Coleoptera: Chrysomelidae) is a major pest of eucalypt plantations in Queensland, including areas planted with *Corymbia citriodora* subsp. *variegata* (CCV), an important specie for hardwood plantations that presents desirable field performance, wood quality and form and suits a range of site conditions. *Paropsis atomaria* can cause severe defoliation in young trees, reducing plantation productivity and quality.

Studies with *Corymbia* spp demonstrated that plant secondary metabolites, such as terpenes, are correlated with arthropod herbivory and can be effective as insect growth inhibitors. Changes in plant chemistry can occur in plants as a response to herbivory, potentially reducing further damage.

To provide a better understanding of plant-herbivore interactions and possible resistance mechanisms, this study evaluated the chemical response of CCV challenged by *P. atomaria*. Seedlings of CCV were submitted to one of three treatments: no damage; mechanical damage and *P. atomaria* larval damage. After 15 days seedlings were removed from the treatments and leaf samples were analysed to determine the leaf-oil gas chromatography-mass spectrometry. The results revealed that *P. atomaria* larval feeding induced chemical response in CCV with up-regulation of waxes and down-regulation of terpenoids. The same pattern was not observed on plants under mechanical damage, suggesting an interaction between plant-herbivore.

*Wednesday 4 December*  
*14:30 – 14:45*  
*Plaza Room 8*  
**STUDENT**

# Abstract – Insect Declines Symposium

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## **Are insects and other invertebrates in decline in Australia?**

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[Michael F Braby](#)

*Division of Ecology and Evolution, Research School of Biology, The Australian National University, Acton, ACT 2601 and The Australian National Insect Collection, GPO Box 1700, Canberra, ACT 2601, Australia*

The current global rate of extinction is estimated to be several orders of magnitude higher than the normal background rate. A recent review documenting changes in insect richness and/or abundance in both terrestrial and aquatic ecosystems in Europe and North America suggested that insects are threatened. These findings parallel similar trends reporting recent catastrophic declines in insect biomass in the Northern Hemisphere. However, it is not certain if declines in insect biodiversity are truly global. Thus, from an Australian and, more broadly, Southern Hemisphere perspective, there are three key questions that need to be addressed: (1) are Australian insects and other invertebrates in rapid decline and to what extent are they threatened with extinction? (2) If they are in decline, are the drivers or key threatening processes similar to those in the Northern Hemisphere? And (3) given those threats, what can be done to rectify the situation and reverse the trend? However, there are few rigorous monitoring programs for terrestrial insects and invertebrates in Australia to address these questions. Thus, it is difficult to evaluate the extent of decline. Therefore, different approaches are required to evaluate the extent of decline. These approaches include: (1) estimating the extent and rate of extinction; (2) estimating the extent of change, especially decline, based on expert opinion; (3) estimating the extent of change based on historical records; and (4) estimating the extent of change based on temporal replication of surveys. These four approaches are briefly discussed to engender further research, which is so urgently needed to obtain evidence that will ultimately underpin the need for imminent conservation management and action.

*Monday 2 December  
11:45 – 12:15 (30 min)  
Plaza Room 9*

# Abstract – Pest Management

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## **A lifetime in summer pulse entomology – a field entomologist’s memories and perspectives of 40+ years of ever changing pest outbreaks and challenges**

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[Hugh Brier](#)<sup>1</sup>, T.M. Volp<sup>2</sup>, A. Quade<sup>2</sup>, E. Teese<sup>2</sup>, E. Williams<sup>3</sup> & J. Wessels<sup>4</sup>

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<sup>3</sup>Biosecurity Queensland Control Centre, 39 Kessels Rd, Coopers Plains QLD 4108

<sup>4</sup>Ex (retired) Department of Agriculture and Fisheries, Kingaroy, QLD 4610

These are memories and perspectives that have evolved from over 40 years working in summer pulses in regional Queensland. They are unashamedly those of a pragmatic field-based entomologist and outline the practicalities and challenges in implementing IPM in broadacre pulse crops, particularly those whose high quality standards require good pest management.

Historically, summer pulses have relied heavily on chemical insecticides, but the pesticides used have changed markedly over the years. These changes have been driven partly by insecticide resistance developing in key pest *Helicoverpa armigera*, and also by environmental and/or health concerns, prominent examples being DDT and old nasties such as parathion. One major challenge is that IPM is only as strong as its weakest links. These include a lack of really soft options for some major pests, particularly podsucking bugs, and also the sheer attractiveness of pulse crops to many pests. Challenges are also posed by sporadic outbreaks of lesser pests such as soybean moth, populations of which can exceed 1,000 larvae/m<sup>2</sup>. Recent incursions of exotic pests including soybean aphids and silverleaf whitefly have also added flavour to the pulse IPM mix. However, the need for pulse IPM has been periodically strengthened by increased insecticide resistance in *H. armigera*, a key IPM strategy being not to flare *H. armigera* by killing the beneficials that prey on it. Silverleaf whitefly (SLW) have also helped the IPM cause. Because no economically viable insecticides are available for SLW in pulses, the default strategy is allow beneficials to ‘do their thing’ by delaying hard insecticides against other pests as long as possible – i.e. by going soft early.

This paper discusses these and other factors, including the ever-changing parade of pests across the seasons, the rise of mungbeans, the expansion of pulses into new regions, and finally, the need for ongoing strong links between researchers and industry to further the adoption of IPM.

*Monday 2 December  
11:15 – 11:30  
Plaza Room 8*

# Abstract – Systematics and Evolution

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## A test of the proposed synapomorphies defining the tarantula genera *Coremiocnemis* and *Psednocnemis*

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[Ethan Briggs](#)<sup>1</sup>, R. Raven<sup>2</sup> & L. Cook<sup>1</sup>

<sup>1</sup>The School of Biological Sciences, The University of Queensland, QLD, 4072

<sup>2</sup>The Queensland Museum, South Brisbane, QLD, 4101

In 2012, West *et al.* erected a new genus of tarantula, *Psednocnemis*, based on three proposed non-homoplastic synapomorphies. They transferred several species from *Coremiocnemis* into the new genus, defining the revised *Coremiocnemis* by two proposed non-homoplastic synapomorphies. To date, all taxonomy and classification of Australian and southeast Asian tarantulas has been based solely on morphological characters. Here, we use DNA sequence data for the first time from types and other specimens from Australia and southeast Asia to assess whether the characters used by West *et al.* are indeed synapomorphies for the clades specified. In particular, we assess whether the only Australian species currently assigned to one of these genera, *C. tropix*, actually belongs with Asian members of these clades.

*Monday 2 December*

*14:15 – 14:30*

*Plaza Room 11*

**STUDENT**

# Abstract – Pest Management

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## **The pathway to the new classical biological control of invasive *Vespula* in New Zealand**

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[Bob Brown](#)

*Manaaki Whenua – Landcare Research, PO Box 69040, Lincoln 7640, New Zealand*

European *Vespula* wasps have become invasive in several parts of the world, particularly in the southern hemisphere. New Zealand is the worst affected due to the absence of native social wasps, combined with copious carbohydrate resource available to *Vespula* wasps in the endemic honeydew beech forest system. So far, attempts at classical biological control against this group have only been seriously pursued in New Zealand. Three Ichneumonid parasitoids of the genus *Sphecophaga* were introduced starting in the late 1980s.

Unfortunately, shortly thereafter the biocontrol programme was abruptly discontinued. Now with new knowledge of the origins of the invasive wasp populations present in New Zealand, we have gone back to the geographical source to survey for natural enemies. In a recent survey trip to the UK, >90% of *Vespula* nests were parasitized by at least one species, albeit at varying degrees of severity. The species found in the common and German wasp nests were: the hoverflies, *Volucella inanis* & *V. zonaria*; the wasp nest beetle, *Metoecus paradoxus*; the Ichneumonid parasitoid *Sphecophaga vesparum*; and the wasp-grabber fly, *Leopoldius signatus*. This talk will describe the journey through searching for potential new biological control agents in the native range, how we've narrowed down the list of agents and finally how we plan to go about seeking approval for releasing the selected agents in New Zealand.

*Monday 2 December  
14:15 – 14:30  
Plaza Room 8*

# Abstract – Rapid-Fire Talk

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## **Preparation of honey bees (*Apis mellifera*) for scanning electron microscopy to image microbial passengers**

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[Martin E. Brummell](#) & R. Rader

*University of New England, Armidale NSW 2351*

Insects visiting flowers carry pollen and microorganisms between plants, contributing to the assembly of a community of bacteria, fungi, and other microorganisms on flowers. When a bee visits a flower, various parts of the bee's anatomy make contact with floral surfaces, creating an opportunity for microorganisms to disperse between flowers. Scanning electron microscopy (SEM) offers the ability to measure and count microorganisms attached to specific regions of insect exoskeletons. However, preparation of insect specimens for SEM includes dehydration and surface coating with a conductive layer of gold, processes that may dislodge attached microorganisms or distort insect morphology, preventing accurate investigation of microbial passengers. We compared five methods of honey bee specimen preparation for SEM: 1. air dried on pins; 2. 95% ethanol; or SEM specimen preparation techniques: 3. fixation in glutaraldehyde and dehydration in acetone; 4. freeze-drying; or a technique used to wash microorganisms from plant surfaces: 5. washed in 0.1 M  $\text{KH}_2\text{PO}_4$  followed by air-drying. All treated bees were coated with gold in a gold-sputterer operating at very low atmospheric pressure. Images of a standardised set of exoskeleton parts, including legs and abdominal and thoracic segments were obtained at standardised magnifications in the SEM and bacteria, fungi, and other microorganisms were counted. The development of a standard methodology will enable quantification of the identity and abundance of microorganisms on honeybees to inform research relevant to microbial dispersal and pathogen transmission.

*Monday 2 December  
16:15–17:30 [13× speakers]  
Plaza Room 8*

# Abstract – Invasive Ants Symposium

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## **Eradication of African big-headed ant, *Pheidole megacephala* (Formicidae) from Tryon Island, a coral cay in the southern Great Barrier Reef, and accompanying changes in the island's ant fauna**

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[Chris J. Burwell](#)<sup>1</sup>, J. Olds<sup>2</sup>, A. Nakamura<sup>3</sup> & A. McDougall<sup>4</sup>

<sup>1</sup>Biodiversity and Geosciences Program, Queensland Museum, PO Box 3300, South Brisbane, Qld 4101

<sup>2</sup>Queensland Parks and Wildlife Service, Department of Environment and Science, PO Box 697, Gympie, Qld 4570

<sup>3</sup>CAS Key Laboratory of Tropical Forest Ecology, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Mengla, Mengla, Xishuangbanna, Yunnan 666303, China

<sup>4</sup>Queensland Parks and Wildlife Service, Department of Environment and Science, PO Box 3130, Red Hill Qld, 4701

The coral cays of the Capricornia Cays National Park in the southern Great Barrier Reef (GBR) support 75% of all nesting seabirds in the GBR World Heritage Area. Much of the seabird breeding in the Capricornia Cays occurs within forests of *Pisonia grandis* trees. Since 1993, outbreaks of a soft scale insect, *Pulvinaria urbicola* (Coccidae), have been observed on some coral cays. Outbreaks were associated with large numbers of the exotic and invasive African big-headed ant, *Pheidole megacephala*, which occurs on most islands of the Capricornia Cays. Tryon Island was worst affected with scale outbreaks causing the death of *Pisonia grandis* trees; only 12% of the island's *Pisonia* forest remained in 2000. Following the collapse of Tryon Island's *Pisonia* forests, the Queensland Parks and Wildlife Service conducted insecticide baiting (2006, 2008 and 2009) targeted at eradicating *P. megacephala*, combined with a *Pisonia* revegetation program. Prior to the baiting program, observations suggest that *P. megacephala* was the only ant species present on the island during the scale outbreaks. Here, using data from several invertebrate surveys conducted on Tryon Island between 2004 and 2018, we conclude that *P. megacephala* has been successfully eradicated from the island. We also document progressive changes in the ant fauna of Tryon Island following the successful eradication program. Tryon Island's ant fauna now resembles that of other islands of the Capricornia Cays which are free of *P. megacephala*. Ants that have since colonised the island include both native and exotic species.

Monday 2 December  
11:45 – 12:00  
Plaza Room 10

# Abstract – Behaviour #3

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## **The blowfly waltz: field and laboratory observations of novel and complex dipteran courtship behaviour**

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[Nathan Butterworth](#), P.G. Byrne & J. Wallman

*School of Earth, Atmospheric and Life Sciences, University of Wollongong, Northfields Avenue, Wollongong, NSW 2522*

Complex courtship has been well documented in the Diptera. However, studies have focused on a limited number of taxa and mostly using lab populations, where behavior can differ substantially compared to nature. To broaden our understanding of dipteran courtship, studies are required in a wider range of species, across both wild and captive populations. The blow flies (Diptera: Calliphoridae) include some of the most commonly encountered flies, yet courtship has been documented in less than 1% of species and is reported to be brief and simple throughout the family. To further investigate blow fly courtship, and to assess the effect of captivity on behavior, this study aimed to document the courtship of a habitat specialist that is endemic to Australasia, *Chrysomya flavifrons*. Video footage of wild and captive groups was recorded and analyzed using behavioral analysis software. The specific aims were 1) to quantify the behavioral sequences that constitute courtship and 2) to compare courtship between wild and captive flies. We found that the courtship behavior of *Ch. flavifrons* was complex and stereotyped, consisting of five discrete behaviors, which starkly contrasts with the simple courtship observed in most calliphorids. All of these stereotyped behaviors were observed in both wild and captive groups. However, the proportion of time males spent on these behaviors differed substantially. These findings highlight that blow fly courtship behavior may be more complex than currently perceived, and that careful consideration should be given to the influence of the laboratory environment in future studies of fly behavior.

*Wednesday 4 December  
14:45 – 15:00  
Plaza Room 9  
**STUDENT***

# Abstract – Systematics and Evolution

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## **The Caterpillar Key – An interactive key for identifying families of Lepidoptera larvae, including those of Australian biosecurity concern**

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[Catherine Byrne](#)<sup>1</sup> & D. Moyle<sup>2</sup>

*Tasmanian Museum & Art Gallery, GPO Box 1164, Hobart TAS 7001*

Incursions of the larvae of exotic lepidopteran pest species present a potential major threat to Australian biosecurity. The identification of caterpillars can be particularly difficult because of the need for detailed training and expertise to effectively use standard dichotomous keys and lack of knowledge of immature Lepidoptera. In general, there is a paucity of diagnostic tools to identify caterpillars collected from field survey work or at the border.

A useful way to facilitate invertebrate identification by non-entomologists is by the use of a Lucid Key - an interactive, multiple-entry (*i.e.* non-dichotomous) program that offers a relatively straightforward process requiring only basic training for the end-user. The key can be programmed to account for common mistakes in identification of morphological features. Unlike dichotomous keys, Lucid Keys are not hierarchical and a user can start with any feature with which they feel confident.

In this project, we have constructed a Lucid Key for the identification of 79 families of lepidopteran larvae with a focus on those of quarantine concern for Australian Biosecurity. Families that were omitted were mostly those with very little or no data available on caterpillars. We have minimised the use of highly technical characters by directing users in the initial stages of the key to more easily identifiable features. Ultra-high resolution photographs and/or line drawings of the relevant characteristics and gross morphology are included for most taxa. A major advantage of this online key is that it will be updated and more data and taxa added dynamically.

*Monday 2 December*

*15:45 – 16:00*

*Plaza Room 11*

# Abstract – Pest Management

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## Selectivity of some novel insecticides against *Trichogramma chilonis* Ishii. (Hymenoptera: Trichogrammatidae)

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[Muhammad A. Chaudhary](#)<sup>1</sup>, T. Shanwar<sup>1</sup>, M.D. Gogi<sup>2</sup>, M. Azeem<sup>1</sup> & D. Hussain<sup>3</sup>

<sup>1</sup>Department of Zoology, Government College University, Faisalabad, Pakistan

<sup>2</sup>Department of Entomology, University of Agriculture, Faisalabad, Pakistan

<sup>3</sup>Entomological Research Institute, Ayub Agriculture Research Institute, Faisalabad, Pakistan

The main objective of present study was to assess comparative selectivity of seven insecticide viz., Belt, Pyriproxyfen, Voliam flexi, Nitenpyrum, Lufenuron, Chlorantraniliprole and Flonicamid at their recommended doses against *Trichogramma chilonis* by egg card bioassay and dipped surface residue bioassay under laboratory conditions. The experiment was carried out in the toxicological laboratory Entomological Research institute Ayub Agricultural Research Institute (AARI) Faisalabad. The insecticides were classified into harmless (< 30% mortality), slightly-harmful (30-79% mortality), moderately-harmful (80-99% mortality) and harmful (> 99% mortality) categories according to the International Organization for Biological Control (IOBC) codes for beneficial species tested under laboratory conditions. The results of egg card bioassay revealed that Tight<sup>®</sup> (Lufenuron) demonstrated 71.5% *T. chilonis* adult emergence (28.5% mortality) and was categorized as harmless insecticides *T. chilonis*. However, egg card bioassay reveal 65.5% (34.5% mortality), 42% (58% mortality), 39.5% (60.5% mortality), 58% (42% mortality), 63.5% (36.5% mortality) and 62% (38% mortality) *T. chilonis* adult emergence from eggs treated with Belt<sup>®</sup> (Flubendiamide), NyLar<sup>®</sup> (Pyriproxyfen), Sega<sup>®</sup> (Nitenpyrum), Voliam-Flexi<sup>®</sup> (Chlorantraniliprole and thiamethoxam), Tight<sup>®</sup> (Lufenuron), Coragen<sup>®</sup> (Chlorantraniliprole) and Nicotinamid<sup>®</sup> (Flonicamid). On the basis of these results, Belt<sup>®</sup>, NyLar<sup>®</sup>, Sega<sup>®</sup>, Voliam-Flexi<sup>®</sup>, Coragen<sup>®</sup> and Nicotinamid<sup>®</sup> were categorized into slightly harmful insecticides against *T. chilonis* in egg card bioassay. Similarly, the results of dipped surface residue bioassay reveal that Tight<sup>®</sup> (Lufenuron) (28% mortality) proved harmless while Belt<sup>®</sup> (44% mortality), NyLar<sup>®</sup> (72% mortality), Sega<sup>®</sup> (48% mortality), Voliam-Flexi<sup>®</sup> (68% mortality), Coragen<sup>®</sup> (44% mortality) and Nicotinamid<sup>®</sup> (44% mortality) proved slightly harmful insecticides against *T. chilonis* when *T. chilonis* adult were exposed to treated surface 4 hrs post application interval. However, at 24 hrs post application exposure, all tested insecticides (0-8% mortality) proved harmless against *T. chilonis* adults. On the basis of these results, it can be concluded that augmentative releases of *T. chilonis* adults can be recommended 24 hours post application of these insecticides.

Tuesday 3 December  
12:00 – 12:15  
Plaza Room 8

# Abstract – Rapid-Fire Talk

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## **Effect of tree architecture and planting density on mango scale, *Aulacaspis tubercularis* Newstead and its natural enemies**

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[Jodie Cheesman](#)<sup>1</sup>, S. De Faveri<sup>1</sup>, C. Wright<sup>1</sup>, I. Bally<sup>1</sup>, P. Ibell<sup>1</sup> & M. Kare<sup>2</sup>

<sup>1</sup>Department of Agriculture and Fisheries Queensland, 28 Peters St Mareeba, Qld 4880

<sup>2</sup>Department of Agriculture and Fisheries Queensland, 24 Experimental Station Rd, South Johnstone, Qld 4859

Mango trees are traditionally grown in densities of about 100-200 trees per hectare. It has been shown for other commodities that yields can be increased dramatically if orchards are planted in higher densities. The Department of Agriculture and Fisheries Queensland are trialling higher density plantings of up to 1250 trees per hectare in combination with different training systems. However, different training systems and planting densities may also affect insect pests and natural enemies. Trials were conducted to monitor the effects of different densities and training systems on the mango scale, *Aulacaspis tubercularis* and its associated beneficial insects. The training systems that were monitored were a conventional (closed vase) tree training system at low (208 trees / ha); and high (1250 trees/ ha) densities; a medium density (416 trees/ha) single leader training system and; a single-leader, high-density training system on trellis (1250 trees/ha). The experiment included three mango varieties, cv. Keitt, cv. Calypso and the yet to be named, cv. NMBP 1243. Mango leaves were collected monthly and observed under binocular microscope for live scales and beneficial insects. The trial design was a randomised complete block split-split-plot with density at the main plot, training system at the sub-plot and variety at the sub-sub-plot. Data were collected from four replicates of each treatment combination and replicated four times. Initial results showed lower scale populations in the high density treatments than in the medium and low densities. The cv. Calypso had less scale than cv. NMBP 1243 and cv. Keitt. Mango scale populations peaked in December coinciding with increases in temperature and relative humidity. The most important parasitoid was *Encarsia citrina*, followed by *Aphytis* spp. The latest results and the benefits of high density planting systems for insect control will be discussed.

*Monday 2 December  
16:15–17:30 [13× speakers]  
Plaza Room 8*

# Abstract – Insects and Plants

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## Impacts of endophytic and mycorrhizal fungi on silicon uptake and anti-herbivore defences: threesomes can have unintended consequences?

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[Ximena Cibils-Stewart](#)<sup>1,2</sup>, J.R. Powell<sup>1</sup>, C.R. Hall<sup>1</sup>, W.J. Mace<sup>3</sup> & S.N. Johnson<sup>1</sup>

<sup>1</sup>Hawkesbury Institute for the Environment, Western Sydney University, Hawkesbury Campus, Richmond NSW, Australia

<sup>2</sup>Instituto Nacional de Investigación Agropecuaria (INIA-Nacional Institute of Agricultural Research), Colonia del Sacramento Colonia, Uruguay

<sup>3</sup>AgResearch, Grasslands Research Centre, 11 Dairy Farm Road, Palmerston North, New Zealand

Pastures are economically important and provide a range of ecosystem services. Grasses associate with several symbiotic fungi, including endophytes (Clavicipitaceae: *Epichloë*) and arbuscular mycorrhizal (AM) (Glomeromycotina), in roots and shoots, respectively. Endophytes and AM fungi often affect insect herbivores by influencing the overall chemistry of their host plant (e.g. alkaloid-production by endophytes). Furthermore, many grasses have the ability to accumulate large amounts of silicon from the soil. Silicification of plant tissues alleviates a wide range of stresses, including herbivory, and recent evidence suggests that both endophytes and AM fungi may facilitate silicon uptake. The consequences of this for herbivores, and whether endophytes and AM fungi interact in this regard, are currently unknown. We therefore conducted a factorial greenhouse experiment to evaluate whether these components, acting alone or in combination, altered population dynamics and fecundity of the bird-cherry oat aphid (*Rhopalosiphum padi*; Hemiptera: Aphididae) feeding on *Festuca arundinacea*. Results confirm that endophyte-associations had the greatest effect and reduced all aphid performance parameters. However, the presence of AM fungi countered these reductions to the extent that aphids performed better on plants associated with both types of fungi. This potentially reflects reductions in alkaloids in these plants relative to plants with just endophytes. Despite evidence that both types of fungi increased silicon uptake, silicon had no discernible impacts on aphids. In conclusion, symbiotic fungal associations may be beneficial to plants, but they might have deleterious effects on herbivore defences when acting in combination. These interactions may, however, prove more effective against other herbivores (especially chewers).

Wednesday 4 December  
13:15 – 13:30  
Plaza Room 8  
**STUDENT**

# Abstract – Behaviour #3

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## **Adenotrophic viviparity in an Australian bat fly (Nycteribiidae)**

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[Shannon Close](#) & D. Merritt

*School of Biological Science, University of Queensland, St Lucia, Brisbane, QLD 4072.*

Adenotrophic viviparity is a reproductive strategy known only from the superfamily of parasitic flies, Hippoboscoidea. Translating to “gland-fed live birth”, a single offspring develops entirely within the female reproductive tract until pupation. To date, the vast majority of literature concerning adenotrophic viviparity has focused on the economically important tsetse flies (Glossinidae). Little attention has been given to the three related families (Nycteribiidae, Streblidae and Hippoboscidae) that display traits more divergent from other dipterans than Glossinidae, such as winglessness.

The female reproductive system of Australian nycteribiid *Cyclopodia albertisii* was examined using scanning electron and light microscopy, and histological sectioning. Additionally, chitin, genetic material and actin contained in tissue was observed through wheat-germ agglutinin, DAPI and phalloidin-conjugated fluorophore staining, respectively. At an organ-level, the female reproductive system of *C. albertisii* was found to adhere to the dipteran reproductive ground plan, yet proportions were greatly altered to reflect the specialised requirements of adenotrophic viviparity. Most notable was the expansive accessory gland occupying a large proportion of the abdominal cavity. Several features were observed for the first time at the cellular level, such as high levels of actin in gland cell reservoirs, and evidence of gland extension through development of new secretory units within the accessory gland. These novel findings add to the limited knowledge of the adenotrophic viviparity reproductive strategy in Hippoboscoidea.

*Wednesday 4 December  
15:00 – 15:15  
Plaza Room 9*

# Abstract – Pest Management

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## **Fungal endophytes producing lolitrem B and ergovaline offer protection against *Metopolophium dirhodum* on perennial ryegrass**

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[Nicholas Collinson](#)<sup>1,2</sup>, I. Valenzuela<sup>1</sup>, S. Vassiliadis<sup>1</sup>, K. Giri<sup>1</sup>, M. Malipatil<sup>1,2</sup>, G. Spangenberg<sup>1,2</sup> & R. Mann<sup>1</sup>

<sup>1</sup>Agriculture Victoria, AgriBio, 5 Ring Road, Bundoora, VIC 3083

<sup>2</sup>School of Applied Systems Biology, College of Science, Health and Engineering, La Trobe University, Kingsbury Drive, Bundoora, VIC 3083

Perennial ryegrass is an important feed base for the dairy and livestock industries around the world. It is often infected with fungal endophytes that confer the plant with protection against biotic and abiotic stresses. Specifically, endophytes can produce alkaloids that are known to protect the host plant from insect damage. The aim of this study was to use an *in-planta* bioassay to investigate the insecticidal effects of five strains of *Epichloë* endophyte-infected perennial ryegrass plants on the mortality of the Rose Grain Aphid *Metopolophium dirhodum* (Walker), compared to endophyte-free controls. The life history effects were also correlated with the alkaloid profiles, which were quantified by liquid chromatography-mass spectrometry (LC-MS). Endophyte-infected perennial ryegrass produced varying types and concentrations of alkaloids, between strains and individual plants. The quantified alkaloids were lolitrem B, ergovaline, epoxy-janthitrem I and peramine, in concentrations ranging from 0.05 to 138.45 parts per million (ppm). Aphids feeding on the plants with endophytes producing both lolitrem B and ergovaline showed significantly increased nymph mortality (83-100%) compared to the control and those that did not produce these alkaloids (38-63%). Nymph mortality was observed throughout the concentration range of the alkaloids, even when produced in low levels (particularly for ergovaline). Our study showed that endophytes producing both lolitrem B and ergovaline are particularly effective at controlling *M. dirhodum* through increased nymph mortality, even when concentrations were low.

*Tuesday 3 December*  
*15:30 – 15:45*  
*Plaza Room 8*  
**STUDENT**

# Abstract – Systematics and Evolution

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## Changes in Australian large planthoppers or evolution of our knowledge?

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[Jérôme Constant](#)

*Royal Belgian Institute of Natural Sciences, O.D. Phylogeny and Taxonomy, Entomology, Vautier street 29, B-1000 Brussels, Belgium*

The families Fulgoridae and Eurybrachidae contain most of the large and spectacular planthoppers of Australia, including the famous lanternflies. Fulgoridae groups 142 genera and 767 species worldwide (Bourgoin 2019), mostly tropical, with 7 genera and 20 species in Australia (3% of the family); Eurybrachidae often superficially resemble fulgorids and are distributed in Old World tropics and subtropics with 15 of 42 genera and 53 of 200 species in Australia (25+% of the family). Eurybrachidae are well known in Australia by their egg masses covered in white wax on trunks of *Eucalyptus* and *Acacia*. Altogether, they represent a characteristic component of the Australian planthopper fauna. However, the knowledge of their taxonomy, species diversity and biology remains extremely poor and impedes assessment of the effects of changes of climate and habitat that could affect them. Although the first Australian Eurybrachids were described in 1775, the first biological data only mentioned they were living on *Eucalyptus* until 1924 when Hacker documented some species around Brisbane, on *Eucalyptus* and *Acacia*. He also described strong sexual dimorphism in two species and hence proposed new synonymies and gave insights into the biology, development, predators and parasites of these species. The situation of Fulgoridae was even worse but I recently started to review the Eurybrachidae and Old World Fulgoridae. This allowed addition of one genus and seven species of Fulgoridae, description of five genera and eleven species of eurybrachids and several taxonomic changes. New host plants, behaviour, habitats or mimicking data were added thanks to the help of several Australian “citizen scientists” and colleagues. However, an estimate 70% of the taxa in these families remain undescribed. Reasonably supported surveys of these insects need acceleration of taxonomic work (= more scientists), and more fieldwork to document their natural history, that could involve citizen scientists in specific projects.

*Tuesday 3 December  
15:30 – 15:45  
Plaza Room 11*

# Abstract – Insects and Plants

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## **Birds and bees and how they shape peas**

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[Lyn Cook](#)<sup>1</sup>, A. Toon<sup>1</sup> & M. Crisp<sup>2</sup>

<sup>1</sup>*School of Biological Sciences, The University of Queensland, Brisbane, QLD 4072*

<sup>2</sup>*Research School of Biology, The Australian National University, Canberra, ACT 2600*

There have been repeated evolutionary switches from an ancestral bee pollination syndrome to bird pollination among the Australian egg-and-bacon peas (Fabaceae tribes Mirbelieae and Bossiaceae). This group therefore provides an opportunity to test ideas about the role of pollinators in driving the evolution of flower morphology, and how different pollinators affect population structure and evolution of species. Here, we use the Western Australian poison-pea genus *Gastrolobium* as our study system to specifically test several hypotheses. Firstly, we use phylogenetic comparative methods to test whether bird-pollinated species have larger geographic range sizes than bee-pollinated species (expected if birds connect pea population over larger scales than do bees). We then test whether there are differences in seed set among pea species with different pollination syndromes co-occurring in the Stirling Range National Park and, finally, we use DArTSeq data to determine the scale of gene flow across the landscape in these species.

*Wednesday 4 December  
13:45 – 14:00  
Plaza Room 8*

# Abstract – Systematics and Evolution

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## Speciation underground in desert aquifers or just another case of hybridisation by blind beetles?

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B. Langille<sup>1</sup>, J. Hyde<sup>1</sup>, E. Fagan-Jeffries<sup>1</sup>, W. Humphreys<sup>2,3</sup>, A. Austin<sup>1</sup> & [Steve Cooper](#)<sup>1,4</sup>

<sup>1</sup>*Australian Centre for Evolutionary Biology and Biodiversity and School of Biological Sciences, The University of Adelaide, Adelaide, SA 5005*

<sup>2</sup>*Western Australian Museum, Welshpool DC, WA 6986*

<sup>3</sup>*School of Animal Biology, University of Western Australia, Crawley, WA 6009*

<sup>4</sup>*Evolutionary Biology Unit, South Australian Museum, Adelaide, SA 5000*

Phylogeographic studies have provided evidence for speciation underground within the confines of a cave environment, questioning the assumption that cave animals evolved from surface ancestors. However, for many of these studies, it is difficult to rule out the possibility that phylogeographic patterns may have resulted from multiple colonisation events by the same ancestral surface species, introgressive hybridisation among related species, and/or the extinction of surface ancestral lineages. Such is the case for the subterranean diving beetle species (Dytiscidae) of the groundwater calcrete archipelago of central Western Australia, where more than 100 species have been described that appear to have evolved by a combination of ecological/allopatric speciation and in some cases possibly sympatric speciation. We have further explored these speciation hypotheses by phylogeographic analyses of nuclear gene data from 86 species in the genera *Limbodessus* and *Paroster*, including analyses of a gene (long wavelength opsin) involved in phototransduction for select *Paroster* taxa. These analyses provide further support for the presence of sympatric sister species, thus, rejecting the hypothesis that previous phylogeographic patterns, based on mitochondrial DNA, resulted from introgressive hybridisation. Our analyses also uncovered deleterious frameshift and stop mutations in a long wavelength opsin gene that mapped to the common ancestor of a sympatric sister triplet of stygobiont species, providing strong evidence that this ancestor was already adapted to living underground and that the species triplet evolved within the confines of a single groundwater calcrete, a process we refer to as ‘endogenous speciation’. Our analyses show that while the majority (~75%) of these stygobiont beetle species evolved from surface ancestors, a significant number diversified underground through a process of either sympatric or parapatric speciation.

*Tuesday 3 December*

*17:00 – 17:15*

*Plaza Room 11*

# Abstract – Ecology and Interactions #2

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## Seasonality and community composition of parasitoid wasps of four agromyzid leafminers (Diptera: Agromyzidae) in Victoria

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[Marianne Coquilleau](#)

*Department of BioSciences, The University of Melbourne, Parkville VIC 3010*

The vegetable leafminer, *Liriomyza sativae* Blanchard (Diptera: Agromyzidae) was first detected in Australia in the Cape York Peninsula in 2015, from where it has yet to spread. This polyphagous leafminer represents a major threat to the ornamental and horticultural plant industries in Australia and chemicals are unlikely to be the best method of control due to increasing insecticide resistance. Secondary pest outbreaks due to the reduction in natural enemies have been a common experience worldwide. In Australia, we still know little about the abundance and seasonality of hymenopteran parasitoids of exotic and endemic agromyzid species, information needed to include them as biocontrol agents in future Integrated Pest Management (IPM) programs against *Liriomyza* spp. I have been sampling four common non-pest leafminers in Victoria (*L. brassicae*, *L. chenopodii*, *Phytomyza plantaginis* and *P. syngenesiae*) between August 2018 and September 2019, at six different sites around Melbourne. The adult flies and parasitoids were reared out of infested plant matter and morphologically identified. Species-specific peaks of abundance were in spring or in fall with the exception of *P. plantaginis* which was found year-round. All hosts were parasitized by a wide range of wasps, the majority of them eulophids (Hymenoptera: Eulophidae). Important biocontrol agents *Diglyphus isaea* and *Hemiptarsenus varicornis* were present but the most abundant parasitoids across all hosts were *Chrysocharis pubicornis* and *Closterocerus mirabilis* (Hymenoptera: Eulophidae). These agromyzid populations are reservoirs for microhymenopterans of economic interest and their parasitism rates and dispersal into crops should be further studied.

*Wednesday 4 December*

*13:45 – 14:00*

*Plaza Room 10*

**STUDENT**

# Abstract – Invasive Ants Symposium

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## **Preventing new invasive insects: a community contribution to biosecurity**

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[Andrew Cox](#)<sup>1</sup>, D. Palmer<sup>2</sup>, C. McGrannachan<sup>2</sup>, C. Booth<sup>1</sup> & M. McGeoch<sup>2</sup>

<sup>1</sup>*Invasive Species Council, PO Box 166, Fairfield, Vic 3078*

<sup>2</sup>*School of Biological Sciences, Monash University, Clayton, Vic 3800*

Invasive insects in Australia are costing both the environment and economy dearly. Given the difficulties and costliness of managing invasive species, one over-riding biosecurity priority must be to prevent more harmful species arriving and establishing. To do this, biosecurity authorities need to know which insects overseas represent the greatest invasion risks for Australia and how they are likely to arrive here. Prevention priorities have not yet been systematically identified for the natural environment.

In 2017, with philanthropic funding, the McGeoch Research Group of Monash University and the Invasive Species Council embarked on a project to fill that gap. The first objective was to identify high-priority potential insect invaders that could harm Australia's natural environment, their pathways and likely impacts. A second objective was to establish a best-practice process – comprehensive, robust, transparent, repeatable, updateable – for identifying environmental biosecurity priorities (high-risk species and pathways) across all species groups.

Of more than 2800 species reported by countries as having an environmental impact, there is sufficient evidence of negative impacts for about 250 species to rate the severity of their impacts. A very few groups dominate this pool of invaders, with just 6 insect orders represented by 2 or more species. The social Hymenoptera, accounting for half the pool species, should be a particularly high biosecurity priority.

Ten unintentional pathways are commonly used by invasive insects. The unintentional spread of invasive insects makes it difficult to predict which species will arrive, so there should be a strong biosecurity focus on minimising the risks of these prevalent pathways. Another high priority is to establish a national exotic and invasive species data platform that is updateable, repeatable and accessible to all (except for restricted data) and provides comprehensive information to support biosecurity risk assessments.

*Monday 2 December  
13:15 – 13:30  
Plaza Room 10*

# Abstract – Systematics and Evolution

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## **A phylogenetic analysis of the eucalypts using targeted genes**

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[Michael Crisp](#)<sup>1</sup>, C. Kulheim<sup>2</sup>, A. Toon<sup>3</sup>, R. Edwards<sup>4</sup>, Y.-P. Lin<sup>5</sup>, K. Meusemann<sup>6</sup>, M. Bui<sup>1</sup> & L. Cook<sup>3</sup>

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<sup>2</sup>*Michigan Technological University, School of Forest Resources and Environmental Science, Houghton, MI, 49931-1295, USA*

<sup>3</sup>*The University of Queensland, School of Biological Sciences, Brisbane, QLD, 4072*

<sup>4</sup>*Smithsonian Institution, National Museum of Natural History, National Mall 10th St. & Constitution Ave, Washington, DC, 20560, USA*

<sup>5</sup>*The University of Queensland, School of Biological Sciences, Brisbane, QLD, 4072*

<sup>6</sup>*University of Freiburg, Biology I, Evolution & Ecology, Hauptstrasse 1, Freiburg, D-79104, Germany*

We will present a preliminary analysis of sequence data from 101 targeted nuclear genes from about 500 samples representing most of the phylogenetic diversity across *Eucalyptus*, *Corymbia* and *Angophora*, plus Myrtaceae outgroups. We identified and targeted low copy exons using reciprocal blasting between the annotated genome of *E. grandis*, and a transcriptome and two whole-genome shotgun sequences from three *Melaleuca* species. We will discuss results from testing the phylogenetic informativeness of the selected loci, including conflict among gene trees, and minimisation of errors due to paralogy in some loci. Missing data was also an issue, resulting in degraded resolution and clade support. Overall, strong support was found for the existing classification of the eucalypts, with some exceptions. Support for recognition of the segregate genus *Corymbia* will be explored in particular. Implications for perianth evolution and generic classification in the eucalypts will be discussed.

*Monday 2 December  
11:30 – 11:45  
Plaza Room 11*

# Abstract – Pest Management

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## **Flight activity and frequency of phosphine resistance genes in *Rhyzopertha dominica* (Coleoptera: Bostrichidae) at two nearby bulk grain depots**

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[Greg J. Darglish](#)<sup>1</sup>, R. Jagadeesan<sup>1</sup>, V. Singarayan<sup>2</sup> & M.K. Nayak<sup>1</sup>

<sup>1</sup>Department of Agriculture and Fisheries, Queensland, Ecosciences Precinct, GPO Box 267, Brisbane, QLD 4001

<sup>2</sup>School of Biological Sciences, The University of Queensland, St. Lucia, QLD 4072

The lesser grain borer, *Rhyzopertha dominica* (F.), is a common pest of stored grain in Australia. A pheromone trapping program was undertaken from January 2018 to March 2019 at two bulk grain depots (25 km apart) in southern Queensland. This provided information on flight activity in this species, and beetles for screening for genes for resistance to the fumigant phosphine. Beetles were trapped at approximately monthly intervals throughout the study, and there was a positive correlation between trap catch between the two depots. Within each depot, there was also a positive correlation between trap catch and mean daily temperature for each trapping period. Molecular screening for a common variant of the *rph2* phosphine resistance gene in trapped beetles, by traditional resistance marker visualisation and advanced sequencing techniques, showed the presence of the resistant allele in a small proportion of flying adults throughout the study. The results for flight activity and resistance gene frequency have implications for pest and resistance management.

*Monday 2 December  
15:15 – 15:30  
Plaza Room 8*

# Abstract – Phil Carne Student Prize

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## **No evidence for nestmate recognition in the only social bee in the family Colletidae, with implications for very early stages in social evolution**

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[Olivia K. Davies](#), M.G. Gardner & M.P. Schwarz

*College of Science and Engineering, Flinders University, GPO Box 2100, Adelaide, SA 5001, Australia*

Nestmate recognition has been widely studied in Hymenoptera as an ability that may be important for modulating reproductive skew and inclusive fitness returns in social species. An important question arises: is the ability to discriminate between kin and non-kin a prerequisite for the development of sociality, or is it a mechanism that evolves once societies are in place? Although some studies have suggested nestmate recognition in simple forms of sociality, such as casteless insects, results have often been difficult to interpret, and some casteless species are likely to be derived from semisocial or eusocial ancestors. *Amphylaeus morosus* is the only species in the large bee family Colletidae that is known to nest socially, and exhibits a very simple form of casteless society, rarely exceeding three adult females per nest. We used blind-observer circle tube experiments to investigate differences in interactions between familiar and unfamiliar individuals, but found no evidence for nestmate recognition. Our results suggest that the maintenance of simple forms of sociality need not require kin or nestmate recognition. We suggest that if the benefits of social living and the costs of desertion are small, the benefits of a kin recognition system may also be small. In such cases the fitness costs of maintaining kin recognition capabilities could become an important barrier to the evolution of strong altruism that requires a high level of intra-colony relatedness.

*Tuesday 3 December  
14:15–15:00 [3× speakers]  
Plaza Room 8  
**STUDENT***

# Abstract – Systematics and Evolution

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## Population structure in a bee species with no mitochondrial DNA diversity

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[Olivia K. Davies](#)<sup>1</sup>, T. Bertozzi<sup>2</sup>, R.L. O'Reilly<sup>1</sup>, L.R. Hearn<sup>1</sup>, M.I. Stevens<sup>2,3</sup>, M.G. Gardner<sup>1,2</sup> & M.P. Schwarz<sup>1</sup>

<sup>1</sup>Flinders University, GPO Box 2100, Adelaide, SA 5001

<sup>2</sup>South Australian Museum, North Terrace, Adelaide, SA 5000

<sup>3</sup>University of South Australia, GPO Box 2471, Adelaide, SA 5001

Mitochondrial DNA is a commonly used marker for assessing molecular diversity and is used for many applications such as phylogenetics, population structure and species delineation. However, in some cases mitochondrial variation can be problematic due to deviations from strictly maternal inheritance and the effects of intra-cellular parasites that can lead to mitochondrial sweeps. *Amphylaeus morosus* Smith is an Australian native bee in the highly diverse and cosmopolitan family Colletidae. Unusually, it has almost no mitochondrial variation throughout its large range from southwestern Victoria through to southern Queensland. Additionally, it has widespread and consistent mitochondrial heteroplasmy, where every individual has the same two mitochondrial haplotypes. This would indicate that *A. morosus* forms a single large population which has undergone a mitochondrial selective sweep event removing all mitochondrial variation except for heteroplasmy. However, using genome-wide SNP (single nucleotide polymorphism) analyses obtained with the sequencing platform DArTseq (Diversity Arrays), genetic population structure is very clear. This raises some major issues: in particular, how can processes such as mitochondrial sweeps over-ride significant barriers to gene flow that are suggested by nuclear markers? Our findings suggest that in *A. morosus*, mitochondrial DNA has been subjected to a very different evolutionary trajectory compared to the nuclear genome and that the selection dynamics of mitochondria are able to overcome the barriers to gene flow that otherwise restrict the exchange of nuclear genes.

*Wednesday 4 December*

*11:15 – 11:30*

*Plaza Room 11*

**STUDENT**

# Abstract – Rapid-Fire Talk

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## **Systematics of the chalcid wasp genus *Psyllaephagus* (Hymenoptera: Encyrtidae): parasitoids of lerp insects**

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[Alana Delaine](#), G. Taylor & A. Austin

*The University of Adelaide, Adelaide, South Australia 5005*

The host specific wasp genus *Psyllaephagus* (Encyrtidae) is the principal natural enemy of lerp-forming psyllids. The genus contains approximately 240 described species worldwide, of which approximately 60 are known from Australia, and comprises obligate parasitoids of lerp forming psyllids which are ubiquitous on eucalypt species across the continent. As such, they are important for regulating natural psyllid populations as well as biocontrol of pest lerps. However, the taxonomy of the Australian fauna is in a state of confusion, with species being poorly described and mostly unidentifiable, partly because of their tiny size and highly conservative and cryptic morphology.

Gaps in the knowledge of the Australian chalcidoid wasps, and particularly the Encyrtidae, are a major shortcoming in our understanding of Australian hymenopteran biodiversity, which limits successful use of this group in biological control programs. It is likely that the taxonomy of *Psyllaephagus* can only be accurately resolved by employing a combined approach that integrates morphology, multi-gene sequencing and verified host data. Therefore, the three primary components of this PhD study are: 1) detailed field collecting and rearing of parasitoids from authoritatively identified host psyllids; 2) multi-gene sequencing for all specimens including the barcode COI gene, and 3) examining the morphology of freshly collected, and pinned museum material and comparing these to holotype material, particularly types that have associated host data. These components will provide a starting point to answer key questions regarding the diversity, identification and host relationships of the genus *Psyllaephagus*

*Monday 2 December*  
*16:15–17:30 [13× speakers]*  
*Plaza Room 8*  
**STUDENT**

# Abstract – Insects and Humans #3

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## **Bed bug deltiology: a history to erotica**

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[Stephen L. Doggett](#)

*Department of Medical Entomology, NSW Health Pathology, Westmead Hospital, Locked Bag 9001, Westmead, NSW, 2145, Australia*

‘Popular Culture’ refers to cultural activities or products that are aimed at ordinary people, and reflect fads, fashions, and even life’s challenges, at a particular point in history. Thus popular culture is an important source of historical information, even that of medically important arthropods.

One example of popular culture is postcards, and postcards depicting bed bugs were common during the late 1800s to WWII. Such cards provide insights into the past when bed bugs were part of our everyday life. As the cards were so popular, they show that bed bug infestations were extremely common. The decline in bed bug postcards WWII is reflective of the time when powerful insecticides such as DDT began to be used, such that bed bug infestations became rare.

Postcards (and letters) were a major form of social media during the early 1900’s and many stories relating the woes of bed bugs are mentioned in the writings to friends and family. Furthermore, many cards even mention the hotel where bed bugs were encountered. In the UK, many bed bug postcards were sent from popular seaside holiday destinations and had the name of the town printed on the front. Such locations had a huge influx of tourists, and suffered badly with bed bugs, as high tourist areas do now. Other postcards depict bed bug management, from searching and killing the insects, even to the use of chemical control options such as ‘Keating’s Powder’. Perhaps one of the most unusual uses of bed bugs on postcards is that of erotica.

A range of bed bug postcards will be depicted along with their historical significance. More on bed bugs and popular culture can be found in the first academic text book on bed bugs for 50 years, ‘*Advances in the Biology and Management of Modern Bed Bugs*’ ([www.abmmmbb.com](http://www.abmmmbb.com)).

*Wednesday 4 December*

*14:30 – 14:45*

*Plaza Room 11*

# Abstract – Insects and Humans #3

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## Edward Scissorhands and habitat jumping larvae; World's Weirdest Mosquitoes

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[Stephen L. Doggett](#)<sup>1</sup>, J. Kasper<sup>2</sup>, P. Whelan<sup>3</sup>, A. Faraji<sup>4</sup> & C. Liew<sup>5</sup>

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<sup>4</sup>Salt Lake City Mosquito Abatement District, 2020 North Redwood Road, Salt Lake City, Utah 84116-1248, USA

<sup>5</sup>Environmental Health Institute, National Environment Agency, 11 Biopolis Way, #06-05/08, Helios Block, Singapore 138667

Mosquitoes are amongst the most despised creatures on the planet, because of their propensity to bite and transmit agents of disease and death. Yet most are harmless, and if all species were eradicated, the consequences on the world's ecology would be profound. Engaging the public, through processes such as Citizen Science, is now being seen as vital in helping to save the future of the globe. Digitally capturing weird and unusual mosquitoes, can provide more 'mass appeal science', which may not make people like the insect, but would at least allow them to appreciate mosquitoes and understand their role in the environment.

In a textbook in development, titled '*World's Weirdest Mosquitoes*', two very weird mosquito species were recently digitally captured. *Uranotaenia diagonalis* grows in the flower bracts and leaf axils of the wild ginger, *Colocasia australasica*. If the larvae find themselves without water, instead of aimlessly wriggling about like most larvae, their bodies go through peristaltic movements and they can move in a snake-like fashion in the one direction. The result is that the larvae can cover considerable distances, to move into an adjacent bract or axil. It is thought that this adaptation allows them to find a new habitat if their development site desiccates.

Male *Opifex fuscus* mosquitoes exhibit a very unusual mating behaviour. They sit on the water surface and are on constant watch for rising pupae. When one reaches the surface, males scramble over the water in a race to be the first to grab the pupa. It is then held with the elongated front tarsal claws of the males. Eventually the pupa is transferred to the claspers, where the male waits for the female to emerge from the pupal case, to then mate with it. These and other species will be discussed in the new text.

Wednesday 4 December  
14:15 – 14:30  
Plaza Room 11

# Abstract – Ticks & Lice Symposium

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## Fragmented mitochondrial genomes of two blood-sucking lice of Old World monkeys, *Pedicinus obtusus* and *Pedicinus badii* (Phthiraptera, Anoplura)

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[Yalun Dong](#)<sup>1</sup>, Y.-T. Fu<sup>2</sup>, W. Wang<sup>1</sup>, G.-H. Liu<sup>2</sup> & R. Shao<sup>1</sup>

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<sup>2</sup>Hunan Provincial Key Laboratory of Protein Engineering in Animal Vaccines, College of Veterinary Medicine, Hunan Agricultural University, Changsha, Hunan Province 410128, PR China

Mitochondrial genome fragmentation has been observed in 12 species of blood-sucking lice (Anoplura) including human lice, chimpanzee louse, rodent lice, pig lice, horse lice. To understand mitochondrial genome evolution in the Old World monkey lice, we assembled the mt genomes of *Pedicinus obtusus* and *Pedicinus badii*, which comprise 12 and 14 minichromosomes, respectively. Only five minichromosomes are common between the two species. All of the other minichromosomes differ between the two species in gene content and gene order. For instance, each minichromosome in *P. obtusus* contains at least two genes but in *P. badii*, the *trnS2* minichromosome has only one gene. *nad2* and *cox2* are in the same minichromosome in *P. obtusus* but are in two different minichromosomes in *P. badii*. These two *Pedicinus* lice diverged likely ~17MYA when their hosts, macaques and colobuses, diverged. Comparison of the mt genome structure of the monkey lice with the inferred ancestral mt genome structure of sucking lice (Anoplura) showed that minichromosome split occurred in both *P. obtusus* and *P. badii* whereas minichromosome merge occurred only in *P. obtusus*.

Wednesday 4 December  
14:15 – 14:30  
Plaza Room 9  
**STUDENT**

# Abstract – Systematics and Evolution

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## Genetic evidence from an endemic Fijian bee suggests a major impact on population size from Quaternary climate changes

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[James B. Dorey](#)<sup>1,2</sup>, S.V.C. Groom<sup>3</sup>, A. Castellón<sup>2</sup>, M. Lee<sup>1,2</sup>, M.I. Stevens<sup>2,4</sup> & M.P. Schwarz<sup>1</sup>

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<sup>3</sup>School of Agriculture, Food and Wine, The University of Adelaide, Waite Campus, Urrbrae, SA, 5064, Adelaide, Australia

<sup>4</sup>School of Pharmacy and Medical Sciences, University of South Australia, Adelaide, Australia

There are substantial grounds to expect tropical ectotherms, such as insects, to evolve narrower thermal niches than their temperate and boreal counterparts and therefore be more strongly impacted by changing climates. However, detecting such impacts can be difficult, particularly in the absence of extensive museum or fossil records that span significant changes in past climates. Here we use molecular techniques to infer the historical demography of an endemic Fijian bee, *Homalictus fijiensis* (Hymenoptera, Halictidae), going back to at least the last glacial maximum using synonymous substitutions in a fragment of the mitochondrial gene COI. This bee species is common in lowland areas across the Fijian archipelago and is a supergeneralist pollinator. Both Bayesian skyline and mismatch analyses are consistent with a rapid increase in the population size of *H. fijiensis*. Coalescent analyses indicate that the onset of this likely predates the arrival of humans in Fiji and is concordant with a warming climate after the last glacial maximum. The marked increase in population size conflicts with a strong decrease in subaerial land mass following the last glacial maximum. This suggests that the role of climate was not mediated by changes in sea level, which is a commonly invoked mechanism for understanding the role of Quaternary climates on island populations. We argue that thermal niche conservatism in the face of past climate change may be an important factor for understanding historical demography in this bee, and a phenomenon that has been largely neglected in other tropical ectotherms. Tropical ectotherms are the most biology diverse animal group and our data provides an example of how population demography can be inferred and calibrated into the past.

Wednesday 4 December

11:00 – 11:15

Plaza Room 11

**STUDENT**

# Abstract – Ecology and Interactions #1

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## **Farmer nurseries for the Australia-wide dispersal and establishment of the newly introduced spring-active dung beetle *Onthophagus vacca***

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[Bernard M. Doube](#)

*Dung Beetle Solutions International, 37 Cave Avenue, Bridgewater SA 5155*

The European spring-active dung beetle *Onthophagus vacca* was introduced from France to the CSIRO quarantine laboratories in 2012. In 2014, small numbers were released to mass rearing field nurseries at three locations in South Australia (about 80 per location). The beetle failed to breed at one location on a heavy clay soil, survived in moderate numbers at a second location and bred well at the third. In order to maximise the rate of dispersal of this species across southern Australia, the concept of ‘Farmer Nurseries’ has been developed and implemented. Farmer Nurseries, as the name implies, are local mass rearing facilities situated on carefully selected farms in target release regions selected using the current predictions about where the beetles are likely to best prosper (CLIMEX analysis). The volunteer collaborating producers will manage the plots during the 20-month course of the trial (two beetle generations).

In spring 2019, *O. vacca* in breeding condition were established in twenty-one Farmer Nurseries across WA, SA, Vic, NSW and Tas. A total of 3500 beetles were released into these nurseries. The next generation will emerge in 8–10 weeks’ time and the success of these nurseries will be reported.

The Farmer Nursery concept allows the widespread establishment of new species of dung beetles with small numbers in the initial inocula.

This trial is being run as part of the Dung Beetle Ecosystems Engineers Project, supported by Meat & Livestock Australia, through funding from the Australian Government Department of Agriculture and Water Resources as part of its Rural R&D for Profit program.

*Tuesday 3 December  
16:30 – 16:45  
Plaza Room 10*

# Abstract – Ticks & Lice Symposium

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## **Tricks used by the kangaroo tick, *Ornithodoros gurneyi*, to survive in Australian deserts**

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[Bernard M. Doube](#)

*Dung Beetle Solutions International, 37 Cave Avenue, Bridgewater SA 5155*

The kangaroo soft tick, *Ornithodoros gurneyi*, is a parasite of the red kangaroo (*Macropus rufus*) in desert regions of central Australia. There it has overcome a range of threats to survive as a parasite of a scarce and nomadic host in an arid region with highly unpredictable rainfall.

The tick is found in sandy soil depressions – ‘kangaroo wallows’ around the base of isolated desert trees, where kangaroos rest in the shade during the heat of a summer’s day. Ticks recognise the presence of a host by the carbon dioxide on its breath, and then emerge from the sand and attach to the recumbent host.

*O. gurneyi* can absorb water from unsaturated air and so can survive long periods without feeding. Adults and late instar nymphs can live for some years without feeding. Larvae are the most vulnerable stage of development but even these can live 100 days or more in mild conditions.

Kangaroos occupy wallows only during hot times of the year. The adult female tick has a facultative reproductive diapause with the result that eggs are laid during late spring and early summer and not at other times. This ensures that the relatively vulnerable larvae are produced when they are most likely to find a host.

Eggs are laid underground in the wallow and the hatched larvae wait for the arrival of a kangaroo. Larvae then emerge from the soil, locate and attach to a host and remain attached for 4–6 days while the host goes about its daily business. A circadian rhythm of detachment causes engorged larvae to leave their host during the middle of the day, when the host is likely to be in a wallow, thus ensuring that the engorged tick is returned to a wallow, where it burrows into the sand, moults into a first instar nymph and awaits another host. First and second instar nymphs also feed for several days and then detach in the middle of the day. This pattern of feeding and detachment not only maximises the chances of the tick’s finding a host but also serves to disperse it between wallows.

*Wednesday 4 December  
10:45 – 11:00  
Plaza Room 9*

# Abstract – Ticks & Lice Symposium

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## **Toxic secretions in cuticular washings from the Australian paralysis tick, *Ixodes holocyclus***

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[Bernard M. Doube](#)

*Dung Beetle Solutions International, 37 Cave Avenue, Bridgewater SA 5155*

The secretion of Folin reactives from the dermal glands onto the cuticular surface of engorged nymphs and females of the Australian paralysis tick, *Ixodes holocyclus*, is described and the toxicity of these secretions was examined by intra-peritoneal injection into young mice. Two toxins were shown to be present. One was a yellowish, low molecular weight substance which caused rapid death at 25 mg/kg and was secreted following the detachment of the engorged female. The second toxin caused paralysis and was present in cuticular washings obtained from engorged ticks immediately upon detachment but was not detected in the cuticular washings obtained subsequently from the same ticks. Similarities between this toxin and the paralysis toxin found in the salivary gland of the ticks were demonstrated in that both extracts induced the typical paralysis syndrome. The molecular weight of the paralysing fraction from the cuticular washings was 55 kDA, which is similar to that of the paralysis toxin from the salivary gland.

We concluded that the paralysis toxin found in the first cuticular washings was very similar to that found in the salivary gland extracts. The former toxin was either secreted by the dermal glands or was a tick salivary extract that leaked from the feeding lesion onto the tick's cuticle.

This work was conducted at the CSIRO Long Pocket Laboratories in the late 1970s in association with Drs Bernard F Stone, Brian V Goodger and James Nolan but not published at the time.

*Wednesday 4 December  
11:00 – 11:15  
Plaza Room 9*

# Abstract – Systematics and Evolution

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## A potential new genus of scale insects that induce galls on *Melaleuca*

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[Craig Rathjen](#), A. Toon & L. Cook

*School of Biological Sciences, The University of Queensland, St. Lucia Qld 4072, Australia*

Five described species of scale insect are reported to induce galls on *Melaleuca* in Australia. Originally, all five were placed in *Sphaerococcus*, but it has since been recognised that the type species of this genus is a mealybug, which these galls are not. However, there is uncertainty about to which family the galls belong, with one ("*S.*" *ferrugineus*) being referred to the Beesoniidae and the others ("*S.*" *froggatti*, "*S.*" *tepperi*, "*S.*" *morrisoni* and "*S.*" *socialis*) to the Eriococcidae on the basis of gall form and female morphology. In contrast, analyses of 18S rDNA place "*S.*" *ferrugineus* with "*S.*" *socialis* in the Eriococcidae. Here, we combine transcriptomic data, along with PCR-derived sequences from *COI*, *DYN*, *ENOL* and *18S*, from the five described galls with multiple families of scale insect and several newly discovered *Melaleuca*-galls to test their placement and erect a new genus if appropriate.

*Tuesday 3 December*  
*11:30 – 11:45*  
*Plaza Room 11*  
**STUDENT**

# Abstract – Ecology and Interactions #2

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## Why are *Homalictus* bees stuck on mountains in Fiji? Modelling climate and niche with NicheMapR

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[Matt Elmer](#)<sup>1</sup>, M.I. Stevens<sup>2,3</sup> & M.P. Schwarz<sup>1</sup>

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<sup>3</sup>School of Pharmacy and Medical Sciences, University of South Australia, Adelaide, Australia

Climate is one of the most important factors that determines the distribution of a species. It can play a significant role in determining the fundamental niche and can have large influences over evolution and diversification. Fijian *Homalictus* bees provide an excellent study system for the role of climate in distribution and evolution. These bees are the only endemic bees in Fiji, nest in the soil and are important pollinators. They have diversified remarkably quickly in evolutionary time, with current studies suggesting these species evolved from a single dispersal event to Fiji approximately 400 ka. There are now over 25 known species, with more continuing to be discovered. Interestingly, the vast majority of these species are restricted to highland mountains ranges, at elevations greater than 800 m above sea level, which comprise only 2% of the total land surface area of Fiji. Most of these species also have very small ranges with some only being found on a single mountain top. To understand the large species richness, highland restriction and small range size of Fijian *Homalictus* bees we have used a combination of modelling and phylogenetics. We used NicheMapR, a recently published package for the R programming environment, which facilitates fine scale modelling of climate both above ground, where adult bees forage, and below ground, where larvae develop. This has allowed us to investigate if and how climatic niche differs between each species, between the highlands and lowlands and also whether climate differences are more significant above or below ground. In combination with phylogenetics, these findings can also facilitate investigations into how climatic niche is associated with the phylogeny and the prediction of ancestral climatic niches which can inform predictions about possible evolutionary scenarios that could explain the patterns observed today.

Wednesday 4 December

14:15 – 14:30

Plaza Room 10

**STUDENT**

# Abstract – Ticks & Lice Symposium

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## **Advances in artificial feeding systems for native Australian ticks**

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[Kimberly Evasco](#)<sup>1,2</sup>, T. Greay<sup>3</sup>, L. Ahlstrom<sup>4</sup>, U. Ryan<sup>3,5</sup>, C. Oskam<sup>3,5</sup> & P. Irwin<sup>1,5</sup>

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<sup>3</sup>*College of Science, Health, Engineering and Education, Murdoch University, South St, Murdoch, WA 6150*

<sup>4</sup>*Bayer Australia Limited, Animal Health, 875 Pacific Highway, Pymble, NSW 2073*

<sup>5</sup>*Vector and Waterborne Pathogens Research Group, Murdoch University, South St, Murdoch, WA 6150*

For over a century, researchers have sought solutions to overcome their reliance on laboratory animals for live tick experimentation. Artificial feeding systems have several applications, including acaricide testing, vaccine candidate screening, and pathogen transmission studies. Occasional reports of artificial feeding methods have been applied to Australian ticks over the past forty years, however, no successful voluntary attachment, life cycle development, such as moulting and oviposition, have been reported, to the authors' knowledge. This study serves as a proof-of-concept for artificial feeding of native Australian ticks, targeting two species that bite humans and domestic animals: *Amblyomma triguttatum* (ornate kangaroo tick) and *Ixodes holocyclus* (eastern paralysis tick). Live, unfed *A. triguttatum* (nymphs and adults) were sourced from southwest Western Australia, and *I. holocyclus* (adults) from New South Wales and Queensland. Ticks were placed on a 'skin substitute', a silicone membrane treated with host stimuli. The hypostome of the ticks were able to penetrate the skin substitute to imbibe bovine blood beneath. Tick attachment, engorgement, mating and mortality values were recorded twice daily. Individual ticks were tracked post-engorgement, measuring incubation duration, moulted adult sex, and oviposition. Fifty percent of *A. triguttatum* nymphs attached to the skin substitute within 48 h. Of the replete nymphs, 38% moulted to adults, an outcome comparable with laboratory animal studies. Adult feeding assays were also developed, 87% of *A. triguttatum* females attached by 48 h. The system successfully fed 40% of *I. holocyclus* females to repletion leading to oviposition. This is the first report of an artificial membrane-based feeding system for native Australian ticks which relies entirely on natural host-attachment behaviours. This artificial feeding system provides an inexpensive and controlled environment for conducting live tick experimentation involving blood meals.

*Wednesday 4 December*

*11:30 – 11:45*

*Plaza Room 9*

**STUDENT**

# Abstract – Systematics and Evolution

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## **The curly case of *Cotesia* (Hymenoptera: Braconidae): a hyperdiverse genus of lepidopteran parasitoids**

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[Erinn P. Fagan-Jeffries](#) & A.D. Austin

*Australian Centre for Evolutionary Biology & Biodiversity, School of Biological Sciences, The University of Adelaide, SA 5005.*

Species in the genus *Cotesia* are parasitoid wasps which, like all members of the subfamily Microgastrinae, are endoparasitoids of lepidopteran larvae. Of all the members of the subfamily in Australia, *Cotesia* is perhaps the easiest to identify to genus level, but the most difficult to untangle at species level due to conserved morphology. There are currently nine confirmed native species and at least four species introduced to Australia for use as biological control agents, however the genus is certainly many times larger than currently described. In this study, *COI* DNA barcoding and host data were used to provide more clarity on the current status of the genus in Australia, seven new species were described, and several new questions were raised, including the possible presence in Australia of a parasitoid of *Spodoptera exigua* (Noctuidae), an agricultural pest. This presentation will also provide an overview of pilot projects being undertaken to involve school students in entomology and taxonomy through running Malaise traps at rural schools.

*Wednesday 4 December  
10:45 – 11:00  
Plaza Room 11*

# Abstract – Insect Declines Symposium

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## Long-term responses of desert ant assemblages to climate

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[Heloise Gibb](#)<sup>1</sup>, B.F. Grossman<sup>1</sup>, C.R. Dickman<sup>2</sup>, O. Decker<sup>1</sup> & G. Wardle<sup>1</sup>

<sup>1</sup>*Department of Ecology, Environment and Evolution, La Trobe University, Melbourne, Victoria 3086, Australia*

<sup>2</sup>*Desert Ecology Research Group, School of Life and Environmental Sciences A08, The University of Sydney, Sydney, NSW 2006, Australia*

Productivity is a key driver of ecosystem structure and function, so long-term studies are critical to understanding ecosystems with high temporal variation in productivity. In some deserts, productivity, driven by moisture availability, varies immensely over time (rainfall) and space (landscape factors). At high productivity, species richness may be driven in opposing directions by abundance (More Individuals Hypothesis – MIH), and competition. The impacts of temporal variability on productivity are poorly understood. We tested how well rainfall predicted the activity, species numbers and assemblage composition of ants (Hymenoptera: Formicidae) and if responses were moderated by landscape position. We also asked whether the number of species responded directly to rainfall or was moderated by ant activity or competition from dominant ants. Over a 22-year period (annual rainfall range: 79 - 570 mm), we sampled ants using pitfall traps in paired dune and swale habitats in the Simpson Desert, Australia. We used climate records to model changes in ant assemblages. Activity of dominant ants responded primarily to long-term rainfall, increasing exponentially, while subordinate ants responded to short-term weather and time. Consistent with the MIH, the number of ant species was best predicted by activity, particularly of subordinate ants. Dominant ant activity had a declining positive effect on numbers of species. Landscape position strongly predicted species composition, while long-term rainfall determined composition at genus- but not species-level. Over time, species composition fluctuated, but several genera consistently increased in activity. Productivity moderators such as long-term rainfall and landscape position are key drivers of ant activity and composition in the study ecosystem, acting indirectly on numbers of species. Numbers of species were explained largely by ant activity, making a strong case for the MIH, but not competition. Long periods of low rainfall may indirectly reduce species richness in desert ecosystems. However, a trend to increasing richness over time may indicate that conservation management can ameliorate this impact.

*Monday 2 December*

*14:00 – 14:15*

*Plaza Room 9*

# Abstract – Ticks & Lice Symposium

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## How much do we really know about tick-borne pathogens in Australia?

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[Telleasha Greay](#)

*College of Science, Health, Engineering and Education, Murdoch University, 90 South Street, Perth, WA 6150*

Hard ticks (ixodids) are vectors of pathogens that cause morbidity and mortality in companion animals, livestock, and humans throughout the world. Several microbial disease-causing agents have been detected in Australian ticks, with infections diagnosed in people and animals either using conventional detection methods (e.g. microscopy) or more modern molecular approaches (e.g. polymerase chain reaction (PCR) and sequencing). However, studies confirming the transmission and vector capacity of Australian tick species for tick-associated microorganisms, including those that cause rickettsial infections (caused by *Rickettsia* spp.) and Q fever (caused by *Coxiella burnetii*) in humans are lacking. Several reviews have been published in recent years on tick-borne pathogens and diseases in Australia, with much of the focus on humans and whether increasing reports of ‘Lyme disease-like illness’ or ‘Debilitating Symptom Complexes Attributed to Ticks’ (DSCATT) in Australians are caused by local infections with *Borrelia burgdorferi* s.l. species. Several recent studies have utilised modern molecular screening approaches, next-generation sequencing, for microorganisms that do not require *a priori* hypotheses for the microbes targeted, therefore allowing for a broad-scale and unbiased approach for bacterial, viral, and parasite screening that would allow for the detection of known and novel microbes. In this presentation, tick-borne microorganisms that have been demonstrated as pathogens that are vectored by ticks will be discussed, with knowledge gaps highlighted, and future research directions for tick-borne pathogen studies in Australia will be explored.

*Wednesday 4 December  
13:30 – 13:45  
Plaza Room 9  
**STUDENT***

# Abstract – Insects and Plants

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## **Bee community composition relative to crop quality across Australian apple production areas**

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[Scott V.C. Groom](#)<sup>1</sup>, L. Kirkland<sup>2</sup>, J. Brown<sup>3</sup>, S. Cunningham<sup>3</sup>, R. Rader<sup>2</sup> & K. Hogendoorn<sup>1</sup>

<sup>1</sup>*School of Agriculture, Food and Wine, University of Adelaide: Waite Campus, Urrbrae, SA 5064, Australia*

<sup>2</sup>*School of Environmental and Rural Science, University of New England, Armidale NSW 2351, Australia*

<sup>3</sup>*Fenner School of Environment and Society, Australian National University, Acton ACT 2601, Australia*

Apples typically require the transfer of pollen from other compatible cultivars to effectively set seed and develop uniform fruit – a key determinant of their market value. In Australian production systems this service is predominantly provided by the European honey bee (*Apis mellifera*) from either managed hives or abundant feral colonies found throughout the landscape. But a suite of other unmanaged species are also found on flowers of apple orchards, with their presence influenced by factors such as the availability of resources and land management practices. Across production areas located in the Adelaide Hills of South Australia, Stanthorpe in Queensland, and the Yarra Valley in Victoria we compare bee abundance and diversity during apple flowering and investigate how this reflects the quality of apples at harvest. We find great variability across the regions in the composition of pollinator communities, their relative proportions, and orchard designs with multiple levels of hail protection. Honey bees are by far the most abundant visitor across sites, but we still find large differences in total numbers between regions. Ground-nesting bees (Halictidae: *Lasioglossum*) represent the next most common visitor in the Adelaide Hills and Stanthorpe, while reed bees (Apidae: *Exoneura*) are more common in the Yarra Valley. Due to their nesting preferences, both native bee groups represent opportunities to develop strategies to enhance within-crop abundances. This is particularly pertinent as the industry shifts toward protected systems that may influence the capacity of honey bees to pollinate effectively. Prioritising a broadening of our understanding of the resource requirements of these native groups may increase supplementary pollination and reduce dependence on honey bees.

*Wednesday 4 December  
13:30 – 13:45  
Plaza Room 8*

# Abstract – Insect Declines Symposium

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## Conservation biological control as a response to global declines of arthropod ecosystem service providers

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[Geoff M. Gurr](#)

*Graham Centre for Agricultural Innovation, School of Agricultural and Wine Sciences, Charles Sturt University, Orange, New South Wales 2800, Australia*

Arthropods are among the planet's most important ecosystem providers, contributing to pest control, pollination, nutrient cycling and other processes that support agriculture. Recently reported global declines in arthropod numbers represent a worrying erosion of our capacity to harness arthropods for the benefit of humanity. Conservation biological control has developed over the last decade as a major discipline in pest management so has established a suite of approaches for conserving natural enemies of pests in farmlands. These approaches offer scope to address declines in arthropod numbers and are especially apposite because agricultural practices such as pesticide use and clearing of non-crop vegetation are themselves important drivers of arthropod declines. Notably, conservation biological control interventions - such as intercropping – can readily be integrated into ‘conventional’ farming systems, allowing large reductions in pesticide use, delivering increases in focal crop yield, and profitability, at the same time as promoting numbers and activity of arthropod ecosystem providers and alleviating adverse impact on farmland biodiversity.

*Monday 2 December  
13:15 – 13:30  
Plaza Room 9*

# Abstract – Chemical Ecology Symposium

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## **Patterns of volatile compound emission among parasitoid-attracting angiosperms.**

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P. Zhu & [Geoff M. Gurr](#)

*Graham Centre for Agricultural Innovation, School of Agricultural and Wine Sciences, Charles Sturt University, Orange, New South Wales 2800, Australia*

The use of nectar-producing plants to provide nourishment to parasitoids has become an important aspect of biological control this century. In several cases, these studies have translated from laboratory phenomenon into real-world systems for promoting the ecosystem service of biological control. Such translation has, however, been hampered by a lack of generally applicable criteria for the selection of optimal nectar plant species. Each crop-pest-parasitoid system addressed has required costly rounds of laboratory and field evaluation of candidate plants. Accordingly, a key challenge for the discipline is to identify plant traits that are linked to strong benefit to parasitoids. In this study, flower volatiles were analysed for 49 plant species from 26 angiosperm families and representing eight major inflorescence architectures (e.g., panicle, umbel) as well as varying flower colours. A total of 347 volatile compounds were identified. Results will be discussed in relation to whether volatile composition is linked to aspects such as plant taxon, inflorescence architecture, and colour. Moreover, we assess whether volatiles of flower origin are likely to offer scope as a rapid screen by which parasitoid-benefitting plants can be identified without the need for laborious bioassays of longevity and fecundity.

*Tuesday 3 December  
12:15 – 12:30  
Plaza Room 9*

# Abstract – Insects and Plants

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## **Silicon uptake alters chemical defence and aphid-parasitoid interactions in a pasture grass**

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[Casey Hall](#)<sup>1</sup>, S. Hartley<sup>2</sup> & S. Johnson<sup>1</sup>

<sup>1</sup>Hawkesbury Institute for the Environment, Western Sydney University, Richmond, NSW, Australia

<sup>2</sup>Department of Biology, York Environment and Sustainability Institute, University of York, York, UK

Many grasses take up large amounts of silicon which acts as a potent physical defence against insect herbivores. Silicon supplementation has also been linked to the jasmonic acid (JA) signalling pathway, which underpins a wider array of anti-herbivore defences. We recently found that Si supplemented plants, contrary to previous reports, have lower jasmonic acid (JA) responses to herbivory. Silicon induced changes in phytohormone signalling and subsequent changes in plant quality may not only affect herbivores but also their natural enemies. To date, only a few studies have investigated the effect of silicon uptake on tritrophic interactions and none have linked this to defensive phytohormonal pathways. We investigated the effect of Si on a plant-aphid-parasitoid system, using a common pasture grass, *Phalaris aquatica*, which is known to produce a range of toxic alkaloids. The aphid, *Rhopalosiphum padi*, and its hymenopteran parasitoid (*Aphidius colemani*) were reared on plants grown with and without Si. Silicon, alkaloid and phytohormone concentrations were quantified in response to Si supplementation and aphid infestation. We found that aphids significantly reduced Si uptake due to lower endogenous JA. Host aphid (mummy) size was significantly reduced on Si supplemented plants. Fewer and smaller parasitoids emerged from aphids reared on plants supplemented with Si. The difference in plant quality due to Si supplementation reduced host aphid quality and subsequent parasitoid development. Previously Si has been found to enhance direct plant defence against herbivory, however it may come at the cost of indirect defences.

*Wednesday 4 December  
11:45 – 12:00  
Plaza Room 8*

# Abstract – Systematics and Evolution

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## **A molecular phylogeny of the fealloid pseudoscorpions (Feaellidae and Pseudogarypidae) reveals ancient Pangean diversification**

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[Mark S. Harvey](#)<sup>1,2</sup> & J.A. Huey<sup>1,2,3</sup>

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<sup>2</sup>*Adjunct: School of Animal Biology, University of Western Australia, Crawley, Western Australia 6009, Australia*

<sup>3</sup>*Adjunct: School of Natural Sciences, Edith Cowan University, Joondalup, WA 6027, Australia*

The Fealloidea represent one of the most intriguing pseudoscorpion clades. They possess several unique morphological traits that have confounded their systematic placement; they have been variously treated as members of the Monosphyronida, the Neobisiinea, sister to Chthonioidea, or sister to Iocheirata. Available molecular data provides best support for the latter hypothesis. Fealloids currently possess allopatric distributions, with Feaellidae found in Africa, Madagascar, Seychelles, the Indian subcontinent, SE Asia, NW Australia and Brazil, and Pseudogarypidae in North America and Tasmania (Australia). Both families have been found in mid-Cretaceous amber deposits (Feaellidae in Burmese amber and Pseudogarypidae in Rhenish Massif amber), and have also been found in Eocene Baltic amber, suggesting co-existence during the Tertiary. Fealloids appear to have poor powers of dispersal and are absent from oceanic islands. The presence of both families in mid-Cretaceous amber deposits explains their widespread modern distribution, with post-Pangean vicariance the most reasonable explanation of the Holocene fauna. Multi-locus sequence data from 59 specimens exhibit deep separation between each family, and significant divergence within the Feaellidae. The subfamilies Cybellinae and Feaellinae are reciprocally monophyletic, and the Australian feaellids are sister to all other sampled feaellines. Deep genetic divergence among the species from Africa and Sri Lanka demonstrate a hitherto unreported diversity in this fauna. Finally, the most widespread fealloid, *Pseudogarypus bicornis*, from western USA, is found to have little genetic substructuring across its range, suggesting relatively recent range expansions.

*Monday 2 December  
13:30 – 13:45  
Plaza Room 11*

# Abstract – Pest Management

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## **An external attractant trap for the small hive beetle (*Aethina tumida*), a pest of European honeybees**

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[R. Andrew Hayes](#)<sup>1</sup>, B. Amos<sup>2</sup>, S. Rice<sup>3</sup>, K. McGlashan<sup>3</sup>, D. Baker<sup>3</sup> & D. Leemon<sup>3</sup>

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The Australian honeybee industry contributes over \$101 million annually to the national economy through honey products, and an estimated \$1.7 billion through pollination services to crops and horticulture. European honeybees (*Apis mellifera*) (Hymenoptera: Apidae) are threatened by a variety of pests and diseases, including the exotic small hive beetle *Aethina tumida* Murray (Coleoptera: Nitidulidae). This beetle is a significant pest in Australia and the USA. The larvae are the destructive life-stage, causing damage to hives when they feed on bee brood and pollen stores. Small hive beetles carry a yeast (*Kodamaea ohmeri*) (Ascomycota: Saccharomycotina) which is primarily responsible for the fermentation of hive products associated with beetle larval development. Our GC-MS analyses of these fermenting hive products found that they consist of typical fermentation volatiles, many of which are known insect attractants. A range of in-hive control options are used by beekeepers, but there is additional need for out of hive control measures such as an external attractant trap that can stop the beetles entering hives, using a lure based on these fermentation odours. We used GC-MS and behavioural bioassays to identify the attractive components of fermenting hive products, which were then tested in the laboratory and field to develop an attractant lure. A simple yeast fermentate was used to study the impact of environmental conditions on beetle hive-finding behaviour in the field to develop targeted trapping for beekeepers, reducing the need for year-round monitoring and control. An external attractant trap will also be useful for biosecurity as a surveillance tool for monitoring small hive beetle in areas of uncertain infestation or to demonstrate area freedom in areas where they are not yet known to occur.

*Monday 2 December  
13:30 – 13:45  
Plaza Room 8*

# Abstract – Behaviour #2

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## Extreme parasitism in a social bee: using a whole-of-life-cycle approach to assess selection dynamics at different stages of a bee's life-cycle

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[Lucas R. Hearn](#)<sup>1</sup>, O.K. Davies<sup>1</sup>, B.A. Parslow<sup>1</sup>, M.I. Stevens<sup>2,3</sup> & M.P. Schwarz<sup>1</sup>

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<sup>3</sup>South Australian Museum, GPO Box 234, SA 5001, Adelaide, Australia

Defence against parasitism has been emphasised as an important factor promoting the evolution of sociality in early insect societies. The Australian hylaeine bee *Amphylaeus morosus* is the only species of the short-tongued bee family Colletidae to exhibit social behaviour, and represents a key species for understanding the earliest stages of social evolution in insects. Previous studies indicate that sociality in *A. morosus* is very simple, with no kin recognition, no apparent morphological or behavioural differences among nestmates and low intracolony relatedness. These characteristics conform to a growing number of casteless and communal bee species where group living involves minimal benefits, and suggests that *A. morosus* has been able to evolve sociality under conditions that are close to those posited for the earliest stages of insect social evolution. Our results indicate that *A. morosus* is strongly pressured by three different parasite species operating at different colony phenology phases – *Gasteruption primotarsale* during the very early stages of brood provisioning, *Anthrax maculatus* throughout the middle, and *Ephutomorpha tyla* towards the end. These three temporal selection agents could have important implications for understanding why unrelated *A. morosus* females choose to nest together and also how reproduction is partitioned. Using the linear nest structure of *A. morosus*, we show that social dynamics are likely to vary based on brood cell placement and hence time. This unique model suggests that selection for social living has the potential to change over a colony's lifecycle depending on the optimal strategy at a given time and provides a perspective that has largely been ignored in social evolution studies.

*Tuesday 3 December*

*17:00 – 17:15*

*Plaza Room 9*

**STUDENT**

# Abstract – Ecology and Interactions #2

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## **The Conservation and management of the Australian freshwater ‘gnammas’, a keystone arid-lands habitat**

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[Brock Hedges](#), A. Austin & P. Weinstein

*Australian Centre for Evolutionary Biology and Biodiversity, Department of Ecology and Evolutionary Biology, the University of Adelaide, SA 5005, Australia*

The granite gnammas (rock-holes) across the north of the Eyre Peninsula, are a unique ephemeral freshwater habitat. A complex but understudied community of invertebrates is known to be associated with these sites. Due to projected drying over the next 100 years, the security of ephemeral freshwater habitats in southern Australia is uncertain. The aim of my PhD project is to assess vulnerability of the invertebrate populations associated with the Hiltaba granite gnammas, and identify the degree to which these gnammas are used as refugia, and provide resources to vertebrate species of conservation interest. My specific research question is: What are the mitigatable threats to the role of ephemeral freshwater bodies in the Australian environment? Extensive sampling of the Hiltaba gnammas, and NGS sequencing will be used to compile an invertebrate species inventory and CO1 barcode library. Specimens generated during initial collection trips will then be used to investigate what impact the dispersal capacity of the species has on gene flow. Individuals of species with differing dispersal capacity will be sequenced, and haplotype networks produced to assess gene flow. Dispersal capabilities of the gnamma fauna will be further investigated through the use of a series of mesocosms, randomly placed throughout Hiltaba Nature Reserve. Invertebrate colonisation and succession will be monitored amongst these mesocosms, and island biogeography theory will be used to assess the longterm viability of the system. To assess the greater role of the Hiltaba gnammas in the environment, camera traps will be deployed at granite outcrops to monitor visitation by vertebrate species of conservation interest.

*Wednesday 4 December*

*11:15 – 11:30*

*Plaza Room 10*

**STUDENT**

# Abstract – Insect Declines Symposium

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## The conservation of the green carpenter bee in current and future climates

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A.A. Santos<sup>1,2</sup>, [Katja Hogendoorn](#)<sup>1</sup>, R.V. Glatz<sup>1,3,4</sup> & R. Leijs<sup>1,4</sup>

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<sup>3</sup>D'Estrees Entomology & Science Services, PO Box 17, Kingscote, SA

<sup>4</sup>South Australian Museum, North Terrace Adelaide SA 5000

Due to extinctions from mainland South Australia and Victoria, the green carpenter bee (*Xylocopa aerata*) has a disjunct distribution in the southeast of Australia and is Regionally Endangered on Kangaroo Island. The species relies on dead, soft wood from a small selection of plant species for making its nests. Habitat fragmentation, combined with deleterious fire events, are thought to have negatively impacted on nesting substrate availability and recolonization chances. Here, we use MaxEnt software to model both the current distribution, and the simultaneous effect of climate change scenarios on the distribution, of *X. aerata* and four plant species that provide most of its nesting substrate: *Banksia integrifolia*, *B. marginata*, *Xanthorrhoea arborea*, and *Xa. semiplana* subsp. *tateana*. We show that annual mean temperature is the strongest climatic predictor of the distribution of *X. aerata* and its host plants. The modeled distribution of the bee under current climatic conditions indicates that climatic factors are unlikely to have caused local extinctions. In all future scenarios, suitable areas for *X. aerata* and each of its nesting hosts are expected to contract towards the southeast of mainland Australia. The suitability of Kangaroo Island for the bee and its current local host species is maintained in all scenarios, while Tasmania (outside of the natural distribution) will become increasingly suitable for all species. The Grampians National Park, where the bees were last seen in the 1930s, is predicted to support *X. aerata* and several host plants under all scenarios. Therefore, this area may be suitable for reintroduction as part of future conservation efforts.

*Monday 2 December*

*15:30 – 15:45*

*Plaza Room 9*

# Abstract – Orthoptera Symposium

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## Preparing a database of range maps for Australian grasshoppers from 54 years of field observations

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[Anwar M. Hossain](#), J.J. Lahoz-Monfort, M. Kearney

*School of BioSciences, The University of Melbourne, Parkville, Victoria, Australia*

Global insect decline has sparked wide interest among scientists around the world. Grasshoppers are a representative group of insects about which we know little, but which also has economic and conservation significance. Australia harbours over 1000 species of grasshoppers under four families (Acrididae, Morabidae, Pyrgomorphidae, and Tetrigidae) of which 93% are considered endemic to Australia including a completely endemic group under the family Morabidae. It is important to have baseline data on the historic distributions of Australian grasshoppers to detect changes in their current distributions. In this study we used the species records from field observations of Ken Key. Key and associates conducted 223 field surveys in 54 years (1936–1989) across Australia and collected grasshopper specimens at roughly 10-mile intervals during their surveys. Field logbooks have been kept on each of Key's collecting trips. Both collecting stops and identifiable geographical features and referenced points are recorded by the odometer (originally in miles, later in kilometres) corresponding to these points. Using the distance and direction of each stop from a suitable reference point and the odometer reading we collected geographical coordinates from Google Earth (currently done for surveys conducted in Tasmania and Western Australia) which we used to prepare range map of each species as convex hull polygons. In total we have identified distribution information for 535 species of grasshoppers (170 genera) from WA and 39 species from Tasmania (25 genera) based on Key's field survey; and prepared range maps for 275 species altogether for WA and Tasmania. We then prepared species and genus richness maps to visualise their distributions across biogeographic regions of Australia. It is hoped that this study will enable us to better conserve and manage an important part of Australia's biodiversity under changing environmental conditions.

*Tuesday 3 December*

*11:45 – 12:00*

*Plaza Room 10*

**STUDENT**

# Abstract – Rapid-Fire Talk

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## **The second species of *Demysus* Pascoe, 1872: an Australian cycad weevil pest's one hundred years of solitude (Coleoptera, Curculionidae, Molytinae)**

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[Yun Hsiao](#)<sup>1,2</sup> & R.G. Oberprieler<sup>1</sup>

<sup>1</sup>*Australian National Insect Collection, CSIRO National Research Collections Australia, GPO Box 1700, Canberra, ACT 2601*

<sup>2</sup>*Division of Ecology and Evolution, Research School of Biology, The Australian National University, Canberra, ACT 2601*

*Demysus* Pascoe, 1872 is a monotypic weevil genus endemic to Australia. The larvae of *Demysus* develop in trunks and caudices of *Macrozamia* and *Lepidozamia* cycads, generally proliferating rapidly in populations of dead or dying plants in the wild. They have been considered as cycad pests since they were found infesting planted cycads of exotic genus and had invaded Italy and South Africa. Only one species has been included in this genus so far, namely *D. meleoides* Pascoe, 1872, which was described from 147 years ago. Recently, a new species of *Demysus* has been identified from North Queensland based on the male genitalia, without external difference could be recognised from *D. meleoides*, highlighting the existence of externally 'cryptic' species in Australian cycad weevils that can be readily distinguished on genital characters.

*Monday 2 December*  
*16:15–17:30 [13× speakers]*  
*Plaza Room 8*  
**STUDENT**

# Abstract – Systematics and Evolution

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## Phylogenomic data reveal a complex biogeographic history for tropical and arid zone trapdoor spiders

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[Joel Huey](#)<sup>1,2,3</sup>, M. Hillyer<sup>1</sup>, J. Carvajal<sup>1</sup> & M. Harvey<sup>1</sup>

<sup>1</sup>Department of Terrestrial Zoology, Western Australian Museum, Locked Bag 49, Welshpool DC, WA 6986

<sup>2</sup>School of Biological Sciences, University of Western Australia, Crawley, WA 6000

<sup>3</sup>School of Natural Sciences, Edith Cowan University, Joondalup, WA 6027, Australia

In Australia, climate and continental drift have given rise to a complex biota comprised of mesic specialists, arid adapted radiations, and taxa that have arrived on the continent from Asia. The relatively recent formation of the Australian arid zone, starting ca. 15 Ma, and the presence of many lineages in the arid zone with tropical and mesic origins raises questions about adaptation to the Australian arid zone, and subsequent diversification within. Here we explore the phylogenomic diversity and biogeographic history of the widespread Australian trapdoor spider genus *Conothele* (Halonoproctidae), which has a tropical and arid distribution in Australia and is found through SE Asia. In particular, we focus on the Pilbara bioregion, an area of topographic complexity in the arid zone that has previously been found to harbour high phylogenetic diversity in mygalomorph spiders. This study adds a large exon-capture dataset to a previously published multigene dataset to further explore the patterns of diversification, and to test putative species concepts based primarily on mtDNA. Molecular clock analyses revealed that *Conothele* diversified concurrently with the formation of the arid zone, and that the genus likely colonised Australia from Asia. Ancestral state reconstructions revealed complex biogeographic histories, with multiple unrelated clades within the Pilbara. The Pilbara has been proposed as a climate refuge for many vertebrate species. These results suggest that the Pilbara likely played a similar role for mygalomorphs during climatic fluctuations in the Plio-Pleistocene.

*Monday 2 December*

*14:30 – 14:45*

*Plaza Room 11*

# Abstract – Orthoptera Symposium

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## **The effects of human activity on outbreaks of wingless grasshoppers (Orthoptera: Acrididae) in the Tablelands of New South Wales**

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[David Hunter](#)

*President, Orthopterists' Society, 125 William Webb Drive, McKellar, ACT 2617*

Grasshopper outbreaks are common in the Tablelands of New South Wales and the most important species is the Wingless Grasshopper (*Phaulacridium vittatum*). Wingless grasshoppers have been studied extensively and have proven to be model organisms for how biotic factors can affect distribution and abundance of pest species. Outbreaks are common in areas with median annual rainfall of about 450-600 mm with more rain during winter. In non-outbreak periods, there is enough rain for good ground cover and high parasitism that limits population growth but during dry years, parasitism declines and bare areas with favoured broad-leafed plants become much more widespread and outbreaks soon follow.

Human activities have favoured wingless grasshopper. Originally *P. vittatum* was mainly in cleared areas along margins of forest but widespread clearing of land for pastures and crops greatly expanded the area that can be infested by this species. In addition, native grasses have often been replaced with improved legume-based pasture that includes the broad leaf plants such as clover that *P. vittatum* prefer. And during drier years, there is often overgrazing that increases the bare areas that encourage outbreaks, while parasites can be detrimentally affected by draining of the wetter areas where parasites are always present and by the use of chemical pesticides that reduce both parasites as well as grasshopper pests. Following application of the biopesticide Green Guard (active ingredient *Metarhizium acridum*) to valuable crops such as vineyards, the percent parasitism increased as grasshopper populations declined while leaving parasites unaffected. Two months after treatment, grasshopper numbers declined by 79% and 7.1% of the residual population was parasitised. In untreated areas, grasshopper numbers declined by only 3% and parasitism was 1.9%. The importance of a higher instantaneous level of parasitism in a species that is present for 4 months during a year is discussed.

*Tuesday 3 December  
15:45 – 16:00  
Plaza Room 10*

# Abstract – Ecology and Interactions #2

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## **Fungicides and their effects on bees: a review of assessments, impacts and interactions**

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[Jay M. Iwasaki](#), E. Fung & K. Hogendoorn

*The University of Adelaide, School of Agriculture, food and Wine, Adelaide SA 5005*

The widespread use of synthetic pesticides is of increasing concern due to their detrimental effects on wild and managed pollinators worldwide. While the impacts of insecticides, particularly neonicotinoids are well researched, we know less about the effect of fungicides or their combinatory effects with insecticides. Fungicides are usually relatively harmless to bees on their own. However, they have the potential to interact with different insecticide groups to enhance their effects on bee physiology from previously sublethal to highly lethal. In addition, a comprehensive literature review of the effects of fungicides and their interactions with pesticides is as yet non-existent. This is an important gap because a variety of pesticides are generally used in agricultural landscapes, and therefore bees are rarely exposed to single chemical. In order to summarise and aggregate what is known regarding fungicide impacts on bees, we conducted a systematic literature review on the methods and outcomes used to assess fungicide impacts on bees. This included studies that integrated the interactive effects with other fungicides and insecticides. We categorised the variety of methods used, quantified outcomes for each experiment, and created a novel index of harm for individual chemicals and chemical combinations. Honey bees (*Apis mellifera*) were the primary subject in fungicide experiments. Mainly focused on the worker stage, they comprised approximately 70% of experimental outcomes. Outcomes reflected the general understanding that fungicides in themselves may be relatively harmless but highlighted the interactive potential of sublethal combinations. The results provide a better understanding of the range of fungicide impacts and directions for further research, particularly regarding the importance of including a wider array of bee species and life stages.

*Wednesday 4 December  
14:00 – 14:15  
Plaza Room 10*

# Abstract – Pest Management

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## Combinatorial RNAi: a potential tool for the management of whitefly

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[Ritesh G. Jain](#), K.E. Robinson & N. Mitter

*Queensland Alliance for Agriculture and Food Innovation, Centre for Horticultural Sciences, The University of Queensland, St Lucia, Queensland 4072.*

Silverleaf whitefly (SLW), *Bemisia tabaci* (Hemiptera: Aleyrodidae), is a highly polyphagous and invasive agricultural pest distributed worldwide. *B. tabaci* causes substantial losses in Australian cotton, vegetable and ornamental plant industries as an efficient vector for plant viruses, and voracious phloem feeder which results in the excretion of copious amounts of honeydew supporting the growth of sooty moulds. In the vegetable industry, economic losses are estimated to be over \$500 million due to infestation and cost of insecticide control and is further complicated by the development of robust resistance mechanism against several high use chemical pesticides. In an effort to fight *B. tabaci*, double-stranded RNA (dsRNA)-mediated gene silencing or RNA interference (RNAi), is emerging as a feasible and sustainable technology for the management of insect pests. In the present study, 22 candidate genes were selected as RNAi targets and tested in artificial diet (AD) bioassays for mortality and gene silencing efficacy. We identified nine RNAi targets, causing moderate-to-high mortality in whiteflies up to six days post-feeding. To further enhance gene silencing and/or mortality rates we combined two of the most effective dsRNA constructs into a single bioassay. Two approaches were used to test combinatorial RNAi effects AD including; (i) mixing individual dsRNA effectors together or (ii) ‘stacking’ dsRNAs into one expression construct. The most effective gene silencing was observed with the stacked dsRNA effector approach, which we surmise triggers additive suppression of both target genes resulting in significantly increased whitefly mortality. These promising results offer valuable insight for the potential application of multiple gene target RNAi in the development of dsRNA-based biopesticides against *B. tabaci* and potentially, other hemipteran pests of agricultural importance.

*Monday 2 December*  
*15:30 – 15:45*  
*Plaza Room 8*  
**STUDENT**

# Abstract – Systematics and Evolution

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## Genomic mining of museum collections: mitogenomic phylogeny of Australian longhorn beetles (Coleoptera: Cerambycidae: Prioninae)

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[Mengjie Jin](#)<sup>1,2</sup>, A. Zwick<sup>2</sup>, R. de Keyzer<sup>3</sup>, H. Pang<sup>1</sup> & A. Ślipiński<sup>2</sup>

<sup>1</sup>State Key Laboratory of Biocontrol, School of Life Sciences, Sun Yat-Sen University, Guangzhou 510275, China

<sup>2</sup>Australian National Insect Collection, CSIRO, GPO Box 1700, Canberra, ACT 2601, Australia

<sup>3</sup>Research Associate, Entomology, Australian Museum, 1 William Street, Sydney, NSW 2010, Australia

The subfamily Prioninae is one of the smaller but morphologically well recognised subfamilies of longhorn beetles and include several of the world's largest species of beetles. Prioninae larvae develop in mostly decaying wood and some species are of economic importance in forest and timber industries. However, very little is known about the evolution of this subfamily and the lack of a robust phylogeny substantially impedes the phylogenetic classification of this taxonomically difficult group. In particular the Australian fauna, while being relatively isolated and constituting a taxonomically important component of the world fauna, has not received much attention over the past decades.

We applied a Whole Genome Shotgun (WGS) sequencing approach to 213 historical museum specimens, representing all morphological Prioninae species from Australia. Complete or partial mitochondrial genomes were acquired for 166 specimens and used to investigate phylogenetic relationships among the genera of Australian Prioninae. Based on our studies of the molecular phylogeny and morphological characters, we have revised the tribal composition of the Australian genera and produced a generic classification of the largest Prioninae tribe Macrotomini. Additionally, while looking at the phylogenetic relationships and utilising various molecular species delimitation tools, we have recovered seven potential new genera and 41 new species, suggesting the species level diversity of Australian Prioninae has been greatly underestimated.

*Tuesday 3 December  
16:30 – 16:45  
Plaza Room 11  
**STUDENT***

# Abstract – Insects and Plants

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## **Toughen up or get toxic? Chewing insects on the receiving end of silicon-based plant defences**

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[Scott N. Johnson](#)<sup>1</sup>, A. Frew<sup>2</sup> & C. Hall<sup>3</sup>

<sup>1</sup>Hawkesbury Institute for the Environment, Western Sydney University, Locked Bag 1797, Penrith, NSW 2751

<sup>2</sup>Charles Sturt University, Faculty of Science, Wagga Wagga, NSW 2678

Herbivorous insects are amongst the most abundance multicellular organisms on the planet. Moreover, plants and insect herbivores have been locked in an evolutionary arms race for over 300 million years. Plants deploy an array of defences which deter feeding or otherwise cause harm to herbivores and herbivores, in turn, develop counter-adaptations to evade their effects. Many plants, especially the grasses, acquire large amounts of silicon (Si) which can be used for herbivore defence. Silicification of plant tissues makes them physically tougher and reduces the nutritional quality of foliage. Recently, Si has been linked to other chemical defences in the plant but this relationship remains poorly understood. Most anti-herbivore defences are under the control of the jasmonic acid (JA) pathway which is triggered following herbivore attack. Using the model grass *Brachypodium distachyon*, we demonstrate that chewing herbivores (*Helicoverpa armigera*; Lepidoptera: Noctuidae) induce Si uptake whereas phloem-feeding aphids (*Rhopalosiphum padi*; Hemiptera: Aphididae) do not. Similar results using methyl jasmonate suggest that induction of the JA pathway drives Si uptake. Chewers were negatively affected when feeding on plants with Si (+Si plants) which also possessed higher densities of leaf macro-hairs. Removal of these macro-hairs restored chewer performance. Crucially, attack by chewing herbivores triggered a much weaker JA response in +Si plants compared to plants without Si. We hypothesise that certain grasses use Si physical defences constitutively or in response to either chewing herbivory or triggering of the JA pathway, *in lieu* of other metabolically costly secondary metabolites. Dampened JA responses may be sufficient to stimulate Si uptake and deposition, which is irreversible, without requiring levels of JA activity needed for continued synthesis of secondary metabolites.

*Wednesday 4 December  
11:15 – 11:30  
Plaza Room 8*

# Abstract – Phil Carne Student Prize

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## **Directed chemical spray of the peppermint stick insect (*Megacrania batesii*) is induced when predation risk is at its highest**

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[Braxton R. Jones](#) & M.W. Bulbert

*Macquarie University, Balaclava Road, North Ryde, NSW, 2109*

The risk of mortality during a predator–prey sequence is at its greatest when a predator makes contact with the prey. Theoretically then, if prey have an active secondary defence, it makes strategic sense that prey should attempt to deter or dissuade a predator prior to contact. Here, we investigated the triggers for the dynamic spraying behaviour of the peppermint stick insects (*Megacrania batesii*) relative to predatory threat status. A variety of non-contact and contact cues representing an escalation in predation risk were applied to the insects. None of the non-contact treatments elicited a spraying response, but instead contact was required. Contrary to our expectations, the likelihood of a spraying event depended on the type of contact and even the particular body regions contacted. The strongest response came from contact that prevented escape, while contact with body regions of higher survival significance (i.e. thorax, abdomen) elicited significantly higher response to body parts less vital to survival (such as tarsi). Staged ‘attacks’ revealed that contact with the initially less ‘vital’ body regions was more likely to trigger a spray response when ‘vital’ regions were subsequently contacted. In light of our findings, we argue that waiting to spray upon contact potentially increases the likelihood of successively deterring predators and we highlight the need to establish a predation risk paradigm for the strategic deployment of chemical defences.

*Tuesday 3 December*  
*14:15–15:00 [3× speakers]*  
*Plaza Room 8*  
**STUDENT**

# Abstract – Rapid-Fire Talk

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## Investigating behavioural challenges for environmental generalists through a study of Australian stick insects

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[Braxton R. Jones](#) & M.W. Bulbert

*Macquarie University, Balaclava Road, North Ryde, NSW, 2109*

The unique landscape of Australia means that we have an unusually large range of habitats, from deserts in Central Australia to tropical rainforests in Northern Queensland. These varied habitats have produced an equally diverse set of insects. The Australian stick and leaf insect (Phasmatodea) fauna are some of the most biodiverse in the world. The study of these genera, which thrive across the whole of Australia, enables us to ask larger questions on the evolution of traits and how these traits facilitate survival across disparate habitats. We are therefore looking at two genera of stick insect, *Hyrtacus* and *Denhama*, which live throughout Australia. These species mimic grasses and can be found in both desert and tropical environments. They are also considered some of the most understudied groups of phasmids in Australia because of their cryptic appearance. By sampling populations over a five-year period throughout the whole of Australia, we will describe behaviours, new species and evolutionary traits of these long-forgotten species. By mapping traits onto a phylogeny, we aim to piece together what makes these two genera so resistant to desiccation in the most extreme deserts of Australia, whilst also being able to thrive in tropical habitats.

*Monday 2 December*  
*16:15–17:30 [13× speakers]*  
*Plaza Room 8*  
**STUDENT**

# Abstract – Systematics and Evolution

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## **Phylogeography of *Plesiastrea versipora* (Cnidaria: Scleractinia: Plesiastreidae): an integrated taxonomic approach reveals a cryptic species**

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[David J. Juszkiewicz](#)<sup>1</sup>, N.E. White<sup>1</sup>, N. Wilson<sup>2</sup>, J. Stolarski<sup>3</sup>, F. Benzoni<sup>4</sup>, R. Arrigoni<sup>5</sup>, A. Baird<sup>6</sup>, M. Bunce<sup>1</sup> & Z. Richards<sup>1</sup>

<sup>1</sup>*Coral Conservation and Research Group, Trace and Environmental DNA Laboratory, School of Molecular and Life Sciences, Curtin University, Kent Street, Bentley, WA 6102, Australia*

<sup>2</sup>*Western Australian Museum, Welshpool, WA 6106*

<sup>3</sup>*Institute of Paleobiology, Polish Academy of Sciences, Twarda 51/55, Warsaw PL-00-818, Poland*

<sup>4</sup>*University of Milano-Bicocca, Piazza della Scienza 2, Milano 20126, Italy*

<sup>5</sup>*Red Sea Research Centre, Division of Biological and Environmental Science and Engineering, King Abdullah University of Science and Technology, Thuwal 23955-6900, Saudi Arabia*

<sup>6</sup>*James Cook University, Townsville, QLD 4811, Australia*

Scleractinian corals are one of the most speciose organisms in coral reef ecosystems. However, species-level identification can be very problematic as a result of morphological plasticity. A recent influx of molecular studies has transformed scleractinian systematics and highlighted that there might be more unidentified cryptic species than previously understood. To detect these cryptic species, robust integrated molecular and morphological studies are required. However, few phylogeographic studies have been attempted. In this study, we test the hypothesis that *Plesiastrea versipora*, a species currently considered to occur throughout the Indo-Pacific in tropical, sub-tropical and temperate waters, is a single species. Molecular and morphological analyses were conducted on 80 samples collected from 29 sites spanning the east, west, and south coast of Australia, Lord Howe Island, Papua New Guinea, Maldives, Red Sea, Gulf of Aden and Madagascar. We initially assembled 12 mitogenomes to identify informative regions of the protein-coding genes; this facilitated the construction of mitochondrial and nuclear phylogenies to examine intraspecific genomic variation. This in addition to multivariate morphometric analysis, based on 13 characters and skeletal microstructure, indicated that cryptic speciation is occurring along a tropical and temperate gradient within the genera *Plesiastrea*. Thus we describe *Plesiastrea peroni*, a tropical member of the *Plesiastrea* complex which may have important implications for biodiversity conservation. A preliminary dated mitochondrial phylogeny of 13 protein-coding genes indicates species divergence occurred in the early Miocene (ca. 17.8 Ma), likely coinciding with a rise in climatic temperatures and an increase in coral reef carbonate platforms and habitat potential in the Indian Ocean. This study has reinforced the importance of using a total evidence approach when dealing with intraspecific scleractinian taxonomy and provides a benchmark for future studies.

*Monday 2 December*

*12:00 – 12:15*

*Plaza Room 11*

**STUDENT**

# Abstract – Behaviour #1

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## Endosymbionts manipulate sex allocation through adjustment of egg size in a haplodiploid thrips

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[Alihan Katlav](#)<sup>1</sup>, D.T. Nguyen<sup>2</sup>, J.M. Cook<sup>1</sup> & M. Riegler<sup>1</sup>

<sup>1</sup>Hawkesbury Institute for the Environment, Western Sydney University, Locked Bag 1797, Penrith, New South Wales 2751, Australia

<sup>2</sup>Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Private Bag 4008, Narellan, New South Wales 2567, Australia

Haplodiploid insects are very diverse and display extraordinary sex ratios. For example, females can regulate offspring sex ratio by controlling sperm access to their eggs. It has recently been established that females of a mite species only fertilize large eggs and can, therefore, control sex allocation via egg size. In addition, endosymbionts may also manipulate sex allocation. For example, maternally inherited endosymbionts (e.g. *Cardinium* and *Wolbachia*) can bias the sex ratio towards females in haplodiploid hosts. However, the egg size-mediated sex allocation hypothesis and its manipulation by endosymbionts have not yet been tested in haplodiploid insects.

Here we investigated if *Cardinium* and *Wolbachia* can influence egg size-mediated sex allocation in a haplodiploid thrips, *Pezothrips kellyanus* (Thysanoptera). This species originates from Australia where individuals have both endosymbionts, and has invaded New Zealand and the Mediterranean region, where individuals only have *Cardinium*. *Pezothrips kellyanus* exhibits a bimodal sex ratio pattern with fertilised females producing broods with either male-only/biased or female-only/biased sex ratio. We found that egg size predicted the fertilization probability and therefore offspring sex, regardless of endosymbiont status. Egg size also influenced offspring fitness parameters such as survival rate, larval and adult size, and survival under stressful condition. Consistent with previous findings, endosymbiont infections led to higher female-only/biased brood production and fewer male-only/biased brood production. Furthermore, comparison of egg size across infection types revealed that *Cardinium* induced higher maternal resource allocation towards eggs and thereby increased female-only/biased brood production and offspring fitness (compared to uninfected status). However, these fitness benefits were either masked or reduced when individuals were co-infected with *Wolbachia*, suggesting a cost of *Wolbachia* infection. Overall, our findings reveal complex cost-benefit interactions among endosymbionts in *P. kellyanus*, which may explain why *Wolbachia* has been lost in some populations of this host species.

Monday 2 December

14:30 – 14:45

Plaza Room 10

**STUDENT**

# Abstract – Insect Declines Symposium

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## **A grave situation for Key’s Matchstick Grasshopper (*Keyacris scurra*)?**

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[Michael R. Kearney](#), V. White & A.A. Hoffmann

*School of BioSciences, The University of Melbourne, Parkville Vic, 3010*

Insect declines are being reported on a global scale but in Australia we have limited historical baseline data on which to base inferences of changes in abundance and distribution. One exception to this is Key’s Matchstick Grasshopper *Keyacris scurra* (family Morabidae), which was studied intensively in the 1950s and 1960s and the subject of textbook studies on the evolutionary process. At the time of these studies, the species was noted to have suffered significant range contractions due to its associating with *Themeda* grasslands which had been severely overgrazed throughout the grasshopper’s range in southeastern Australia. The early researchers had most success finding the species in remnant grassland patches in the cemeteries of country towns, where it could still be found at high abundance. Here we report on the results of a resurvey of the current distribution of *K. scurra*, based on a survey of over 80 locations both old and new across its range. We show that it has suffered significant further declines but also that the remaining populations hold some of the major genetic (cytological) variants noted in the early studies. We discuss how the species could be a valuable test case for developing new techniques and approaches in restoring threatened insects.

*Monday 2 December  
13:45 – 14:00  
Plaza Room 9*

# Abstract – Orthoptera Symposium

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## **Matchstick grasshoppers as model systems for studying local adaptation**

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[Michael R. Kearney](#)

*School of BioSciences, The University of Melbourne, Parkville Vic, 3010*

The process of local adaptation reflects the selective power of the environment and the constraints of genetic variation. Its study therefore occurs at nexus of ecology and evolution. An understanding of the process of local adaptation is fundamental to inferring the persistence of species under environmental change and the dynamics of the speciation process. A number of taxa have proven to be excellent models for studying local adaptation, including cichlid fishes, drosophilid flies and Caribbean anoles. In this talk I will argue that the uniquely Australian matchstick grasshoppers (family Morabidae) have much potential to contribute to the study of local adaptation. The main reasons for this are both intrinsic and pragmatic. The intrinsic reasons relate to their diversity both taxonomically (~250 species) and ecologically (almost all Australian habitats), as well as the extensive background knowledge we have of their taxonomic and evolutionary status. I will provide illustrations of the potential of this group from studies my colleagues and I are doing on climatic adaptation in the group.

*Tuesday 3 December  
11:30 – 11:45  
Plaza Room 10*

# Abstract – Invasive Ants Symposium

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## Utilising molecular techniques to aid eradication of Red Imported Fire Ants (*Solenopsis invicta*)

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[Hadley Keast](#)<sup>1</sup> & J. Oakey<sup>2</sup>

<sup>1</sup>National Red Imported Fire Ant Eradication Program, Department of Agriculture and Fisheries, Health and Food Science Precinct, 39 Kessels Rd, Brisbane, QLD 4108

<sup>2</sup>Biosecurity Qld, Department of Agriculture and Fisheries, Health and Food Science Precinct, 39 Kessels Rd, Brisbane, QLD 4108

The Red Imported Fire Ant (*Solenopsis invicta*) is a globally significant invasive species, with incursions in North America, Asia and Australia. Predictive climatic modelling indicates that RIFA has potential to spread across Australia<sup>1</sup> causing estimated economic impact of Billion\$1.65 annually<sup>2</sup>. In response to the 2001 discovery of RIFA in Brisbane, the National Red Imported Fire Ant Eradication Program (“the program”) was formed. Since 2007, one component of the program applies molecular techniques to facilitate informed decision making. Here, we demonstrate the application of microsatellite genotyping to answer practical genetics questions.

Product movement controls are an essential aspect of the program, preventing the movement of material which could carry fire ants outside of the eradication boundary. As fire ants can be translocated in common material such as soil or mulch, detection of such activities is difficult. Microsatellite genotyping is used to assign a unique genetic fingerprint to nests. The genotype of the outlying nest is compared to the database of nests sampled in the program using pedigree software Kingroup<sup>3</sup>. The location of close relatives to the outlier is then used to focus investigation efforts.

The microsatellite data is applied also to provide answers to population genetics questions. Analysis shows the Brisbane population is not a single homogenous population, but has formed spatially segregated genetic sub-clusters. This technique was used also to show that the Gladstone incursions of 2006 and 2013 (both successfully eradicated) did not result from product movement of the Brisbane incursion and were both independent and external in origin. Further analysis of the microsatellite data demonstrates the prolonged maintenance of genetic bottleneck through the eradication effort, suggesting the effects of the program are preventing genetic establishment and hindering genetic fitness.

*Monday 2 December  
12:00 – 12:15  
Plaza Room 10*

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<sup>1</sup> Bureau of Rural Sciences 2008

<sup>2</sup> Wylie & Janssen-May 2016

<sup>3</sup> KoNovalov 2004

# Abstract – Ticks & Lice Symposium

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## **Phylogenies from mitochondrial genomes of 120 species of ticks: insights into the evolution of families of ticks and of the genus *Amblyomma***

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[Samuel Kelava](#)<sup>1</sup>, D. Barker<sup>2</sup>, R. Nakao<sup>3</sup> & S. Barker<sup>1</sup>

<sup>1</sup>*Department of Parasitology, School of Chemistry and Molecular Biosciences, The University of Queensland, QLD 4072 Australia*

<sup>2</sup>*School of Veterinary Science, The University of Queensland, Gatton, Australia. QLD 4343*

<sup>3</sup>*Department of Disease Control, Graduate School of Veterinary Medicine, Hokkaido University, Hokkaido 060-0818, Japan*

Entire mitochondrial genome sequences have been remarkably instructive about the evolutionary-history (phylogeny) of ticks and indeed other Acari. At present the tick-community has published entire mt genomes for 125 species of ticks. I will present my analyses of 18 newly sequence mt genomes (143 genomes in total). The aims of my project were: (i) to discover the phylogenetic position of the family Nuttalliellidae; (ii) to discover the phylogenetic position of the sub-genera *Aponomma* and *Africaniella* (ticks of reptiles); and (iii) to identify approximate dates-of-origin of the sub-genera *Aponomma*, *Africaniella* and the genus *Amblyomma*.

*Wednesday 4 December  
13:15 – 13:30  
Plaza Room 9*

# Abstract – Ecology and Interactions #2

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## Diversity of soil inhabiting Oribatida (Arachnida: Acari) from different agro-ecological zones of Punjab, Pakistan

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[Ahmad Kamran Khan](#)<sup>1</sup>, M.H. Bashir<sup>2</sup>, S. Ali<sup>1</sup>, S. Ahmed<sup>3</sup>, S.A. Hameed<sup>4</sup>, R. Ajmal<sup>3</sup>, M. Zahid<sup>5</sup>, S.F. Honey<sup>6</sup> & I. Ahmed<sup>7</sup>

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<sup>3</sup>Department of zoology, fisheries and wildlife, University of Agriculture, Faisalabad, Pakistan

<sup>4</sup>Department of zoology, Ghazi University, Dera Ghazi Khan, Punjab, Pakistan

<sup>5</sup>Department of Agriculture Extension, Government of Punjab, Pakistan

<sup>6</sup>Center for Agriculture and Biosciences International (CABI), Central and West Asia

<sup>7</sup>Yunnan Provincial Key Laboratory of Animal Nutrition and Feed, Yunnan Agricultural University, Kunming 650201, Yunnan, PR China

Soil is a very complex ecosystems comprising of interaction of different arthropods including mites. Soil mites are a highly diverse group, having important role in agricultural productivity by increasing the soil fertility through the process of decomposition, mineralization and having a good potential of biological control of different pests. Suborder Oribatida is extensively distributed geographically in all terrestrial ecosystems. Family richness, diversity, abundance and evenness of soil inhabiting Oribatid mites in soil type I (undisturbed soil) and soil type II (disturbed soil type) were estimated from ten different localities of Punjab, Pakistan. Soil sampling was done after two months interval. Overall, 9 families of Oribatida from both types of soils were reported. Oribatida was the most prominent group with 50% individuals followed by Mesostigmata 38%, Prostigmata 8%, and Astigmata 8%. In Oribatida, families such as Oribatellidae, Oppiidae, and Scheloribatidae reported the dominating families. Soil type I has more richness ( $S=07$ ), abundance ( $46.01\pm 2.61$ ) and Shannon diversity index ( $H'=1.77\pm 0.03$ ) as compared to soil type II with richness ( $S=5$ ), abundance ( $25.35\pm 1.14$ ) and Shannon index ( $H'= 1.47\pm 0.03$ ). Maximum mean value of abundance ( $62\pm 11.87$ ) was recorded in Murree from soil type I while in soil type II, it was recorded from Faisalabad ( $29.83\pm 7.28$ ). The maximum family richness of Oribatid was observed in Faisalabad and Chakwal locality ( $S=07$ ) while minimum was ( $S=05$ ) from T.T. Singh locality.

Wednesday 4 December  
11:30 – 11:45  
Plaza Room 10

# Abstract – Rapid-Fire Talk

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## Does bee diversity improve with restoration effort?

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[Dona Kireta](#)<sup>1</sup>, K. Hogendoorn<sup>2</sup>, K.v. Dijk<sup>1</sup> & A.J. Lowe<sup>1</sup>

<sup>1</sup>*School of Biological Sciences, The University of Adelaide, Adelaide SA 5005*

<sup>2</sup>*School of Agriculture, Food and Wine, The University of Adelaide, Adelaide SA 5005*

In Australia, many habitats are degraded through clearing or grazing. Efforts to restore native vegetation vary from simple tree plantings to complex revegetation. However, it is questionable whether and to what extent the simple approach can restore ecosystem functionality. Pollination is an essential ecosystem function, as it assists plant recruitment. It is mainly performed by bees and other insects.

We have assessed how different styles of restoration influence the recovery of native bee diversity within restored areas that utilised two common planting methods – direct seeding and tube stock plantings. We investigated bee diversity within four restoration sites - each containing direct seeded and tube stock restoration. We undertook bee and flower surveys each month from October 2018 to February 2019. Bee diversity within simple revegetation treatments was not much higher than negative controls, and diversity within complex revegetation treatments was higher than positive controls. This strongly supports the notion that restoration quality is vital for restoring bee diversity, subsequent pollination services, and hence seed set and plant recruitment.

*Monday 2 December  
16:15–17:30 [13× speakers]  
Plaza Room 8  
**STUDENT***

# Abstract – Insects and Humans #3

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## **Variation in decomposition stages and carrion insect succession in a dry tropical climate and its effect on estimating post-mortem interval**

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K. Griffiths<sup>1</sup>, [Matthew N. Krosch](#)<sup>2</sup> & K. Wright<sup>3</sup>

<sup>1</sup>*Scientific Section, Forensic Services Group, Queensland Police Service, 200 Roma Street, Brisbane, QLD 4000*

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<sup>3</sup>*Genomics Research Centre, Institute of Health and Biomedical Innovation, Queensland University of Technology, 60 Musk Avenue, Kelvin Grove, Queensland, 4059, Australia*

Insects have an important role in minimum post-mortem interval (PMI<sub>min</sub>) estimation. An accurate PMI<sub>min</sub> estimation relies on a comprehensive study of the development and succession of local carrion insects. No published research on carrion insect succession exists for tropical north Queensland. To address this, we aimed to obtain preliminary data concerning the rate of decomposition and insect succession on pig carcasses in Townsville and compare these with other regions of Australia and overseas. Adult insects were collected daily from three pig carcasses for 30 days during summer and identified to family level. Decomposition was rapid: all carcasses were at the dry/remains stage by day five, which was substantially quicker than all other regions in the comparison. Differences were also observed in the presence/absence of insect families and their arrival and departure times. Given the rapid progression through early decomposition, we argue that later-arriving coleopteran taxa may be more forensically informative in tropical Australia, in contrast with temperate regions where Diptera appear most useful. This research contributes invaluable data to understanding insect succession patterns in tropical Australia and demonstrates the critical need for comprehensive local succession data for each climatic region of Australia to enable accurate PMI<sub>min</sub> estimation.

*Wednesday 4 December  
13:45 – 14:00  
Plaza Room 11*

# Abstract – Insects and Humans #2

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## Collecting permits, ethical research, and Native Title

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[Christine Lambkin](#)

*Queensland Museum, Entomology, South Brisbane, QLD 4101*

Biological research in Queensland's most biologically significant areas, especially those under National and State protection is increasingly affected by permit issues. In post-Wik areas that have valid Native Title determinations, permit applications are being blocked as Queensland Parks & Wildlife Service does not have the authority to grant scientific collecting Permits until there is an authorised Validation Indigenous Land Use Agreement or Indigenous Management Agreement. The UN Conference of the Parties 13, Convention on Biological Diversity 2017; Australian Institute of Aboriginal and Torres Strait Islander Studies Guidelines for Ethical Research in Australian Indigenous Studies 2012; and state requirements when working with Native Title holders and landowners affect our ability to take specimens from areas owned, managed or co-managed by Indigenous people without greater investment in relationships and Traditional Owner support. Chris Lambkin (Entomological Society of Queensland Permit Officer) has been in direct discussion with more than 10 Queensland Aboriginal groups concerning biological research, permits, and collection of specimens on country. Chris will outline and explain a set of protocols and procedures that researchers might follow when working on country, focused on potential benefits for Traditional Owners through two-way communication and knowledge transfer, integrating their cultural knowledge and best scientific practice. Enhanced interactions may hopefully lead to greater satisfaction for both researchers and Traditional Owners not just for Queensland but possibly for Australia.

*Tuesday 3 December  
16:15 – 16:30  
Plaza Room 10*

# Abstract – Pest Management

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## **Biological control of Australian-origin eucalypt plantation pests requires international collaboration**

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[Simon A. Lawson](#), H.F. Nahrung & M.A. Healey

*University of the Sunshine Coast, Forest Industries Research Centre, 90 Sippy Downs Drive, Sippy Downs, QLD 4556.*

Australian-origin pests of eucalypts have been moving around the world since 1873. Since the 1990's, the invasion of new eucalypt pests has increased almost exponentially with rapid subsequent invasion of these pests into new countries and across continents. Traditional approaches to classical biological control, where individual countries or regions funded natural enemy searches and carried out the required specificity testing and released the agents, were effective when rates of invasion were low and with slow subsequent movement between countries and continents. These approaches are less able to cope with multiple new pests arriving in rapid succession. A more collaborative and coordinated approach to biological control of these pests was thus required, where funds and expertise can be more cost-efficiently pooled and shared to develop effective biological control for eucalypt plantation pests. The Biological Control of Insect Pests Alliance (BiCEP) was developed by industry and researchers worldwide to attempt to solve this problem. BiCEP carries out collaborative research in Australia and overseas on biological control of the key invasive pests prioritised by its industry partners. Approaches used in this collaboration include conventional surveys for endemic natural enemies in Australia, genetic characterisation of these agents and climate matching with invaded countries. Key outcomes from current research and future directions will be presented.

*Tuesday 3 December  
12:15 – 12:30  
Plaza Room 8*

# Abstract – Orthoptera Symposium

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## Land degradation and grasshoppers: a hierarchical patch dynamics approach

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[Douglas Lawton](#)<sup>1</sup>, T. Deveson<sup>2</sup>, C. Waters<sup>3,4</sup> & A. Cease<sup>1,4</sup>

<sup>1</sup>*School of Life Sciences, Arizona State University, Tempe, AZ, United States*

<sup>2</sup>*Australian Plague Locust Commission, Fyshwick ACT, Australia*

<sup>3</sup>*Dubbo District Office, NSW Department of Primary Industries, Dubbo, NSW, Australia*

<sup>4</sup>*School of Sustainability, Arizona State University, Tempe, AZ, United States*

The field of ecology has historically viewed life as balanced with disturbances being countered with stabilizers, but this has rarely been supported by evidence. This equilibrium theory is unable to account for many factors such as the scaling of ecological processes. To account for this disharmony of nature, the hierarchical patch dynamics framework allows for linkages between spatial and temporal scales through a nested model of patches within patches. Grasshoppers are an excellent model to investigate multi-scale phenomena due to how behavioral and small level decisions on the micro-habitat/climate scale influence large population and landscape levels. In this presentation, I will introduce the concept of hierarchical patch dynamics in relation to 1) locust (Orthoptera: Acrididae) gregarization and 2) current field work investigating the multi-scale effects of land degradation on grasshopper diversity in Eastern Australia.

1) Since locust gregarization is an individual physiological change with impacts on regional to landscape levels, the hierarchical patch dynamics framework has great potential in explaining the ecological underpinnings of locust swarms due to a nested design approach. We will show this by looking at the relationship between landscape structure (e.g. grass spatial and nutritional clumpiness) on locust gregarization

2) Land degradation through overgrazing decreases soil fertility by interrupting the connectivity of a landscape and this can affect grasshopper diversity. The current hypothesis is that overgrazing decreases plant diversity which negatively impacts insect herbivore diversity. Since ecological phenomena rarely scale linearly, the hierarchical patch dynamics framework can be used to describe the impact of land degradation on grasshopper diversity. This study investigates the multi-scale impacts of land degradation on grasshopper diversity.

*Tuesday 3 December*

*16:00 – 16:15*

*Plaza Room 10*

**STUDENT**

# Abstract – Ecology and Interactions #2

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## **An under-recognised achievement of Australian parasitoids: new data confirms occurrence of *Megastigmus zvimendeli* in China, India, Israel and Kenya**

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[Ngoc Hoan Le](#), H.F. Nahrung & S.A. Lawson

*Forest Industries Research Centre, University of the Sunshine Coast, QLD, Australia*

Within the last twenty years, nineteen species of *Megastigmus* Dalman (Hymenoptera: Megastigmidae) have been identified as potential biocontrol agents against *Leptocybe* spp. gall wasps. *Megastigmus zvimendeli* and *M. lawsoni* from Australia have established as biocontrol agents in the invasive range of *Leptocybe* spp. In addition, twelve species have been reported to occur “locally” in association with *Leptocybe* spp. in Africa, Asia, Europe and South America, among which exist several species that are hard to distinguish from *M. zvimendeli* based on morphological data, including *M. sichuanensis* and *M. icipeensis*. We examined variation of size of body characters of *M. zvimendeli* in Australian-collected specimens using morphometric measurement and compare its body characters to a closely related congener as reference species. Molecular markers (mitochondrial cytochrome oxidase I DNA) was used for DNA based species delimitation; and Genbank searches were conducted to find data matching identities of the target species. Our data revealed high variability in many characters that are relied on in species discrimination of *Megastigmus* that associate with *Leptocybe* galls, e.g. *length of club* or *combined length of funicle 5, 6 and 7*. *ocellocular length*, *eye length* and *eye breadth* were the characters that performed best in discriminating *M. zvimendeli* from the reference species. DNA data confirmed the occurrence of *M. zvimendeli* in China, Kenya and Israel, while the Genbank search identified specimens of *M. zvimendeli* in Kenya and India. The newly generated knowledge on morphology and DNA justified the synonymizing of *M. icipeensis*, *M. judikingae* and *M. sichuanensis* with *M. zvimendeli*, but rejected the link between *M. viggianii* and *Leptocybe* spp. In addition to the reported occurrence in Israel, *M. zvimendeli* is now recorded in China, India and Kenya, revealing its under-recognised use as a biocontrol agent.

*Wednesday 4 December  
13:30 – 13:45  
Plaza Room 10  
**STUDENT***

# Abstract – Insect Declines Symposium

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## Conservation success: provision of nesting substrate for green carpenter bee *Xylocopa aerata* on Kangaroo Island

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[Remko Leijts](#)<sup>1,3</sup>, R. V. Glatz<sup>1,2,3</sup> & K. Hogendoorn<sup>1</sup>

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<sup>2</sup>D'Estrees Entomology & Science Services, PO Box 17, Kingscote, SA

<sup>3</sup>South Australian Museum, North Terrace Adelaide SA 5000

The green carpenter bee *Xylocopa aerata* has a disjunct distribution in bushland around Sydney and on western Kangaroo Island (KI). Extinction of the species in Victoria and mainland South Australia is thought to have resulted from a combination of habitat clearing and large-scale bushfires. On Kangaroo Island, dead trunks of mature silver Banksias (*Banksia marginata*) are the main nesting substrate for the species. These bushes do not survive bushfires - they grow back from seed. After a fire, it takes about 25-30 years for new dead trunks to become available to the bees to nest in.

In 2007, a large-scale bush fire burnt the entire Flinders Chase National Park (FCNP). As a consequence, very little natural nesting substrate is currently available in the park. In an effort to conserve the KI population, we developed artificial nesting stalks and placed these at various sites within and close to FCNP. The bees first reproduced in the stalks in 2016. Since that time, we follow the uptake of substrate and monitor reproductive success by X-raying nests in winter. Bees started nests in more than 150 stalks. Substrate uptake varied (5-95%) among sites and seems to depend on availability of remaining natural substrates

Due to the large scale of the 2007 fire, it seems likely that the population on FCNP would not have survived without our intervention. Because the shortage of nesting substrate is ongoing, we aim to continue to supply the bees with nesting substrate until natural substrate is once more available in FCNP.

To our knowledge, this is the first time that provision of nesting substrate leads to the conservation of a native bee population. We acknowledge the financial support private donors and are grateful to the AES the help in raising funds that allow us to continue this project.

*Monday 2 December*

*15:45 – 16:00*

*Plaza Room 9*

# Abstract – Systematics and Evolution

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## A preliminary phylogeny of Bombyliidae using anchored enrichment data (Brachycera)

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[Xuankun Li](#)<sup>1,2</sup>, L.C. Teasdale<sup>1</sup>, B.D. Lessard<sup>1</sup>, K. Bayless<sup>1</sup>, M.D. Trautwein<sup>3</sup>, C.L. Lambkin<sup>4</sup>, N.L. Evenhuis<sup>5</sup>, C.J.E. Lamas<sup>6</sup>, A. Zwick<sup>1</sup>, B.M. Wiegmann<sup>7</sup> & D.K. Yeates<sup>1</sup>

<sup>1</sup>*Australian National Insect Collection, CSIRO National Research Collections Australia, Canberra, ACT 2601, Australia*

<sup>2</sup>*Australian National University, Canberra, Australia*

<sup>3</sup>*California Academy of Sciences, San Francisco, U.S.A.*

<sup>4</sup>*Queensland Museum, South Brisbane, Australia*

<sup>5</sup>*Bishop Museum, Honolulu, Hawaii, U.S.A.*

<sup>6</sup>*Museu de Zoologia da Universidade de São Paulo, São Paulo, Brazil*

<sup>7</sup>*North Carolina State University, Raleigh, U.S.A.*

The Bombyliidae is a very species-rich and widespread family of parasitoid flies with more than 250 genera divided into 15 extant subfamilies. Transcriptomes of 15 species and anchored hybrid enrichment (AHE) data of 86 species, representing 94 bee fly species and representing all but one of the extant subfamilies, was used to reconstruct the phylogeny of Bombyliidae. Analyses of four different data sets (nucleotides and amino acids of 550 and 216 loci) using species from 12 lower Brachycera families as outgroup generated similar and well-resolved phylogenetic trees. Our overall results show strong consistency with the internal taxonomic architecture of the family, with 11 out of 15 subfamilies recovered as monophyletic. Heterotropinae and Mythicomysiinae are successive sister-groups to the remainder of the family. The Anthracinae, Antoniinae, Lordotinae, *Neosardus* Roberts (Cythereinae) and the core Bombyliinae form a well-supported clade. Cythereinae and Bombyliinae were broadly polyphyletic. While most nodes received strong support, a minority of nodes were weakly supported and some of these differed between trees generated from the four data sets. Hence the Toxophorinae, Mariobezziinae, Tomomyzinae and Lomatiinae are monophyletic but their inter-relationships differed between data sets. We reinterpreted the evolution of key morphological characters on the tree, and these indicated the sand chamber evolved once but was lost multiple times. The cup-shaped postcranium is more labile, evolving at least four times independently and being lost twice. Therefore, both “sand chamber subfamilies” and “Tomophthalmae” are not monophyletic on our phylogenomic trees.

*Wednesday 4 December*

*13:30 – 13:45*

*Plaza Room 11*

# Abstract – Rapid-Fire Talk

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## Macroevolution of a hyperdiverse invertebrate group at continental scales

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[Yun Li](#)<sup>1,2</sup>, A. Ślipiński<sup>2</sup>, A. Zwick<sup>2</sup> & C. Moritz<sup>1</sup>

<sup>1</sup>*Research School of Biology, The Australian National University, Acton, ACT 2601*

<sup>2</sup>*Australian National Insect Collection, CSIRO, GPO Box 1700, Canberra, ACT 2601*

Australia is unique in its forms of biodiversity, but the big question is WHY? Previous hypotheses have identified geological events, climate history, trait innovation and co-diversification as main drivers, but without systematically testing the contribution of each factor. Additionally, a lack of representative studies on terrestrial invertebrates prevents us from addressing it for the fauna as a whole. This project will fill this gap using a hyperdiverse invertebrate group, darkling beetles (Coleoptera: Tenebrionidae; ~200 genera, ~1600 species), as a model system to test multiple forces which have shaped their diversity over an entire biogeographic region. The overarching goal of my PhD project is to answer how Australia's tenebrionid fauna has evolved within the contexts of geological history, environmental change and ecological co-diversification. Specifically, I will address two main questions: what is the spatio-temporal diversification pattern across Australia? which factors have driven the diversification rate variations among lineages, across biomes and through time? Fieldwork and museum visiting will be conducted to collect samples for molecular analyses and to compile ecomorphological datasets (distribution, morphological traits). I will generate genome-wide datasets to establish a backbone phylogeny for Australian darkling beetles. By combining these datasets, I will reconstruct their evolutionary history, explore macroevolutionary trends and test which processes have driven their diversification.

*Monday 2 December  
16:15–17:30 [13× speakers]  
Plaza Room 8*

# Abstract – Systematics and Evolution

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## **An undescribed species of soft scale (Hemiptera: Coccidae) found in Brisbane city centre**

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[Yen-Po Lin](#)<sup>1,4</sup>, H. Tanaka<sup>2</sup>, C.J. Hodgson<sup>3</sup> & L.G. Cook<sup>4</sup>

<sup>1</sup>*National Chiayi University, College of Agriculture, Department of Plant Medicine, Chiayi City, Taiwan 60004*

<sup>2</sup>*Ehime University, Faculty of Agriculture, Tarumi, Matsuyama, Ehime, Japan 790-8566*

<sup>3</sup>*The National Museum of Wales, Department of Biodiversity and Biological Systematics, Cardiff, UK CF10 3NP*

<sup>4</sup>*The University of Queensland, School of Biological Sciences, Brisbane, QLD 4072*

Specimens of what appear to be an undescribed species of soft scale (Coccidae) were found on the leaves of street trees in the Brisbane Central Business District (CBD) and several inner suburbs. The coccids are bisexual and have been found on species of Meliaceae, Myrtaceae and Proteaceae, indicating a lack of strict host specificity. Here, we show the morphologies of adult females and males, and compare these with supposedly closely related Australian endemic species such as *Ceronema* spp. and *Pulvinaria dodonaeae* Maskell. We sequenced specimens from different locations for mitochondrial and nuclear loci to determine their species and generic status.

*Tuesday 3 December  
12:00 – 12:15  
Plaza Room 11*

# Abstract – Chemical Ecology Symposium

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## **The role of plant volatile organic compounds in mediating the response of sweet potato weevil (*Cylas formicarius* (Fabricius)) to crop-protecting barrier plants**

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[Jian Liu](#)<sup>1</sup>, G. Malambo<sup>2</sup>, P. Weston<sup>1</sup> & G. Gurr<sup>1,2</sup>

<sup>1</sup> *Graham Centre for Agricultural Innovation, School of Agricultural and Wine Sciences, Charles Sturt University, Orange, New South Wales 2800, Australia*

<sup>2</sup> *School of Agricultural and Wine Sciences, Charles Sturt University, Orange, New South Wales 2800, Australia*

Plant volatile organic compounds (VOCs) are recognised as metabolites that play important roles in communication with conspecific and other plants, as well as other life forms including herbivores, natural enemies of herbivores, and microorganisms. There is increasing research interest in VOCs because they offer scope to reduce the agricultural impacts of pest herbivores including by direct repellency or masking the olfactory cues that pests use to locate host plants. Here we report work on the sweetpotato weevil (*Cylas formicarius* (Fabricius)). Laboratory studies using multi-arm, still-air olfactometer identified several plant species that reduced the numbers of weevils that reached the terminal ends of olfactometer arms in which sweetpotato plants were located. VOCs samples from these plants were collected using dynamic headspace volatile collection system, then analysed using GCMSD. Results of VOC analyses will be presented to explain the significance of these compounds in mediating the response of weevils and the scope to develop pest management tactics based on using repellent plants as borders to reduce the numbers of pests entering newly-planted sweetpotato crops.

*Tuesday 3 December  
12:00 – 12:15  
Plaza Room 9*

# Abstract – Systematics and Evolution

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## Taxonomy and phylogenomics of the Australian bristle fly genus *Rutilia* Robineau-Desvoidy (Diptera: Tachinidae)

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[James Lumbers](#), B. Lessard, K. Bayless, D. Rowell & D.K. Yeates

The Australian National Insect Collection, CSIRO Canberra 2601 and the Research School of Biology, Australian National University, Canberra 2600, Australia

Bristle flies (Tachinidae) are important insect parasitoids and play a significant role in regulating insect populations in natural and agricultural landscapes. The family is currently recognised to include four subfamilies, the Dexiinae, Exoristinae, Phasiinae and Tachininae, which are further divided into a total of 50 tribes. The impressive metallic-coloured genus *Rutilia* Robineau-Desvoidy (subfamily Dexiinae, tribe Rutiliini) are parasitoids of scarab beetle larvae in the soil. The genus comprises 57 recognised species, with 52 of these being found in Australia. *Rutilia* Robineau-Desvoidy is further divided into seven subgenera: *R. (Ameniamima* Crosskey), *R. (Chrysorutilia* Townsend), *R. (Donovanius* Enderlein), *R. (Grapholostylum* Macquart), *R. (Microrutilia* Townsend), *R. (Neorutilia* Malloch) and *Rutilia sensu stricto*, and two species are currently not assigned to a subgenus. The genus is largely confined to Australia, but six described species are known from the Indomalayan and Oceanic ecozones. The genus has not been revised for more than 40 years since the work of Crosskey and consequently at least 40 undescribed species have since accumulated in Australian collections. This PhD project aims to revise *Rutilia* by describing new species and generating a modern identification key to species. For the first time, anchored hybrid enrichment data has been used to build a preliminary phylogenetic framework for the genus, as well as providing insights into the subgeneric boundaries for such a charismatic group of flies.

Wednesday 4 December  
12:15 – 12:30  
Plaza Room 11  
**STUDENT**

# Abstract – Pest Management

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## **Host-recognition of *Cotesia urabae*: enhancing risk analysis of biological control agents through electrophysiological and chemical profiling**

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[Lee-Anne Manning](#) & K. Park

*The New Zealand Institute for Plant and Food Research Limited, Private Bag 4704, Christchurch 8140, New Zealand*

*Cotesia urabae* (Hymenoptera: Braconidae) is an endoparasitoid of the gum-leaf skeletoniser, *Uraba lugens*, and less frequently other moth species such as *Nyctemera annulata*. We used these species as a model to see if host range prediction may be enhanced by chemical profiling and electrophysiology. Testing the potential host range of a biological control agent (BCA) is challenging, it requires relatively large resources and is often time consuming. Therefore, it is useful to develop a new technique to enhance and facilitate the current host range testing of BCA.

In this research, we compared the olfactory sensory system of *C. urabae* with the volatile compounds produced by two moth species, *U. lugens* and *N. annulata*. We characterised the olfactory sensilla of *C. urabae*. Volatile extractions of host and non-host larvae were prepared and the compounds present identified by gas chromatography mass spectrometry (GCMS). Gas chromatography coupled electroantennogram detection (GC-EAD) was used to identify olfactory active compounds in the extracts. Work was done in parallel by colleagues who used a testing sequence for host specificity in the laboratory and semi-field conditions to determine host specific volatile cues in hosts and non-host species.

Our results showed that two morphological types of olfactory sensilla were abundant in the antennae of *C. urabae*, and four volatile compounds produced by the larvae of *U. lugens* were olfactory active on the antennae of *C. urabae*. However, those four compounds were not detected in the larval extracts of *N. annulata*, it produced other compounds that were EAD active to *C. urabae*. We found that the volatile profile of a small proportion (4%) of *N. annulata* differed from the majority of the *N. annulata* tested, which could be why some *N. annulata* are attacked by *C. urabae*.

Our study demonstrates that electrophysiology and chemical profiling can be used in parallel as a tool to identify host-specific olfactory active compounds for BCA.

*Tuesday 3 December  
15:15 – 15:30  
Plaza Room 8*

# Abstract – Systematics and Evolution

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## Grasping the diversity of the *Doris* ‘*kerguelenensis*’ species complex within the Southern Ocean

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[Paige Maroni](#)<sup>1</sup> & N.G. Wilson<sup>2</sup>

<sup>1</sup>The University of Western Australia, Stirling Highway, Crawley, WA 6009

<sup>2</sup>The Western Australian Museum, Kew Street, Welshpool, WA 6106

The Southern Ocean benthic sea slug, *Doris kerguelenensis*, was long thought to be a single species that showed reduced dispersal potential. This slug lacks a free-swimming larval stage and can only crawl along the seafloor as an adult. More recently however, a combination of mitochondrial and nuclear DNA sequencing combined with metabolics, has revealed a multitude of highly divergent lineages within that ‘species’, signalling an explosive marine adaptive radiation comprising of over 32 putative species. This radiation was thought to reflect speciation through a unique combination of selection and allopatry facilitated through millions of years of episodic glacial cycles. This resulted in the segregation of previously widespread species into smaller, reduced populations which in turn, increased vulnerability to predation pressure. This study was dedicated to comprehend the extent of diversity of the *Doris* ‘*kerguelenensis*’ species complex within the Southern Ocean. This project sequenced the mitochondrial gene Cytochrome Oxidase I (COI) from over 1,000 *D.* ‘*kerguelenensis*’ nudibranchs and used maximum-likelihood phylogeny and species delimitation methods to produce a phylogeny consisting of over 50 putative species. This work supports the idea that Antarctica is a cradle of diversity, promoting high speciation rates.

*Monday 2 December*

*11:45 – 12:00*

*Plaza Room 11*

**STUDENT**

# Abstract – Insects and Plants

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## **The endemics behind the pests: how the iMapPESTS detection program can provide information on a number of Australian native insects and why this is important**

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[Francesco Martoni](#), I. Valenzuela, L. Rako, L. Eow, A. Piper, R. Mann, E. Nogarotto, J. Edwards, C. Trollip, B. Rodoni & M. Blacket

*Agriculture Victoria Research Division – AgriBio Centre for AgriBio Science, 5 Ring Road, Bundoora 3083, VIC, Australia*

Australia is home to a high number of native and introduced insects of great interest to Agriculture, amongst these, some are considered pests, while others are vectors of plant pathogens.

The iMapPESTS project was launched in 2018 aiming to improve Australian biosecurity and plant pest management through deployment of smart sensors, an implemented morphological and molecular diagnostic program, and forecasting. This national project adopts advanced surveillance technologies, such as automated trapping and sampling, for detecting and monitoring endemic and exotic plant pests and pathogens.

A major focus of iMapPESTS is to improve current diagnostics, used to support pest and disease surveillance programs. In the context of the Australian insect fauna, this can be problematic due to the high number of both described and undescribed endemic taxa that can slow down the identification process of pest species.

A fast, reliable, cost-effective means to detect individual species, capable of processing large volumes of specimens is required. At the same time, however, it is fundamental to preserve samples as voucher specimens for future morphological examination and to provide distribution records of both pest and non-pest species.

A high throughput sequencing (HTS) metabarcoding approach, combined with non-destructive DNA extraction methods and a curated database of sequences, is presented here as a possible solution. This enables differentiation of closely related species and identification of immature stages and partial specimens while generating a curated database of DNA sequences allowing links between molecular data and morphological voucher specimens.

Here, we focused on targeting psyllids and aphids, both native and adventive to Australia, as a model to test the HTS metabarcoding system. We highlight challenges and possible limitations of the HTS method, together with key aspects to be considered when implementing this approach in biosecurity and plant pest management.

*Wednesday 4 December  
12:00 – 12:15  
Plaza Room 8*

# Abstract – Insects and Plants

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## **Invasive fig longhorned borer *Trichoferus griseus* (Fabricius, 1792) (Coleoptera: Cerambycidae) in north-east Libya**

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[Ayad Masry](#)<sup>1</sup>, I.M. El Ghariani<sup>2</sup> & A.-H.A. Gleo<sup>2</sup>

<sup>1</sup>Faculty of Science, Tobruk University, Tobruk, Libya.

<sup>2</sup>Plant Protection Department, Faculty of Agriculture, Omar Al-Mukhtar University, El-Beida, Libya

Fig longhorned borer *Trichoferus griseus* is one of the most serious pests on fig trees in the eastern coastline of Libya where is an environmentally suitable area for common fig (*Ficus carica* L.) cultivation. *T. griseus* Larvae bore into the main trunk and branches of fig trees and consequently cause greater damage to the crop. Although there is a concern about the risk of invading *T. griseus*, there is no measure of its impact on fig trees in the eastern region of Libya. The aim of the current study is to estimate the level of insect infestation and understanding of how agricultural practices influence on an invasive level. Based on a field survey using the technique of adult exit holes, we estimate the invasive rates as the number of exit holes on 180 randomly chosen trees within fig orchards located at three main wadis (Al-Khaberi, Janzour and Al-Terfawi) with different agricultural practices. Overall, 65% of 180 fig trees were invaded, despite significant differences in invasion between the three sites. Significantly more exit holes were found on fig trees in Wadi Janzour compared to Wadi Al-Khaberi and Wadi Al-Terfawi, whereas the number of exit holes were the lowest on irrigated trees in Wadi Al-Terfawi. We provide the first documented infestation data for the common fig in the target area, which would improve the chances of effective control.

*Wednesday 4 December  
11:30 – 11:45  
Plaza Room 8*

# Abstract – Systematics and Evolution

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## Phylogeographic structure in Tasmanian glow-worms

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[Zack McIntyre](#), L. Cook, A. Toon & D. Merritt

*School of Biological Sciences, The University of Queensland, Brisbane, Qld*

Larval fungus gnats of the genus *Arachnocampa* are predators that use bioluminescence to attract flying prey to their silk webs. The adults are very short-lived (3–5 days) and are weak flyers. Most species are troglophiles, i.e. they are capable of living and reproducing in caves as well as suitable epigeal habitats such as rainforest. A recent investigation of population genetic structure of the Tasmanian species, *Arachnocampa tasmaniensis*, from two caves within a few kilometres of each other and a nearby forest site in the Ida Bay region of SE Tasmania found that no mitochondrial DNA (mtDNA) haplotypes were shared between the three populations (Claudia Schipp, BSc honours, UQ, 2019). On the other hand, analyses of RADseq data (nuclear DNA) showed less geographic structure and was consistent with isolation-by-distance. One interpretation is that females have a reduced tendency to disperse compared to males. Here, we test whether phylogeographic structuring of mtDNA present in the Ida Bay region applies across the species' broader distribution. We present data on COI haplotypes in populations of *A. tasmaniensis* collected from caves and forest sites throughout the island state of Tasmania.

*Wednesday 4 December*  
*13:15 – 13:30*  
*Plaza Room 11*  
**STUDENT**

# Abstract – Invasive Ants Symposium

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## Using non-target “citizen science” detections to infer absence of red imported fire ants

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[Matt McKinney](#) & M. McNaught

*National Red Imported Fire Ant Eradication Program, Qld Department of Agriculture and Fisheries, Wayne Goss Drive, Berrinba QLD 4118*

Widespread and structured surveillance data are often not available for non-bird, non-charismatic species in Australia, particularly invertebrates. Therefore, passive surveillance by the public (so-called “citizen science”) is a primary means of estimating species distributions. However, citizen science data typically provide presence-only information and often cannot easily be associated with any measure of search effort, presenting challenges for inferring true absences. Bird lists are a notable exception to both scenarios.

The National Red Imported Fire Ant Eradication Program has collated a novel citizen science dataset of public reports of red imported fire ants (*Solenopsis invicta*; hereafter fire ants) from throughout a region of Southeast Queensland. This region is believed to encompass the entire Australian fire ant distribution. The data are novel because they are significantly comprised of incorrect, or “negative” samples, and are therefore not presence-only. For the first time, we show a method to exploit these negative data, by using them in conjunction with positive (i.e. presence correctly identified) samples within a hierarchical mixture-modelling framework, in order to better estimate the probability of absence of fire ants in locations where positive reports are absent. We demonstrate that a high incidence of negative-only reporting can increase certainty that fire ants are not present in a particular area. This method has the potential to enhance inference from citizen science data, and can be used within the context of an eradication program to prioritise areas for treatment and structured surveillance.

*Monday 2 December  
13:30 – 13:45  
Plaza Room 10*

# Abstract – Ecology and Interactions #2

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## Monitoring honey bee health during pollination services

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[Aimee C. McKinnon](#)<sup>1</sup>, L. Collins<sup>1</sup>, J. Wood<sup>2</sup>, M. Clarke<sup>1</sup>, A. Franks<sup>2</sup>  
& M.J. Steinbauer<sup>1</sup>

<sup>1</sup>Department of Ecology, Environment & Evolution, La Trobe University, Melbourne, VIC 3086

<sup>2</sup>Department of Physiology, Anatomy & Microbiology; La Trobe University, Melbourne, VIC 3086

Certain crops depend upon pollination services for fruit-set and of these, almonds are the most valuable in Australia. This reliance on European honey bees *Apis mellifera* (Hymenoptera: Apidae), has resulted in the need for studies to identify the risk factors associated with colony health for improving industry management practices. While various interacting biological stressors such as diseases, pests and nutrition may contribute to any decline in colony health, there is evidence that agricultural pesticides applied to crops can have a significant impact, even in sublethal quantity. Recent studies in the United Kingdom, Europe and North America have quantified pesticide residues from pollen and assessed for effects of pesticides on foraging behaviour. In Australia, however, field studies are still required to monitor and determine realistic levels of pesticide exposure and to ascertain the risk to bee health. The Australian environment is unique, systemic insecticides may still be used and the *Varroa destructor* mite is absent, presenting an opportunity to study pesticide exposure in the absence of and prior to an incursion of this profound pest. The aim of this study was to monitor honey bee colony health before, during and after pollination services. Hives placed on almond, canola and/or native bush were monitored in-field for activity during seasonal exposure to the pesticide regimes applied by growers. Forager movement was quantified over time using Eyesonhives™ scout cameras (Keltronix, Inc.). Bee-collected pollen was sampled weekly for comprehensive pesticide residue analyses. To complement residue data, plant species present in pollen were identified using DNA metabarcoding of pollen to determine where bees may go apart from the target crop. Finally, bees from study hives were tested using molecular methods to investigate the incidence of *Nosema* spp. disease at the onset and conclusion of the trial, to assess for effects of pesticide exposure on disease susceptibility.

Wednesday 4 December

14:30 – 14:45

Plaza Room 10

# Abstract – Invasive Ants Symposium

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## **Join the Ant Hunt: the power of passive surveillance in the search for red imported fire ants in South East Queensland**

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[Melinda K. McNaught](#) & R. Wylie

*National Red Imported Fire Ant Eradication Program, Qld Department of Agriculture and Fisheries, Wayne Goss Drive, Berrinba QLD 4118*

The red imported fire ant (*Solenopsis invicta*) has been the focus of a national eradication program since its first official detection in Australia in 2001. From the beginning of the program, the Brisbane public have been encouraged to look for fire ants and report what they find. As such, investment in community engagement has been significant throughout the life of the program, resulting in tens of thousands of ant specimens and the discovery of new detections of fire ants.

Analysis of these public detections (including physical specimens and digital images) provided evidence of pest traits linked to public reporting. The introduction of ant photos has been widely beneficial, both as an engagement tool and in increasing the efficiency of the program's targeted surveillance.

Overall, the fire ant program's passive surveillance campaign has been a worthwhile investment and provided a valuable dataset that not only provides information on fire ant distribution, but also has the potential to inform future surveillance efforts and priorities as the program moves into the final stages of eradication.

*Monday 2 December  
13:45 – 14:00  
Plaza Room 10*

# Abstract – Systematics and Evolution

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## **Ten species in one: no single data source differentiates all species of the *Apiomorpha ovicola* species complex**

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[Penelope Mills](#)

*School of Biological Sciences, The University of Queensland, Brisbane, Qld 4072*

High levels of genetic and chromosomal variation, in conjunction with varying levels of host specificity within currently described species, suggests that most species of *Apiomorpha* represent cryptic species complexes. Here, I focus on one of the fourteen recognised species groups (the *Apiomorpha nookara* species group) because previous studies have shown that at least one of the four described species (*A. ovicola* Schrader) in the group is a cryptic species-complex. Some putative species have been difficult to distinguish because of little to no DNA sequence variation despite having very different karyotypes, and there is a lack of clear morphological differentiation among most mtDNA lineages. I use independent datasets (host use, karyology, mtDNA, morphology and three independent nuclear loci) to attempt to delimit species in the *A. ovicola* species-complex, and to assign historical specimens, for which no DNA is available, to species based on PCA and historical records.

*Tuesday 3 December  
11:45 – 12:00  
Plaza Room 11*

# Abstract – Insect Declines Symposium

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## **Coextinction risk of herbivorous insects in a biodiversity hotspot**

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[Melinda L. Moir](#)<sup>1,2</sup> & P.A. Vesk<sup>2</sup>

<sup>1</sup>*Ecosystem Restoration and Intervention Ecology Research Group, School of Plant Biology, The University of Western Australia, Crawley, WA 6009, Australia*

<sup>2</sup>*ARC Centre of Excellence for Environmental Decisions, School of BioSciences, University of Melbourne, Parkville, VIC 3010, Australia*

Coextinction, or the loss of dependent species due to declines in the population of the host, is possibly one of the greatest threats to biodiversity. This is particularly so in the 34 global biodiversity hotspots, where the number of potential endemic host species is the highest in terrestrial systems. We provide the first empirical evidence from a global hotspot, the south west of Australia, to test predictions of a high coextinction threat for areas of high floristic diversity. We quantified the realized host use of 957 insect species on 104 plant species of varying threat status, and modelled the species richness of insects that use each plant species. The estimated host breadth of dependent taxa ranged from zero to over 60 hosts, with few highly host-specific taxa. There was a slight shift to more generalised host breadth when host plant species increased in threat status, but once critically endangered status was reached, the insect assemblage became more specialised. There was no general trend of number of insect species per plant species changing with threat status, but this depended on the genus or family of plant considered. Given the overall lower levels of specialisation of insects, coextinction may have been over-emphasized for the majority of plant hosts and their dependent insect assemblages for this global diversity hotspot. Coextinction still remains a threat for particular insect assemblages, however, as removing more plant species of mid-range threat status from the system increased the number of both monophagous and oligophagous insect species that were lost. Furthermore, the sheer number of herbivorous species involved, and the high proportion of endemic plant species under threat, ensures that coextinction is one of the most likely forms of extinction for the herbivorous insects of southwestern Australia.

*Monday 2 December*

*15:15 – 15:30*

*Plaza Room 9*

# Abstract – Invasive Ants Symposium

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## **Join The Electric Ant Hunt: where size really does matter**

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[Gary Morton](#) & N. Cox

*National Electric Ant Eradication Program, Biosecurity Queensland, 21-23 Redden Street, Portsmith, Cairns, QLD 4870*

The electric ant (*Wasmannia auropunctata*) has been the focus of a national eradication program since its first official detection in Australia in 2006. The Cairns public have been an integral part of the success in detecting electric ant in Far North Queensland with 40% of all detections the result of public reporting.

Historically, as a smaller, less well-resourced program, the National Electric Ant Eradication Program (the electric ant program), has utilised the knowledge and resources of the fire ant eradication program community engagement strategy to tailor their engagement campaigns. However, this has not always been beneficial. For example, the advent of readily available, mobile digital imagery has been hugely beneficial to the fire ant program; not so much for the electric ant program.

The electric ant program has had to adapt its message to suit the size and cryptic nature of its target pest. We will discuss these adaptations, their success and failure, and how the message will change as we get closer to our goal of the eradication of electric ants from Australia.

*Monday 2 December  
14:00 – 14:15  
Plaza Room 10*

# Abstract – Pest Management

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## **Predicting *Sirex* biocontrol success in subtropical Australia: can *Deladenus siricidicola* take the heat?**

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[Helen F. Nahrung](#)<sup>1</sup>, M. Ramsden<sup>2</sup> & M. Griffiths<sup>3</sup>

<sup>1</sup>Forest Industries Research Centre, University of the Sunshine Coast, Queensland

<sup>2</sup>HQPlantations Pty Ltd, Beerburrum, Queensland

<sup>3</sup>Horticulture & Forestry Sciences, Queensland Department of Agriculture and Fisheries, Queensland, Australia

The invasive exotic woodwasp *Sirex noctilio* (Hymenoptera: Siricidae) established in the temperate pine plantation estate (*Pinus radiata* and *P. taeda*) in southern Queensland in 2009, fifty years after first reaching Australia. If it spreads further northwards, the wasp will encounter warmer climatic conditions and completely different host taxa - synthetic hybrids between *P. elliottii* and *P. caribaea* – than in its current range. However, subtropical conditions and these new potential host trees may impact substantially on the efficacy of existing successful biological control, in particular the major biological control agent, the nematode *Deladenus siricidicola*. We tested the performance of this important bicyclic nematode under subtropical conditions and in hybrid pine hosts. We also used probes to measure internal tree temperatures in the field in healthy and stressed trees to ascertain the conditions to which nematodes would be exposed in subtropical climate and hosts, and used these data to further predict nematode survival. Our results suggested that *D. siricidicola* may not be as effective in hybrid pine taxa as it is in current host taxa, possibly because of reduced growth of its mycetophagous-phase food source, *Amylostereum areolatum*, in hybrid pine. If *Sirex* reaches the coastal subtropical hybrid plantation estate, new nematode strains and/or alternative biological control agents may be required.

*Tuesday 3 December  
11:15 – 11:30  
Plaza Room 8*

# Abstract – Rapid-Fire Talk

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## **How are we going to protect the coffee industry from Coffee Berry Borer (*Hypothenemus hampei* (Ferrari); Coleoptera: Curculionidae: Scolytinae) in Papua New Guinea and Australia?**

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[Ian Newton](#)

*Department of Agriculture and Fisheries, PO Box 1054, Mareeba QLD, 4880*

Coffee is one of the most important crops in Papua New Guinea (PNG) with some 87,000 Ha producing 60,000t/year, making it one of PNG's major exports and sources of foreign income. Until recently, PNG was one of the last major coffee producing nations free of the Coffee Berry Borer (CBB) *Hypothenemus hampei*. However, CBB has now entered coffee production areas in PNG and could potentially have a major impact on the livelihoods of millions of people, including farmers, farm workers, processors etc. and their families and communities. CBB is the most serious and destructive pest of coffee production in the world, and while currently absent from Australia, it poses a significant biosecurity threat.

In PNG, the pest has now become well established and future priorities will now focus on managing the pest, or "living with CBB". A five-year project is aiming to limit CBB damage and protect the coffee industry by managing CBB infestations with world's best practices and to find long-term sustainable IPM solutions. The project is a partnership between the Department of Agriculture and Fisheries Queensland, the PNG Coffee Industry Corporation and the Australian Centre for International Agricultural Research.

Developing of a package of management practices will begin with an expert review panel, which will evaluate the current management and control methods; From this review, a recommended best management practice package will be developed for immediate implementation to selected extension teams and farmers. Research will also be conducted on CBB monitoring methods, cultural control, agronomic practices, biological control, chemical pesticides and biopesticides. Research activities in Queensland will complement this work by further investigating insect pathology biological control methods.

*Monday 2 December  
16:15–17:30 [13× speakers]  
Plaza Room 8*

# Abstract – Ticks & Lice Symposium

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## **The lesser known members of the ecto-parasitic communities from a long-term study of sleepy lizards across an ecological gradient in South Australia**

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[Gerrut Norval](#)<sup>1</sup>, R.D. Sharrad<sup>1</sup>, K.E. Ross<sup>1</sup> & M.G. Gardner<sup>1,2</sup>

<sup>1</sup>College of Science and Engineering, Flinders University, Adelaide, South Australia, Australia

<sup>2</sup>Evolutionary Biology Unit, South Australian Museum, North Terrace Adelaide 5000, South Australia, Australia

Parasites are major elements of biodiversity and play important roles in ecology by influencing host population dynamics, interspecific competition, and energy flow. Spatial variations in temperature and/or humidity create ecological gradients, which influence the distribution of various species and their parasite communities. These ecological gradients therefore provide natural experiments for how species associations may change with climate perturbations. However, the influences of ecological gradients on the parasite communities of wildlife is poorly understood. This knowledge gap is in part due to limited data on host/parasite associations within different ecosystems. My research forms part of the long-term field surveys on the sleepy lizards (*Tiliqua rugosa*) at a study site near Mt. Mary in the Mid North region of South Australia. For this I utilize established transects, which cross a precipitation-induced natural ecological gradient, to study the ecto-parasite (ticks and mite) communities of the lizards that inhabit this locality. Earlier research at the study site focussed on the ticks, *Amblyomma limbatum* and *Bothriocroton hydrosauri* and their interactions with each other as well as their primary host, the sleepy lizard. My research incorporates the other more rarely encountered ecto-parasites that I have observed parasitising sleepy lizards to provide a more comprehensive description of the ecto-parasite community of these lizards.

*Wednesday 4 December*  
*13:45 – 14:00*  
*Plaza Room 9*  
**STUDENT**

# Abstract – Pest Management

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## **Pesticide regime can negate the positive influence of native vegetation on natural enemy abundance in adjacent crop fields**

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[Sunita Pandey](#)<sup>1,2</sup>, A.C. Johnson<sup>1,2</sup>, G. Xie<sup>3</sup> & G.M. Gurr<sup>1,2</sup>

<sup>1</sup>*School of Agricultural and Wine Sciences, Faculty of Science, Charles Sturt University, P.O. Box 883, Orange, NSW 2800*

<sup>2</sup>*Graham Centre, Charles Sturt University, P.O. Box 883, Orange, NSW, 2800*

<sup>3</sup>*Quantitative Consulting Unit, Charles Sturt University, Wagga Wagga, NSW 2678, Australia*

The benefits of non-crop vegetation to conservation biological in adjacent crops has often been demonstrated but this capacity could be compromised by chemical pesticide use in crops. Here we assessed the spatial distribution of natural enemies in brassica crop fields with varying pesticide use intensity and with one edge bordering perennial native vegetation. For predators as a whole and in particular ground active taxa, namely Araneae, Carabidae, Dermaptera and Formicidae, the donor habitat effect of the adjacent vegetation was overridden by pesticide use. Natural enemies were uniform within crops with intense insecticide regimes. Perennial vegetation only influenced natural enemies in fields with a relatively low pesticide use. Natural enemies such as parasitoids with a high dispersal capacity were not affected by pesticide use, reflecting their ability to rapidly recolonize a field. Integrated pest management strategies need to consider pesticide use and dispersal capacity of key natural enemies.

*Tuesday 3 December  
16:30 – 16:45  
Plaza Room 8  
**STUDENT***

# Abstract – Behaviour #2

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## Why do honey bees collect fungal spores?

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[Jorgiane B. Parish](#), E.S. Scott & K. Hogendoorn

*School of Agriculture, Food and Wine, The University of Adelaide, Adelaide, South Australia 5005, Australia*

The collection of fungal spores by honey bees, *Apis mellifera*, can be classified as active or passive. Active collection refers to the sole collection of spores and passive collection occurs when spores are associated with pollen, nectar or honey dew. While low quality and shortage of pollen have been raised as hypotheses for fungal spore collection, the impact of consumption of spores on honey bee health has not been experimentally investigated. In this study, we investigated the effects of consumption of fungal spores in combination with pollen on the survival, ovarian activation and development of the hypopharyngeal glands (HPGs) in honey bee workers. Two pollen diets (*Eucalyptus* sp. pollen and a multifloral pollen) containing or without spores of *Botrytis cinerea*, *Cladosporium* sp. or *Colletotrichum acutatum* were used. Consumption of diets that contained fungal spores increased the lifespan of honey bee workers but had no significant effect on ovarian activation or the development of HPGs. This demonstrates that fungal spores may have nutritional value for honey bees and that the consumption of fungal spores may compensate for nutritional imbalances of poor-quality pollen diets.

*Tuesday 3 December*  
*16:45 – 17:00*  
*Plaza Room 9*  
**STUDENT**

# Abstract – Systematics and Evolution

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## Phylogenomics and biogeography of the parasitic wasp family Gasteruptiidae (Hymenoptera: Evanioidea).

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[Ben A. Parslow](#)<sup>1</sup>, E.A. Sadler<sup>4</sup>, J. Rodriguez<sup>5</sup>, S. Van Noort<sup>6</sup>, C. van Achterberg<sup>7</sup>, J.P. Pitts<sup>8</sup>, M.P. Schwarz<sup>1</sup> & M.I. Stevens<sup>2,3</sup>

<sup>1</sup>Biological Sciences, College of Science and Engineering, Flinders University, Adelaide, SA 5001, Australia

<sup>2</sup>South Australian Museum, North Terrace, GPO Box 234, Adelaide, SA 5000, Australia

<sup>3</sup>School of Pharmacy and Medical Sciences, University of South Australia, Adelaide, SA 5001, Australia

<sup>4</sup>Department of Biology, Utah State University, 5305 Old Main Hill, Logan, UT 84322-5305, USA

<sup>5</sup>Australian National Insect Collection, CSIRO, Canberra, Australian Capital Territory, Australia

<sup>6</sup>Research and Exhibitions Department, Iziko South African Museum, P.O. Box 61, Cape Town, 8000, South Africa

<sup>7</sup>Research Associate, Department of Terrestrial Zoology, Naturalis Biodiversity Center, Postbus 9517, 2300 RA Leiden, The Netherlands

<sup>8</sup>Department of Biology & Ecology Center, Utah State University, Logan, Utah, United States of America

The wasp family Gasteruptiidae (Hymenoptera: Gasteruptiidae) is an easily recognised, diverse group of wasps whose larvae are predator-inquilines of cavity nesting bees and wasps. Although they are readily collected and there is an abundance of material in collections, there is limited information on their systematic relationships, biodiversity, taxonomy and the evolutionary relationships with their hosts. The family exhibits a puzzling distribution with the largest genus *Gasteruption* found across all biogeographical regions. The smaller genera are all restricted to specific regions (e.g. *Pseudofoenus* is restricted to a Gondwanan distribution, *Spinolafoenus* is only found in the Neotropical region). There has been no strong consensus for the phylogenetic relationships or biogeography of the family, with only two studies including more than singleton taxa in large scale family level studies. We used the sequencing of Ultraconserved Elements (UCE) from freshly collected and museum preserved material to infer phylogenetic relationships, estimate divergence dates and test biogeography boundaries for the family across the world. Our dataset recovered the most robust phylogeny for the family to date with almost unanimous support across the tree confirming the monophyly of the genera *Gasteruption*, *Hyptiogaster* and *Pseudofoenus*. We were also able to estimate the divergence age of the family during the Paleocene, coinciding with the divergence of their host taxa but revealing a complex and confusing biogeographical history within this family. The data demonstrates the utility of UCE's for museum preserved material with loci recovery correlated with specimen age.

Tuesday 3 December

16:45 – 17:00

Plaza Room 11

**STUDENT**

# Abstract – Chemical Ecology Symposium

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## **Chemical ecology for managing ecosystem services in conservation biological control of insect pests**

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[John A. Pickett](#)

*School of Chemistry, University of Cardiff, CF10 3AT, Wales, UK*

With the widely accepted need for sustainable intensification of agricultural food production, there will be increased pressure on ecosystem services to deliver more, probably by land sparing strategies. In addition to reducing the impact of insecticides on pollinators such as honey bees by methods already conceived, we must consider enhancing populations of other beneficial Hymenoptera such as the parasitoids used against pests by conservation biological control. Although slow to be developed in regions practicing industrialised agriculture, conservation biological control of insect pests by managing parasitoids using semiochemicals delivered by companion cropping is a clear option. This opportunity has been realised in the push-pull system for controlling lepidopterous stem borers and more recently the fall armyworm in smallholder cereal cropping agriculture in sub-Saharan Africa and dramatically demonstrates the value of such approaches. However, for high input broad acre agriculture as is the main route to food production in industrialised regions we must consider ways to maximise the ecosystem service of reliably high parasitoid populations. Simply growing marginal strips of plants to encourage beneficial insects, as with so-called beetle banks, does not work in practice and leaves the beneficials happily living in their refugia. For aphid parasitoids, we can draw them into the crop, using plant stress related semiochemicals, as with the push-pull. Here is described an opportunity by which to create a push from the ecosystem service so that the learning by parasitoids of chemical cues, associated with the value of the ecosystem service directly to parasitoid development, is overcome thereby promoting foraging where they are needed.

*Tuesday 3 December  
11:00 – 11:30 (30 min)  
Plaza Room 9*

# Abstract – Pest Management

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## **Towards quantitative and high-throughput insect surveillance using DNA metabarcoding**

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[Alexander M. Piper](#)<sup>1,2</sup>, J. Batovska<sup>1,2</sup>, F Martoni<sup>1</sup>, N.O.I. Cogan<sup>1,2</sup>, J.P. Cunningham<sup>1,2</sup> & M.J. Blackett<sup>1</sup>

<sup>1</sup>*Agriculture Victoria Research, AgriBio, Bundoora, Vic, Australia*

<sup>2</sup>*School of Applied Systems Biology, La Trobe University, Bundoora, Vic, Australia*

Trap based insect surveillance forms a key component of plant biosecurity and pest management programs, aiming to detect newly arrived exotic taxa as well as track the population levels of established or endemic pests. However even when targeted lures are used, surveillance traps generally capture many more native species than the target pests and the extensive specimen sorting required prior to identification forms a major diagnostic bottleneck.

DNA metabarcoding has recently emerged as a method for conducting simultaneous, multi-species identification of complex mixed communities. By analysing bulk DNA extracts rather than single specimens Metabarcoding circumvents the ‘needle in a haystack’ problem of previous diagnostic methods and allows a dramatic scale up of both the quantity of traps that can be processed concurrently, and the number of species that can be monitored for. While recent proof of concept studies have demonstrated the effectiveness of metabarcoding in detecting low-abundance invasive insect species, biased amplification of certain taxa currently inhibits its ability to quantify species abundances within mixed trap samples. Here we summarise our recent work developing a quantitative framework for metabarcoding, and applying it to the simultaneous identification and quantification of thousands of insects trapped in ongoing surveillance programs. We anticipate the future integration of this technology into routine diagnostics laboratory operations will enable biosecurity agencies and industry to receive accurate and timely insect identifications to facilitate both large-scale surveillance and precision integrated pest management programs.

*Tuesday 3 December*

*11:30 – 11:45*

*Plaza Room 8*

**STUDENT**

# Abstract – Insects and Humans #1

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## **Entomophagy in Australia: could insects solve the impending food security challenge?**

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[Rocio Ponce-Reyes](#)<sup>1</sup> & B. Lessard<sup>2</sup>

<sup>1</sup>*CSIRO Land & Water, EcoSciences Precinct, 41 Boggo Rd, Dutton Park 4102, Queensland*

<sup>2</sup>*CSIRO National Research Collections Australia, Clunies Ross Street, Acton, ACT 2601*

Producing sufficient protein to feed our growing population is a global challenge that will not be met using current food sources alone. Currently the dominant protein sources in the western world have high environmental and production costs. In contrast, entomophagy (eating insects) promises significant health, cultural and environmental benefits.

Entomophagy is an emerging, rapid growth market in Europe, and the USA, however, Australia lags behind with only a handful of early adopting local industries farming insects, even though eating insects has a long tradition in Australia.

In August 2019, we held the 'Developing Australia's edible insect research and industry to improve environmental, health and cultural outcomes' symposium in Brisbane. We brought together leading scientific and traditional knowledge of native Australian edible insects. The purpose of the symposium was to promote their inclusion in our diet, and drive commercialisation opportunities. During the symposium we identified the research priorities of edible insects in four major topics: culture, environmental benefits, health and diet and commercialisation. In this talk we will present our findings, including a roadmap to farming novel Australian insect species and implementing insect-derived protein into our diet.

*Tuesday 3 December*

*16:15 – 16:30*

*Plaza Room 9*

# Abstract – Behaviour #1

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## Foraging of the Leyburn ant in Bulloak woodland near Leyburn, QLD

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[Adelaide Power](#) & L. Cook

*School of Biological Sciences, The University of Queensland, Brisbane, Qld 4072, Australia*

The Bulloak Jewel (*Hypochrysops piceatus*) is a rare butterfly that occurs in only a few small patches of bulloak (*Allocasuarina leuhmannii*) woodland in SE Queensland. The butterfly has an obligate association with a currently undescribed species of ant, the "Leyburn ant", about which very little is known. The ant nests in large trees and is known to attend larvae of three butterfly species and an eriococcid scale insect feeding on the bulloak. Occurrence of the ant in high density is thought to be a cue for oviposition by the butterfly, and the ant is thought to be dependent on having access to old-growth trees for nesting. Here, we assess the foraging of the ant in the Ellengowan Nature Reserve, with a particular emphasis of determining whether the ants are especially tied to old-growth trees.

*Monday 2 December*

*14:15 – 14:30*

*Plaza Room 10*

**STUDENT**

# Abstract – Ecology and Interactions #2

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## Diversity of dung beetles in lowland forests of Pangandaran Nature Reserve, West Java, Indonesia

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[Windra Priawandiputra](#)<sup>1</sup>, Y. Tsuji<sup>2</sup>, K.A. Widayati<sup>1</sup> & B. Suryobroto<sup>1</sup>

<sup>1</sup>*Department of Biology, Faculty of Mathematics and Natural Sciences, IPB University (Bogor Agricultural University), Jl. Raya Dramaga Bogor, West Java, Indonesia*

<sup>2</sup>*Primate Research Institute, Kyoto University, Inuyama City, Aichi, Japan*

The dung beetles (Scarabaeidae) play crucial role as decomposer and bioindicator in tropical mountainous and lowland forests. However, the information on the dung beetle fauna in lowland/coastal forest in Java Island is still lacking. Pangandaran Nature Reserve (PNR) area, which is recognized as lowland forest habitat of wildlife, including exotic plants and introduced ungulates, support dung beetles. The study aims to examine the dung beetle community in coastal forests of PNR. The dung beetles were collected using baits traps with mammal feces and on the road, for five times (September 2016, August 2017, October 2017, February 2018 and August 2018). During the study, 853 individuals of dung beetles from 17 species were collected. The two dominant species were *Onthophagus babirussa* with 434 individuals (50.8%) and *O. tricolor* with 301 individuals (35.2%). Both species were not dominantly presented in three mountainous forests of West Java (Gunung Gede Pangrango National Park, Gunung Halimun Salak National Park and Ciremai National Park) and in lowland forest of Southeast Sulawesi and East Kalimantan. The highest number of dung beetle individuals was found in dry season (August): 335 individuals in 2017 and 286 in 2018. The abundance of dung beetles in this study was mostly higher in the dry season than in the wet season. Our result was different with most studies from other regions where abundance of dung beetles mostly collected in the high precipitation. In the future study, we will conduct research on dung beetles using different feces of various mammal species as baits in other tropical lowland forests, West Java, Indonesia.

*Wednesday 4 December  
11:00 – 11:15  
Plaza Room 10*

# Abstract – Rapid-Fire Talk

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## How silicon indirectly affects plant nutritional quality for an insect herbivore via impacts on nitrogen-fixing bacteria

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[Rocky Putra](#)<sup>1</sup>, J.R. Powell<sup>1</sup>, S.E. Hartley<sup>2</sup> & S.N. Johnson<sup>1</sup>

<sup>1</sup>Hawkesbury Institute for the Environment, Western Sydney University, Locked Bag 1797, Penrith, NSW, 2751, Australia

<sup>2</sup>York Environment and Sustainability Institute, Department of Biology, University of York, York YO10 5DD, United Kingdom

Legumes (Fabaceae) are one of the most important crops worldwide. Legumes form an intimate relationship with nitrogen-fixing bacteria (rhizobia), particularly when availability of soil nitrogen is scarce. Nitrogen is usually the limiting nutrient in the diet of insect herbivores, so fluctuations in the nitrogen content of legume tissues can alter the performance and population dynamics of such herbivores. Nitrogen fixation by rhizobia takes place within nodules in the roots, which occupy the highly complex soil environment. Silicon is the most abundant metalloid element in soil, some of which (bioavailable silicon) can be taken up by plants, especially the grasses. Little, however, is known about how silicon affects legumes or their relationships with rhizobia. Recently, we showed that silicon supplementation in soil increased nitrogen fixation in three different genotypes of the model legume barrel medic *Medicago truncatula* inoculated with a model rhizobial strain *Ensifer meliloti* SM1021. Silicon-promotion of nitrogen fixation may alter host quality (nutritional and defensive), potentially affecting aboveground insect herbivores, as was reported for the pea aphid (*Acyrtosiphon pisum*). Our current research aims to pinpoint the mechanisms for how silicon indirectly affects insect herbivores of legumes, focussing on changes in nitrogen availability in the plant. Plants were grown in soil with low bioavailable silicon and either supplemented or non-supplemented with silicon. All genotypes were singly inoculated with two closely related rhizobial strains of *E. meliloti*. One-month old plants were infested with the larvae (neonates) of cotton bollworm *Helicoverpa armigera* (Lepidoptera: Noctuidae). Insect performance (e.g. larval biomass) was recorded every other day for two weeks. Two-month old plants were harvested and key symbiotic traits, such as root nodulation and nitrogen fixation were analysed. These results, together with host nutritional quality (e.g. amino acids), will be discussed in the context of herbivore performance.

Monday 2 December  
16:15–17:30 [13× speakers]  
Plaza Room 8  
**STUDENT**

# Abstract – Pest Management

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## **A mycoinsecticide for lesser mealworm (*Alphitobius diaperinus*) control**

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[Steven J. Rice](#), D.K. Baker, D.M. Leemon

*Queensland Department of Agriculture and Fisheries, Ecosciences Precinct, Dutton Park, Qld 4102*

Lesser mealworm (*Alphitobius diaperinus*) (PANZER) (Coleoptera: Tenebrionidae) is a significant pest in commercial meat-chicken houses. Vast numbers occur in the flock's bedding litter, mostly under feed pans and along walls. This pest can vector avian pathogens and food safety pathogens and tunnels into the chicken-house floors and insulation causing significant damage. Current control relies on chemical insecticides, however insecticide resistance is compromising their efficacy and residues in litter are of concern, particularly with public demand for chemical-free, safe food. Mycoinsecticides based on entomopathogenic fungi offer a solution; these fungi are non-toxic to humans and birds and leave no chemical residues. We identified local strains of the entomopathogenic fungi *Metarhizium anisopliae* and *Beauveria bassiana* that are virulent to lesser mealworm. Laboratory investigations determined that granular formulations of both fungi were the most effective, with >90% mortality of larvae within seven days, when applied to soil. A field trial evaluated the granular formulations against lesser mealworm, in comparison to industry standard insecticides, in eight commercial meat-chicken houses over five consecutive flocks. The granules were applied to the house floor-soil in 0.9m bands under feedlines and along walls before each flock, at a mean rate of  $2 \times 10^{10}$  spores/ m<sup>2</sup>. The insecticide treatments were applied by industry contractors. Litter was sampled from under the feed pans in each house, each week over the time of each flock, and live lesser mealworms in samples were counted. Houses treated with *Beauveria* granules, and *Metarhizium* granules had mean lesser mealworm populations 72% and 50% lower than the control (respectively) while the insecticides reduced populations by 48%. Further trials aiming to support commercialisation will commence in 2020 evaluating *Beauveria* formulations in different chicken meat production systems. Targeted application of a mycoinsecticide offers the poultry industry a novel, economic and safe control option for lesser mealworm.

*Tuesday 3 December  
16:15 – 16:30  
Plaza Room 8*

# Abstract – Systematics and Evolution

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## **Phylogeny and biogeography of the open-holed trapdoor spider genus *Namea*: a highly diverse mygalomorph lineage from Australia's tropical eastern rainforests**

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[Michael G. Rix](#)<sup>1</sup>, J.D. Wilson<sup>1,2</sup>, R.J. Raven<sup>1</sup> & M.S. Harvey<sup>3</sup>

<sup>1</sup>*Biodiversity and Geosciences Program, Queensland Museum, South Brisbane, QLD 4101, Australia*

<sup>2</sup>*Division of Arachnology, Museo Argentino de Ciencias Naturales "Bernardino Rivadavia", Av. Ángel Gallardo 470 (C1405DJR), Buenos Aires, Argentina*

<sup>3</sup>*Department of Terrestrial Zoology, Western Australian Museum, Welshpool, Western Australia 6106, Australia*

The tropical and subtropical rainforests of Australia's eastern mesic zone have given rise to a complex and highly diverse biota. Numerous old endemic, niche-conserved groups persist in the montane rainforests south of Cooktown, where concepts of serial allopatric speciation driven by the formation of xeric inter-zones have largely driven our biogeographic understanding of the region. Among invertebrate taxa, studies on less vagile arachnid lineages now complement research on vertebrate taxa, and phylogenetic studies on mygalomorph spiders in particular are revealing significant insights about the biogeographic history of the Australian continent since the Eocene. One mygalomorph lineage entirely endemic to Australia's tropical and subtropical eastern rainforests is the open-holed trapdoor spider genus *Namea* Raven, 1984 (family Anamidae). We explore, for the first time, the phylogeny and biogeography of this group of spiders, with the aims of understanding patterns of rainforest diversity in *Namea*, and of exploring the relative roles of lineage overlap versus *in situ* speciation in driving high levels of congeneric sympatry. Sequences were newly obtained for three mtDNA and four nuDNA markers from 81 specimens of *Namea*, and these sequences were combined and analysed with a legacy dataset consisting of 53 taxa. We recovered a monophyletic genus *Namea* sister to the genus *Teyl* Main, 1975, and monophyletic species clades corresponding to 30 morpho-species OTUs, including 22 OTUs nested within three main species-complex lineages. Remarkable levels of sympatry for a single genus of mygalomorph spiders were revealed in rainforest habitats, with upland subtropical rainforests in south-eastern Queensland often home to multiple (up to six) congeners of usually disparate phylogenetic affinity living in direct sympatry or close parapatry, likely the result of both simultaneous allopatric speciation in already co-occurring lineages, and more recent dispersal across 'leaky' barriers in a minority of taxa. *In situ* speciation, in contrast, appears to have played a relatively minor role in generating sympatric diversity within rainforest 'islands'. We further reveal a huge undescribed diversity of *Namea* species from tropical and subtropical rainforest habitats, and an old endemic fauna which is beginning to shed light on more complex patterns of rainforest biogeography.

*Monday 2 December*

*14:00 – 14:15*

*Plaza Room 11*

# Abstract – Pest Management

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## Field management to support beneficial arthropods for IPM on vegetable farms

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[Syed Rizvi](#)<sup>1,2</sup>, O. Reynolds<sup>3,7,8</sup>, M.J. Furlong<sup>4</sup>, J. Mo<sup>5</sup>, J. Page<sup>6</sup>, A. Haque<sup>1</sup>, M. Melo<sup>4</sup>, V. Sandoval<sup>4</sup>, S. Munro<sup>5</sup>, A. Johnson<sup>1,2</sup>, T. Osborne<sup>7</sup> & G. Gurr<sup>1,2,8</sup>

<sup>1</sup>Charles Sturt University, Orange, NSW, Australia

<sup>2</sup>Graham Centre for Agricultural Innovation, Wagga Wagga, Australia

<sup>3</sup>Cesar Australia, Parkville, VIC, Australia

<sup>4</sup>University of Queensland, Brisbane, QLD, Australia

<sup>5</sup>New South Wales Department of Primary Industries, Yanco, NSW, Australia

<sup>6</sup>IPM Technologies, Hurstbridge, VIC

<sup>7</sup>Australia, New South Wales Department of Primary Industries, Menangle, Australia

<sup>8</sup>International Joint Research Laboratory on Ecological Pest Management, Fuzhou, China

The colonization of arthropods, in an agricultural field, depends on the arrangement of land-cover types (landscape complexity) and its effects on the factors that control the exchange of species between the habitats. Landscape complexity almost always increases the abundance and diversity of natural enemies by providing resource subsidies such as shelter, nectar, alternative food sources, and pollen. Many natural enemies are influenced by the non-crop habitats surrounding the agricultural fields. We surveyed around 500 fields including sweet corn, brassica, carrot, lettuce, capsicum, and beans field, across Australia, to determine if, and what scale, adjacent land-use types influence the abundance and diversity of pests and natural enemies. We identified and measured the pests and natural enemies' populations in each nearby edges of different habitats. We found that the diversity and density of both pests and natural enemies are significantly influenced by the adjacent land-use types. Non-crop vegetation such as, riparian strips and shelterbelts tended to be associated with higher numbers of natural enemies and lower numbers of pests, in the nearby edges of vegetable crop fields. Field centres, in contrast, had more pests and fewer natural enemies, suggesting that (i) riparian vegetation and shelterbelts are donor habitats for beneficial arthropods and that could be associated with pest suppression and (ii) the spatial scale at which vegetation patterns on farmlands affect in-crop pest and beneficial densities is small, at least for many key taxa. Crops of a given vegetable species planted contiguously tended to have fewer beneficial arthropods and more pests but separating crops by areas of other land uses, including crops of other species, improved the composition of arthropod communities. Notably, pests were not significantly numerous in organic fields than in conventionally managed crops, whereas natural enemies were significantly higher in organic fields. This suggests that synthetic insecticides may not be essential; natural enemies can adequately check pest outbreaks in the absence of synthetic insecticide use.

*Monday 2 December*

*14:00 – 14:15*

*Plaza Room 8*

# Abstract – Systematics and Evolution

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## **Evolution of chemical defences in dalodesmid millipedes**

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[Juanita Rodriguez](#)<sup>1</sup>, H. Zurcher<sup>1,2</sup>, O. Evangelista<sup>1</sup>, J. Nicholls<sup>1</sup>, A. Zwick<sup>1</sup> & B. Mesibov<sup>3</sup>

<sup>1</sup>*Australian National Insect Collection, CSIRO National Research Collections Australian, Canberra, ACT 2601, Australia*

<sup>2</sup>*Research School of Biology, Australian National University, Canberra, ACT 2601, Australia*

Through the course of more than 500 million years of evolution, all but five millipede orders have evolved to produce more than nine unrelated molecule types independently. The only chemical analyses so far performed for Australian millipedes, have been performed in the polydesmidan family Dalodesmidae and have revealed the production of ketones - a molecule type never before recorded for millipedes. These molecules produce a pungent smell that has given some species within Dalodesmidae the common name: stinky pinkies. These chemicals, however, seem to be found almost exclusively in ground-dwelling species, which suggests a potential correlation between chemical production and substrate. In order to study the evolutionary history of ketone production in Australian dalodesmids and its potential association to habitat type we performed a phylogenetic analysis of all genera of Tasmanian dalodesmid millipedes and estimated ancestral chemical and habitat type. For this, DNA was extracted from 48 species belonging to 13 genera within the Dalodesmidae. Whole genome shotgun sequencing was performed to recover whole mitochondrial genomes. Ribosomal RNA genes 28S, 18S and 5.8S and the spacers ITS1 and ITS2 were also recovered. Genes were extracted from the assemblies, aligned separately and manually refined. Three concatenated matrices were generated: a mitochondrial-only matrix, a nuclear-only matrix and an all genes supermatrix. Bayesian reconstruction was performed on each concatenated matrix. Chemical production and habitat type were mapped onto the resulting phylogeny. The ancestral condition in Dalodesmidae was the production of Benzaldehyde. From there, there was a switch to the production of phenols from which there was a switch to the production of ketones. The ancestral condition of habitat type was ground-dwelling, with independent switches to log-dwelling and leaf litter-dwelling.

*Monday 2 December  
15:30 – 15:45  
Plaza Room 11*

# Abstract – Chemical Ecology Symposium

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## Physiological and molecular interactions between Queensland fruit fly larvae, *Bactrocera tryoni*, and tomato fruit

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[Shirin Roohigohar](#), A.R. Clarke & P. Prentis

*School of Earth, Environmental and Biological Sciences, Science and Engineering Faculty, Queensland University of Technology, QLD 4000*

The Queensland fruit fly *Bactrocera tryoni* is a highly polyphagous crop pest, its success due in part to its ability to cope with a wide variety of fruits' defensive mechanisms. However, the physiological and molecular interactions between *B. tryoni* larvae and host-fruit is largely unknown. This study investigates *B. tryoni* larval performance in tomatoes during different larval instars, studying the effect of different tomato cultivars (Roma and Cherry), ripening stages (colour-break and fully ripe), and fruit position (on and off the plant). In addition to larval phenotype effects, 15 genes from the defensive pathway of the tomato and 30 genes with possible detoxification roles in *B. tryoni* larvae were examined to determine if there was a correlation between gene-expression and larvae mortality under different experimental treatments. Tomato cultivar had no significant effect on larvae survival, but ripening stage and fruit position did significantly effect on survival rates of different instars. In both cultivars at colour-break stage larval survival was greater in fruit off the plant than on the plant. Gene expression results found significantly differentially expressed genes over time, and with fruit location. Results are discussed in the context of herbivorous insects and plant defensive genes.

*Tuesday 3 December*

*15:45 – 16:00*

*Plaza Room 9*

**STUDENT**

# Abstract – Ecology and Interactions #2

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## Nymphal life history influences adult head shape variation in Dermaptera and Plecoptera

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[Peter T. Rühr](#) & A. Blanke

*Morphological Dynamics Group, Institute for Zoology, Biocenter, University of Cologne, Zùlpicher StraÙe 47b, 50674 Cologne, Germany*

A complex life cycle (CLC) with discrete life phases is a pervasive trait in animals, and it is found in all insect groups. The shift from one phase to the next is called metamorphosis, a process accompanied by changes in morphology, physiology, behaviour and ecology. The prevalence and persistence of CLCs throughout Metazoa is explained by the adaptive decoupling hypothesis: alternative life phases within a species can occupy separate ecological niches and are thus able to respond in relative independence to changing selection pressures. For insects, it is currently unknown whether the shape variation in adults is influenced by the an ecologically decoupled nymphal phase in contrast to taxa with ecologically similar nymphs and adults. We studied this question by comparing earwigs (Dermaptera) and stoneflies (Plecoptera). Even though both taxa lack the pupal stage of Holometabola, the last molt separating the aquatic stonefly nymph from its terrestrial, often airborne imago, is accompanied by strong changes in lifestyle and morphology. In contrast, earwig nymphs resemble their adults from the earliest instar onward, and both often share habitat and diet. By combining  $\mu$ CT-based three-dimensional geometric morphometrics of the head shape of 122 earwig and 64 stonefly genera with an extensive literature screening of various ecological traits, we show how strong the higher degree of adaptive decoupling in stoneflies influences the head shape variation of the adult heads in comparison to earwigs. Additionally, we are able to identify further important ecological predictors for head shape variation. We also investigated the speed of shape evolution in these taxa in a phylogenetic comparative framework in order to identify rate shifts in shape diversification over time and analysed them in the framework of the adaptive decoupling hypothesis and ecological novelties.

*Wednesday 4 December  
12:00 – 12:15  
Plaza Room 10  
**STUDENT***

# Abstract – Insect Declines Symposium

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## Drivers of the worldwide decline of the entomofauna

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[Francisco Sánchez-Bayo](#)<sup>1,2</sup>

<sup>1</sup>*Honorary Associate, The University of Sydney, Eveleigh, NSW 2015*

<sup>2</sup>*Department of the Environment & Energy, Civic, ACT 2600*

A review of 73 reports from across the globe has shown that biodiversity of insects is threatened worldwide. Declines affect 41% of species in the major insect taxa, while a third of them are threatened and may become extinct over the next few decades. In terrestrial ecosystems, Lepidoptera, Hymenoptera and dung beetles (Coleoptera) appear to be the taxa most affected, while four major aquatic taxa (Odonata, Plecoptera, Trichoptera and Ephemeroptera) have already lost a considerable proportion of species. Diptera and Hemiptera species also show declines in some regions. In addition, insect biomass has decreased at a rate of 2.5% annually in the past four decades in regions as different as Europe and the Caribbean. The main drivers of species declines appear to be in order of importance: i) habitat loss and conversion of natural landscapes to intensive agriculture and urbanisation; ii) pollution, mainly that by synthetic pesticides and fertilisers; iii) biological factors, including pathogens and introduced species; and iv) climate change, particularly in tropical regions and mountainous areas. The implications of such declines for the sustainability of ecosystems and the actions needed to stem the current trends will be discussed.

*Monday 2 December  
11:15 – 11:45 (30 min)  
Plaza Room 9*

# Abstract – Insect Declines Symposium

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## **Reigniting interest: citizen science as a platform for addressing declines in insects and entomologists**

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[Chris Sanderson](#)<sup>1,2</sup> & M.F. Braby<sup>1,3</sup>

<sup>1</sup>*Division of Ecology and Evolution, Research School of Biology, The Australian National University, Acton, ACT 2601*

<sup>2</sup>*University of Queensland, St Lucia, QLD 4072*

<sup>3</sup>*The Australian National Insect Collection, GPO Box 1700, Canberra, ACT 2601*

Recent literature has suggested that insect populations around the world may be declining, some with alarming rapidity. At the same time, interest in the field of entomology also appears to be on the decrease, with many major academic institutions decreasing or cancelling entomology-related jobs and university subjects. Citizen science has the potential to address both of these concerns. In the short term, it is possible to collect baseline data across whole continents, as well as use targeted projects to discover causes of insect declines. In the medium to long term, engaging the community in entomology will lead to greater interest in study and research opportunities. As an example of the power of this approach, in October this year we have launched a major national project collecting citizen science butterfly sightings records. We will discuss the nature of the data collected in the first few months of operation, and also some information on the citizen scientists themselves. We will talk about the future of the project, and how it could apply to other taxa within the entomological field.

*Monday 2 December*

*14:15 – 14:30*

*Plaza Room 9*

# Abstract – Insect Declines Symposium

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## **The Insect Apocalypse narrative: evidence, engagement ethics and research opportunities**

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[Manu E. Saunders](#)<sup>1</sup>, J.K. Janes<sup>1,2</sup> & J.C. O’Hanlon<sup>1</sup>

<sup>1</sup>*School of Environmental and Rural Science, University of New England Armidale NSW Australia*

<sup>2</sup>*Biology Department, Vancouver Island University, Nanaimo, BC, Canada*

Recent studies showing temporal changes in local and regional insect populations have received exaggerated global media coverage. At what cost? Confusing and inaccurate science communication on this important issue could have counter-productive effects on public support for insect conservation. The ‘insect apocalypse’ media narrative is built on limited scientific evidence, i.e. a handful of studies that are very restricted geographically (predominantly the UK, western Europe and the USA) and taxonomically (predominantly bees (mostly *Bombus* spp.), macrolepidoptera, and ground beetles). Biases in sampling and analytical methods mean these studies do not show evidence of overall global insect decline, contrary to global media coverage. Rather, the value of existing research lies in highlighting important areas for priority investment. Evidence-based insect conservation depends on greater investment in research and public engagement, with the aim of increasing understanding of insect ecology and population dynamics. Most importantly, we urgently need a balanced perspective in science communication to better serve both public and scientific interests.

*Monday 2 December*

*12:15 – 12:30*

*Plaza Room 9*

# Abstract – Insects and Plants

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## **The Mealybugs Strike Back: the return of *Heliococcus summervillei* and Queensland pasture dieback**

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[Mark K. Schutze](#)<sup>1</sup>, D.J. Tree<sup>2</sup>, C. Hauxwell<sup>3</sup>, A.B. Dickson<sup>3</sup> & P.J. Gullan<sup>4</sup>

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<sup>2</sup>c/o Queensland Primary Industries Insect Collection (QDPC), Queensland Department of Agriculture and Fisheries, GPO Box 267, Brisbane, Qld 4001

<sup>3</sup>School of Earth, Environmental and Biological Sciences, Science and Engineering Faculty, Queensland University of Technology, Brisbane, Qld 4000

<sup>4</sup>Division of Ecology & Evolution, Research School of Biology, The Australian National University, Acton A.C.T. 2600

Mealybugs were collected by W.A.T. Summerville (Entomological Branch, Queensland Dept. Ag.) during a 1920s pasture dieback event in the Cooroy district of Southeast Queensland. Undescribed at the time, this mealybug was implicated as the cause of the dieback characterised by yellow and purple colouration of leaves prior to death. Later, the mealybug was described as *Heliococcus summervillei* by H.M. Brookes in 1978; Pakistan specimens collected from sugar-cane were included in her description. *Heliococcus summervillei* was later associated with pasture dieback in New Caledonia from 1998-2003; as for the earlier Australian incident, mealybugs reduced in number due to apparently natural causes.

Recently, much of Queensland from the southeast to the northern tropics has experienced widespread pasture dieback reminiscent of early last century's incident in the Cooroy district; and late last century's outbreak in New Caledonia. Once again, mealybugs are implicated, with contemporary specimens differing slightly in their morphology from historical material; this lead to early suspicions that the latest material may represent a new species.

Here, we discuss historical and contemporary 'outbreaks' of *H. summervillei*, specifically regarding how this species relates to other *Heliococcus* species and to what extent their morphology varies across collections made almost 100 years apart.

Wednesday 4 December  
11:00 – 11:15  
Plaza Room 8

# Abstract – Systematics and Evolution

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## **Taxonomy and identification of *Carpophilus* (Nitidulidae, Coleoptera) species from south eastern Australian almond orchards**

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[Linda Semeraro](#)<sup>1</sup>, L. Rako<sup>1</sup>, M. Hossain<sup>1</sup>, A. Piper<sup>1</sup>, M.J. Blacket<sup>1</sup> & P. Cunningham<sup>1,2</sup>

<sup>1</sup>*Agriculture Victoria Research, AgriBio, Bundoora, Victoria, 3083, Australia*

<sup>2</sup>*School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, 3083, Australia*

The taxonomic diversity of Australian *Carpophilus* beetles is currently poorly known. Previous studies of this group in Australia has focussed on pest species in stone fruit orchards. A project funded by Hort Innovation and Agriculture Victoria (2015 - 2018) aimed to identify the predominant economic pest species of *Carpophilus* in almond orchards. Of additional interest, was the identification of other non-pest nitidulids occurring in Victoria, New South Wales and South Australia found in these orchards and collected from nuts (in trees or on the ground) or in pheromone traps. In recent years, one main species of *Carpophilus* (both adults and larvae) has been found damaging almond kernels and is currently present in around 70% of almond plantings in south eastern Australia. However, the identification of this serious pest has been hampered due to gaps in taxonomic knowledge and few taxonomic experts studying this group. Furthermore, misidentifications of *Carpophilus* can easily occur due to the overall morphological similarities between some species. Therefore, a combined approach, using both morphological and molecular methods, was employed to identify 11 species of nitidulids associated with these orchards. This included the main pest species in almonds, which appeared to be close to *C. dimidiatus* (a species also associated with almond) but differed from it morphologically in the shape of the male hind tibia and the male paramere. It was also found to be 12% divergent from *C. dimidiatus* based on the COI (barcoding gene) sequence data. A reference specimen-based DNA sequence (of the COI gene) library was produced from the 11 nitidulid species identified and included more than 90 specimens. This verified DNA sequence library now provides valuable baseline data for the development of mixed-species sampling metabarcoding tests, an approach which could be adopted in future for large scale monitoring of *Carpophilus* in Australian orchards.

*Tuesday 3 December*

*16:15 – 16:30*

*Plaza Room 11*

# Abstract – Pest Management

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## **Efficacy of ethyl formate against coffee bean weevil, *Araecerus fasciculatus* (Coleoptera: Anthribidae)**

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[Lara Senior](#)<sup>1</sup>, P. Wyatt<sup>1</sup>, C. Wright<sup>2</sup>, R.A. Hayes<sup>3</sup> & M. Moradi<sup>4</sup>

<sup>1</sup>Department of Agriculture and Fisheries, PO Box 267, Brisbane, QLD 4001

<sup>2</sup>Department of Agriculture and Fisheries, Mareeba, QLD 4880

<sup>3</sup>University of the Sunshine Coast, Locked Bag 4, Maroochydore DC, QLD 4558

<sup>4</sup>Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Dutton Park, QLD 4102

Coffee bean weevil, *Araecerus fasciculatus* (Coleoptera: Anthribidae) is a globally widespread pest of a large number of stored products and some field crops. Postharvest control options have included fumigation with methyl bromide or phosphine, and insecticide treatments. Laboratory bioassays were conducted to assess the efficacy of ethyl formate, a GRAS (general recognised as safe) fumigant that has been shown to be effective against other weevil species. Eggs, larvae, pupae and adults of *A. fasciculatus* were exposed to a series of doses of ethyl formate, with the aim of determining the most tolerant life stage. This information will be useful for future large-scale trials for fumigation of produce infested with this pest. Insects were exposed to ethyl formate in airtight glass flasks for a six hour duration under ambient laboratory conditions. Bioassays indicated that pupae were the most tolerant to ethyl formate. The highest dose (298 mg/L) caused only 87% mortality for pupae, resulting in an unreliable estimate for the effective dose for 99% mortality (ED99). Eggs were the second most tolerant stage, with an ED99 at the 95% confidence level of 117.6 mg/L. The ED99 for larvae was 80.8 mg/L and adults were the most susceptible with an ED99 of 54.6 mg/L.

*Tuesday 3 December  
11:00 – 11:15  
Plaza Room 8*

# Abstract – Insects and Humans #3

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## **Conspecific density and diet dependent effects on development rate and survival of *Aedes aegypti***

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[Majeed Shahid](#)<sup>1</sup>, R.R. Khan<sup>1,2</sup>, A. Ali<sup>1</sup>, M. Binyameen<sup>3</sup> & H. Qadeer<sup>1</sup>

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<sup>3</sup>*Department of Entomology, Bahauddin Zakariya University, Punjab, Pakistan*

The tropical and subtropical regions of the world are over burden by various acute mosquito-borne viral infections including dengue. It was estimated that dengue was responsible for the global economic burden of US\$8.9 billion in 2013. The survival of the virus and immatures are dependent on the conspecific density and quality of the habitats. So, the current work investigated the association between the population density and survival of mosquito's population as well as examine the diet dependent growth of the mosquito's population by performing the experiments under controlled conditions. The results depict that the larval mortality significantly increased with the increasing conspecific population density as well as the larval and pupal growth significantly enhanced with the gradual increase in diet as well as the development time significantly dependent on the diet and conspecific density. Moreover, the significant variations have been observed in body length, width and wing size of population per density/diet. In addition, oviposition preferences were also examined, which shows that the gravid female of *Ae. aegypti* prefer to lay their eggs in moisture filter paper cups containing *Ae. aegypti* larval water compared to *Culex* or distilled water.

*Wednesday 4 December  
14:00 – 14:15  
Plaza Room 11*

# Abstract – Pest Management

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## Testing alternative host *Opuntia* species as potential target for biocontrol agents (*Dactylopius* sp.) previously established in Queensland

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[Shamli Shamli](#)<sup>1,3</sup>, T. Taylor<sup>2</sup> & M. Day<sup>3</sup>

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<sup>2</sup>*Biosecurity Queensland, Department of Agriculture and Fisheries, Ecosciences Precinct, Brisbane, Queensland, Australia*

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Introductions of cactus in Australia have been occurring since the late 1700's. Some species were brought in for commercial cultivation and others as ornamental plants. Since then, many species have become invasive, with 27 opuntoid cacti now listed as Weeds of National Significance (WoNS). Cacti in Australia can form dense thickets that impact on Agriculture by reduce grazing activities, as well as reducing habitat for native species. Biological control of invasive cactus has been on-going in Australia since the 1920s, resulting in the release of insect agents targeting numerous cactus species. However, there are several cactus species currently present in Australia that have not been studied as potential targets for biocontrol. Some of these species are major threats in the State of Queensland where they are not currently established – with an increase in the number of confiscations of these restricted cacti made by Biosecurity Queensland officers over the last few years. In Queensland, Cochineal bug (*Dactylopius* sp., Dactylopiidae, Hemiptera) have been successfully used to control invasive *Opuntia* species. The aim of this study was to test alternative hosts for *Dactylopius opuntiae*, which is currently used in Queensland as a biological control agent for *Opuntia stricta* and *O. tomentosa*. In no choice host tests, development of *D. opuntiae* on cladodes of *Opuntia microdasys*, *O. rufida*, *O. robusta* and *O. puberula* were compared with development on the target host for this species, *O. tomentosa*. Initial results indicate that *D. opuntiae* may be effective as a biocontrol of some of our test species, however efficacy trials on whole plants will need to be completed. This research will allow an assessment of whether biological control agents currently released in Queensland may be effective in preventing establishment of additional opuntoid cactus species, and provide information to other States about potential biological control for species naturalized outside Queensland.

*Monday 2 December  
12:00 – 12:15  
Plaza Room 8*

# Abstract – Ticks & Lice Symposium

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## **Mitochondrial genome analysis provides novel insights into the high-level phylogeny and classification of parasitic lice (Phthiraptera)**

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[Renfu Shao](#)

*GeneCology Research Centre, School of Science and Engineering, University of the Sunshine Coast, Sippy Downs, Queensland 4556 Australia*

The ~5,000 species of parasitic lice (order Phthiraptera) are currently classified into four suborders: Anoplura, Amblycera, Ischnocera and Rhyncophthirina. Ischnocera is the most species-rich among the four suborders with 2,737 species parasitizing birds and 383 species parasitizing eutherian mammals. While the monophyly of Anoplura, Amblycera and Rhyncophthirina, respectively, is supported by morphological and molecular evidence, there is controversy whether Ischnocera is monophyletic. Using Illumina HiSeq platforms, we have sequenced the mitochondrial genomes of 25 species of parasitic lice of birds and mammals from all of the four suborders. Genes in the mitochondrial genomes of parasitic lice are highly rearranged in comparison to other insects. Furthermore, the mitochondrial genome organization differs drastically between bird lice and eutherian mammal lice. The typical one-chromosome mitochondrial genome is retained in bird lice but is fragmented into many minichromosomes in the eutherian mammal lice in the Anoplura, Ischnocera and Rhyncophthirina. The shared character of mitochondrial genome fragmentation supports the mammal lice of Ischnocera (family Trichodectidae) to be more closely related to Anoplura and Rhyncophthirina than to the bird lice of Ischnocera (family Philopteridae). Together, they form a clade, which we name as Mitodivisia for having fragmented mitochondrial genomes. This novel clade is also supported by four types of shared derived mitochondrial minichromosomes and by phylogenetic analysis of mitochondrial genome and gene sequences. We propose that the Ischnocera as a suborder should be rejected, and the mammal lice currently in the family Trichodectidae be elevated to a new suborder Trichodectera, in parallel with Amblycera, Anoplura and Rhyncophthirina.

*Wednesday 4 December  
14:00 – 14:15  
Plaza Room 9*

# Abstract – Systematics and Evolution

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## **Deciphering the dermanyssine mites (Acari: Dermanyssiae)**

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[Matthew D. Shaw](#)

*South Australian Museum, North Terrace, Adelaide SA 5000*

The diverse mite superfamilies Dermanyssoidea and the Eviphidoidea include free-living forms plus a vast array of phoretic and parasitic forms associated with arthropods and vertebrates. Existing systematics was built upon ideas of morphological and ecological similarity and rooted according to assumptions about “primitive” forms and habits. However the first detailed morphological analysis of these groups shows several previous assumptions are unfounded. Despite the variation associated with disparate and often specialised lifestyles, there are useful characters that diagnose groups and provide a basis for future molecular and morphological work.

*Monday 2 December*

*15:15 – 15:30*

*Plaza Room 11*

# Abstract – Ticks & Lice Symposium

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## **Revisiting the status of morphologically divergent populations of *Amblyomma triguttatum* (Acari: Ixodidae)**

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[Saba Sinai](#)

*Central Queensland University*

*Amblyomma triguttatum* (Koch, 1844) commonly known as the ‘ornate kangaroo tick’, is one of 17 species of Australian ticks in the genus *Amblyomma*. *Amblyomma triguttatum* has been associated with a vast host range including kangaroos, cattle, horses, dogs and humans. *Amblyomma triguttatum* is also thought to play a role in the transmission of *Coxiella burnetti*, the pathogenic bacteria responsible for Q fever. Yet despite the importance of *Amblyomma triguttatum* to animal and human health, many questions remain about the status of the four morphologically divergent subspecies. Although the work on determining the geographical distribution of *Amblyomma triguttatum* subspecies is limited, the data that exists suggests that a sympatric distribution of three of the four subspecies in parts of central Queensland. The work presented here will discuss efforts to collect, identify and map *Amblyomma triguttatum* in in this region and expand on the work of Roberts (1962) and others in resolving the status of morphologically divergent populations of *Amblyomma triguttatum*.

*Wednesday 4 December  
12:15 – 12:30  
Plaza Room 9*

# Abstract – Insects and Plants

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## The composition of psyllid communities in Bell miner-associated dieback

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[Julia Smith](#)<sup>1</sup>, B. Horton<sup>2</sup> & M. Steinbauer<sup>1</sup>

<sup>1</sup>La Trobe University, Plenty Road, Bundoora, VIC 3086

<sup>2</sup>Department of Planning, Industry and Environment, Moonee Street, Coffs Harbour, NSW 2450

Bell miner-associated dieback (BMAD) is a unique Australian macroecological phenomenon involving eucalypts, psyllids and birds which also has implications for the diversity of hymenopteran parasitoids. BMAD is a key threatening process and affects tens of thousands of hectares of forest, however, its incidence and severity is patchy making it difficult to fully understand. The role of lerp-forming species of psyllid (Hemiptera: Aphalaridae: Spondyliaspidae) in BMAD is the subject of much speculation. Psyllid genera differ in host plant preferences, leaf age requirements, damage to host leaves and the attractiveness of lerps to Bell Miners. Therefore, it is important to understand the composition of psyllid communities and how psyllid biology influences mechanisms behind BMAD.

This study focused on psyllid communities and host associations in BMAD and non-BMAD affected forests within the Gondwana Rainforest World Heritage Area of NSW. Using a combination of lerp morphology and CO1 barcoding, we found seven *Cardiaspina* species, five *Glycaspis* species and four other psyllid genera across five *Eucalyptus* host species. Host species *E. sideroxylon* had the highest rate of psyllid infestation and *Glycaspis* was the most abundant psyllid genus on this eucalypt in both BMAD and control plots. BMAD affected plots had an overall psyllid infestation rate of more than double that of control plots. A maximum of three genera co-occurred on some individual leaves, however, the majority of infested leaves were occupied by a single genus of psyllid only. These findings will be used to test the strength of the relationships between psyllid communities and the incidence and severity of BMAD as well as provide an indication of psyllid diversity on different species of eucalypt in northern NSW.

Wednesday 4 December  
14:15 – 14:30  
Plaza Room 8  
**STUDENT**

# Abstract – Orthoptera Symposium

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## **From cricket songs to swarming locusts: elucidating patterns and processes of orthopteran evolution**

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### [Hojun Song](#)

*Department of Entomology, Texas A&M University, College Station, Texas, U.S.A.*

Orthoptera is the most diverse order within Polyneoptera with more than 28,000 species known worldwide. Throughout 300 million years of evolution, orthopteran insects have diversified into numerous lineages that occupy every conceivable terrestrial habitat outside the polar regions and play integral roles in their ecosystems. Such diversity in form and function has attracted researchers who use these insects as model systems for studying anatomy, bioacoustics, chemical ecology, evolutionary ecology, life history traits, neurobiology, physiology, and speciation. In recent years, large-scale molecular phylogenetic studies have become available for major orthopteran lineages, which have collectively provided new insights into understanding the evolution of these insects. Furthermore, the application of high throughput sequencing technologies has enabled the generation of genomic and transcriptomic data to build more robust phylogenies and to gain deeper understanding of the molecular basis of orthopteran evolution. In this presentation, I provide two fascinating examples of how orthopteran insects can be used as model systems for elucidating patterns and processes of evolution. For the first example, I consider the entire order as a whole to discuss about how hearing and sound production have evolved based on a new phylogenomic analysis and ancestral character reconstruction. For the second example, I zoom into one particular genus of grasshoppers to discuss about the evolution of density-dependent phenotypic plasticity by integrating phylogenetics, transcriptomics, and manipulative behavioral experiments. Finally, I highlight some striking examples of Australian Orthoptera that can be developed into new model systems for understanding various aspects of ecology and evolution.

*Tuesday 3 December  
11:00 – 11:30 (30 min)  
Plaza Room 10*

# Abstract – Chemical Ecology Symposium

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## Exploring a chemo-discrimination tool for *Gonipterus* weevils

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[Natalia M. Souza](#)<sup>1</sup>, M.L. Schröder<sup>2</sup>, R.A. Hayes<sup>1</sup>, J.E. Bello<sup>3</sup> & H.F. Nahrung<sup>1</sup>

<sup>1</sup>Forest Industries Research Centre, University of the Sunshine Coast, Australia

<sup>2</sup>Forestry & Agricultural Biotechnology Institute, University of Pretoria, South Africa

<sup>3</sup>Department of Entomology, University of California, Riverside

*Gonipterus* is a genus of *Eucalyptus*-feeding weevils from Australia containing several cryptic species. Thus, species identification in this genus has become a taxonomic challenge in both its native range and in countries where it is an invasive pest. In this study, we explored cuticular hydrocarbons (CHCs) of different *Gonipterus* species to assess their potential for species discrimination. Adult weevils were collected from various sites across Australia and kept in identical conditions prior to the study, and species were identified by examination of male genitalia and mitochondrial CO1 sequencing. Whole body hexane washes of the adult weevils were performed and analysed by GC-MS, and the peaks in the resulting chromatograms were analysed by comparison of their relative areas, retention indices, and MS fragmentation patterns. Our results show that the CHC profiles of the seven species of *Gonipterus* used in this study were significantly different from each other. The closely-related weevil genus *Oxyops* was used as an outgroup and its CHC profile was distinct from all *Gonipterus* species. Within *Gonipterus*, the compounds that contributed to species' dissimilarities were alkanes, alkenes and methyl branched alkanes, known to be semiochemicals in other groups. Within species, collection locality impacted CHC profiles. These findings demonstrate CHC analysis as a promising chemotaxonomic tool for the genus *Gonipterus*.

*Tuesday 3 December  
16:00 – 16:15  
Plaza Room 9*

# Abstract – Insects and Plants

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## **Specialisation on old eucalypt leaves by *Cardiaspina albitextura* (Hemiptera: Aphalaridae): characterising sources of variation in the quality of hosts and possible implications for nymphs**

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[Martin J. Steinbauer](#)<sup>1</sup>, R.T. Najafabadi<sup>1</sup> & J.-P. Salminen<sup>2</sup>

<sup>1</sup>*Department of Ecology, Environment and Evolution, La Trobe University, Melbourne, Victoria 3086, Australia*

<sup>2</sup>*Department of Chemistry, Laboratory of Organic Chemistry and Chemical Biology, University of Turku, 20014 Turku, Finland*

Plant quality is fundamentally important to the survival and performance of all insect herbivores. *Cardiaspina* is a genus of lerp-forming psyllid (starchy lerps) that induce discolouration and necrosis of feeding lesions on host leaves leading to serious defoliation, especially during outbreaks. Members of the genus are reported to prefer to oviposit on leaves that are between 1.5 to six months old but the quality of such leaves and the implications of variations in quality (e.g. canopy *versus* understory hosts and leaf age) have not been investigated.

Using an outbreak of *Cardiaspina albitextura* on remnant River red gums (*E. camaldulensis*) in a Melbourne reserve, we conducted a six-month longitudinal study of the abundances of nymphs on tagged leaves in the canopy as well as on leaves of saplings/regrowth in the understory. We nested our surveys by the relative age of infested leaves, i.e. those nearer the apical bud/apex of a branchlet (“younger”) and those further away (“older”). We also quantified the concentrations of foliar sugars and phenolic metabolites in leaves representative of those hosting nymphs.

Greater numbers of eggs were recorded on older than on younger leaves of both canopy and understory hosts. Greater numbers of I and II instar nymphs were recorded on younger than on older leaves of both types of host however from the III instar onwards abundances were greater on older leaves. Quantitative differences in sugars and phenolic metabolites were more pronounced between leaves of different age than between leaves from different hosts. Leaf quality in terms of sugars was higher for younger leaves than older leaves but younger leaves were also higher in phenolic metabolites with greater oxidative activity. We characterise the components of leaf quality correlated positively and negatively with the abundance of the immature lifecycle stages of this damaging species of psyllid.

*Wednesday 4 December*

*14:45 – 15:00*

*Plaza Room 8*

# Abstract – Chemical Ecology Symposium

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## **Sex, Drugs and Ecosystem Services: the paradox of plant toxins in nectar**

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[Philip C. Stevenson](#)

*Royal Botanic Gardens, Kew, Surrey, TW9 3AB, UK & Natural Resources Institute, University of Greenwich, Chatham, Kent, ME4 4TB, UK*

Plants produce an extraordinary diversity of secondary metabolites that protect against diseases and herbivores. Secondary compounds also occur in nectar and pollen and are typically the same as those produced for defense elsewhere in the plant because individual species are restricted to just a few biochemical pathways and therefore limited products. Thus pollinators may encounter toxic compounds in floral rewards. However, evidence from our labs suggests that nectar metabolites can benefit pollinators or optimise pollination. For example, (i) caffeine enhances memory for floral traits associated with food, (ii) the diterpenoid grayanotoxin filters preferred pollinators through selective toxicity to flower visiting bees and (iii) aconitine protects *Aconitum* flowers against nectar robbery. How floral metabolites enhance pollination is informed further by two additional recent studies from our labs. We showed that thrips, a taxon typically associated with herbivory, actually pollinates the commercially important elderflower (*Sambucus nigra*). Floral visitation was mediated by volatiles with peak levels coinciding with flower opening and pollen dehiscence. Deterrent cyanogenic glycosides, however, accumulate as fruits develop repelling thrips and preventing fruit damage. In a second study we showed that antimicrobial compounds in nectar protected against disease acquisition in bees. Callunene, a megastigmene in Ling heather (*Calluna vulgaris*) nectar prevented bumblebees acquiring the common trypanosomatid pathogen *Crithidia bombi*. Exposure to the nectar compound caused flagellum loss preventing the parasite from anchoring to the epithelial cell wall of the gut. Ultimately more research is required to determine impacts of floral chemicals in free flying bees, and how compounds are metabolized, sequestered or excreted by flower feeding insects to understand how they may then affect the pollinators or their parasites. More work is also required on how plants regulate nectar and pollen chemistry to better understand how secondary metabolites and their defensive and pollinator supporting functions are controlled, evolve and adapt.

*Tuesday 3 December  
11:30 – 12:00 (30 min)  
Plaza Room 9*

# Abstract – Phil Carne Student Prize

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## **How rapidly do litter decomposition and decomposer invertebrates return during rainforest restoration on disused pastures?**

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[Marisa Stone](#), L. Shoo, N. Stork, F. Sheldon & C. Catterall

*Environmental Futures Research Institute, Griffith University, Nathan, QLD 4111*

Converting rainforest to pasture can have large impacts on many ecological processes. It could be expected that these processes could be recovered by restoration of native vegetation communities. However, there is little available evidence to clarify such recovery patterns. We deployed open mesh bags containing forest leaves across a network of 25 sites to experimentally quantify the decomposition rates (mass loss) of litter in old growth forest, grazed pasture and two pathways of vegetation recovery: unassisted regeneration and assisted regeneration 1-10 years after interventions to accelerate vegetation development. Both regeneration site-types consisted of woody regrowth aged 20-50 years on former pasture with complete livestock exclusion 11 years prior. We found that decomposition occurred 50 % slower when rainforest had been converted to pasture, but that 83 % of old-growth values had returned within all regenerating site-types. Invertebrates are known to play an important role in decomposition processes. So, to investigate this role we also sampled the potential decomposer community at each site from independently collected samples of ground surface litter. The abundance of invertebrate decomposers in pasture sites was much lower than in old growth forest but had substantially recovered in all regenerating sites. Decomposer community composition at a broad taxonomic level differed strongly between pasture and all other site-types. Further results will be presented that assess the effect of excluding macro-detrivores in open versus closed 1mm mesh bags on litter decomposition rates, meso-decomposers, and how their abundance corresponded with decomposition rate. This study shows a relatively rapid partial recovery during rainforest restoration, of both decomposition rates and communities of decomposer invertebrates, both of which had likely occurred prior to woody regrowth reaching 20-50 years of age.

*Tuesday 3 December  
14:15–15:00 [3× speakers]  
Plaza Room 8  
**STUDENT***

# Abstract – Rapid-Fire Talk

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## Glacier genetics: phylogenetic placement and species delimitation of the Rocky Mountain locust, *Melanoplus spretus* Walsh (Orthoptera: Acrididae), using glacier-preserved samples

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Oliver P. Stuart<sup>1</sup>, L. Qiu<sup>2</sup>, T. McNary<sup>3</sup> & A.S. Mikheyev<sup>1,2</sup>

<sup>1</sup>Research School of Biology, Australian National University, Acton ACT 2601

<sup>2</sup>Okinawa Institute of Science and Technology, Okinawa 904-0495, Japan

<sup>3</sup>C.P. Gillette Museum of Arthropod Diversity, College of Agricultural Science, Colorado State University, Fort Collins CO 80523-1177

The Rocky Mountain locust, *Melanoplus spretus* Walsh (Orthoptera: Acrididae), was once the most abundant agricultural pest in North America, reportedly appearing in trillions-strong swarms to feed on agricultural crops. Despite this hyperabundance, the species suddenly declined at the end of the 20<sup>th</sup> century, was last seen in 1902, and in 2014 was formally declared extinct. The causes of its extinction are unknown.

The term ‘locust’ refers to a transient behavioural and colour phenotype displayed by some Acridid grasshoppers in response to high conspecific density; a usually solitary species will shift into a gregarious phase, change colour, and aggregate in swarms. It has been hypothesised that *M. spretus* is the gregarious phase of another *Melanoplus* species and that it persists today, hiding in plain sight under another name. Few well-preserved *M. spretus* specimens appear in entomological collections, making molecular species delimitation or phylogenetic study challenging. Recently, specimens washed out of the Grasshopper Glacier, Montana US, were identified as *M. spretus*. Only fragmented mitochondrial sequences could be recovered from these specimens with Sanger sequencing, and the information they contained proved ambiguous. The synonymy hypothesis remains unresolved.

We leveraged hybrid-capture RAD sequencing to generate a multispecies SNP dataset for a subset of the *Melanoplus* genus. By comparing samples of glacier-preserved and contemporary *Melanoplus sanguinipes* Fabricius, a close congener, we isolated loci containing accurate species-level information and tested species delimitation hypotheses with glacier *M. spretus* samples using PCA-based and phylogenetic approaches.

*Monday 2 December*  
*16:15–17:30 [13× speakers]*  
*Plaza Room 8*  
**STUDENT**

# Abstract – Pest Management

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## Optimising a combined mealybug pheromone lure for use in New Zealand vineyards

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[Nicola J. Sullivan](#)<sup>1</sup>, V.A. Bell<sup>2</sup>, R. Wallis<sup>3</sup>, R.C. Butler<sup>1</sup>, L.M. Manning<sup>1</sup>, A.M. Twidle<sup>1,4</sup> & D.M. Suckling<sup>1,5</sup>

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<sup>3</sup>The New Zealand Institute for Plant and Food Research Limited, 55 Old Mill Road, RD 3, Motueka 7198, New Zealand

<sup>4</sup>School of Chemical Sciences, University of Auckland, Private Bag 92019 Auckland, New Zealand

<sup>5</sup>School of Biological Sciences, University of Auckland, Auckland 1010, New Zealand

Mealybugs (Hemiptera: Pseudococcidae) are phloem feeding insects that are pests in many crops internationally, due to black sooty mould growing on the sugary secretions produced by feeding mealybugs. They also transmit viruses such as Grapevine Leafroll associated Viruses (GLRa-V); economically important pathogens in vineyards around the world. In New Zealand, the most important of these is GLRaV-3, which is transmitted from diseased to healthy vines by two mealybug species: the longtailed mealybug (*Pseudococcus longispinus*, LTMB) and the citrophilus mealybug (*P. calceolariae*, CMB). Monitoring both species would allow growers to target management responses to areas where they are problematic rather than applying insecticide treatments in areas where they are largely absent. Synthetic pheromones offer growers a potentially very effective monitoring tool for mealybugs that requires far less labour than the alternative of physically inspecting multiple vine leaves. The sex pheromones produced by female LTMB and CMB were identified in 2009 and 2010, respectively. Parameters (e.g. optimal dose, longevity, active space) for use of the CMB pheromone for monitoring for males is well understood in New Zealand, however, some parameters related to the effective use of the LTMB pheromone remained unresolved. Here, we present trapping experiments conducted in two separate New Zealand vineyards to evaluate the dose response and lure longevity of the LTMB pheromone, and the efficacy of combining the two mealybug pheromones into one lure. The optimum loading (considering both sensitivity and monetary cost) was 20 µg, with lure longevity being up to 60 days. Combining the pheromones in a single lure had no significant effect on trap catch of either species.

*Tuesday 3 December  
15:45 – 16:00  
Plaza Room 8*

# Abstract – Behaviour #1

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## Host discrimination of a larval parasitoid - millisecond behaviour of *Microplitis demolitor*

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[Shun-ichiro Takano](#)<sup>1,2</sup> & N.A. Schellhorn<sup>1</sup>

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<sup>2</sup>Faculty of Agriculture, Kyushu University, 744 Motoooka, Fukuoka, 819-0395, Japan

Oviposition into a host that is already parasitised often has dire consequences for the offspring. In solitary parasitoids in which only one offspring can survive in one host, many species are known to be able to discriminate hosts to avoid oviposition in previously parasitised ones. Yet, it is believed that parasitoids that attack aggressive hosts do not examine host condition carefully and do not discriminate because such parasitoids attack hosts very quickly to avoid being attacked. *Microplitis demolitor* (Hymenoptera: Braconidae) is a solitary koinobiont larval endoparasitoid of *Helicoverpa armigera* (Lepidoptera: Noctuidae). In this study, we investigated oviposition behaviour of *M. demolitor* to reveal host discrimination of a parasitoid that attacks hosts very quickly. Previously parasitised or unparasitised hosts were given to a female wasp and attacked larvae were dissected to investigate existence of parasitoid eggs. Female wasps inserted their ovipositor into both previously parasitised and unparasitised larvae and proportion of female wasps that inserted ovipositor did not differ between parasitised and unparasitised hosts. However, 95% of females that inserted their ovipositors into unparasitised hosts actually laid eggs, while that was only 31% for parasitised host. This indicates that female wasps examined internal host condition with their ovipositor sensing the existence of previously parasitised conspecifics and avoid laying eggs. Analysing video footage of the oviposition behaviour revealed that it took 0.4 sec for oviposition insertion when wasps actually laid eggs, while it took 0.3 sec for oviposition insertion when wasps didn't lay eggs. This suggests that *M. demolitor* took 0.3 sec for investigating internal condition of hosts and took 0.1 sec for laying eggs. Effects of previous experience on host discrimination were also investigated. Female wasps that had experienced "host rich" environments readily rejected parasitised hosts, while wasps with experience of low host availability tended to accept parasitised hosts.

*Monday 2 December*  
*15:30 – 15:45*  
*Plaza Room 10*

# Abstract – Ecology and Interactions #2

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## Population demographic of Queensland fruit fly in subtropical region of Australia

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[Shahrima Tasnin](#)

*Queensland University of Technology, 2 George St, Brisbane City, QLD 4000, Australia*

Although, temperature is not limiting, the predictable phenology patterns seen in temperate insects are still often seen in tropical insects. Most tropical phenology studies stop at correlating biotic and abiotic variables with insect abundance, and the study of mechanisms underpinning phenology are rare. Here we applied the captive-cohort method to examine demography and phenological adaptive mechanisms of Queensland fruit fly, *Bactrocera tryoni*, a multivoltine tropical insect which exhibits a distinct seasonal pattern of population abundance. To generate the “captive cohorts”, wild *B. tryoni* males were collected four times during a year in spring, early summer, late autumn and late winter; periods of the year when marked changes occur in the population abundance of *B. tryoni* in subtropical Australia. At the same time as captive cohort collections, infested fruits were collected which provided subsequent “reference cohorts” of adult flies. Both captive and reference cohorts were then held under optimum laboratory conditions until death, providing population mortality data which was used to estimate age-structure of male flies. Results show that the age-structure of field populations varies depending on season, indicating population breeding is not continuous throughout the year. Age-structure heterogeneity increases with spring population growth, hence early summer and autumn population’s exhibit mixed age flies. During late autumn, very young age individuals were lacking but middle- and old-age flies were common. In contrast, late winter and early spring populations were uniformly old, with only a few young individuals which indicate low reproductive activity during winter. In summary, our results show that from spring to autumn Queensland fruit fly continuously breeds and produces relatively short-lived overlapping generations, but their reproductive activity reduces during winter while adult longevity increases, which may be linked to complex physiological and behavioural mechanisms in response to environmental changes.

*Wednesday 4 December  
13:15 – 13:30  
Plaza Room 10  
**STUDENT***

# Abstract – Systematics and Evolution

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## **Molecular phylogeny of the minute water bug genus *Nesidovelia* (Hemiptera: Veliidae)**

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[Nikolai J. Tatarnic](#)<sup>1,2</sup>

<sup>1</sup>*Department of Terrestrial Zoology, Western Australian Museum, 49 Kew St, Welshpool, WA 6106*

<sup>2</sup>*Centre for Evolutionary Biology, University of Western Australia, Crawley, Perth, WA 6009*

The minute water strider genus *Nesidovelia* (Hemiptera: Veliidae) is found in freshwater streams, creeks and ponds throughout Australia. *Nesidovelia* are characterised by elaborate male and female sexually dimorphic traits, which are thought to have arisen through sexual conflict. The current phylogeny of the genus is based almost entirely on these secondary sexual traits, making studies of trait evolution problematic. In some species these sexual traits vary only subtly, making species delimitation difficult. Using molecular data, I revisit the phylogeny of *Nesidovelia*, testing species boundaries and providing a framework for assessing the coevolution of male and female sexual traits.

*Tuesday 3 December*

*12:15 – 12:30*

*Plaza Room 11*

# Abstract – Pest Management

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## **Biological control of Queensland weeds: long-term achievements**

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[Dianne B.J. Taylor](#), K. Dhileepan, M. Day & T. Pople

*Biosecurity Queensland, Department of Agriculture and Fisheries, Ecosciences Precinct, Boggo Road, Dutton Park, Qld 4102*

Weeds costs Queensland over \$600 million a year. Almost all major Queensland weeds are of overseas origin and biological control is the most cost-effective long-term management option. The Queensland Government has been involved in weed biological control for over a century. Target weeds for biological control are prioritised in consultation with stakeholders, accounting for target weed impact and feasibility of success. Biological control is a complex, expensive and long-term program, involving sourcing (native range surveys), testing (host specificity testing and non-target risk assessment), introducing (mass-rearing and field releasing) and evaluating (impact assessment) specialist natural enemies from the weed's native range. Sourcing of biological control agents from the native range has involved collaboration with research agencies from over 20 countries. Once sourced, host specificity tests are done in a quarantine facility. Once the agents are approved for field release, mass-rearing and field release of agents are undertaken in partnership with community groups and local governments. Successful examples of biological control in Queensland include prickly pear, rubber vine, Harissia cactus, parthenium, groundsel bush, annual ragweed, Noogoora burr and giant sensitive plant. The average benefit:cost ratio of weed biological control in Australia has been estimated to be 23:1. Currently, Queensland conducts research on the biological control of over 13 restricted invasive plants, including many Weeds of National Significance. Based on their success in Queensland, many of the biological control agents have been introduced into other countries around the world.

*Monday 2 December  
14:30 – 14:45  
Plaza Room 8*

# Abstract – Behaviour #1

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## **Impact of cage size on the oviposition of *Stomphastis* sp. (Lepidoptera: Gracillariidae)**

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[Dianne B.J. Taylor](#) & K. Dhileepan

*Biosecurity Queensland, Department of Agriculture and Fisheries, Ecosciences Precinct, GPO Box 267,  
Brisbane, Qld 4001, Australia*

Host specificity testing is an essential component of assessing the suitability of potential weed biological control agents. Testing under quarantine conditions necessitates the use of cages or other forms of confinement and this can interfere with the host selection behaviour of an insect. Host selection involves a series of steps that ultimately results in the acceptance or rejection of a potential host. Where the sequence of selection behaviours cannot be fully expressed, normally unacceptable species may be accepted, which may result in the needless rejection of a host specific agent. In the case of oviposition, indiscriminate egg lay can occur not only on non-host species but also on surfaces such as cage walls. Many insects particularly Lepidoptera are known to indiscriminately dump eggs in confinement. This can be problematic for determining host range. *Stomphastis* sp. nov. is a potential biocontrol agent for *Jatropha gossypifolia* in Australia. Under no-choice conditions in quarantine, females laid eggs on 34 of the 50 non-target species tested, though none of the emerged larvae completed development on any of the non-target species. This prompted the need for further choice trials using the species on which oviposition occurred during no-choice trials. In this study, we examine the impact of cage size on host selection. Females were given the choice of four test species plus the target in a standard sized testing cage and a significantly larger walk-in cage. The results from this trial and the implications are discussed.

*Monday 2 December  
15:45 – 16:00  
Plaza Room 10*

# Abstract – Insect Declines Symposium

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## **Strategic nomination of insects and allied invertebrates for conservation management in Australia**

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[Gary S. Taylor](#)

*Australian Entomological Society Conservation Committee (AESCC), and Australian Centre for Evolutionary Biology & Biodiversity, School of Biological Sciences, The University of Adelaide, S.A. 5005, Australia*

Insects and allied invertebrates are the most numerous and diverse organisms in terrestrial and freshwater environments. They play critical roles in ecosystem function including pollination, herbivory, nutrient cycling, parasitism and predation, and providing food for most invertebrates and vertebrates. The Australian fauna is highly endemic, with numerous ancient lineages, relicts and evolutionary radiations. Yet, under increasing environmental stress, they may be disappearing rapidly, undocumented, in the face of key threatening processes such as habitat loss and fragmentation, exotic and invasive species, pollution and climate change. As impediments to conservation, terrestrial invertebrates are impacted by the Public dilemma (too small, too hidden and too little known), the Political dilemma (too little attention from decision-makers), the Scientific dilemma (too few scientists and scarce funding), the Linnean shortfall (many undescribed species), the Wallacean shortfall (too little known about distribution), and the Prestonian shortfall (too little known about abundance). Of the 285 species of insects and allied invertebrates listed under State/Territory Acts, the *EPBC Act* and *IUCN Red List* shows a highly biased (mis)representation across the Australian landscape. Of the 89 IBRA regions, six had more than 18 species, 23 had less than five species and thirty-six (40%) had no species at all. For a more uniform representation, the AESCC proposes a novel regional approach by selecting a relatively small number (3-5) ‘flagship taxa’ from each IBRA region to engage scientists, government agencies, local community groups and the general public in conservation management. The Australian entomological community is here encouraged to nominate iconic flagship species from under-represented IBRA regions. These may include threatened species at risk of extinction, or species of important scientific, social or cultural value. Nominations will be evaluated by the AESCC and selected species will be further promoted for conservation listing under the *EPBC Act*. Nominations will be progressively posted on the AES website at [www.austentsoc.org.au](http://www.austentsoc.org.au).

*Monday 2 December  
14:30 – 14:45  
Plaza Room 9*

# Abstract – Ticks & Lice Symposium

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## **Why do ticks in Australia live where they live, and do not live where they do not?**

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[Ernest J.M. Teo](#) & S.C. Barker

*Department of Parasitology, School of Chemistry and Molecular Biosciences, The University of Queensland, QLD 4072 Australia*

Although the geographic distribution of ticks in Australia is more or less well known, we still do not know why these ticks live where they live, and do not live where they do not. The answer to the fundamental biological question as to why these ticks live where they live is not only crucial but is also vital in the prediction of where these ticks might be in the future, especially the ticks of medical and veterinary importance. Projections of where these ticks might be in the future would inform control measures which might reduce morbidity and mortality of men and other animals. I would be using *Ixodes holocyclus*, the eastern paralysis tick, as an example as to how we might be able to predict the geographic distribution of these ticks of medical and veterinary importance in Australia, and how the findings from this study might tell us more about the biological responses of *I. holocyclus* to climate change, and perhaps, other ticks in Australia.

*Wednesday 4 December  
11:15 – 11:30  
Plaza Room 9*

# Abstract – Ecology and Interactions #1

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## Challenges of mass rearing of dung beetles in controlled environments

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[Agasthya Thotagamuwa](#)<sup>1</sup>, P.A. Weston<sup>1</sup>, G.M. Gurr<sup>1,2</sup> & G. Burgess<sup>1</sup>

<sup>1</sup>Graham Centre for Agricultural Innovation, Charles Sturt University, Wagga Wagga, NSW 2650, Australia

<sup>2</sup>School of Agricultural and Wine Sciences, Faculty of Science, Charles Sturt University, P.O. Box 883, Orange, NSW 2800, Australia

Rearing dung beetles in controlled environments poses many challenges. Even when conditions such as temperature and light regime are optimised, other factors may have significant impact on brood production, notably the quality of the dung provided, the moisture content of the rearing medium, and the presence of sciarids and other dipterans. In a preliminary experiment, brood production by the Moroccan strain of *Onthopagous vacca* was compared on two types of cattle dung: dung from hay fed cattle ('HF') and dung from cattle grazing on irrigated pasture ('IP'). Beetles produced significantly more brood when provisioned with IP dung. The moisture of the rearing medium (sand and vermiculite mix) is another critical factor. When the medium was too dry (<4%), brood ball production dropped significantly; a moisture level of 10% proved to be most suitable for this species for increased brood production. Moreover, the evaporative water loss from the mesocosms could be minimised by maintaining a relative humidity of 50% in the growth chambers. Growth of fungus on dung is inevitable as the dung used for feeding the beetles is not pasteurised. It was observed that the growth of fungus starts after four days if the dung has not been shredded by the beetles, particularly towards the end of the life cycle of beetles, when provisioned dung remains undisturbed. The control of flies is another challenge as the moist rearing containers inside humid growth chambers provide ideal breeding grounds for dipterans. Fungus gnats can become a serious problem when their numbers are high as their larvae can feed on the developing brood. Providing high quality dung, maintaining the rearing medium at the appropriate moisture level and limiting attack by dipteran pests by appropriate hygiene practices are key to maximizing production of progeny by dung beetles in controlled environments.

*Tuesday 3 December*

*16:45 – 17:00*

*Plaza Room 10*

# Abstract – Insects and Plants

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## Natural edge effects on larval mortality of the Diamondback Moth

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[Jessa H. Thurman](#) & M. Furlong

*School of Biological Sciences, University of Queensland, St. Lucia, QLD 4072*

Conserving biodiversity may become increasingly important as many current biological control programs are predicted to be disrupted by climate change. The conservation of arthropod natural enemies and the pest suppression that they have the potential to deliver may be achieved through synergistic use of conservation and augmentative biocontrol strategies. However, previous studies in conservation biocontrol have failed to directly relate conservation of biodiversity in agricultural systems to pest suppression. In reviewing the effect of these biocontrol strategies, we have measured the relationship between natural field edges and larval mortality of the major economic pest, the diamondback moth (*Plutella xylostella* L.) in organic *Brassica* farms in Queensland. First, we surveyed the arthropod diversity in the field and the adjacent natural area. We then used natural enemy exclusion or exposed cages to measure absolute predation and parasitism of diamondback moth cohorts on sentinel experimental *Brassica* plants. Cages were also placed at varying distances (one, thirty, and ninety meters) from the field edge to record potential edge effects. In predator exposed cages, we observed larvae surviving at significantly lower rates on average when located one (16.67%  $\pm$  4.81) and 90m (26.52%  $\pm$  7.66) from the field edge compared to 30m (40.69%  $\pm$  11.74). Of these larvae which pupated, however, the majority were parasitized by the biocontrol agent, *Diadegma semiclausum* Hellen (Hymenoptera: Ichneumonidae) at each distance, with significantly higher parasitism at one (54.17%  $\pm$  5.83) and 90m (75%  $\pm$  14.43). This suggests that augmentative biocontrol may be supported by natural field margins. The use of ‘nature strips’ composed of nectar-rich flowers throughout the field may be able to obtain similar ecosystem services, but further study is needed to develop an applied biocontrol program targeted for diamondback moth and other major pests.

*Wednesday 4 December*  
*14:00 – 14:15*  
*Plaza Room 8*  
**STUDENT**

# Abstract – Systematics and Evolution

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## Species boundaries in *Macrozamia* cycads

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[Alicia Toon](#)<sup>1</sup>, P.I. Forster<sup>2</sup> & L.G. Cook<sup>1</sup>

<sup>1</sup>*School of Biological Sciences, The University of Queensland, Brisbane, QLD 4072*

<sup>2</sup>*Queensland Herbarium, Department of Environment & Science, Brisbane Botanic Gardens, Mount Coot-tha Road, Toowong, Qld 4066*

Hybridization and introgression are powerful evolutionary forces that can lead to speciation, extinction and fusion of divergent lineages. Currently, we know very little about the evolutionary processes leading to the extant diversity of cycads, partly because standard molecular markers show little differentiation among taxa that are considered to be distinct species. Here, we test perceived species boundaries of two species of Australian cycads, *Macrozamia lucida* and *M. macleayi*, that occur patchily in broadly overlapping populations in south-east Queensland. Where they occur sympatrically, parental and intermediate (presumed hybrid) phenotypes have been reported. We measured phenotypic (leaf) traits and genetic (genotype-by-sequencing) admixture to test for the extent of gene flow between what is currently accepted as two different species.

*Monday 2 December  
11:15 – 11:30  
Plaza Room 11*

# Abstract – Systematics and Evolution

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## **Integrative species delimitation of the Australian jumping spider genus *Cytaea* (Araneae: Salticidae)**

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[Łukasz Trębicki](#)<sup>1,2</sup>, M. Dabert<sup>3</sup> & M. Żabka<sup>2</sup>

<sup>1</sup>*Department of Biodiversity Studies and Bioeducation, Faculty of Biology and Environmental Protection, University of Lodz, Banacha 1/3, 90-237 Lodz, Poland*

<sup>2</sup>*Siedlce University of Natural Sciences and Humanities, Department of Zoology, Prusa 12, 08-110, Siedlce, Poland*

<sup>3</sup>*Molecular Biology Techniques Laboratory, Faculty of Biology, Adam Mickiewicz University, Umultowska 89, 61-614 Poznan, Poland*

Salticidae are the most diverse spider family in Australia, with almost 500 species recorded and about 1000 estimated. Within the genus *Cytaea*, there are 41 species known, but the taxonomy of the genus is still poorly understood, and the real number of species is far from being complete. Based on types, new material and field research, we discovered as many as 60 new species of *Cytaea* from Australia alone. To clarify monophyly of the genus we provide phylogenetic analysis (MP, ML) based on morphological (82 characters) and molecular (COI, 16S, 28S) data. In result, number of species in *Cytaea* have significantly decreased (18 nominal species in monophyletic group) and divided into five groups. The species across groups shows individual variation in genital morphology and body coloration, thus their delimitation is highly difficult. To solve the problem, we examined some ultra-structures with LM, SEM and X-ray micro tomography and revealed new morphological characters in genitalia of some representative species. Furthermore, we performed standard DNA barcoding, calculated barcoding gap for *Cytaea* and compared with distances between studied taxa. The analysis indicated that species which do not differ in morphology, genitalic structures and distribution, differ in body colouration in males. It seems that sexual selection across the species of *Cytaea* is based on visual and probably olfactory signals.

*Monday 2 December*

*13:15 – 13:30*

*Plaza Room 11*

# Abstract – Pest Management

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## **Yield losses associated with Russian wheat aphid infestation; field experiments in Horsham, Victoria**

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[Piotr Trebicki](#)<sup>1</sup>, O. Fung<sup>1</sup>, R. Pasam<sup>2</sup>, S. Kant<sup>1</sup>, J. Koh<sup>1</sup>, G. Hollaway<sup>1</sup>, M. Hayden<sup>2</sup> & J. Tibbits<sup>2</sup>

<sup>1</sup>*Agriculture Victoria, 110 Natimuk Road, Horsham, VIC 3400*

<sup>2</sup>*Agriculture Victoria, AgriBio, 5 Ring Road, Bundoora, VIC, 3083*

Russian wheat aphid, RWA (*Diuraphis noxia*), is a global pest of cereal crops, capable of causing high economic losses through yield reduction and insecticide inputs. Russian wheat aphid entered Australia in 2016, first detected in South Australia, then quickly spread across Victoria, New South Wales and Tasmania. Although it is now common across south eastern Australia, its distribution, population dynamics and associated yield and quality losses are poorly understood. The negative effects of RWA infestation can be effectively suppressed by use of resistant cultivars which Australia is currently lacking. To increase the resilience of Australian wheat to this new pest, Agriculture Victoria aimed to develop and validate high-throughput phenotyping tools for in-field detection of RWA infestation, monitoring of RWA symptom progression and yield losses and large-scale screening of potentially resistant wheat genotypes. In 2018, a large scale, replicated field experiment was established in Horsham, Victoria with 150 wheat lines infested with, and free of, RWA, in three replications. Over the growing season, RWA symptom expression was measured on multiple occasions using visual assessments and digital RGB and multispectral cameras mounted on unmanned aerial vehicles (UAVs). Post-harvest trait measures like biomass, yield and grain quality were recorded. Russian wheat aphid infestation had substantial effects on symptom expression and caused significant yield losses, particularly on wheat cultivars commonly grown in southern Australia. Some wheat cultivars of exotic origin have shown high level of tolerance and reduced symptom expression for RWA.

*Monday 2 December*

*11:30 – 11:45*

*Plaza Room 8*

# Abstract – Orthoptera Symposium

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## Australia's high-country Orthoptera

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[Kate Umbers](#)

*School of Science and Health & Hawkesbury Institute for the Environment, Western Sydney University, Hawkesbury, Richmond, NSW 2753*

Australia's high-country is a surprising biological treasure-trove of Orthopteroid insects with species that exhibit diverse anti-predator strategies and complex mating systems. In this talk I will showcase the mountain katydid (*Acripeza reticulata*) and the thermocolour grasshopper (*Kosciuscola tristis*) which I have been building into model systems for behavioural ecology, thermal physiology, and mountain phylogeography for the past 10 years. Mountain katydids are large tettigoniids abundant across the entire great dividing range. Their most conspicuous trait is their startling startle display in which they lift their tegmina to reveal blue, red and black stripes on their abdomens. I am currently investigating the variation in this display across the species range and its efficacy against predators. The thermocolour grasshopper inhabits Australia's highest peaks and has an equally remarkable life history. Males change colour from black to turquoise depending on their body temperature via the movement of intracellular granules and also have extremely ferocious fighting behaviour - both traits previously unknown in grasshoppers. These two species have wonderful rich natural histories which have the pizzazz to become powerful flagship species for this highly threatened Australian Alps fauna.

*Tuesday 3 December  
12:15 – 12:30  
Plaza Room 10*

# Abstract – Rapid-Fire Talk

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## **Double trouble: can silicon improve plant resistance to insect herbivory and drought?**

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[Rebecca K. Vandegeer](#)<sup>1</sup>, D.T. Tissue<sup>1</sup>, S.E. Hartley<sup>2</sup> & S.N. Johnson<sup>1</sup>

<sup>1</sup>Hawkesbury Institute for the Environment, Western Sydney University, Locked Bag 1797, Penrith, NSW 2751;  
<sup>(2)</sup> York Environment and Sustainability Institute, Department of Biology, University of York, York YO10 5DD, UK

Silicon (Si) is abundant in soils, where it is taken up by plant roots, transported within the plant, and deposited into organs as silica bodies (SiO<sub>2</sub>). Si supplementation has been reported to improve plant resistance to biotic (e.g. herbivory) and abiotic (e.g. drought) stress. However, few studies have tested for interactive effects of Si-induced drought tolerance and insect herbivore performance. We grew tall fescue (*Festuca arundinacea*, Poaceae) in a hydroponic system with or without Si. After 8 weeks, half the plants from each Si treatment were treated with a 20% polyethylene glycol treatment (PEG; osmotic stress), to simulate drought conditions. After 14 days, half the plants were harvested for plant physiological parameters (e.g. photosynthesis, water potential, Si content, specific leaf mass). The other half of the plants were each exposed to an individual 4<sup>th</sup> instar cotton bollworm larva (*Helicoverpa armigera*, Lepidoptera) for an additional 7 days to determine herbivore relative growth rate (RGR). Contrary to previous studies, we found little evidence that Si alleviates the negative effects of osmotic stress on plant physiological performance. In fact, Si further reduced leaf water potential and photosynthesis of plants exposed to osmotic stress. In contrast, both Si supplementation and osmotic stress reduced herbivore RGR. Our findings show that Si plays a role in the resistance of grasses to herbivory during osmotic stress, but that the role of Si during drought may be limited.

*Monday 2 December  
16:15–17:30 [13× speakers]  
Plaza Room 8*

# Abstract – Pest Management

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## All quiet at the Russian front?

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[Maarten van Helden](#)<sup>1</sup>, T. Heddle<sup>1</sup>, F. Al-Jawahiri<sup>1</sup>, J. Maino<sup>2</sup>, E. Pirtle<sup>2</sup>, J. Lye<sup>2</sup>, P. Umina<sup>2</sup> & G. Baker<sup>1</sup>

<sup>1</sup>PIRSA-SARDI, Hartley Grove, Urrbrae SA 5064

<sup>2</sup>Cesar pty ltd, 293 Royal Parade, Parkville Victoria 3052

After the initial detection of the Russian Wheat Aphid (*Diuraphis noxia* Kurdjumov - RWA), in 2016 in South Australia, RWA has spread, south-eastwards (SA, VIC, Tas, NSW) and northwards, approaching Queensland as predicted by Climex modelling.

Because agronomists and farmers expected the risk for substantial yield damage to be high, most have opted for prophylactic neonicotinoid seed treatments. These will protect the young seedlings efficiently against possible RWA installation.

Industry funded research aims to understand RWA ecology in the Australian environment, determine the regional risk, and establish intervention thresholds.

Over the last three seasons, the actual pressure of RWA has been low. Few reports were received of (treated or untreated) crops with significant RWA populations causing economic yield loss.

Close to 1000 grass samples belonging to >100 species were Berlese extracted in 2018/2019. Most grasses seem able to harbour some RWA in spring, but Barley Grass and Brome grasses were the main alternative hosts, together with volunteer cereals. Over the dry summer, few grasses survived and hence RWA declined sharply.

Field trials using RWA *inoculations* show large differences in aphid establishment and development on cereals according to region, with (drought) stress being a major aggravating factor. Populations in these trials are largely above American-derived economic thresholds, but even then, economic yield losses are not always observed.

Findings to date indicate the risk of yield loss from RWA may be constrained in most cereal-cropping regions, since it would require wet summer (high green bridge) followed by a dry growing season. With plant feeding symptoms being very easy to monitor an IPM/FITE (Find, Identify, Threshold, Enact) approach, seems feasible and more sustainable for RWA management.

Wednesday 4 December  
10:45 – 11:00  
Plaza Room 8

# Abstract – Chemical Ecology Symposium

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## New chemistry testing on beneficials

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J. Page<sup>1</sup>, L. Senior<sup>2</sup>, [Maarten van Helden](#)<sup>3</sup> & Z. Hall<sup>2</sup>

<sup>1</sup>*Integrated Pest Management Technologies 994 Heidelberg-Kinglake Rd, Hurstbridge VIC 3099*

<sup>2</sup>*Department of Agriculture and Fisheries, PO Box 267, Brisbane QLD 4001*

<sup>3</sup>*PIRSA-SARDI, Hartley Grove, Urrbrae SA 5064*

Beneficials (whether introduced for biological control or naturally occurring) play an important role in integrated pest management in horticultural crops. However, they are exposed to pesticides used to manage pests or diseases, so the choice of appropriate chemistry is critical to conserve their populations. Many of the more recently registered pesticides are claimed to have a lesser impact on beneficials but knowledge is incomplete.

In an industry-funded project we are testing the effect of (recent) pesticides on a range of beneficials (predators and parasitoids, adults and larvae), recording both acute toxicity and sub lethal effects. A simple petri-dish/potter tower bioassay was developed for contact exposure studies, and compared with exposure to leaves from plants sprayed in a semi-field set-up (track sprayer).

Effects of pesticides on different beneficials were very variable, with some killing 100% of the beneficials in < 48h. In some cases, low acute mortality was obtained but, in the subsequent sub-lethal test, reproduction was completely inhibited. Petri-dish bioassays present a ‘worst case’ scenario and mortality is generally higher than on leaves sprayed in semi-field conditions

These results show that the off-target effects of pesticides on beneficials need to be tested on a wide range of beneficials and in crop realistic setups to assess the suitability of different pesticide options as part of an Integrated Pest Management Strategy.

*Tuesday 3 December  
15:30 – 15:45  
Plaza Room 9*

# Abstract – Pest Management

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## **The introduction, establishment and spread of *Tamarixia triozae*, a parasitoid of *Bactericera cockerelli*, in New Zealand**

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[Jessica Vereijssen](#)<sup>1</sup>, L. Watkins<sup>1</sup>, N. Agnew<sup>2</sup>, T. Sachtleben<sup>2</sup>, F. MacDonald<sup>3</sup>, A. Chhagan<sup>3</sup>, G. Avila<sup>3</sup>, A. Tringham<sup>4</sup> & M. Davidson<sup>1</sup>

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<sup>3</sup>Plant and Food Research, Auckland 1025 New Zealand

<sup>4</sup>McNicol Rd, Clevedon, Auckland 2585 New Zealand

Industries (potato, tomato, capsicum, and tamarillo) affected by the pest *Bactericera cockerelli* (tomato potato psyllid, TPP) received approval from the Environmental Protection Agency (New Zealand) to import its parasitoid, *Tamarixia triozae* in an attempt to help regulate populations of the pest. The F1 and subsequent generations of the parasitoid were approved for release from quarantine in July 2017. Adult *T. triozae* were released at sites in three regions (Auckland (n=810), Hawke's Bay (n=610) and Canterbury (n=1061)) from December 2017 – February 2018. At the three Hawke's Bay and two Canterbury sites, *T. triozae* adults were released on TPP infested *Lycium ferocissimum* (African boxthorn). In Auckland *T. triozae* adults were released on vegetation surrounding a commercial tomato greenhouse. *T. triozae* survived over the winter in Hawke's Bay and Canterbury as it was recovered from TPP nymphs collected from African boxthorn in December 2018. No *T. triozae* were recovered from TPP nymphs (n=50) collected from the Auckland site. Further releases were carried out by industry personnel in Auckland (same site), Hawke's Bay (four new sites) and Canterbury (three new sites) from December 2018 – April 2019. Concurrent to these additional releases, surveys of TPP host plants surrounding the release sites were carried out in Hawke's Bay and Canterbury to evaluate spread of the parasitoid. In Hawke's Bay, parasitised TPP nymphs were observed 16.7 km away from the nearest release site. In Canterbury a parasitised TPP nymph was observed 500m from the original release site. The abundance of TPP host plants was markedly higher in Hawke's Bay than Canterbury, which could help explain the difference in spread of the parasitoid in the two regions.

*Monday 2 December*

*13:45 – 14:00*

*Plaza Room 8*

# Abstract – Systematics and Evolution

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## **New Zealand pirates: Evolutionary origins and diversity of Zealandia's mimetid spider fauna revealed through morphology and molecular data**

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[Cor J. Vink](#)<sup>1,2</sup>, N. Dupérré<sup>2</sup>, M.A. Townley<sup>3</sup> & D. Harms<sup>2</sup>

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<sup>2</sup>Department of Arachnology, Centre of Natural History, Universität Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany

<sup>3</sup>University Instrumentation Center, University of New Hampshire, 46 College Road, Durham, NH 03824, USA

The evolutionary origins and phylogenetic affinities of Zealandia's (New Zealand & New Caledonia) biota are the subject of ongoing debate. Many studies have suggested that most of Zealandia's fauna results from recolonisation events that have occurred since a major drowning episode in the Oligocene, but few data are presently available to evaluate both mode and direction of such dispersal events. We investigated the evolutionary origins of Zealandia's fauna of pirate spiders through a combination of molecular phylogenetic analyses (3 genes: COI, H3 and 28S), spinneret morphology and taxonomy. We find that New Zealand's fauna of pirate spiders is polyphyletic and represents three independent colonisation events of a single genus (*Australomimetus*) from mainland Australia, whilst the fauna of New Caledonia comprises a single species, which is unrelated to the New Zealand fauna. There is evidence for in-situ speciation in one of the New Zealand clades, and of the eight species found there, only two are shared with Australia. We further discuss an "out-of-Australia" biogeographical model for *Australomimetus* in which this genus evolved in Australia and dispersed northwards into Southeast Asia and further east to several Pacific islands. We document the fauna of Zealandia at the species level through taxonomy and detailed morphological investigations of the spinneret structures. We further document biogeographical patterns of this genus in Australia, such as major divergences in the fauna between eastern and western Australia.

*Monday 2 December  
13:45 – 14:00  
Plaza Room 11*

# Abstract – Pest Management

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## **Diagnosics response to the 2019 detection of Queensland fruit fly *Bactrocera tryoni* on Auckland's Northshore, New Zealand**

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[Dave Voice](#), S. George, D. Gunawardana, S. Bennett, D. Li, R. Balan, G. Gill, R. MacLellan & A. Flynn

*Plant Health & Environment Laboratory, Biosecurity New Zealand, Ministry for Primary Industries, PO Box 14018, Christchurch, 8544 | New Zealand*

Biosecurity New Zealand operates a national surveillance programme for exotic fruit fly (Diptera: Tephritidae). In February 2019 a male Queensland fruit fly was detected with a further 10 trapped over the following five months up to mid-July. The July trap catch indicated that in favourable conditions flies are still trappable midwinter in the maritime climate of Auckland's Northshore.

No immature life stages were detected during the February-July period despite extensive larval surveys.

This paper discusses the role of the Ministry for Primary Industries Entomology team in this response.

*Monday 2 December  
13:15 – 13:30  
Plaza Room 8*

# Abstract – Pest Management

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## Managing *Helicoverpa* spp. in north-eastern Australian grain crops: what is the current state of play?

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[Trevor M. Volp](#)<sup>1</sup>, H. Brier<sup>2</sup>, A. Quade<sup>1</sup>, E. Teese<sup>1</sup>, E.R. Williams<sup>3</sup> & M. Miles<sup>1</sup>

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The Noctuid moths *Helicoverpa armigera* and *Helicoverpa punctigera* are major pests of broadacre cropping in north-eastern Australia. *Helicoverpa armigera* has the capacity to rapidly evolve resistance to insecticides, which almost caused the collapse of the cotton industry in the 1980's/1990's before the introduction of transgenic cotton. In the Australian Grains industry there is still a heavy reliance on conventional insecticides to control *Helicoverpa* spp. in crops. Subsequently, resistance levels of *H. armigera* to the frequently used insecticides indoxacarb and chlorantraniliprole are low, but increasing.

The threat of resistance places an increased emphasis on Integrated Pest Management (IPM) for not only *Helicoverpa* spp., but all grain crop pests. To manage the potential of resistance in *H. armigera* there are several IPM tactics currently in play:

1. Wide-scale pheromone trapping is used to detect mass moth movements and inform industry.
2. Economic thresholds have been developed for *Helicoverpa* spp. in several summer and winter grain crops.
3. Alternative insecticide groups have been evaluated to be used in conjunction with the at-risk products.
4. Substantial work has been conducted around the use of NPV (Nuclear polyhedrosis virus) as a biological control.
5. Non-disruptive insecticide options and management strategies have been evaluated for numerous other grain pest species, whose management influences *Helicoverpa* spp.
6. The lead industry body, the Grains Research & Development Corporation has recently released a resistance management strategy for *H. armigera*.

However, there are still major limitations to the adoption of IPM of *Helicoverpa* spp. in Australian grain crops. These limitations include: the inexpensiveness of broad-spectrum insecticides, the current inability to incorporate natural enemies into management decisions, and a changing climate that may increase the risk of resistance evolving.

This presentation examines the current status and challenges of adopting IPM for *Helicoverpa* spp. in north-eastern Australian grain crops.

Tuesday 3 December  
16:45 – 17:00  
Plaza Room 8

# Abstract – Invasive Ants Symposium

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## **Monitoring for invasive insects in the Anthropocene: Increasing border detection rates to mitigate risk of pest species establishment**

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[Erin L. Wallace](#)<sup>1</sup> & M. Janes<sup>2</sup>

<sup>1</sup>*National Red Imported Fire Ant Eradication Program, Qld Department of Agriculture and Fisheries, Wayne Goss Drive, Berrinba, QLD 4117*

<sup>2</sup>*Department of Agriculture and Fisheries Prevention and Preparedness Unit, Kessels Road, Coopers Plains, QLD, 4108*

Globalisation and increased international trade has resulted in increased opportunity for invasive invertebrates to ‘hitch a ride’ and establish in areas outside their native distributions. While the frequency of port intercepts of invasive invertebrate species is likely to further increase, the establishment potential of these species also rises under climate change. Invasive species’ establishment in new environments has major implications for conservation; agriculture and business lifestyle; and human and animal health. It is well recognised that no individual sampling method collects all invertebrate species effectively. As such, successful monitoring is contingent on having a functional understanding of the target species, and deploying monitoring methods to suit their biology and habitat. Using a one-size-fits-all approach to monitoring for invertebrates reduces the likelihood of successful intercepts, particularly when the species of interest is relatively unknown or understudied. Indeed, the extent of time between arrival and identification increases the risk of human-assisted movement of these species into more sensitive areas, and subsequent establishment in a new environment. Current monitoring options for invertebrate biota are limited and generally deployed dependant on cost effectiveness and ease of sample processing. Recent identification of an understudied tramp ant, browsing ant (*Lepisiota frauenfeldi*), at the Port of Brisbane, raises questions about whether our reliance on existing passive monitoring options are capturing the desired data in an effective timeframe and whether active surveillance, such as the use of odour detection dogs, may be better utilised. Here we investigate the potential to develop and include new, innovative methods of surveillance to support national biosecurity and compliment the increasing propagule pressure we face in the Anthropocene.

*Monday 2 December*

*12:15 – 12:30*

*Plaza Room 10*

# Abstract – Insect Declines Symposium

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## **The Australian Bogong moth (*Agrotis infusa*, Lepidoptera: Noctuidae) 1951-2020: decline and crash**

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K. Green<sup>1</sup>, P. Caley<sup>2</sup>, M. Baker<sup>3</sup>, D. Dreyer<sup>4</sup>, [Jesse Wallace](#)<sup>5</sup> & E. Warrant<sup>4,5</sup>

<sup>1</sup>*Australian National University, College of Asia and the Pacific, Canberra, ACT 2601, Australia*

<sup>2</sup>*Data 61, Commonwealth Scientific and Industrial Research Organisation, Canberra, ACT 2601, Australia*

<sup>3</sup>*Bayside, Melbourne, Vic 3193, Australia*

<sup>4</sup>*Lund Vision Group, Department of Biology, University of Lund, Lund, Sweden*

<sup>5</sup>*Australian National University, Research School of Biology, Canberra, ACT 2601, Australia*

The Bogong moth (*Agrotis infusa*) is well known for its long-distance migration – a return journey from the plains of southeast Australia to the mountains of south-eastern Australia. It has been estimated that over 4 billion moths arrive in mountain areas to aestivate in cool caves each Spring, bringing with them a massive annual influx of energy and nutrients that is critical for the health of the alpine ecosystem. However, a massive decline in moths present in their aestivation caves has occurred over the 2017/18 and 2018/19, with only a few individuals present where hundreds of thousands could be found just two year earlier. In order to understand the possible sources of decline, we analysed historical records of Bogong moth numbers at aestivation sites in the Australian Alps, including observations on Mt. Gingera (ACT/NSW) in the early 1950s, observations from 1980 onwards in the Snowy Mountains, and an almost-unbroken series of observations each summer over the past 53 years in Mt. Buffalo. This analysis shows that moth numbers were probably steady over 1951-1980, but began to fall from then until 2016 before the dramatic crash beginning in 2017. The analysis also revealed that until 2016 declining moth numbers likely led to a greater availability of space at more favourable aestivation sites at higher elevation, thereby leading to the gradual abandonment of sites at lower elevations. We found little evidence that increasing global temperatures *per se*, and thus climate change, were responsible for the steady decline from 1980-2016, but that changes in farming practice which currently removes almost half a billion moths from the annual migration compared to pre-1980 levels, and an elevated use of insecticides, was more likely responsible. The crash in moth numbers from 2017 is almost certainly due to the recent severe drought in the moth's winter breeding grounds.

*Monday 2 December*

*13:30 – 13:45*

*Plaza Room 9*

# Abstract – Ticks & Lice Symposium

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## **Rapid host expansion of the introduced spiny rat louse *Polyplax spinulosa* (Phthiraptera) among endemic rodents in Australia**

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[Wei Wang](#)<sup>1</sup>, L.A. Durden<sup>2</sup> & R. Shao<sup>1</sup>

<sup>1</sup>GeneCology Research Centre, School of Science and Engineering, University of the Sunshine Coast, Sippy Downs, Queensland 4556, Australia

<sup>2</sup>Department of Biology, Georgia Southern University, Statesboro, Georgia 30458, USA

Historical European exploration and colonization introduced four species of rodents to Australian continent from Eurasia since 1600s: the brown rat, *Rattus norvegicus*, the black rat, *R. rattus*, the Pacific rat, *R. exulans*, and the house mouse, *Mus musculus*. The spread of these rodents created opportunities for their co-introduced sucking lice to parasitize and adapt to endemic rodents in Australia. We investigated the host expansion of introduced sucking lice among endemic rodents in Australia. We found that the spiny rat louse, *Polyplax spinulosa*, had nearly doubled its host range by parasitizing at least six endemic rodent species in Australia. The other two introduced lice, *Polyplax serrata* and *Hoplopleura pacifica*, however, have apparently failed to expand to any endemic rodents in Australia. Our analysis of mitochondrial *rrnL* gene sequences divided *P. spinulosa* into two genotypes (European vs Southeast Asia), which differ by 7.5%; both genotypes were introduced into Australia and then expanded their host ranges to include endemic rodents. The expansion of *P. spinulosa* to at least six endemic rodent species in Australia has occurred in the timeframe of 200 to 400 years, which is extremely rapid relative to its host expansion to eight native rat species in Eurasia in ~16 millions of years since it diverged from *P. serrata*. The host expansion of *P. spinulosa* is remarkable for a blood-sucking louse, and is in stark contrast to the no host expansion of *P. serrata* and *H. pacifica*. Comparison among these three introduced sucking lice indicated that both louse-specific factors and host-specific factors can contribute to the success or failure of host expansion.

Wednesday 4 December  
14:30 – 14:45  
Plaza Room 9  
**STUDENT**

# Abstract – Pest Management

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## Understanding and incorporating aphid parasitoids within IPM strategies in Australian grain crops

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[Samantha Ward](#)

*The University of Melbourne, Parkville, VIC 3010*

Aphids (Hemiptera: Aphididae) can be particularly devastating to grain crops, with their economic importance weighted on their ability to cause significant yield losses through a variety of methods. From feeding damage alone in 2012, cereal aphids caused an average annual loss of \$14 million in Australian wheat crops. For over a century, growers have relied upon host plant resistance and chemical treatments to control invertebrate pests, however suppression of beneficial organisms and increased resistance within targeted species has created an ongoing battle with pest suppression. In Australia the polyphagous green peach aphid (*Myzus persicae* (Sulzer)), often a pest of Canola crops, has developed resistance to over 74 insecticides including carbamates, pyrethroids, and organophosphates. Due to these issues, control of agricultural pests is now focussed on integrated pest management (IPM) programs, within which natural enemies can play a role as biological controls. Parasitic Hymenoptera have had the most success as biological control organisms in the past, likely due to their host specificity. There are several trophic levels to understand regarding aphid parasitism; the primary parasitoids, the secondary parasitoids (including hyperparasitoids and mummy parasitoids), and other natural enemies such as predators and pathogens. Three years' worth of data collected on aphid pests and their associated natural enemies, with particular emphasis on hymenopteran parasitoids, within Australian grain production landscapes, will be presented. I aim to determine the diversity, abundance and activity of grain aphids and their associated natural enemies within grain production landscapes, and how these change over the growing seasons of various grain crops. Furthermore, an updated taxonomy, phylogeny and distribution mapping of aphidiine wasps (Hymenoptera: Aphidiinae) parasitizing aphids in Australian grain production will be presented. Finally, I discuss effects of seed treatments on specific natural enemies associated with grain pests.

*Tuesday 3 December  
16:00 – 16:15  
Plaza Room 8  
**STUDENT***

# Abstract – Ecology and Interactions #2

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## **Where, oh where can my dung beetle be? The problem of mapping insect distributions using random occurrence records**

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[Paul A. Weston](#)<sup>1</sup> & G.M. Gurr<sup>1,2</sup>

<sup>1</sup>*Graham Centre for Agricultural Innovation, Charles Sturt University, Wagga Wagga, NSW 2678*

<sup>2</sup>*School of Agricultural and Wine Sciences, Charles Sturt University, Orange, NSW 2800*

Mapping the spatial distribution of insect species is a straightforward task if occurrence records have been collected in a systematic fashion across uniformly spaced coordinates. If the occurrence records are the result of random observations collected using different methods, the task of producing a meaningful distribution map becomes quite unwieldy. One of the objectives of the Dung Beetle Ecosystem Engineers project is to produce distribution maps of the twenty-three species of dung beetles introduced to Australia from 1966-1982 and known to have become established on the continent. Unfortunately, occurrence records for these species that are publicly available have been collected by different means by a range of collectors from locations that are not at all uniformly distributed across the landscape. This talk will focus on approaches to mapping species distributions in general and the methods being used to produce meaningful distribution maps of the introduced species of dung beetles in Australia, given the serious limitations imposed by the non-systematic nature of the available occurrence records.

*Wednesday 4 December  
10:45 – 11:00  
Plaza Room 10*

# Abstract – Invasive Ants Symposium

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## **The good in amongst the bad and the ugly: how invasive species further knowledge on understudied native species**

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[Elizabeth R. Williams](#)

*National Red Imported Fire Ant Eradication Program, Qld Department of Agriculture and Fisheries, Wayne Goss Drive, Berrinba QLD 4118*

Insects are among the least defined and studied animals on Earth. This is particularly true for those of limited economic importance. Indeed, a search of 2019 publications relating to insects in Australia resulted in 69% of studies directly examining species that were either agricultural pests, invasive species or those of importance to human health. Although the scope of such research appears relatively limited, it does further scientific knowledge of understudied native insect species and other biota. Examples of indirect scientific knowledge garnered from invasive species research include:

1. native species distributions, dominance hierarchies and food preferences
2. taxonomic definition and accuracy
3. host plant biology and other habitat information
4. life cycle biology of parasitoids or other biocontrol agents
5. further untargeted invasive species incursions.

This talk will explore this concept, with case studies relating to ants and other insects in the Australasian region.

*Monday 2 December  
11:15 – 11:30  
Plaza Room 10*

# Abstract – Rapid-Fire Talk

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## Reliability of feral honey bee hive density estimates using drone sampling

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[Elisabeth Williamson](#), S. Groom & K. Hogendoorn

*School of Agriculture, Food & Wine, University of Adelaide, Adelaide, Australia*

The European honey bee (*Apis mellifera*) is the most economically important crop pollinator in agriculture, and many primary industries (e.g. almond, Lucerne, canola, apple, pear, cherries) are heavily dependent on the pollination services of these bees. In Australia a significant amount of crop pollination is performed by feral honey bees, but the reliance of this free pollination is yet to be quantified. Using feral hive density estimates growers can determine their reliance on feral hives. This can aid biosecurity responses for the likely invasion of the parasitic mite *Varroa destructor* which will decimate feral hives, hence free pollination is threatened. Advancements in molecular science have allowed the development of indirect methods that estimate population density based on a drone sampling using a Williams trap. This method utilizes the haplo-diploid nature of honey bees to determine maternity. Microsatellites are the genetic markers used for this analysis and allow a determination of the mother queen's genotype. However, this method has several underlying assumptions on the nature of drone production and capture that need verification. The assumptions that are the focus of this Honours research are: the area that density estimates cover is known (44km<sup>2</sup>); all colonies will be presented in a drone sample (>300 drones); and all colonies produce drones. My project will address these assumptions to investigate the reliability of density estimates using drone samples. This will be achieved by locating > 30 feral hives surrounding a sample site, and sampling workers using a novel method. Using worker DNA, microsatellites will be analyzed to obtain the colony's queen genotype. The sons of these queens will be correlated with the drones to determine the colony's contribution to sample. The effect of relative size hive and the distance to the sample site on a colony's drone contribution will be analyzed.

*Monday 2 December*  
*16:15–17:30 [13× speakers]*  
*Plaza Room 8*  
**STUDENT**

# Abstract – Systematics and Evolution

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## **Australia's first monoplacophoran (Mollusca): diving deep off Western Australia**

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[Nerida G. Wilson](#)

*Molecular Systematics Unit, Western Australian Museum, 49 Kew St, Welshpool 6106, WA*

Science has not been long acquainted with the extant members of the class Monoplacophora, and their enigmatic nature is still being slowly unravelled. The lack of morphological diversity among living species has led to them being described as 'living fossils'; however, that has been contrasted with the hypothesis that the extant group may instead represent a relatively recent radiation. Despite continuing controversy around their deeper evolutionary relationships, there remain problems with lower level classification as well. The single extant family Neopilinidae contains seven currently accepted genera. To date, the monophyly of these genera has not been tested extensively, although *Laevipilina* appeared polyphyletic in previous studies. The discovery of a new monoplacophoran off Western Australia allows discussion of the limitation of currently used characters. Despite being brought up in a rock dredge from nearly 4300m, the newly collected specimen was in very good condition, and molecular data was generated to place it in a phylogenetic framework. Field-work planned for early 2020 will revisit the site of collection with a Remotely Operated Vehicle, and further study of the new species may be possible at that stage.

*Monday 2 December*

*12:15 – 12:30*

*Plaza Room 11*

# Abstract – Orthoptera Symposium

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## **Environmental effects on local adaptation, and genetic connectivity of generalist (*Phaulacridium*) versus specialist (*Kosciuscola*) Australian grasshoppers**

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[Sonu Yadav](#), A.J. Stow & R.Y. Dudaniec

*Department of Biological Sciences, Macquarie University, Sydney, Australia*

Environmental variables can exert strong effects on a species' neutral, and adaptive genetic variation. Understanding how environmental variables affect species' genetic connectivity and adaptive genetic responses has implications for conserving species subject to climate change and habitat fragmentation. With a landscape genomics approach applied to endemic Australian grasshoppers, we compare how patterns of gene flow and selection interact in a generalist grasshopper agricultural pest, *Phaulacridium vittatum*, versus two specialist grasshoppers of the genus *Kosciuscola* (*K. usitatus* and *K. tristis*), restricted to alpine regions. For *P. vittatum*, we identified mean annual temperature had a stronger positive non-linear effect on genetic connectivity compared to land cover, and despite high gene flow across the 900 km sampling gradient. Environment Association Analysis (EAA) detected signatures of selection in relation to mean annual temperature, latitude and body size. Candidate adaptive SNPs were annotated to gene functions for olfaction, metabolic detoxification and ultra-violet shielding that may be important for environmental adaptation. For the two specialist *Kosciuscola* grasshopper species, EAA analysis indicated that climatic variables were more strongly associated with selection signatures in both species compared to soil or terrain variables. However, *K. tristis*, with a narrow elevational niche and lower cold tolerance, showed stronger genetic structure and more pronounced signatures of local adaptation compared to the more widely found *K. usitatus*. Some candidate loci putatively under selection were shared by both species with a greater number associated with elevation, indicating the likelihood of parallel adaptation driven by climatic variables. The highest number of candidate outlier loci were annotated to genes involved in lipid metabolism and development. The study suggests that species with wider environmental niches are likely to maintain higher gene flow and exhibit weaker signatures of selection than species with narrower niche breadths. We demonstrate that generalist species are more likely to successfully move and adapt under shifting environments due to land use or climate change than specialist.

*Tuesday 3 December*  
*15:30 – 15:45*  
*Plaza Room 10*  
**STUDENT**

# Abstract – Ecology and Interactions #2

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## **Ecology, life history, and the effect of fire on an endemic Australian tarantula, *Selenotypus* sp. nov. (Araneae: Theraphosidae)**

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[Martha Yanez](#) & M.P. Zalucki

*School of Biological Sciences, The University of Queensland St. Lucia, Australia 4072*

The taxonomy of the Australian tarantulas has been relatively well studied. In contrast, the study of natural history and ecology of populations have been largely ignored. The capture of tarantulas is regulated in all states of Australia, but illegal trade and illegal export still occur. Management and conservation require an understanding of a species biology and ecology. So, it is crucial to study the natural history and habitat requirements, especially of recently described species, the endemic *Selenotypus* sp. nov. in the North Central Queensland. The species is located in both a protected reserve and adjacent unprotected areas. On the 28 of November 2018, a fire occurred in the area, where a population was well established. The effect of the fire was quantified; pre-adult stages and females were resilient to the fire. Months later, the area was populated by spiderlings and juveniles. Comparison of the structure of the burrows over three field trips in spring, summer and autumn, showed differences in the quantity of silk: around, in between, and inside the walls of the burrow. Differences were seen not just in different seasons but also in each of the developmental stages. A hemi-view camera was used to capture the quantity of light and solar radiation falling on burrows compared to areas where burrows were absent. Evidence suggests a possible interspecific mutualism between ants, *Iridomyrmex rufoniger* and *Selenotypus* spp., where the ant gets the prey items left by the spider, and the tarantula gets the protection from ants against wasps or other insects. Further studies needed to test this speculation.

*Wednesday 4 December  
11:45 – 12:00  
Plaza Room 10  
**STUDENT***

# Abstract – Invasive Ants Symposium

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## **Fipronil concentration, forager exposure, and bait shyness in yellow crazy ant management**

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[Peter Yeeles](#) & L. Lach

*College of Science & Engineering, James Cook University, PO Box 6811, Cairns QLD 4870, Australia*

The use of pesticides for the management of undesirable insects requires land managers to balance achieving sufficient mortality of the target species against causing unintended off-target impacts. This balance is particularly important when managing invasive ants because high concentration insecticide may kill foragers before they return to their colony, where they would share the toxin with non-foraging nest-mates, including queens. We investigated the toxicity of fipronil, a frequently used neurotoxin, on yellow crazy ants, *Anoplolepis gracilipes*. We examined the LC<sub>50</sub> of fipronil and whether it varies with sugar matrix concentration, the effect of the proportion of a colony exposed to the bait on colony mortality over two weeks, and whether treatment survivors would exhibit bait shyness. We found that the 24 hour LC<sub>50</sub> was 99 µg/L irrespective of the sucrose concentration of the matrix in which the toxin was offered. As expected, none of the colonies with treatments applied at the LC<sub>50</sub> concentration had total worker mortality after one week. When provided with baits at a more typical management concentration of 6400µg/L only the two treatments with the highest number of foragers, between 12% and 30% of the colony, achieved worker mortality approaching 100%. Only 8 of 60 queen ants died during the course of the experiment, and queen death did not correspond with treatment. Workers in colonies previously exposed to either fipronil treatment showed limited interest in food resources compared to workers from control colonies, regardless of whether the resource had fipronil. Our results suggest that interactions between the number of foragers exposed to bait and the concentration of fipronil can have strong effects on colony mortality, even when the toxin is presented at many times the target species' LC<sub>50</sub>. Foraging reluctance following exposure to bait suggests that re-baiting within a short time period will not be effective.

*Monday 2 December  
11:30 – 11:45  
Plaza Room 10*

# Abstract – Behaviour #1

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## **Hymenopteran game of thrones: power shifting in nests of Mud dauber wasp *Sceliphron formosum***

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[David Yuan](#)<sup>1,2</sup>, J. Florez<sup>2</sup> & J. Rodriguez<sup>2</sup>

<sup>1</sup>Research School of Biology, Australian National University, Canberra, ACT 2601, Australia

<sup>2</sup>Australian National Insect Collection, CSIRO National Research Collections Australian, Canberra, ACT 2601, Australia

### Abstract

*Sceliphron* are a unique group of sphecoid wasps that build mud nests for reproduction and commonly inhabit human constructions. Many *Sceliphron* species are well studied in terms of their nesting behaviour and prey selection. However, despite being a common insect in urban areas, *Sceliphron formosum* occurring in ACT, has never been comprehensively studied. In this study over 650 mud nests of *S. formosum* were collected, analysed and examined to establish prey preference, nest ecology and interspecific relations taking place in mud nests. Prey preference was evaluated in terms of spider abundance, diversity and morphology. Preference in terms of morphology was estimated using body length to leg span ratio. Prey preference was compared to vegetation coverage and potential factors that affect spider composition in mud nests and how urbanization can influence prey selection are discussed. Moreover, as a novel study direction of *Sceliphron* species, this study discovered that the enclosed mud nests can become a micro niche that supports a wide variety of insects. Fourteen families and 21 species of insects were found associated with the use of mud nests, comprising three insect orders: 1. Hymenoptera: Ichneumonidae, Chrysididae, Crabronidae, Vespidae, Eulophidae, Torymidae, Chalcididae, Megachilidae, Colletidae and Gasteruptiidae; 2. Diptera: Bombyliidae, Acroceridae and Sarcophagidae; and 3. Coleoptera: Dermestidae. More importantly, the composition of these communities revealed the presence of important pollinators, new species and native species that have never been recorded in the past 20 years of mud dauber wasp studies. Therefore, understanding *Sceliphron* nest ecology is essential for assessing how these urban insects influence urban ecosystems and how they could contribute to conservation, ecology and biodiversity studies.

*Monday 2 December  
15:15 – 15:30  
Plaza Room 10*

# Abstract – Pest Management

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## **Exploring the relevance of the ecological traits of parasitoid wasps and nectariferous plants: the new frontier for conservation biological control of pests**

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[Pingyang Zhu](#)<sup>1,2,3</sup>, Z. Lu<sup>2</sup>, G. Chen<sup>3</sup> & G.M. Gurr<sup>1</sup>

<sup>1</sup>*Graham Centre, Charles Sturt University, Orange, NSW2800 Australia*

<sup>2</sup>*State Key Laboratory Breeding Base for Zhejiang Sustainable Pest and Disease Control, Institute of Plant Protection and Microbiology, Zhejiang Academy of Agricultural Sciences, Hangzhou, Zhejiang 310021, China*

<sup>3</sup>*Jinhua Plant Protection Station, Jinhua, Zhejiang 321017, China*

Conservation biological control aims to protect and enhance natural enemies through rational design of the farming system. This can be achieved through many practices such as selective pesticides and biopesticides, artificial food sprays, and ecosystem services by habitat management. An important example of manipulating ecosystem services is the enhancement of biological pest control using nectar plants to nourish natural enemies. However, studies of this type have relied upon the empirical testing of multiple candidate plants to identify suitable species for each pest—parasitoid interaction in each agroecosystem. It is of significant applied value to determine whether there are general principles that could guide the selection of plant species in habitat management rather than requiring an empirical research be conducted afresh in each new system. We assessed the benefits of 77 different flower species as nectar sources for 21 parasitoid wasp species of significance in a range of crop systems in the lab, then we processed all the experimental data and available information on the traits of parasitoid and plant species by a pooled analysis approach to determine which plant and parasitoid traits most strongly affect the extent of benefit to parasitoids. Only plant inflorescence-related traits significantly affected response. Among the inflorescence types, compound umbel was the most positively predictive of parasitoid longevity and fecundity enhancement. The inflorescence types of capitulum, solitary and spike showed no (or weak) positive effect on parasitoid longevity and fecundity. This principle offers the prospect of enhancing the ecosystem service provided by parasitoids in agriculture by avoiding the need to empirically screen multiple candidate plants in each new study system.

*Monday 2 December*

*11:45 – 12:00*

*Plaza Room 8*

***STUDENT***

# Poster Abstract

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## **Influence of landscape composition on arthropod assemblages of crop fields**

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[Salma Akter](#)<sup>1</sup>, O. Reynolds<sup>2</sup> & G.M. Gurr<sup>1</sup>

<sup>1</sup>*School of Agricultural and Wine Sciences, Faculty of Science, Charles Sturt University, P.O. Box 883, Orange, NSW 2800, Australia*

<sup>2</sup>*cesar pty ltd, 293 Royal Parade, Parkville, Victoria 3052, Australia*

Increasing landscape heterogeneity in agroecosystems can play an important role in invertebrate pest suppression by enhancing the availability of donor habitats of natural enemies. However, the effects of non-crop vegetation (such as shelterbelts, riparian vegetation, scattered trees, and forest fragments) on natural enemy and pest densities in crops are inconsistent. Crop and non-crop plant identity, spatial scale, climate, arthropod taxon, and local-scale management practices can all exert effects but they are poorly understood. Accordingly, the aim of this study was to better understand the effects of these factors in the context of Australian brassica vegetables. Data on pest and natural enemy densities were collected for sites covering four climatic regions across Australia (Western Australia, New South Wales, Victoria and Queensland). Arthropod data were collected from the centre of brassica fields and from crop margins with differing types of adjacent land use. Landscape composition was analysed from Google Earth images of each site using ArcGIS 10.6 at different spatial scales (250 m, 500 m, 1000 m, 2500 m and 5000 m) from the focal crop. Results will be presented and discussed in relation to optimising pest suppression by promoting natural enemy activity in focal crops by strategies that exploit the effects of vegetation patterns at scales ranging from peri-field to multi-kilometre.

*Poster session:  
Monday 2 December  
17:30 – 18:30  
Plaza Foyer*

# Poster Abstract

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## Phylogenetic position of two aberrant subfamilies of braconid wasps: the Masoninae and Trachypetinae

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D. Quicke<sup>1</sup>, [Andy Austin](#)<sup>2</sup>, E. Fagan-Jeffries<sup>2</sup>, P. Hebert<sup>3</sup> & B. Butcher<sup>1</sup>

<sup>1</sup>*Integrative Ecology Laboratory, Department of Biology, Faculty of Science, Chulalongkorn University, Phayathai Road, Pathumwan, BKK 10330, Thailand*

<sup>2</sup>*Australian Centre for Evolutionary Biology & Biodiversity, School of Biological Sciences, The University of Adelaide, AUSTRALIA 5005*

<sup>3</sup>*Centre for Biodiversity Genomics, Biodiversity Institute of Ontario, University of Guelph, Guelph, Ontario, Canada N1G 2W1*

Although a phylogenetic understanding of relationships among the subfamilies of Braconidae and Ichneumonidae (Ichneumonoidea) has advanced significantly in recent years, the position of several critical groups has remained elusive due to a lack of material for molecular studies. Here we report on studies that have resolved the positions of two somewhat aberrant subfamilies of Braconidae – the Masoninae and Trachypetinae. Members of Masoninae are highly derived and rarely collected; species are tiny in size (2 mm or less), morphologically reduced, with most species being wingless. Discovery of a fully-winged female *Masona* from Australia has enabled a reassessment of its relationships. The specimen yielded sequence data for four genes and when analysed with other Braconidae and Ichneumonidae surprisingly was nested basally among the ophoniform Ichneumonidae and, therefore, is not a member of Braconidae! The Trachypetinae have been recognized as one of the most distinctive groups of Braconidae, comprising seven species of large wasps in three genera which are endemic to Australia. Historically they have been variously treated in braconid classifications, but never satisfactorily and with a growing consensus that they fall outside the rest of the Braconidae. We generated a molecular data set comprising five gene fragments and morphology for a taxonomically broad range of Braconidae and Ichneumonidae. The resultant trees confirm the monophyly of the Trachypetinae (also support by a unique glandular or sensory structure on the mandibles) and robustly place them as sister to the Braconidae. A detailed morphological analysis shows that the trachypetine genera lack several synapomorphies of the Braconidae, and that they possess several symplesiomorphies absent from this family but found in some ichneumonids. We argue that, based on these results, family level status is warranted for the group and, hence, we propose the new family Trachypetidae stat. nov. (type genus *Trachypetus* Guerin de Meneville) for it.

*Poster session:  
Monday 2 December  
17:30 – 18:30  
Plaza Foyer*

# Poster Abstract

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## Phylogeny and taxonomic revision of the Australian spider wasp genus *Cryptocheilus* Panzer, 1806

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[Mahin Chavoshi](#)<sup>1,2</sup>, D. Rowell<sup>1</sup> & J. Rodriguez<sup>2</sup>

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*Cryptocheilus* Panzer, 1806 is a cosmopolitan genus of spider wasps (Hymenoptera: Pompilidae) with the oldest record dating back to 33.9–37.8 million years ago. Australian *Cryptocheilus* spp. are among the most visually distinctive pompilids, being generally large (3–4 cm in length) and with contrasting coloration (orange and black). They are parasitoids of spiders from the families Lycosidae, Araneidae and Sparassidae. Host records are sparse, and not usually identified past generic-level. These spider wasps are pollinators of various plant genera such as *leptospermum*, *Pastinaca* and *Gomphocarpus*.

Of 89 species, there are six in Australia, eight in North, Central and South America, 74 species concentrated in the Palearctic and one in Africa. Within Australia, *Cryptocheilus* can be found in almost any environment, ranging from the interior to the regions in the southeast, although their diversity appears to be highest close to the coast. There is no systematic revision of Australian *Cryptocheilus* and a recent morphological analyses Wahis (2008) suggests that what is known as *Cryptocheilus* in the Australian region, can probably be split up into two genera: *Cryptocheilus* and *Heterodontonyx* Haupt, 1935. Wahis (2008) also suggests the need of molecular data for generic delineation. Preliminary examination of specimens in Australian collections shows that there are undescribed species.

The aims of this project are to: 1) assess the monophyly of Australian *Cryptocheilus* and delimit genera boundaries using ultraconserved element (UCE) data, use morphological and molecular data to perform a systematic revision of Australian *Cryptocheilus*, assigning morphological characters and providing a species level identification key. So far, type materials of Australian species have been studied and imaged and molecular sampling of 150 specimens from major Australian collections has been completed. Sequencing has been performed for a fraction of these specimens. Preliminary results show that *Cryptocheilus* is paraphyletic and that *Heterodontonyx* is nested within Australian *Cryptocheilus*. There are an estimated 2 new species within Australian *Cryptocheilus*.

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## Revision of the planthopper genus *Olonia* Stål, 1862

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The Australian genus of Eurybrachidae Stål, 1862 (Hemiptera, Fulgoromorpha) *Olonia* Stål, 1862 was redescribed and reviewed and seven new species were described: *O. bourgoini* (N Queensland, Chillagoe), *O. danielsi* (N Queensland, Cape York Peninsula), *O. guillaumei* (N Queensland), *O. hochae* (N Queensland, Undara), *O. monteithi* (Queensland), *O. rylandae* (N Queensland, Chillagoe) and *O. soulierae* (N Queensland, Chillagoe). *Platybrachys nobilis* (Stål, 1863) was transferred to *Olonia* while *Olonia ornata* Lallemand, 1928 and *O. apicalis* (Walker, 1851) were removed from *Olonia* and transferred to *Platybrachys* Stål, 1859 and *Maeniana* Metcalf, 1952, respectively. The new genus *Stalobrachys* was described to accommodate *Olonia alboapicata* Jacobi, 1928. The male genitalia of *Olonia* species bear strongly modified, sclerotised gonostyli extremely useful for species identification. Figures of male genitalia and photographs of male and female, a distribution map, biological data and an identification key were provided. The genus *Olonia* currently contains twelve species and seems to be restricted to the eastern part of Queensland, extending to the Great Dividing Range to the west, and mountains might have played a role in the speciation within the genus. Eight host plants belonging to five different families were identified, mostly contributed by citizen scientist's field observations which additionally allowed documenting habitats, egg masses, nymphal stages and parasites of the Lepidoptera family Epipyropidae. The necessary better knowledge of the distribution, host plants, phenology etc. of these species requires more, targeted fieldwork which could involve some citizen scientists.

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## **Systematics and host associations of labenine parasitoid wasps (Hymenoptera: Ichneumonidae: Labeninae) from south-eastern Australia**

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[Madalene Giannotta](#)<sup>1</sup>, S. Klopstein<sup>2</sup> & A. Austin<sup>1</sup>

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The Labeninae is unique among the Ichneumonidae (Hymenoptera) as the only subfamily containing an ecologically divergent tribe specialising in parasitising ground-nesting, solitary bees. Limited studies on their taxonomy (especially of the genus *Labium*), is a significant shortcoming in understanding the evolution of this seemingly ancestral ichneumonid group, and the co-evolution with their aculeate hosts. Currently, 28 species of *Labium*, and a species of *Ozlabium* are known from Australia (mostly from inadequate descriptions), which is only about half of their estimated species-richness.

Using molecular data and morphological traits, this study aimed to assess the diversity and evolutionary history of this understudied group of Australian parasitoid wasps, and document their distribution and host associations. Pinned material was sourced from all major Australian collections, with fresh specimens collected across the southern half of the continent and Tasmania. A molecular phylogeny using the mitochondrial *COI* gene region from 106 specimens (80 *Labium*, 14 other labenines, 10 other ichneumonids), and a set of four morphological characters were used to conduct an analysis of species relationships. The resulting preliminary phylogeny supports the monophyly of Labeninae and the genus *Labium*. Surprisingly, *Ozlabium* was not resolved as sister to *Labium*, as previously hypothesised in earlier studies. Species delimitation analyses (bPTP; K2P divergence distances) estimated the presence of 26 *Labium* species from the 80 successfully sequenced specimens, while morphological analyses recognised 29 putative species, with slightly different species boundaries. Given the potential for *COI* to become saturated, and the frequency of homoplasy, within the Ichneumonidae, future research would benefit from significantly increased taxon sampling and a Next Generation Sequencing approach for robust species delimitation, and resolution of generic and subfamilial relationships.

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## **‘Damsels in excess’ a plant-arthropod interaction between damselflies and a freshwater swamp lily: *Ottelia ovalifolia***

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[Brock Hedges](#)<sup>1</sup>, A. Austin<sup>1</sup>, C. Madden<sup>2</sup>, J. Conran<sup>1</sup>, G. Taylor<sup>1</sup> & P. Weinstein<sup>1</sup>

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<sup>2</sup>*Freshwater Macroinvertebrates*

The granite gnammas (rock-holes) across the north of the Eyre Peninsula, are a unique ephemeral freshwater habitat. A complex community of invertebrates is known to be associated with these sites, but macroinvertebrate predator occurrence is often sporadic, both spatially and temporally. Due to the potential driving effect of predator occurrence/abundance on community structure, the aim of this project was to determine what predicts predator occurrence in the EP gnammas. A total of 14 gnammas were sampled across five granite outcrops along the Eyre Highway in 2016. Sites were classified by depth & size, and extensive dip-net sampling was undertaken to determine damselfly presence. Representative specimens were collected for identification and imaging. Three species of damselfly were recorded from the EP gnammas: *Ischnura aurora*, *Xanthagrion erythroneurum*, and *Astrolestes annulosus*, with all three species co-occurring in a single gnamma at Pildappa Rock. This gnamma was notable as it had the greatest depth of all those surveyed, and the longest predicted hydroperiod. Additionally, this gnamma was the only one containing a floating-leaved, rooted aquatic macrophyte, resulting in a complex, three-dimensional vegetative structure across the whole water depth in the gnamma: swamp lily, *Ottelia ovalifolia* (Hydrocharitaceae). Due to their exclusive co-occurrence, damselflies were hypothesised to be dependent on the presence of *O. ovalifolia*, possibly as a result of the plant providing a complex three-dimensional habitat for the nymphs. The results of this study contribute to the previously very limited ecological information regarding the EP gnammas. Increased understanding of the factors that influence species diversity, is critical in maintaining these threatened habitats.

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## **Physical resistance versus bodyguard recruitment: impacts of silicon on direct and indirect herbivore defences in plants**

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Herbivorous insects account for over 25% of plant and animal species in the world and have been locked in an evolutionary arms race with the plants they consume for over 300 million years. In particular, plants use a vast array of defences against herbivores to which herbivores continually adapt to. Many plants acquire silicon (Si) from the soil which can be deposited within and between plant tissues. Silicification can make plant tissues rigid and tough as well fortifying physical structures (e.g. spines, hairs and phytoliths). These changes can create a formidable physical barrier against invading herbivores. In addition to these direct defences, a few studies have also reported enhanced levels of attraction of natural enemies to Si supplemented plants under herbivore attack (e.g. indirect defence). The underlying mechanisms remain unclear but most likely involve Si-induced changes to the production of herbivore-induced plant volatiles (HIPVs) which attract natural enemies. This poster reports how Si affects direct defences against the cotton bollworm (*Helicoverpa armigera*) feeding on cucumber (*Cucumis sativus*). We also report how Si affects HIPVs and how this relates to a natural enemy (*Phytoseiulus persimilis*) of two-spotted spider mite (*Tetranychus urticae*). In short, is it better to deploy direct (toughening up) or indirect (cry for help) for herbivore defence?

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## **Know thine enemy: culturing two invasive ant species within an eradication program—why do it and what works?**

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[Lance Maddock](#) & E. Wallace

*National Red Imported Fire Ant Eradication Program, Qld Department of Agriculture and Fisheries, Wayne Goss Drive, Berrinba QLD 4118*

Maintaining laboratory colonies of ants within an eradication program is necessary for various reasons. Ants may be used for live displays for education purposes, experimental work, or for producing training materials for odour detection dogs.

The National Red Imported Fire Ant Eradication Program, which has been running since 2001, has successfully cultured fire ant (*Solenopsis invicta*) colonies since early in the program. Fire ants are a highly invasive species, with a large body of research and knowledge about their biology, and whose hardy and aggressive nature makes them easy to maintain in culture.

Recently, the program began culturing a new invasive ant species known as browsing ant (*Lepisiota frauenfeldi*), to determine the viability of cross imprinting detection dogs with multiple invasive ant odour signatures. Browsing ants, as opposed to fire ants, have not been studied in detail and have proven difficult to culture successfully under laboratory conditions.

Through careful observation and investigation into the biology of sister species, suitable methods for culturing browsing ants were eventually determined and have proven successful over the last several years. Now, both species (browsing ants and fire ants) are cultured to produce odour on cloth that is the basis for training detection dogs within the program.

Here, we highlight the importance of understanding differences in the behaviour, biology and dietary requirements in culturing species, particularly when little is known or understood. Culturing invasive ant species is valuable both from an educational perspective and for operational purposes, and is a critical part of the science activities pursued by the program.

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## **What do you mean you've eradicated fire ants? The critical role of population genetics in tracking invasive ant incursions**

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R. Wylie & [Melinda K. McNaught](#)

*National Red Imported Fire Ant Eradication Program, Qld Department of Agriculture and Fisheries, Wayne Goss Drive, Berrinba QLD 4118*

As modern trade continues to spread invasive species across the globe, eradication of these species becomes challenging in the light of the ever present threat of re-introduction. In the case of the red imported fire ant, detailed genetics analysis has allowed the national eradication program to track the origins of all known nests and assign them to their sub-populations. To date, there have been 7 incursions and 3 post-border detections in Australia; all but one of these are no longer present in the country. Due to the efforts of the program, eradication and proof-of-freedom have been claimed for these incursions, with the original Port of Brisbane eradication the largest recorded eradication of any invasive ant species worldwide.

Without genetics, it would be impossible to track these populations or determine their origins. Genetic analysis has been essential in demonstrating whether each detection was a new arrival, or the result of spread from already established populations. Given that there are hundreds of records of fire ants arriving in shipping containers at the Port of Brisbane every year, it is imperative to consider eradication in terms of genetically distinct populations, rather than the presence/absence of the species as a whole. Here we highlight the history of fire ant detections in Australia and the new commitment to eradicate the last known population over the next decade.

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## **Small hive beetle infestation and Cucurbit pollination in Australian stingless bees**

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[Scott Nacko](#)<sup>1</sup>, M. Hall<sup>1</sup>, R. Spooner-Hart<sup>1</sup>, J. Cook<sup>1</sup> & M. Riegler<sup>1</sup>

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Managed stingless bee hives represent a growing industry in Australia, heightening the importance of factors which affect hive health and pollination services. We present findings from the first study to examine Australian stingless bee pollination of cucumbers under protected and field setting. We also present the first detailed study of a small hive beetle infestation in a living hive of the Australian stingless bee *Tetragonula carbonaria*. Nine hives were deployed for use in dwarf cucumber field crop pollination. Stingless bees were not observed visiting crop flowers, and few visits were observed on non-crop resources. After two months on site it was evident that two of nine hives had become weakened, with fewer foragers present and reduced hive weight. Following a sustained heat wave, one hive was removed early from site to recover. After all hives had been returned, one was found to be infested with small hive beetle and was unlikely to recover. All small hive beetle stages except eggs were discovered inside the hive, totaling 14 adults and 133 larvae. Extreme daily maximum temperatures coupled with low humidity appear to weaken stingless bee colonies, elevating the need for careful hive placement in open agricultural settings. A follow-up glasshouse experiment with dwarf cucumber plants revealed bees would visit the crop more readily when given no other alternative food source.

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## **Determining the effects of body size on the population dynamics of a frugivorous pest**

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[Jaye Newman](#)<sup>1</sup>, H. Parry<sup>2</sup>, K. Merkel<sup>1</sup> & A. Clarke<sup>1</sup>

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In insects, the quality and quantity of the larval host diet commonly influences the size of emergent adults. Adult size is an important trait which impacts on population dynamics by influencing individual fecundity, mating success, survival, longevity and movement. However, equating individual variation in size with emergent properties such as local population dynamics is extraordinarily difficult using classical ecological tools. In contrast, individual-based models can be used to explore individual variation in morphology and behaviour among individuals in a dynamic environment, thus offering a way to link individuals with population properties. An individual-based model will be developed for the Queensland fruit fly, *Bactrocera tryoni*, a polyphagous frugivorous pest along the east coast of Australia. The life cycle of the fly is modelled to mechanistically link individual body size with key behavioural/physiological parameters influencing individual fitness (movement, development rate, fecundity) to address variation in individual fitness and the impact on population dynamics.

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## Olfactory ecology of dung beetles: proposed investigation of responses to semio-chemicals and dung volatiles

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[Nisansala Perera](#)<sup>1</sup>, P.A. Weston<sup>1</sup>, L.A. Weston<sup>1</sup>, G. Gurr<sup>2</sup> & R. Barrow<sup>1</sup>

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<sup>2</sup>Charles Sturt University, Leeds Parade, Orange, NSW 2800

Locating patchily distributed food resource and finding a mate are strongly influenced by volatile cues for most insects, including dung beetles. Even though coprophagous dung beetles are considered to be generalists as they can subsist on different types of dung, recent studies have revealed that some species of dung beetles orient more towards one type of dung than others indicating that they can discriminate among different dung odors. Pheromone communication although well documented in many beetle species, has been largely unexplored for dung beetles, the only studies being for the South African genus *Kheper*. Because of the lack of comprehensive studies on the olfactory ecology of dung beetles, we are planning behavioral studies of dung beetle responses to odors using *Bubas bison* and *Onthophagus vacca* (Coleoptera: Scarabaeidae) as model organisms. In the initial phase, responses to odors will be tested in the laboratory using olfactometers. Test insects will be exposed to volatiles from several types of herbivore dung (e.g. cattle, sheep, wombat, kangaroo and horse) and chemicals previously reported to occur in the headspace of dung (e.g. butyric acid, 2- butanone, indole, skatole, p-cresol, phenol and a quinone mixture). The existence of pheromones will be tested by observing the response of beetles of one sex to odor emanating from beetles of the opposite or the same sex. Further studies are planned to pinpoint the active compounds from stimulatory odors using GC-electroantennography. Based on results from laboratory bioassays, testing will be done in the field to verify the ecological relevance of compounds found to be active in the laboratory, with one of the ultimate objectives being the formulation of synthetic lures to improve the consistency and ease of trapping dung beetles in the field.

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## **Integrative taxonomy to unravel a cryptic fruit fly species pair: *Bactrocera musae* (the banana fruit fly) and *B. opiliae* (the false Oriental fruit fly)**

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S.M. Close, [Jane E. Royer](#) & M.K. Schutze

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*Bactrocera musae* (Tryon) and *Bactrocera opiliae* (Drew & Hardy) (Diptera: Tephritidae) are morphologically similar Australian fruit fly species. *Bactrocera musae* is a pest of bananas, while *B. opiliae* is only known from the native *Opilia amentacea*. Both are trapped with the male lure methyl eugenol. Until recently, they were thought to be allopatric, with *B. opiliae* occurring in the dry tropics from Western Australia through to northwest Queensland, and *B. musae* occurring in the northeast Queensland wet tropics. However, recently developed nuclear DNA markers have revealed that some specimens collected in northeast Queensland were *B. opiliae*. This has made identification of methyl eugenol trap catches in this area of sympatry difficult. Accurately distinguishing these two species is critical for defining pest boundaries for horticultural market access. Consequently, we're updating our knowledge of the geographic distribution of *B. opiliae*, whilst refining diagnostic morphological characters to more readily distinguish them. This is being achieved by sequencing suspected *B. opiliae* trapped in northeast Queensland to confirm their identity, and comparing the morphology of undisputable specimens i.e. methyl eugenol-trapped *B. opiliae* from the Northern Territory, and *B. opiliae* and *B. musae* reared from their respective hosts. This is leading to a refined understanding of the morphological characters to separate this species pair and the new distribution of *B. opiliae* in northeast Queensland.

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## **Insecticide resistance status in the field population of *Bemisia tabaci* (Hemiptera: Aleyrodidae) to the new chemistry insecticides in Punjab, Pakistan**

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[Muhammad Saleem](#)<sup>1</sup>, M. ul Hasan<sup>1</sup>, M. Sagheer<sup>1</sup> & M. Atiq<sup>2</sup>

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<sup>2</sup>Department of Plant Pathology, University of Agriculture, Faisalabad

The cotton whitefly, *Bemisia tabaci* Gennadius (Hemiptera: Aleyrodidae) had developed high degree of resistance to various insecticides throughout the world. Because control of *B.tabaci* still depends upon on the application of insecticides in Pakistan, monitoring the insecticide resistance of *B.tabaci* populations is essential for achieving control and for managing resistance. To monitor insecticide resistance in Punjab, Pakistan eight insecticides (Difenturon, Buprofezin, Imidacloprid, Acemaprid, Thiamethoxam, Thiacloprid, Bifenthrin and Chlorpyrifos) from different chemical families were tested using leaf-dip method on three field populations collected from cotton in Bahawalpur, Multan and Faisalabad in 2017, 2018 and 2019. No resistance to difenturon and buprofezin was detected. All of the *B.tabaci* populations exhibited resistance to neonicotinoid insecticides; the resistance was 2.5- to 133.6-fold greater than that of susceptible laboratory strain. The traditional insecticides bifenthrin and chlorpyrifos had very low toxicity. *B.tabaci* populations in some regions exhibited annual difference in resistance to some insecticides. The data presented will be helpful for making on the proper insecticide usage in the field.

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## ***Metcalfa pruinosa*'s time-periodic invasion route in apple orchard and effect of blocking inflow on farm land using Sunflower**

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*Metcalfa pruinosa* were introduced to South Korea in 2009 and continue to cause damage to farm land each year. In order to identify the invasion route of the *Metcalfa pruinosa* in the apple orchard, the transparent sticky trap was installed at the boundary of field and surveyed periodically. The results of the invasion route in apple orchard, *Metcalfa pruinosa* stayed only at the apple orchard boundary and did not enter much inside the orchard. And to control *Metcalfa pruinosa*'s nymphs in an environmentally friendly manner, fence plant was selected to block the inflow into the farm land using sunflower. As a result of testing the blocking effect in the farm land, the *Metcalfa pruinosa*'s nymphs have entered more farm land without sunflower than farm land with sunflower. And also, The density of the *Metcalfa pruinosa*'s nymphs where the chemicals were treated was about 50% less than the density that was not treated by the chemicals. The results confirm that sunflower could be used to block some of the *Metcalfa pruinosa*'s nymphs from entering the farmland.

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## Climate change and its effects on aphid parasitoid *Aphidius colemani*

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Atmospheric carbon dioxide (CO<sub>2</sub>) concentration, currently over 400 ppm, is predicted to double by 2100, likely increasing global temperature by 2.2 °C. Among the main drivers of climate change, elevated CO<sub>2</sub> (eCO<sub>2</sub>) and elevated temperature (eT), significantly affect agricultural crops as well as plant pathogens and insect pests, their predators and parasitoids. Changes to any part of multitrophic systems due to environmental factors will affect the different trophic levels, thus the magnitude and severity of pests and diseases. Therefore, assessing the effects of combining climate change factors in multitrophic interactions is essential to enhance integrated pest and disease management in a global change scenario. Our study evaluated the effects of eCO<sub>2</sub> and eT combined, on the performance of the parasitoid *Aphidius colemani* Vierick (Hymenoptera: Braconidae), when its aphid host, *Rhopalosiphum padi* L. (Hemiptera: Aphididae) was grown on non-infected or *Barley yellow dwarf virus*-infected wheat. Using controlled environment chambers, plant physiology, pest and parasitoid performance were examined under two different climate conditions, ambient (aCO<sub>2</sub>&aT = 400ppm&20°C) and elevated (eCO<sub>2</sub>&eT = 800ppm&22°C). Leaf discoloration and plant biomass reduction due to virus infection were greater under eCO<sub>2</sub>&eT thus, BYDV symptomatology could be magnified under future climate. Under eCO<sub>2</sub>&eT, aphid fecundity and development time decreased on non-infected plants, whereas on virus-infected plants, aphid fecundity decreased but not development time. *Aphidius colemani* shortened its development time under eCO<sub>2</sub>&eT and a potential mismatch with its host life cycle when grown on virus-infected plants could be addressed under future climate. However, parasitism rate, sex ratio and pupal survivorship remained unchanged under eCO<sub>2</sub>&eT, independently of virus infection. Our research provides information about how a virus infection could affect differently a tritrophic system under eCO<sub>2</sub>&eT. This investigation is necessary to better comprehend the impact of climate change in the complex interactions involved in agrosystems.

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## **The effect of elevated CO<sub>2</sub> and nitrogen rates on aphid *Rhopalosiphum padi* development and fecundity**

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The atmospheric carbon dioxide concentration ([CO<sub>2</sub>]) has increased from 277 ppm in the mid-eighteenth century to 411 ppm in July 2019. The main contributors to this rise in atmospheric CO<sub>2</sub> levels are the burning of fossil fuels and deforestation.

Wheat is a staple crop and its cultivation worldwide is of significant importance. Previous research has shown that elevated [CO<sub>2</sub>] affects many biological functions, including plant phenology and carbon and nitrogen dynamics. This will not only impact crop growth and quality of food products but will also affect the development and fecundity of insect pests such as aphids. While the nitrogen content of wheat tissues is generally reduced under elevated [CO<sub>2</sub>], a potential adaptation strategy to maintain the quality of wheat is the increased use of nitrogen fertiliser.

This study examined the effect of three different nitrogen application rates (low, medium and high) and two CO<sub>2</sub> concentration levels (400 ppm and 800 ppm) in controlled environment chambers on wheat physiology and, the development and fecundity of the bird cherry-oat aphid, *Rhopalosiphum padi*, a major pest of cereal crops in Australia and worldwide. We found that aphid fecundity increased with higher nitrogen application rates across both CO<sub>2</sub> treatments whereas elevated [CO<sub>2</sub>] decreased aphid fecundity by about 38% when compared to current CO<sub>2</sub> levels.

As CO<sub>2</sub> concentration levels are projected to increase, this study aims to provide a better understanding of the interactive effects of elevated [CO<sub>2</sub>] and nitrogen application rates on aphid biology.

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## Presence of aphids in Victorian field crops: species identification and population dynamics

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Aphids are important pests of grain crops such as cereals, pulses and canola. They not only cause feeding damage but also spread viruses, therefore aphid monitoring and correct identification is important for the deployment of control measures. During the growing season, crops are visited by many aphid species. During 2018, alate aphid species were trapped from cereal and pulse trials using yellow sticky traps. The aphid species were identified and numbers counted. The species found in abundance were oat aphid (*Rhopalosiphum padi*), corn aphid (*R. maidis*), Russian wheat aphid (RWA) (*Diuraphis noxia*), green peach aphid (*Myzus persicae*), plum aphid (*Brachycaudus helichrysi*), cabbage aphid (*Brevicoryne brassicae*), turnip aphid (*Lipaphis pseudobrassicae*) and blue-green lucerne aphid (*Acyrtosiphon kondoi*). The species trapped in highest numbers was RWA. The species found in low numbers were cotton aphid (*Aphis gossypii*), pea aphid (*Acyrtosiphon pisum*) potato aphid (*Macrosiphum euphorbiae*), green sowthistle aphid (*Hyperomyzus lactucae*), brown sowthistle aphid (*Uroleocon sonchi*), spotted alfalfa aphid (*Therioaphis trifolii* forma maculata), tulip aphid (*Brachycaudus helichrysi*), cowpea aphid (*Aphis craccivora*) and blackberry cereal aphid (*Sitobion fragariae*). Most of these aphids are reported vectors of grain crop viruses. In 2018, the population of aphids started increasing from the first week of October, peaked at the end of October and then declined after mid-November but the RWA population started rising from the end of October peaked in mid-November and declined in early December.

*Poster session:  
Monday 2 December  
17:30 – 18:30  
Plaza Foyer*

# Poster Abstract

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## **Microbes in insect herbivore oral secretions increase senescence around plant wounds**

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Plants have long been exposed to insect herbivore attack and pathogen infections, often simultaneously. Crucial to the plant's ability to defend itself against multiple natural enemies is the correct identification of the biotic agent and deployment of the most appropriate defence response. Distinctive chemical cues, such as those associated with chewing insect oral secretions (OS), activate targeted defence responses against chewing insect herbivores. However, this interaction may be complicated by the fact that these herbivores form associations with microbes that produce their own specific signals which result in alternative processes such as cell senescence, a common response induced by plants to prevent the spread of biotrophic pathogen infection. Here we report that microbes within the OS of the global pest, the cotton bollworm (*Helicoverpa armigera*), activate greater levels of cell senescence in *Brachypodium distachyon* than mechanical wounding alone or OS treated with antibiotics. Nonetheless, plants sealed mechanical wounds more rapidly when treated with herbivore OS regardless of the microbial component. We conclude that microbes within OS have an important role in shaping plant-herbivore interactions through modification of the plant wound response.

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