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# Deep transcriptome insights into cave beetle eyes

*Marcus Friedrich (1,2)*

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Beetles have been exceptionally successful in diversifying into one of the most extreme habitats on earth: the light-secluded and energy-poor environments of caves. The exclusive long-term persistence of any animal lineage in the cave habitat, i.e. the transition to troglobiotic ecology, is associated with a suite of profound changes in morphology, physiology, and life history. Most notable among them is the partial or complete regression of the visual system. Recent years have seen a surge of new insights into the genetic basis of such cave-adaptive phenotypic changes due to the application of high throughput sequencing approaches. Beetles have been no exception to this. I will review first lessons learned from transcriptome-based studies of cave adaptation in this group, focussing on the regressive evolution of the visual system.

# Aedes control: the future is now!

*Hoffmann, A.A.*

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*Aedes aegypti* and *Aedes albopictus* are the major mosquito vectors of dengue and other arboviruses around the world. Both species are invasive and have expanded their ranges in recent times. In the absence of effective vaccines, the major focus of disease prevention has centred around vector population suppression, and more recently on novel ways of altering the composition of target populations through the introduction of genetic constructs and particularly through the invasion of target mosquito populations by *Wolbachia* bacterial endosymbionts. *Wolbachia* programs targeting both *Aedes* species have now moved to the field trial stage. Disease suppression through *Wolbachia* releases can be achieved through multiple modalities. The most direct of these involves blocking of viral transmission by some *Wolbachia* strains; a number of studies have now demonstrated that the titre of dengue and other viruses in salivary glands of both *A. aegypti* and *A. albopictus* is markedly reduced by some strains of *Wolbachia*. After *Wolbachia* have invaded natural populations to reach a high frequency, viral transmission by mosquitoes feeding on infected humans should therefore be substantially decreased. Recent data indicate that *Wolbachia* stably maintains high frequencies following invasion of natural *A. aegypti* populations, resulting in blockage effects being maintained across time. *Wolbachia* can also influence disease transmission by suppressing vector populations as a consequence of post-mating incompatibility and through exerting deleterious effects on their mosquito hosts. Incompatibility is being used in trial field releases against *A. albopictus* but requires ongoing interventions to achieve suppression. Deleterious host fitness effects could be used to suppress and even eliminate local isolated populations following incursions; these effects have now been demonstrated in field cage trials with *A. aegypti*. *Wolbachia*-based approaches therefore provide exciting opportunities for health authorities to suppress disease transmission, and they also provide new tools for dealing with future incursions by invasive *Aedes*.

# The Hemipteroid Tree of Life

*Kevin P. Johnson*

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The hemipteroid insect orders (Psocodea, Thysanoptera, and Hemiptera) are a diverse group of insects, comprising well over 100,000 species. The phylogenetic relationships among these orders and their relationship to other insect groups generally have not been strongly resolved in the past. The Phylogenomics and Morphology of the Hemipteroid Insect Orders Tree of Life project is using both genome scale data and morphology to resolve the higher level phylogenetic relationships of this group. A large morphological data matrix of over 300 characters provides some preliminary resolution of the tree. Preliminary results from transcriptome data for this group provide generally stronger resolution for the backbone of the tree. From whole genome data, a novel approach using an automated Target Restricted Assembly Method (aTRAM) provides strong support for phylogenetic relationships among groups of parasitic lice. In particular, these data suggest that Ischnocera is paraphyletic, and the sucking lice (Anoplura), which parasitize mammals, are closely related to the Ischnocera that parasitize mammals. These same genome sequence data sets are also being used to assemble the genomes of symbionts and mitochondria of these insects.

# Biosecurity in northern Australia

*James A. Walker*

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The biosecurity threats to northern Australia are numerous and often complex to manage. Most of us are familiar with the pathways by which insect pests usually arrive in Australia. Huge volumes of sea and air cargo move through the ports, millions of passenger movement occur annually, and numerous fruits, vegetables and plant material are imported. These pathways represent risk for all parts of the country and are managed through a regulatory approach. However, there are pathways into northern Australia which are more unique and cannot be managed so easily. Our proximity to neighbours, unregulated vessel movements, visitors associated with cultural treaties, seasonal monsoon winds and cyclone events all combine to bring exotic insects into the north.

Unlike much of the insect fauna in southern Australia, our northern fauna is often poorly described or its biology unknown. As agricultural enterprises expand and novel crops are trialled growers experience unexpected attention from endemic insects. This becomes a cruel challenge for crop scouts, extension officers, applied researchers and biosecurity scientists. Beyond the challenge of endemics shifting their hosts, there is a daunting array of exotics that turn up and it often requires the expertise of specialist taxonomists to make judgements regarding what is endemic and what has arrived more recently. Most entomologists are connected to these challenges in one way or another and there are valuable contributions to managing the biosecurity threats that we can all make.

# Seeing at the limits: vision and visual navigation in nocturnal insects

*Eric Warrant*

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Despite their tiny eyes and brains, nocturnal insects have remarkable visual abilities. Our recent work – particularly on fast-flying moths and bees and on ball-rolling dung beetles – has shown that nocturnal animals are able to distinguish colours, to detect faint movements, to learn visual landmarks, to orient to the faint pattern of polarised light produced by the moon and to navigate using the stars. These impressive visual abilities are the result of exquisitely adapted eyes and visual systems, the product of millions of years of evolution. Nocturnal animals typically have highly sensitive eye designs and visual neural circuitry that is optimised for extracting reliable information from dim and noisy visual images. In my talk I will elaborate on these adaptations to show how biological sensors - even very small ones – are capable of high performance at the limits of what is physically possible.

## Dung beetle (Coleoptera, Scarabaeidae) abundance and diversity at nature preserve within hyper-arid ecosystem of Arabian Peninsula

*Abdel-Dayem, M. (1), Kondratieff, B. (2), Fadl , H.(1) and Aldhafer, H. (1)*

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Coprophagous beetles (Coleoptera: Scarabaeidae) play an important ecological role in the management of grazing and cycling of nutrients within different ecosystems. Seasonal variation in abundance, richness, and alpha diversity of the dung beetles were investigated in Rawdhat Khorim Nature Preserve in central Saudi Arabia. Adult beetles were captured using UV light traps biweekly from November 2011 to October 2012 (given 24 nocturnal trapping periods). A total of 2,982 dung beetles were captured, representing 22 species in 9 genera belonging to subfamilies of Aphodiinae and Scarabaeinae. The catch was dominated (58%) by *Aphodius pruinosus* Reitter and *A. wollastoni iranicus* Balthasar, with the Aphodiinae constituting 94% of the total beetle richness. Most of dung beetle species were dwellers (20 species). Four activity periods were distinguished during the course of the year. Significantly high abundance and species richness documented during spring and low alpha diversity during winter. Alpha diversity increased with higher average temperatures, while the dung beetle abundance was positively correlated with the normalized difference vegetation index (NDVI). Our findings may enhance the understanding of dung beetle ecology in the rawdhat network within hyper-arid ecosystems of Arabian Peninsula and sustainable management of dung beetles for nutrient reincorporation through the consumption and storage of dung in the soil.

## Screening of sugarcane cultivars to assess the incidence against *Chilo infuscatellus* (Pyralidae, Lepidoptera)

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Research was conducted to screen out the fifteen sugarcane cultivars with an objective to assess the varietal response against the *Chilo infuscatellus.* The experiment was designed in a randomized complete block designed (RCBD) with three replication. It is evident from the results that the US-394 showed maximum pest infestation (21.90%) while NSG-555 and (21.60%) showed significantly different from other varieties BL-4, US-162, US-394, L-116 and CP-77-400. The variety US-718 showed minimum infestation (15.49%) after US-133 and US-676 with (15.59) and (16.46%). The variety CPF-237 showed (17.81%) which significantly different from US-312, US-1491, US-824 and CPF-246 respectively. The Host Plant Susceptible indices (HPSIs) showed that CPF-237 showed maximum HPSIs (13%) and proved susceptible whereas all the other varieties showed equal response each with 11% HPSIs. The variety US-718 showed minimum HPSIs (10%). It concluded that most of the varieties of sugarcane showed equal response towards population of *Chilo infuscatellus* except CPF-237 that showed maximum HPSIs (13%).

## Microbiology and nutritional composition of some edible insects

*Amadi, E.N.*

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An overview of the microbiology and nutritional composition of four (4) insects, *Bunaea alcinoe*, *Rhychophorus phoenicis*, *Gonimbrasia belina* and *Gryllotalpa Africana*, used as food is given. All the edible insects studied so far have a mixed population of bacteria with *Bacillus* and *Staphylococcus* persistently occurring. The Gram-negative population is much more diverse and included members of the genera, *Acinetobacter*, *Enterobacter*, *Klebsiella*, *Proteus*, *Pseudomonas* and *Serratia*. Available data show that edible insects contain protein in the range 22.06 to 55.2%. The larval forms seem to have a high fat content compared to the adult forms. Macro-elements and micro-elements of *Rhychophorus phoenicis* occur at significant amounts. Thus, sodium, calcium, potassium, copper, cadmium and zinc occur at 773.49 ± 1.02mg/100g, 60.81 ± 0.32mg/100g, 26.65 ± 0.24mg/100g, 1.26 ± 0.04mg/100g, 0.039 ±0.022mg/100g and 10.57 ± 0.89mg/100g, respectively. There seem to be a dearth of information on the macro- and micro-elements of the other insects so far studied. Insects with high protein content can form a good protein supplement in areas where meat or fish protein is scarce, unattainable or dear. Further studies are advocated for a better understanding of the nutritional status of edible insects. For sustainability, insect husbandry/farming is advocated.

## Studies on the mopane worm, *Imbrasia belina* an edible caterpillar

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The caterpillar of the Emperor moth, *Imbrasia belina* is processed by degutting, boiling/cooking and drying in the sun before eaten as food in Southern Africa. Botswana is the largest producer of the mopane worms for the open market. The dried product is available as a street food, being sold by vendors, as a canned food. The proper processing and storage of the worms are essential for extending the shelf-life, which can be up to 20 years. Studies show that, *I. belina* contains > 38% protein, 16% fat, Ca 13% carbohydrate and some chitin. The lipids are made up of C16 and C18 saturated fatty-acids and C18:1, and C18:2 unsaturated fatty acids. The caterpillars are a valuable source of nutrition during pregnancy and lactation and for consumption by children. The caterpillar is rich in minerals such as calcium (0.25%) Phosphorus (0.075%) and iron (0.01%). It has been recommended as supplement for high cereal diets and infant foods. Mopane worm is liable to contamination by various agents of bio-deterioration namely micro-organisms, insects and mites. When the caterpillar is feeding on leaves and later during processing, it gets contaminated with fungi from the leaves and soil. The genera isolated from both the intestinal and laboratory stored dried caterpillars were *Alternaria*, *Chaetomium*, *Drechstera*, *Fusarium*, *Mucor*, *Phoma* and *Penicillium* suggesting contamination during the drying and storage stages. Insects, mostly dipteran flies of the families Muscidae (*Musca domestica*) and Calliphoridae (*Calliphora* spp.) settle on the drying caterpillars hence the importance of keeping the environment clean. During storage, beetles such as *Dermestes maculatus*, *Tribolium castaneum*, *Tribolium confusum* and *Lasioderma serricorne* infest the food product as hidden infestations, which may cause bio-deterioration and reduce the shelf-life of the caterpillars. Hazard analysis critical control point (HACCP) principles should be implemented for effective disease and pest management to minimise contamination.

# DNA barcoding identification of mosquitoes using traditional and next-generation sequencing techniques

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Morphological identification of mosquitoes is time-consuming, requires specialist knowledge and is problematic when trying to identify damaged specimens or distinguish between similar species. DNA barcoding is a species identification technique that targets a short DNA sequence with much less variance within species than between species. The approach has the potential to fundamentally change insect surveillance programs. To evaluate the application of DNA barcoding in mosquito identification, 113 morphologically identified mosquitoes representing 12 genera and 26 species were barcoded. Two DNA regions were targeted, mitochondrial Cytochrome Oxidase I (COI) and nuclear Internal Transcribed Spacer 2 (ITS2). COI was sequenced using traditional Sanger methods, while ITS2 was sequenced via amplicon-based next-generation sequencing due to the presence of multiple alleles and repetitive regions in the ITS2 region. COI and ITS2 sequences produced similar phylogenetic trees, both containing the same barcode clusters. The majority of species formed distinct groups, however a number of species complexes were identified. ITS2 had higher divergence values than COI, which reflects the large number of alignment gaps formed due to microsatellites present in the ITS2 sequences. Barcode data revealed an additional three species that were initially misidentified morphologically, bringing the total species count to 29. This incongruency highlights the accuracy of DNA barcoding and its usefulness in enhancing species identification in surveillance programs. The DNA barcodes produced by this study have been uploaded to the ‘Mosquitoes of Australia – Victoria’ project on the Barcode of Life Database (BOLD), which will serve as a resource for the Victorian Arbovirus Disease Control Program and other mosquito surveillance programs.

# Towards a compelling phylogeny of cyclorrhaphan flies (Diptera) using whole body adult transcriptomes

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Most of the genetic models and agricultural or veterinary pests in the order Diptera are members of Cyclorrhapha. These flies emerge from their puparia via a circular seam and are able to pupate in a wide array of substrates. Within this lineage, evolutionary relationships between the acalyptrate Schizophora have been difficult to reconstruct. The pattern of cladogenesis remains unclear for taxa such as *Drosophila* spp., tephritid fruit flies, and calyptrate flies (house flies, bush flies, blow flies, etc.) despite being subjected to intense research. Previous studies that include robust sampling of genes and taxa yield unresolved or contradictory phylogenetic hypotheses. This is likely because this period in the evolutionary history of flies was characterized by an incredibly fast radiation. This study uses a new approach with unprecedented gene coverage from transcriptome data to provide a framework into an evidence-based, robustly supported phylogeny of the Cyclorrhapha. A dataset including more than three thousand genes and an alignment of over one million amino acid positions was assembled to address this question. cDNA libraries of adult flies were sequenced with Illumina technology. After we assembled the data in to transcriptomes with Trinity, orthology was assessed using profile hidden markov models in the program Orthograph. Maximum likelihood phylogenetic analyses were performed in ExaML and RAxML Although support is low for the relationships between a few lineages, this effort offers insight into several previously intractable problems in the evolution of higher flies. These include the first robust evidence for the monophyly of the heterogeneous family Heleomyzidae, new sister group hypotheses for Fergusoninidae, an Australasian family with unique symbiotic phytophagous nematodes, and for Diopsidae, the stalk-eyed flies, models of sexual selection. We also find moderately strong support for a close relationship between calyptrate flies and *Drosophila,* with tephritid fruit flies distantly related.

# Establishing a population genetics toolbox and regional spatial database to facilitate identifying the incursion origin of the dengue mosquito *Aedes aeqypti* and the Asian tiger *Ae. albopictus*

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Incursions of exotic mosquitoes that can transmit dengue and chikungunya into international ports of Australia are escalating. Identifying the incursion origins of the highly invasive exotic mosquitoes *Aedes aegypti* and *Ae. albopictus* would be vital in understanding the transport nodes and networks driving their arrival – a crucial contribution to reducing biosecurity risk. The last two years has seen the regular appearance of *Ae. aegypti* in Perth, Adelaide, Melbourne and Brisbane international airports and *Ae. albopictus* at the Perth international airport, highlights this escalating problem. To assist federal and state biosecurity bodies establish the incursion ports of origin we are developing a microsatellite-based population genetics toolbox and regional spatial database that now permits genetic analysis of mosquito incursions for both species. This information will better enable quarantine authorities to secure loopholes in transport nodes and networks. We will also attempt to run this service for quarantine authorities but intend to make this technology available to state and federal authorities as well as regional stakeholders.

# A summary of interceptions and additions to the New Zealand fauna, with reference to Australian origins

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A review is given of data from recent years regarding intercepted and established exotic organisms in New Zealand, with specific reference to instances of Australian origin. While detections of significant exotic pests are responded to and well publicised, exotic organisms of lesser significance also find their way into New Zealand each year. Australia is the source of the majority of Post Border interceptions made in New Zealand when country of origin is known, and also the most common country of origin for new to New Zealand organisms.

# The role of nutrition in determining individual and group patterns of behaviour

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One of the many goals of invasion biology is the identification of factors that determine whether a species will establish successfully in a new environment and that predict whether a newly introduced species has the potential to become highly invasive. Invasive ants are ideal subjects to investigate the role of behavior underpinning success of biological invasions. Of these, many have become highly destructive invaders. Rapid colony growth and dispersal are traits shared by many successful invasive ants, and these abilities are believed to be largely conditioned by nutrition. An increase in the quantity and quality of food resources available to a colony can increase worker size, alter body size distributions, increase colony size, and influence behavior. More generally, access to carbohydrate resources is thought to be a key factor in the ecological success of many ants by providing the fuel needed to maintain a larger number of highly active workers. The main goal of this study is to determine how key behavioral mechanisms believed to contribute to invasion success are affected by nutrition. The objectives were to manipulate the macronutrient content of diets provided to colonies of the world's three most widespread highly invasive ant species *Solenopsis geminata*, *Pheidole megacephala*, and *Paratrechina longicornis*, to test how protein and carbohydrate availability influence both individual and colony-level behavioral attributes including aggression, foraging and recruitment rates, and defense. The outcomes from this study will provide the most comprehensive assessment of how ants regulate their behaviors according to aid invasion success.

# Australian millipede diversity: an update

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Almost twenty years ago an assessment of the higher level diversity of Australian millipedes was made based on available literature and museum material. At that stage 20 families of the existing 140+ worldwide were documented for Australia (three introduced), within nine of the 15 orders recognised. Many major gaps in our knowledge were identified, with great disparity noted in the taxonomic interest dedicated to individual orders and families. However, interest in some components of the Australian fauna was beginning to increase, particularly from overseas researchers. Taxonomic studies by Australian workers were also beginning in earnest. This new interest from both sectors has continued in the intervening period, greatly increasing the scope of taxonomic cover of indigenous fauna. The emphasis on diplopod research in Australia shifted from the biology and ecology of one introduced species (the Black Portuguese Millipede) to documentation of regional and taxon specific diversity, particularly in Tasmania. As more international workers became involved, important collaborations have led to an appreciation of the actual diversity of our fauna. Several orders, especially Polyxenida, Polyzoniida and Polydesmida are now much better known. Our largest and most diverse family, Paradoxosomatidae, is finally receiving much needed attention. The net result is that Siphonophorida is the only order for which details remain minimal. Another surprising result of these efforts has been documentation of millipedes in several extreme environments including subterranean systems, moist refugia in central Australia and the edges of the arid zone. However, millipedes of rainforest ecosystems, clearly diverse, remain largely unknown. Mesibov's website compendium of our current taxonomic knowledge, Millipedes of Australia, is a unique and enormously useful resource database. The current work summaries improvements in taxonomic knowledge at the family level and presents an illustrated key to the Australian families.

# Systematics of the African cassava whitefly: getting it 'right' feeds 700 million people

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Species delimitation directly impacts on global biosecurity as accurate identification of species is a critical element in the decision making process of both State and National governments. To illustrate this we use the *Bemisia tabaci* species complex. This group of whiteflies poses a considerable threat to a broad range of agriculture and horticulture food and fiber crops and is named in International Union for the Conservation of Nature and Natural Resources (IUCN) list of 'A hundred of the World's Worst Invasive Alien Species'. Australia, Africa, China, USA and the EU regard them as a regulated species because of the threats they pose to their agriculture.

Here I will present an approach we call 'tip to root' for species delimitation that involves the synthesis of several existing approaches. The analytical approaches included are the commonly used Kimura two-parameter (K2P) distance, as well as four more stringent measures of taxon distinctiveness:

1. Rosenberg's reciprocal monophyly, P(AB)
2. Rodrigo's P(randomly distinct)
3. genealogical sorting index, gsi, and
4. General mixed Yule- coalescent (GMYC).

A comparative analysis of the methods shows that the K2P distance method does not capture the same level of species distinctiveness as the other measures. In particular, in *B. tabaci* there are more distinct groups than previously identified using K2P distances. A consensus of the results from P(AB), P(randomly distinct) and gsi offers greater confidence as to where genetic limits might be drawn. For *B. tabaci*, the results clearly indicate that there is a need for more gene sampling to substantiate the new cohort of species indicated for *B. tabaci*.

I will also present our future *Bemisia tabaci* species delimitation research plan, which is a major aim in the recently funded Bill and Melinda Gates Foundation Grant entitled: "African cassava whitefly: outbreak causes and sustainable solutions" awarded to NRI with UWA, CSIRO and OSU as partners.

# Green mirids: Multiple host-use patterns and population connectivity in native and agricultural habitats

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To understand why insects invade agricultural systems, we need to appreciate the ecology of the species in both its native and agricultural habitats. Green mirids, *Creontiades dilutus* (Stål) (Hemiptera: Miridae), are insects endemic to Australia that feed on a broad variety of native plants, crops, and invasive weeds. In eastern Australia, green mirids are now the primary pests of cotton crops. The ultimate source of green mirids in eastern cotton-growing regions is likely to be from host plants in the arid continental interior, but the factors that lead to agricultural invasions are poorly known.

Green mirid host associations were quantified across a vast geographic range to determine where mirid populations build-up, and thus piece together their spatio-temporal dynamics. Field surveys were conducted in the cotton growing regions of Queensland and New South Wales, as well as portions of their native habitat within western Queensland and the Simpson Desert in South Australia. Molecular analyses of individuals collected during these surveys have assessed the connectivity of green mirid populations in eastern and central Australia.

By understanding the connectivity between mirid populations, crop managers can better prepare for potential invasions when mirid populations are predicted to be building up at distant locations. These findings will be discussed in the context of recent weather patterns and crop management techniques. This study also provides insights into the ecological mechanisms associated with the host plant associations of generalist insect herbivores across diverse habitats.

# Use patterns and damage thresholds of the *Amblypelta lutescens lutescens* (Banana-spotting bug) pheromone trap

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*Amblypelta lutescens lutescens* (banana-spotting bug) is a Coreid bug native to Australia with a wide host range of both native and introduced plants. It is a major pest of tropical and sub-tropical commercial crops. In previous work, a pheromone lure and sticky panel trap for *A. lutescens lutescens* was developed. This aggregation pheromone attracts male and female adults and nymphs; however the attractancy range of the trap was unknown.

In recent field trials, use patterns of the pheromone trap and damage assessments were assessed to refine optimum trap densities and economic injury thresholds. Trials were conducted in commercial orchards of avocado and custard apple. Trap densities of 10 and 20 traps per hectare were compared. At the same time, damage caused by *A. lutescens lutescens* was recorded.

Preliminary analysis of the data indicates that the optimal trap density is between 10 and 20 traps/ha. For orchard management purposes 10 traps/ha would provide sufficient information for monitoring. Insect damage was correlated with trees containing a pheromone trap and proximity to the trap tree. The correlation between trap captures and damage allows the determination of a reliable economic injury threshold.

# The fitness cost of bifenthrin resistance of the redlegged earth mite, *Halotydeus destructor*

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The redlegged earth mite, *Halotydeus destructor* is one of the most important pest affecting a variety of pastures and crops in southern Australia. *Halotydeus destructor* is reputed to commonly have three generations per year in the field, active from April or May to October or November. Then, it survives through the harsh summer as diapause eggs. Pesticides are the most effective method to control *Halotydeus destructor* at this moment and probably in the foreseeable future. However, the continued application of pesticides increases the selection pressure on this species to develop pesticide resistance. The bifenthrin-resistance populations which has been discovered in Western Australia have an amino acid substitution L1024F in the sodium channel, the target site of pyrehroid pesticide. As a result, the fitness cost of this resistant mutation is of concern for pesticides rotation. In this study, both resistant and susceptible strains of RLEM were collected from Boyup Brook, Western Australia and sent to Melbourne in 2014. These mites were mixed by different ratios and were introduced into tubs with pasture plants in the absence of pesticides. After mite introduction, the mite numbers of every tub were counted once per week in order to compare the reproduction of resistant and susceptible mites. The resistant treatment had less offspring number in the next generation. Besides, genotyping data of the offspring showed that there was a fast decline in the resistant homozygote.

# How isolated is the fig pollination system on Lord Howe Island?

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Lord Howe Island (LHI) is situated some 600 km from the Australian mainland. It is a World Heritage area of great conservation significance and home to many endemic plant and animal species. A keystone species in the forests is the banyan fig, *Ficus macrophylla*. This is one form (f. columnaris) of the Moreton Bay fig, with the other form (f. macrophylla) restricted to the mainland. On the mainland *F. macrophylla* is pollinated by the agaonid wasp *Pleistodontes froggatti* and also exploited by several parasitic wasp species. In addition, *F. macrophylla* suffers from periodic outbreaks of the sap-sucking psylloid *Mycopsylla fici*, which forms large sticky lerps on the leaves. Our project explores how this system has diverged genetically and ecologically between LHI and the mainland.

We find that LHI figs are pollinated by the same wasp species, and exploited by the same non-pollinating wasp species, as on the mainland. The psylloid and its parasitoids are also the same species on LHI and mainland. Our preliminary genetic analyses suggest that there is no LHI-mainland gene flow via fig seeds, but does not rule out pollinator (and pollen) gene flow. In contrast, the psylloids of LHI are a genetically distinct offshoot of the mainland insects. Ongoing work is focused on further testing of pollinator and parasitoid gene flow.
Ecologically, the most striking difference between island and mainland comes from our phenology surveys. Most island trees have fruited rarely (if at all) during our study and even those that do fruit, produce small crops. Since pollinator offspring must develop inside fig fruits, the island pollinator population may be at risk of local extinction from extreme events, such as when droughts or outbreaks of psylloids reduce or stop fruit production.

# Australia’s battle with Fire Ants – we can’t afford to lose

*Corcoran, S.*

National Red Imported Fire Ant Eradication Program

The National Red Imported Fire Ant Program has been battling with Fire Ants (Solenopsis invicta) since they were first detected in Queensland in 2001. This presentation will discuss the current situation, the innovations used in the fight to eradicate this pest and what the future may hold.

# Recent insights into the ecology of *Cryptolestes ferrugineus* (Stephens): a new threat to Australia's grain industry

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The rusty grain beetle, *Cryptolestes ferrugineus* (Stephens), is one of several *Cryptolestes* species of the family Laemophloeidae that can infest stored grain in Australia. Until recently, *C. ferrugineus* was considered a minor pest but this changed when populations were discovered in 2007 with a very strong resistance to phosphine ($PH_3$). This fumigant is used widely in Australia in order to meet market demands for insect- and residue-free grain. A program of research has generated new ecological knowledge which is providing insights into the ecology of these pests with implications for understanding infestation threat and the movement of resistance genes on local and regional scales. Research questions include (1) is this pest limited to the storage environment, (2) how far do pests disperse on local and national scales, and (3) how quickly do pests infest stored grain? Field studies have demonstrated that *C. ferrugineus* flight occurs both in the immediate storage environment and further way. Seasonality was evident with periods during the colder months of the year when *C. ferrugineus* flight was reduced or did not occur. *Cryptolestes ferrugineus* readily infested small experimental wheat bulks located 2 km away from the nearest farm stored grain. Samples of beetles were collected from all grain growing regions of Australia, and population genetics was used to estimate the extent of gene flow within and between regions. There is evidence of gene flow on large geographic scales but gene flow is restricted between South Australia and Western Australia. These kinds of results will be integrated into strategies for the management of these pests.

# Effects of local environmental conditions on the spatial and temporal structure of fig-wasp communities

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Figs are keystone species across the tropics and subtropics, and provide a vital food source for many species of birds and mammals. The relationship between figs and associated species of pollinating wasps is a classic and well-studied mutualism. The figs also host diverse communities of galling and parasitoid wasps from four functional groups, which have the potential to disrupt the stability of the mutalism. We predict that variation in local climate may drive patterns of distribution and abundance of these wasp species. We aimed to investigate the impact of local environmental variation on the composition and structure of wasp communities associated with Port Jackson figs (*Ficus rubiginosa*) across a large latitudinal and climatic gradient. We collected >6000 ripe fruits over 18 months from fig trees at coastal and inland sites with contrasting rainfall and temperatures around Sydney and in north Queensland, and recorded the diversity and abundance of pollinating and non-pollinating wasps that emerged. We found key differences in the relative abundances of the different wasp functional groups, both at a local scale and between tropical and temperate sites. In addition, we found marked temporal variation in rates of wasp emergence and community assemblages throughout the year. We also carried out controlled experiments to test how climatic conditions experienced at the Sydney sites impact on the longevity of the pollinating wasp, *Pleistodontes imperialis*. We found that wasp longevity decreases strongly with increasing temperature and decreasing humidity. Furthermore, extreme temperatures impacted on wasp emergence, which sharply declined at temperatures above 42 °C. Such temperature extremes are increasing in frequency in the Sydney region, which may have profound effects on the persistence of pollinating fig wasps. Consequently, predicted climate change scenarios may play an important role in shaping fig-wasp communities, with the potential to de-stabilise this mutualistic interaction.

# Management of insecticide resistance: using leading-edge technologies in on-farm management

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There are a number of challenges in pest aphid management, and while insecticides are the most effect and widely used control method, emerging resistance issues are forcing a reevaluation of current approaches. The green peach aphid (*Myzus persicae,* GPA) has developed resistance to more insecticides than any other insect species. This polyphagous pest attacks a range of horticultural and grains crops, and is a vector for over 100 plant viruses. In Australia, over recent years, there has been increasing occurrence of resistant GPA populations across all states. Communication between researchers and managers is fundamental as chemical control failures can lead to local economic losses (crop failure, unnecessary chemical application) and wider environmental issues. Using state of the art genetic tests, we found many GPA across southern Australia have a high level of resistance to synthetic pyrethroids and carbamates; the use of products from these chemical groups will not provide control against these populations. Genetic testing has also shown widespread (moderate) resistance to organophosphates. Because of these rapid and highly accurate tests, we are able to communicate resistance results, along with control recommendations, to farm managers in less than 7 days. This allows on-farm GPA management decisions to be based on the best available science, demonstrating the value of maintaining open and constructive communication between researchers, industry and managers

# Ecology and biology of *Imbrasia belina* (Westwood) in Southern Africa: with special reference to Botswana

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The African continent hosts a great diversity of edible insects. There is variation found on how these edible insects are harvested, processed and utilized as human and animal feed. Consumption of edible insects in Africa may depend on food preferences and socio-economic bracket, which is reflected in different communities. To ensure the sustainability of these edible insects resources, there is the need to understand their ecology and biology so as to put in place appropriate conservation and management strategies. Thus the ecology and biology of *Imbrasia belina* were studied in Botswana. *Imbrasia belina* is a moth belonging to the family Saturniidae, and it produces edible caterpillars commonly called mopane worms. The results of the study are presented in this paper.

# Population analysis of *Halotydeus destructor* (the red legged earth mite) in crops and pastures

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The redlegged earth-mite, *Halotydeus destructor* occurs in broadacre production landscapes across southern Australia (Ridsdill-Smith, 1997). *H.destructor* is a major establishment pest of crops and pastures. Due to the damage this species can cause, pesticide sprays are often applied without an understanding of the pest density or the risk of damage being caused. The use of insecticides reduces the numbers of natural enemies in fields, potentially leading to damage from other pests and has also led to insecticide resistance problems being discovered in *H.destructor* (Umina et al., 2012).

Like most major agricultural pest species, *H.destructor* is highly opportunistic with the ability to survive in a field during adverse conditions and then rapidly increase in numbers when presented with optimal conditions (Ridsdill-Smith and Annells, 1997). The population density therefore fluctuates greatly depending on important determinants of survival and reproduction.

The factors determining population expansion have been well studied. These factors include food quality (Annells and Ridsdill-Smith, 1994; Maclennan et al., 1998; Umina and Hoffmann, 2004), conditions suitable for breeding, oviposition and egg hatch (Solomon, 1937; Wallace, 1970) and control practices (Gower et al., 2008; Ridsdill-Smith et al., 2005; Ridsdill-Smith et al., 2008).

The life cycle and population dynamics of this species have also been well studied in the laboratory (eg (Ridsdill-Smith and Gaull, 1995; Solomon, 1937)) and in the field (Grimm et al., 1994; Ridsdill-Smith and Annells, 1997). However there is still a lack of understanding about the way these factors determine the density present in the autumn generation, particularly within different field environments.

This presentation will present the results from an analysis of mite density in 112 broadacre fields sampled in different areas of Victoria, following mite emergence in autumn 2014 and 2015. This presentation will then document the applied use of this data in designing a field severity index, which is a tool for farmers to determine the risk of damage being caused to their crops in autumn, by combining pest density with crop susceptibility.

# Investigating diversity in the *Yoyetta* genus of Australian cicadas

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Cicadettini is by far the most diverse of the Australian cicada tribes, comprising the majority of smaller, thin-bodied species (Moulds, 2012). The genus *Yoyetta* Moulds was recently erected to accommodate nine Australian species, previously allocated to the genus *Cicadetta* Amyot. However, this genus of “tickers, ambertails and firetails” (http://dr-pop.net/yoyetta.htm), found predominantly in eastern Australia, has been revealed as highly diverse and likely to comprise more than 50 cicada species. Dissection and description of the species complexity has been approached with a combination of morphotaxonomy, particularly timbals and genitalia, analysis of museum specimens and collecting and recording songs from individuals over the past 30 years. This ongoing investigation has also resolved some outstanding taxonomic issues, involving synonmy and clarification of previously described species[1].

1. Emery, N.J., Emery, D.L., Popple, L.W. (2105). A redescription of *Yoyetta landsboroughi* (Distant) and *Y. tristrigata* (Goding and Froggatt) (Hemiptera: Cicadidae) and description of four new related species. *Zootaxa* 3948: 301–341.

# The phylogeny of the fungal spore-feeding thrips subfamily Idolothripinae (Thysanoptera; Phlaeothripidae)

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The subfamily Idolothripinae (spore-feeding thrips: order Thysanoptera; suborder Tubulifera; family Phlaeothripidae) is a group of over 700 thrips species closely associated with dead plant materials pantropic and subtropics wide. Members of this group are morphologically highly diverse and all sharing only one known synapomorphy of wide laciniae adapted to imbibe whole spores. Subsocial and parasocial behaviour were reported, while many are easily the largest thrips in size. A traditional tribal classification of the 80 recognized genera consists of two tribes and nine subtribes. This system is based on eight morphological characters that partially support relationship hypotheses for four of the purported more-advanced subtribes; while the rest at the basal position are open to questions. Furthermore, this subfamily is ridden with wide range of taxonomic problems from synonyms at species level to nebulous genus definitions subfamily-wide. This talk focuses on recent insights into the Subfamily internal lineages, based on a series of consecutive studies involving taxonomic review for two exemplar genera, morphological phylogenetics analysed with Maximum Parsimony, and multigene molecular phylogenetics analysed with Maximum Likelihood and Bayesian Inference. Current study indicated morphological attributes are highly homoplasious at the subfamily level, one of the main factors contributing to long lasting taxonomic complication.  The phylogenetic framework provided here is not nearly robust, but important as a foundation to promote questions and encourage future critical testing that will benefit revision of this subfamily and hopefully also facilitate the study of evolution history of the nearly 3600 species of Phlaeothripidae in future.

# Borne on the wind; understanding the significance of natural pathways of plant pests into Australia and New Zealand

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This project aimed to identify the pest and pathogen biosecurity risks posed to Australia and New Zealand by long distance natural dispersal pathways. Human-assisted transport of biosecurity threats, quite rightly receives most of the attention, but there has been limited research on the natural dispersal of species across national borders. Long distance wind-borne plant pests and pathogens have been implicated in a number of incursions worldwide.

A literature review and survey of biosecurity personnel was undertaken to assess and quantify the actual and potential biosecurity risk of naturally dispersed plant pests and pathogens, to determine whether biosecurity threats from natural dispersal were being underestimated and to assess whether the perceived risk is commensurate with the actual risk.

Key findings are as follows. Long distance natural dispersal is a real and continual risk which is somewhat underestimated by biosecurity personnel and both normal and extreme weather events (cyclones) were found to be feasible dispersal mechanisms. The important pathways are from "the North' (PNG, Indonesia) into Australia, from Africa into Australia from New Zealand into Australia and from Australia to New Zealand. Surveillance data is biased towards insects, especially Lepidoptera and risks for other taxa are likely to be underestimated. There is no definitive data, sampling protocols or trap types identified as most suitable for capturing key pest and pathogen incursion threats.

The project identified knowledge gaps indicating the need for better quantification of risk for high stake and high impact pathways, and a review of surveillance strategies for high risk pests and pathogens. The Plant Biosecurity CRC is now supporting a new 3-year project to investigate in more detail the risks from natural dispersal and improve surveillance systems and biosecurity preparedness for wind dispersed plant pests and pathogens.

# The leafhopper genus *Amrasca* Ghauri (Cicadellidae: Typhlocybinae: Empoascini) with particular emphasis on the Indian cotton leafhopper

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The genus *Amrasca* Ghauri (Hemiptera: Cicadellidae: Typhlocybinae: Empoascini) includes 11 described species of microleafhoppers (in two subgenera) distributed in the Oriental and Australasian regions. The genus is represented in Australia by *A. terraereginae* (Paoli), the Australian cotton leafhopper in Queensland and northern New South Wales, and an unidentified taxon in Western Australia and Darwin, the result of a 2001 incursion, probably from East Timor. Study of the Oriental fauna has been focussed mainly on Sri Lanka and Vietnam although a number of species are known to occur in mainland China. The genus is of biosecurity interest with the Indian cotton leafhopper a recorded pest of cotton, okra, eggplant, sunflower, radish, tomato, Rhodes grass, sorghum, cowpea and maize in India and surrounding areas. The correct name for the Indian cotton leafhopper, however, is uncertain following Dworakowska's (1970) synonymy of *Amrasca devastans* (Distant) from India, *Empoasca bipuncata* Schumacher (= *E. schumacheri* Metcalf) from Taiwan, *Chlorita bimaculata* Matsumura from Japan and *Empoasca quadrinotatissima* Dlabola from Afghanistan with *A. biguttula biguttula* (Ishida) from Taiwan. An examination of diagnostic genitalia features has begun, focussing initially on the species occurring in Taiwan in an attempt to clarify the identity of *A. biguttula* and hence establish the status of *A. devastans.*

# Recent diagnostics response to the detection and eradication of Queensland fruit fly *Bactrocera tryoni* in Auckland, New Zealand

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The New Zealand Ministry for Primary Industries runs a national surveillance programme for exotic fruit fly (Diptera: Tephritidae). In February – March 2015 Queensland fruit fly males were trapped in an inner city suburb in Auckland. Detection of larvae in fruit nearby provided evidence of a small establishing population and an eradication programme was initiated. This paper discusses the role of the Ministry for Primary Industries Entomology team in this response.

# How effective are Greenfleet $CO_2$ offset forests at supporting moth and beetle diversity?

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The planting of native trees can offset anthropogenic emissions of $CO_2$ and conserve insect diversity. The age at which $CO_2$ offset forests begin to resemble remnant forests with respect to insect species composition is of interest to Greenfleet and their supporters. We examined the effect of planting age of Greenfleet forests on moth (macro-Lepidoptera) and beetle diversity at Mount Worth State Park in south-eastern Victoria relative to insect diversity in nearby remnant forests. Paddocks were sampled to represent 'age zero' sites along with successively older plantings from four years up to 23 years. A light-trap was erected at each of the study sites (paddocks, plantings and remnants) in December 2014, January 2015 and February 2015. We found an increase in moth diversity with planting age in the month of December only, whilst beetle diversity was not influenced by planting age. The species composition of moths in older plantings (six and 23 years) closely resembled remnant forest while the composition of younger plantings was more similar to paddocks. We caught a number of undescribed species of geometrid (genera including *Austroterpna, Chlorocoma, Furcatrox* and *Monoctenia*) and obtained new locality records for *Chrysolarentia euphileta* (Lepidoptera: Geometridae). The composition of beetle communities in Greenfleet and remnant forests were significantly different to paddocks. There was no separation in beetle composition across plantings of different age. Our results indicate that insect diversity is supported by Greenfleet $CO_2$ offset plantings, but it is likely that proximity to remnant forest is an important factor influencing the rate at which they are colonised by moths and beetles. Our results have important implications for Greenfleet and we intend to continue our partnership to acquire stronger evidence for planting age-insect diversity relationships before they offer biodiversity offset credits to their supporters.

# Medical maggots: misunderstood superheroes?

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Diabetic ulcers and pressure sores are a costly chronic infection currently treated with surgical debridement and a course of antibiotics. The increasing occurrence of antibiotic resistant strains of bacteria however, are causing this treatment to require more invasive measures with surgery removing significant amounts of living tissue, and antibiotic treatment to be less effective, resulting in continued and possibly spread infection. The final resort for treatment is often amputation of the infected limb. Maggots have been re-introduced into a hospital setting for their ability to debride a wound, and encourage self-healing through stimulation of new growth cells. In order to be used on a patient, these medical grade maggots are being put through a sterilisation process. Given a maggot's natural environment, in which they are exposed to a number of harmful bacteria, the sterilisation process may be reducing their effectiveness in treatment. By understanding the bacteria naturally present within a maggot, and how the maggot has obtained this, there is the potential to not only improve current treatment and have a more effective, cheaper alternative to surgery; but the potential to manipulate their internal microbes could lead to the production of infection specific medical maggots.

# Development of a strategy to control *Myzus persicae* using *RNAi* technology

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The economic loss in agriculture due to aphids is estimated to be $723 million/year in Australia. The reason for this is two-fold; aphid feeding directly harms plants and aphids transmit plant viruses. Currently chemical insecticides are the main aphid control strategy, however these insecticides are environment pollutants and continually need to be replaced as aphids evolve resistance to them. As part of an Indo-Australian project that is aiming to improve brassica crops (CARiB; Caterpillar and Aphid Resistance in Brassica), we set out to develop transgenes that control aphids using RNA interference (*RNAi*) technology. This follows numerous publications showing that aphids fed upon dsRNA in artificial diet, or fed on transgenic plants expressing dsRNA, or microinjected with dsRNA, not only have reduced target gene expression but have reduced viability and fecundity.

The identification of *RNAi* targets is an important step in this approach and we have been exploring four design considerations to help us chose anti-aphid RNAi transgenes. The target genes should: 1) be expressed in tissues likely to get a high dose of dietary RNAi 2) be stably expressed and required regardless of environmental variables such as host plant exposure 3) maximize the utility of RNAi to target pest species but not other species and 4) minimize the chance of resistance development.

Here we report on transcriptomic analyses of *Myzus persicae* designed to identify midgut genes to be targeted by RNAi. We illustrate the use of a purpose-built bioinformatics tool to choose species-specific dsRNA’s. We also report on our experiments measuring the effectiveness of *dsRNA* delivered to *M. persicae* through artificial diets and through transgenic *Arabidopsis thaliana* plants, and compare them to those published in the literature.

# Rewards and risks in timing of herbicide application date and dose in maximising *Sirex noctilio* (Siricidae) biocontrol

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*Sirex noctilio* Fabricius (Hymenoptera: Siricidae) is an invasive wood wasp that causes significant damage to pine trees (*Pinus radiata*) globally. Trees treated with a herbicide so as to make them attractive to ovipositing *S. noctilio,* are the means by which the nematode biocontrol agent, *Beddingia* (=*Deladenus*) *siricidicola* (Sphaerulariidae), is introduced into the pest population. These trap trees can also be attacked by the bark beetle, *Ips grandicollis* Eichhoff (Coleoptera: Scolytinae) which disrupts *S. noctilio* biocontrol. Two experiments were conducted concurrently in two major pine growing regions of Australia, Tumut (Southern New South Wales) and Adelaide Hills (South Australia). Trees that were first attacked by *I. grandicollis* were not subsequently attacked by *S. noctilio* in both regions. Attack of trees by the bark beetle negatively influenced overall *S. noctilio* nematode parasitism. This talk presents important findings for forest managers on the effect of herbicide dose and timing of application on subsequent attraction of *S. noctilio* to trap trees and colonisation by *I. grandicollis*.

# The effect of temperature on host plant chemistry and how it mediates plant-insect interactions

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Plants have developed a vast array of secondary metabolites, many of which are used in defence against insect herbivory. Increased temperatures, however, can directly affect the concentrations of these compounds. Such changes have the potential to disrupt relationships between plants, herbivores and their natural enemies through a number of direct and indirect pathways. A number of studies have shown that galling insects have the unique ability to actively manipulate plant secondary metabolites for their own benefit. This ability, however, makes them potentially more susceptible to changes in host plant chemistry. We reared galling flies (Cecidomyiidae) and their parasitoids (Hymenoptera) from three plant species sampled along an elevational gradient in subtropical rainforest. In contrast to previous studies, our results show no difference in leaf chemistry between galled and non-galled plants. We did, however, find significant differences in plant chemistry based on site temperature. We also found decreased galling density and increased general herbivory (leaf damage) with increasing temperature. Higher rates of parasitism were also observed with increasing temperature, driven by increased parasitoid effectiveness (positive richness-parasitism relationship). A growing number of studies looking at host plant chemistry and tritrophic interactions have shown that changes in plant chemistry can have indirect effects on higher trophic levels. To test this we experimentally warmed host plants using plastic enclosures along the elevational gradient. We found that increased temperatures have significant bottom-up effects on food chains through changes in host plant chemistry. In accordance with our observational data, warmed plants had reduced galling density, increased general herbivory, and altered chemistry. However, in contrast to our observational data, parasitism rates were lower on warmed plants. This suggests that parasitoids may be particularly vulnerable to increased temperatures and also highlights the importance of field-based experimental manipulations when investigating tritrophic interactions.

# Arrival and spread of vegetable leaf miner (Agromyzidae: *Liriomyza sativae*) in Australia

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Vegetable leaf miner (Agromyzidae: *Liriomyza sativae*) is a polyphagous pest of numerous vegetable and flower crops with potential in Australia to become economically damaging to a wide range of important agricultural and ornamental crops. It has been recorded from nine plant families, although preferred hosts are in the Cucurbitaceae (pumpkin), Fabaceae (bean) and Solanaceae (tomato) families. *L. sativae* is known to transmit a number of plant viruses and causes damage from direct adult-puncturing of leaf tissue but more so from larval-mining. *L. sativae* was first detected in the Torres Strait on Warraber (also known as Sue Island, in the Central Islands group) on 12 August 2008 by the Northern Australia Quarantine Strategy (NAQS) program (Department of Agriculture). *L. sativae* had not previously been detected in Australia. In 2010 *L. sativae* was officially detected by NAQS on three more islands in the Torres Strait and by June 2015, it had been recorded as present on a total of eleven islands including Prince of Wales Island and Thursday Island. On 1 May 2015, routine surveillance detected three vegetable leaf miner larvae in the Cape York Peninsula community of Seisia. They were found in a backyard garden on 'siratro' a widespread leguminous weed, originally introduced as a pasture plant. We outline the movement of this pest through the Torres Strait and hypothesise mechanisms for its spread and establishment.

# The role of bioinsecticides from spider venoms in biosecurity

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Tropical ecosystems are particularly susceptible to arthropod pests, in large part due to moderate environmental conditions (temperature and humidity particularly). In Australia global, cosmopolitan pests of concern include urban pests, agricultural pests, and arbovectors. We have isolated a suite of toxins from the venom of native Australian tarantulas, and screened them for activity against economically important insect pests – including several arthropods of biosecurity concern in Northern Australia. Several toxins with potent activity have been discovered, and one toxin has been comprehensively characterised. The activity and stability of these orally active insecticidal peptides will be discussed.

# *Melophorus* ants (Hymenoptera: Formicidae): really cool thermophiles

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A revision of the *Melophorus* fauna (Hymenoptera: Formicidae) of Australia using both morphological and molecular techniques reveals approximately 92 species in two major clades; 74 of these species being new. One taxon has been removed from genus *Melophorus*. A key to the workers of these 92 species has been devised, based on morphological features. Molecular sequencing (PCR) using one fast evolving mitochondrial gene (COI) and four slow evolving nuclear genes (AA, H3, LR and Wg) provides broad support for the species identifications based on morphology. Two species, *M. turneri* and *M. sulla*, which are part of the *M. fieldi* complex, we are unable to resolve due to their polyphyletic positioning. More confounding is that nest mates may be found in different parts of the phylogenetic tree. The molecular data suggests incomplete lineage assortment within or, possibly, continuing genetic exchange between some members of the highly derived group. These species, coincidentally, are very difficult to categorize using morphological means. We are currently trialing a sixth nuclear gene, RPF, which is evolving slightly faster than the other four in order to clarify the status of doubtful taxa and the positioning of sister groups within *Melophorus*.

# Entomovectoring of *Trichoderma* spores has no noticeable influence on hive health

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Entomovectoring involves the use of insects to bring biological control agents to crops, in lieu of spraying. This can improve the quality of the control and reduce the number of sprays needed, with benefits for both growers and the environment. In addition, the method can increase the demand for managed hives. This is of particular importance in Australia, where growers of pollination dependent crops rely for about 70% of their pollination needs on feral honeybees. Current enhancement of the beekeeping industry will reduce the pollination deficit that is predicted to occur when, due to an incursion of the Varroa mite, the feral honeybees will be decimated. However, for entomovectoring to be adopted by the beekeeping industry, it is essential that there are no major negative impacts of entomovectoring on hive health. We are currently introducing entomovectoring in the cherry and strawberry industries. The bees transport spores of *Trichoderma*-based biological control product to control cherry brown rot and strawberry grey mould, diseases that are caused by *Botrytis cinerea*. Here we investigated how the presence of the dispensers in front of the hive and the daily dispensing of the spore mix affected the number of hive bees, closed brood and foraging activity. We found no effects on activity, brood numbers or hive bees. We also showed that the spores did not germinate in honey.

# Developmental biology of the minute two-spotted ladybird beetle, *Diomus notescens*

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The minute two-spotted ladybird beetle, *Diomus notescens* is a natural enemy of cotton aphid, *Aphis gossypii.* While two-spotted ladybeetles are commonly found in Australian agricultural crops very little is known about its biology. In a series of laboratory experiments we studied aspects of its development, reproduction and prey consumption. At 25°C immature development of *D. notescens* requires 21 days, 5d for egg, 11d for larva and 5 for pupa development. During larval development they consume a total of 130 aphids. Adult lifespan at 25°C last around 77 days and during this period a female ladybeetle can lay an average of 580 eggs. Prey consumption of adults is approximately 30 aphids per day. From this experiment we calculated an intrinsic rate of increase of 0.14 females/female/day for *D. notescens*. The prey preferences of *D. notescens* were tested using the Manly preference index. We compared preference for aphid nymphs or silverleaf whitefly, *Bemisia tabaci* eggs and found the ladybeetle had a strong preference for the aphid nymphs. Our studies into the biology and prey choices of the minute two spotted ladybeetle indicate it plays a valuable role to play in pest management, in particular suppression of cotton aphid populations.

# Darkness down under – diversity and opportunities from subterranean life in Australia

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Over the last two decades the extraordinary diversity of subterranean life and habitats has been recognised throughout Australia. Habitat diversity extends beyond caves in karst and pseudokarst, where subterranean fauna is typically studied, into novel, sometimes superficial, systems such as groundwater and lacustrine calcretes, and the voids and fractures in banded ironstone and its derivatives. Over the same period, especially the last decade, research into the evolution, age and diversity of subterranean faunas has been reinvigorated by new insights into the nature of subterranean environments (darkness is key), becoming subterranean (relictualisation / adaptive shift), the persistence of subterranean lineages through geological time (still an area of major debate), and the contentious question as to the processes driving morphological convergence (genetic drift and/or selection). These questions have become more tractable through newly found ecosystems, new methods for sampling and analysis, and the rise and rise of molecular genetics and evodevo. The recent discovery of the great diversity of subterranean fauna in Australia (hereafter 'this fauna'), perhaps the taxonomically most diverse globally, has created opportunities for research into these large questions posed by these, in Darwin's view, 'wrecks of ancient life'. The bulk of non-taxonomic research on this fauna has been on aquatic systems which are, as elsewhere, dominated by Crustacea, with the notable exception of Dytiscidae in the arid interior. Elsewhere troglobiont hexapods inhabit air-filled voids but few Australian higher taxa are well represented or even known as troglobionts in Australian even globally. Those represented include Collembola, Diplura[1], Zygentoma, Orthoptera, Blattaria[1], Hemiptera[1] and Coleoptera[1], especially those highlighted ([1]) which show well represented grades of troglomorphism (pigment loss and eye size). The diversity of cave carabids, the focus of much research in Europe, is largely absent in Australia, but best represented in Tasmania, the area most subject to Pleistocene glaciation.

# Chemical control of *Frankliniella* spp [Thysanoptera] in Ataulfo mango orchards does not increase yields

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Thrips in the genus *Frankliniella* damage many crops, including mango (*Mangifera indica* L.), where they feed and reproduce on flowers. In Ataulfo mango orchards of Chiapas, Mexico, there is a complex of several species of *Frankliniella* that appear in large numbers during mango blossoming. Growers have associated the presence of thrips with the gradually decline of productivity and they spray insecticides regularly. Our objective was to evaluate the effect of insecticides commonly used against thrips and to assess their impact on yields. The experiment was conducted in a commercial orchard using five treatments (malathion, spinosad, imidacloprid, α-cypermethrin, and the control) with seven replicates. Data were analysed through a one-way analysis of covariance. The results confirmed the presence of ten thrips species on mango flowers, with eight of them being phytophagous. Thrips density ranged from 246 to 1694 thrips/panicle with *F. invasor* being the dominant species with ca. 95% of total individuals. Insecticides significantly reduced the number of thrips, but population recovered immediately. It is possible that eggs and pupae, two biological stages not typically affected by insecticides, and the immigration of individuals from non-treated trees, are important factors in maintaining high densities of thrips on mango panicles. No significant effect among treatments and final number of fruits was found. Insecticides did not increase the number of fruits harvested, nor the crop yield in any of the treatments. We conclude that the economical threshold is higher than the number of thrips that were present in this study.

# The dark side of night: the biological implications of artificial light at night

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The presence of artificial light at night (ALAN) is one of the most profound recent changes in urban ecosystems. Correlated with increases in ALAN are declines in the survival and fitness of species; however, the underlying mechanism driving these changes remains poorly studied. One proposal is that ALAN causes a decline in circulating levels of the hormone melatonin; a key driver of circadian rhythm and a putative antioxidant. Previous data on the field cricket, *Teleogryllus commodus* indicates that constant light at night leads to declines in survival, immune function and reproductive success. Further, experimental manipulation of dietary melatonin suggests that reductions in circulating melatonin concentrations are a likely causal mechanism. In a large scale experimental study, we are rearing families of crickets from eggs through to the adult stage of the lifecycle under bright daytime lighting but with varied and more ecologically relevant intensities of night lighting (0 lux, 1 lux, 10 lux or 100 lux). Our aim is to assess variation in the behaviour, growth and survival of offspring and then compare immune function, markers of oxidative stress and levels of circulating and tissue-bound melatonin (from haemolymph, eggs, sperm and brain) from surviving adults. Preliminary data suggests that even low levels of night lighting are capable of causing shifts in behaviour, physiology and immune function but the nature of these changes is complex and likely to vary considerably across the different types of parameters measured.

# In the footsteps of Wallace: the biogeography of the Breadfruit fruit fly, *Bactrocera umbrosa*, across the Malay Archipelago

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Located just to the north of the Australian continent the Malay Archipelago, which comprises the islands of Indonesia, Malaysia, East Timor, Papua New Guinea, the Philippines and Brunei, represents one the world's great biotic transition zones. It is in this region that members of the Oriental and Australian biotas overlap or abut. Recognition of this transition zone by the 19th Century naturalist Alfred Russel Wallace sparked the beginnings of the modern concept of biogeography, and the 'Wallace Line' demarcates where he considered the disjunction between biotas to occur. It is proposed that this biogeographical feature acted as an historical barrier to dispersal, thereby driving differentiation of species isolated on either side. Other hypotheses (Weber's Line, Lydekker's Line) modified Wallace's original proposition, providing alternate locations for the transition of biotas.

This region represents a hotbed of diversity and endemicity for many faunal and floral groups. It is in this region that the tephritid fruit fly genus *Bactrocera* is most diverse, with well over 400 species known from across the region. Despite this high diversity, only a single species, *B. umbrosa*, has a native (non-invasive) distribution that spans the transition zone, presumably unaided by human movement. The species has a long history of taxonomic changes, including the recent synonymisation of two species that were restricted to either side of the transition zone. This project thus seeks to explore population structure within *B. umbrosa* by integrating morphological and molecular genetic data. We assessed patterns at two mitochondrial loci (COI and COII), along with wing shape geometric morphometrics and aedeagus length to test hypotheses about whether populations separated by the proposed biogeographical barriers are significantly structured and whether these differences may represent species-level divergence.

# Decreased pollen carriage and foraging in European honey bees with a common gut parasite

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Research into loss of pollination capacity has primarily focused on documenting pollinator declines and their causes with comparatively little attention paid to how stressors may affect pollinating behavior of surviving pollinators. The European honey bee, *Apis mellifera*, is one of the world’s most important generalist pollinators, and *Nosema apis* is a widespread microsporidian gut parasite of adult *A. mellifera*. We individually fed 960 newly eclosed *A. mellifera* workers either a sucrose solution or 400 *N. apis* spores in a sucrose solution and tagged them with a unique radio frequency identification (RFID) tag to monitor their foraging behavior. We found spore-fed bees were less likely to forage than those fed sugar only. Those that did forage started foraging when they were older and stopped foraging when they were younger than non-inoculated bees. However, inoculated and non-inoculated bees did not significantly differ in the number of foraging trips taken per day, the total hours foraged over their lifetime, or homing ability. Inoculated returning foragers were 4.3 times less likely to be carrying available pollen than non-inoculated returning foragers and the number of pollen grains carried was negatively correlated with the number of *N. apis* spores in their gut. In an arena of artificial flowers, inoculated bees had a tendency ($p=0.061$) to choose sugar flowers over pollen flowers, compared to non-inoculated bees, which visited pollen and sugar flowers equally. These results demonstrate that even a low dose of a widespread disease of *A. mellifera* may adversely affect bees’ ability to pollinate.

# The common cat flea: a phylogenetic story of the most ubiquitous ectoparasite and an underrated vector

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Fleas are the most common ectoparasite infesting our canine and feline pets around the world. The genus *Ctenocephalides*, which includes the cosmopolitan cat flea (*Ctenocephalides felis*) is particularly ubiquitous. Fleas of this genus are able to harbour and transmit a variety of known human pathogens such as *Bartonella* and *Rickettsia* bacteria. The close relationship between modern man and his pets creates an interactive interface by which flea-borne pathogens are allowed constant transmission opportunities. Despite their importance to both veterinary and public health, the microbial community dynamics of pathogens and endosymbionts within fleas has been poorly studied. Similarly, the taxonomy of the genus *Ctenocephalides* is largely unresolved, an astonishing fact given their ubiquity in family homes, veterinary clinics and animal shelters around the world. We have developed primers for the mtDNA cytochrome c oxidase subunit 1 (cox1) gene as a method for *Ctenocephalides* flea identification and phylogenetic analysis. The four subspecies within the cat flea species are still contended, over 60 years after their initial description. The cox1 genetic barcoding marker has proven to be an effective tool in resolving the genetic relationships between the cat flea, its subspecies, as well as the sister species *Ctenocephalides canis* (dog flea) from around the world. We combine this method with morphological comparisons with reference material of type specimens from museums to create a robust species profile. Relating vector taxonomy and genetics to pathogen carrying capacity is important for understanding the risks associated with certain species or biotypes. Evidence suggests that the oriental cat flea (*C. orientis*) and the dog flea (*C. canis*) are important carriers of *Rickettsia felis* and like strains in regions where these species are relatively common compared to cat fleas (*C. felis felis*).

# Summer and winter diapause in *Helicoverpa punctigera*: adaptations for a changeable climate

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Apparent changes in the ecology of *Helicoverpa punctigera* (Wallengren), including reduced migration from inland Australia and increased proportions of *H. punctigera* overwintering relative to *Helicoverpa armigera* (Hübner) in the Namoi Valley have led to concerns about the possibility of Bt (Bollgard II cotton) resistance arising in the future. We have been investigating potential changes in migration and overwintering to determine whether these effects may be reducing the dilution of resistance alleles in the population, and potentially producing a resistant population.  In this presentation I will focus on overwintering and diapause.

In lab studies 25°C induced the least amount of diapause and the highest percentage of diapause was induced at 19°C or cooler, even under a summer 14L:10D photoperiod. At a 12L:12D photoperiod the highest percentages of diapause where induced below 19°C. Overwintering pupae extracted from Namoi Valley farm “Drayton” were all in diapause based on eye spot development. When half of the captured “Drayton” pupae were exposed to 25°C they all completed diapause development within 5 days, while the other half were kept at 19°C remained in diapause. Diapause was broken by exposure to low temperatures by early winter, but emergence was delayed until temperatures rose in the spring.

Preliminary studies on summer diapause indicated the presence of diapause in pupae in 17-31% of the population at the temperatures of 31-35°C. A reproductive diapause/quiescence was also detected in adults exposed to 32°C, defined by a 73% failure of females to mate, compared to 21% not mating at 25°C. This may explain the discrepancy between late-season pheromone trap catches and light trap catches reported by previous workers, where male moths are not caught in pheromone traps. This effect may have caused other authors to underestimate the population of *H. punctigera* present in late-season crops and bears further investigation.

# Making scents of urban pollination: does air pollution alter honeybee memory?

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Vehicle exhaust contributes significantly to air pollution in cities and may impair the detection of key odours used in insect-plant interactions. We investigated whether petrol exhaust pollution interrupts the formation and retention of floral odour memories in honey bees (*Apis mellifera*). Using appetitive olfactory conditioning (odour-sugar) we trained bees to learn one of three floral odours: linalool, dipentene and myrcene. Odours were unpolluted or, polluted with exhaust collected from a petrol generator. Once bees had learnt the training odour, we tested their memory of that odour 1 hr, 24 hrs and 48 hrs post training. We found it takes significantly longer for bees to learn a polluted odour and, despite attrition of all odour memories over time, bees forgot polluted odours faster than unpolluted ones. We also tested if pollution masks odours. Using EI mass spectroscopy we quantified changes in the chemical profile of polluted versus unpolluted odours and determined whether bees could recognise polluted odours if they were trained using unpolluted ones. Bees could distinguish between polluted and unpolluted odours, suggesting a masking effect of pollution. Our results show that pollution changes the recognition and retention of floral odours by honey bees which, may consequently impact upon a honeybee's foraging efficiency in polluted areas and, therefore, the pollination services that they provide.

# Completing the alpha-level taxonomy of the Australian horse flies

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Horse flies (Diptera: Tabanidae) are important as vectors of disease in livestock and pollinators, with over 250 species occurring in Australia alone. In 1956, Ian Mackerras began an ambitious plan to revise the taxonomy of the entire Australian fauna through a series of large monographs. He succeeded in revising the species and genera of Pangoniinae, Chrysopsinae, and the majority of the species and genera of the Tabaninae, but unfortunately passed away in 1980, leaving only the Diachlorini untreated. An NSF PEET grant awarded in 2007 spawned a recent surge of renewed taxonomic interest in horse flies and enabled the description of over 56 new Australian species and the completed revision of the tribe Diachlorini. Molecular data was also used to provide the first robust phylogenetic hypothesis for the Australian fauna, focusing on the subfamily Pangoniinae, which largely confirmed the morphology-based classification scheme established by Mackerras. Taxonomic keys were also updated to include novel taxa so that all known species of Australian horse fly can be recognised. Ultimately this research completes the essential taxonomic work set out by Mackerras over 60 years ago. Future investigations may now use this taxonomy to match immature stages to adults, identify feeding hosts from blood and nectar meals, and adopt next generation sequencing techniques to increase phylogentic resolution and reconstruct historical biogeography.

# Soldier fly taxonomy is a battlefield

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A war is waging in the taxonomy of the Australian soldier flies (Diptera: Stratiomyidae), with a paucity of attention from previous workers and a lack of comparative material making the fauna virtually impossible to identify. This is undesirable as the family is one of the most morphologically diverse groups of Diptera and have an underappreciated role in pollination. Moreover, they are extremely important nutrient recyclers as most Australian compost bins are powered by soldier fly larvae. The Australian fauna comprises eight subfamilies, 33 genera and over 110 species currently described. These numbers are expected to increase with the renewed interest in the family through ABRS-funded research being conducted by the ANIC and the USNM. Our fragmented current knowledge indicates that a number of the genera and subfamilies are shared with South America, suggesting austral biogeographic relationships. By applying anchored hybrid enrichment (NGS) protocols, over 250 genes will be captured and analysed to produce a robust phylogenetic framework for soldier fly subfamilies. This will be essential, in combination with morphological data, to revise the taxonomic concepts for the Australian genera. New genera and species will be described, illustrated and named, and original keys will be produced for identification.

# Novel insecticide resistant mechanisms in the common bed bug, *Cimex lectularius*

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Research on field strains of the Common bed bug (Hemiptera: Cimicidae: *Cimex lectularius* L.) from Australian infestations has identified widespread resistance to pyrethroid insecticides, but with variability in the magnitude expressed. To determine if differences in resistance mechanisms exist, collected strains were examined for the presence of metabolic detoxification and/or cuticle thickening. To assess the presence and relative contribution of detoxifying esterases or cytochrome P450 monooxygenases, bed bugs collected from Parramatta (NSW), Melbourne (VIC) and Alice Springs (NT) were exposed in topical bioassays employing a high dose (2.5 g/L) of deltamethrin and two pyrethroid synergists: piperonyl butoxide (PBO) and EN16/5-1. PBO inhibits both monooxygenases and esterases, whereas EN16/5-1 will inhibit esterases only, and thus in a competitive bioassay the results can infer the dominant enzyme system. All strains possessed resistance that was inhibited by the synergists, with the Parramatta and Melbourne (n$^{o.}$2) indicating esterase-dominance, and Alice Springs and Melbourne (n$^{o.}$4) indicating cytochrome P450 monooxygenase-dominance. The Parramatta strain was then selected to study the potential presence of cuticle thickening. Nine-day-old male bed bugs were exposed to filter papers treated with the highest label rate of Demand Insecticide® (200 mL/10 L of 25 g/L lambda-cyhalothrin) and were grouped according to time-to-knockdown (‘intolerant’ < 2 hours, ‘tolerant’ ≥ 4 hours, and ‘resistant’ survivors at 24 hours). Electron microscope analysis of the mean cuticle thickness of a transverse section at the midpoint of the second leg tarsus indicated that all three groups were significantly different ($p < 0.001$) and positively correlated ($p < 0.01$, $R^2$ adjusted = 0.337) with time-to-knockdown. These results demonstrate that bed bugs have many more resistant mechanisms than previously identified, which helps to explain why failures in the control of field infestations are so common. This further emphasizes the need for an integrated approach in the control of bed bugs.

# Thrips of tropical areas – how much do we not know?

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Tropical areas host most of insect diversity but, in spite of this, most expertise available to record this diversity is based outside the tropics. For Thysanoptera, the number of species described is usually greater from subtropical than from tropical areas, and data examining this asymmetry will be presented for Brazil, Africa and Australia along with comparisons to adjacent temperate areas. About 90% of Brazilian territory is Tropical, whereas only around 40% of the approximately 560 species recorded in that country comes from the tropics, and in North America, for comparison, more than 1,000 species are recorded. From Central Africa only about 200 thrips species are listed, whereas from South Africa there are 300 species, and in Europe almost 600 species. In Australia, knowledge of thrips has increased greatly in the past 20 years, but scarcely 100 out of 900 described species are from the wet tropics. Very little is known of the thrips in tropical countries north of Australia, particularly New Guinea, although many were named from Java about 100 years ago and remain largely unrecognisable. The lack of faunistic studies on tropical thrips, and the almost complete absence of biological studies on these insects in tropical areas, is likely to become of increasing significance to the Australian economy with progressive climate changes.

# The cryptic diversity and possible origin of Linnaeus' glasshouse scale insect, *Coccus hesperidum*

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*Coccus hesperidum*, the glasshouse scale or brown soft scale, was described by Linnaeus in the 18th century and is the type species of its genus (*Coccus*), family (Coccidae) and superfamily (Coccoidea). This ovoviviparous scale insect is one of the worst invasive pests worldwide and can feed on host plants from more than 103 families. Previous studies incorporating adult female morphology and DNA sequences indicated that cryptic species might be present. Here, we report on whether the currently recognised *C. hesperidum* (which probably is not the same species as that described by Linnaeus) is actually a species complex. We sequenced specimens from different locations around the world for mitochondrial and nuclear loci to assess species boundaries and to determine the possible geographical origin of this cosmopolitan pest. Our results also contribute to our understanding of whether the brown soft scale is strictly parthenogenetic or whether sex occasionally occurs.

# Spatial and temporal dynamics of *Amblypelta lutescens lutescens* Distant (Heteroptera: Coreidae) in avocado crops

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The native banana-spotting bug, *A. l. lutescens,* is a major polyphagous insect pest of many tropical and sub-tropical horticultural crops in Australia, including high valued commodities such as avocados (*Persea americana*). The cryptic nature of *A. l. lutescens* makes it difficult to sample and much about its ecology and behaviour remains poorly understood. An attractant lure based on the main components of the semio-chemicals emitted by male *A. l. lutescens* has been developed and incorporated into a trap and this has created opportunities to investigate *A. l. lutescens* in the field.

An ongoing two year study is investigating spatial and temporal dynamics of the pest in avocado crops using a grid of traps (36 m x 36 m) across two 4-6 ha avocado (cv. 'Shepard') blocks. We present data for the first year. Higher *A. l. lutescens* populations were recorded from October through to June with peaks occurring in October, February and May. Spatial Analysis by Distance IndicEs (SADIE) indicated very low occurrences of aggregated adult (6-9%) and nymph populations (8-16%) based on weekly pheromone trap counts; most weekly trap counts were randomly distributed. Year-end summary count data indicated significant adult and nymph spatial aggregations in both avocado blocks. Adult male and female count data indicated biased sex ratios 2.9:6.1 and 4.5:1.9. Significantly more *A. l. lutescens* adults were captured in traps positioned less than 18 metres from the edge of the crop than elsewhere in the crop in only one of the avocado blocks. The implications of these results for pest management are discussed.

# The mopane worm as a model to study cryptococcal virulence

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Cryptococcosis is one of the deadliest opportunistic infections that affect individuals with impaired immune system. This disease is especially ravaging in Sub-Saharan Africa, where mortality is surpassing the death rates from tuberculosis and tropical cluster diseases. A recent study from the US Center for Disease Control and Prevention identified cryptococcal meningitis as the third most common cause of death of HIV/AIDS patients in Africa, and estimated that the rate of cryptococcosis is approaching one million cases per year. The mopane worm is an edible larval stage of *Imbrasia belina* Westwood moth. The worm is a culinary delicacy in various regions of Southern Africa, and feed solely on the mopane tree (*Colophospermum mopane*) leaves. Previous studies have established that at least 30% of the mopane trees harbor *Cryptococcus neoformans,* the etiologic agent of cryptococcosis. The mopane worm can therefore serve as an important intermediary in the transmission and dissemination of the pathogen to the consuming populace. In the present study, mopane worm were infected with varying amounts of *Cryptococcus neoformans* in the laboratory over a three week period and then a death curve plotted. From the death plots, it was abundantly evident that more than 85% of the mopane worms survived to the pupa stage. Neither did the excreta of the worms yield any positive culture nor the gut of the dead worms after they were swabbed and cultured in *Cryptococcus* selective medium. This study, which was a first attempt at studying cryptococcal virulence in the mopane worm, suggests that the mopane worm has a proficient immune system which clears the pathogen upon entry into the worm. Although this study sheds some light into the pathogen-host coevolutionary dynamics, further studies as to how this happens are warranted.

# Spider communities in cities: have we underestimated the biodiversity value of private gardens?

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Maintaining biodiversity in urban areas is essential for both the conservation of native species and the wellbeing of people living in cities. While the broad scale habitat destruction associated with urbanisation often leads to localised extinctions and decreased biodiversity, green space within the urban matrix may still support a wide range of species. The aim of this study was to evaluate the biodiversity of spiders in a range of urbanised landscapes and natural habitats, identifying the landscape variables associated with diversity. Spider diversity was surveyed in 67 private gardens and compared to extensive surveys within 6 urban parks, 6 patches of remnant vegetation and 5 continuous bushland sites. We identified over 150 morphospecies from 13 families and analysed the associations between spider communities and both fine and coarse scale landscape characteristics. We found that while some species are limited by environmental constraints and were only found in natural bush habitats, many groups of spiders showed a preference for highly modified urban habitats. Abundance also increased with urbanisation although spiders preferred gardens with a higher percentage of vegetation. Our research shows that gardens in urban areas can harbor diverse communities of spiders and can be of value for the conservation of native species.

# The long and the short of mate attraction in a psylloid: do semiochemicals mediate mating in *Aacanthocnema dobsoni* Froggatt (Hemiptera: Triozidae)?

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Mating is preceded by a series of interdependent events that can be broadly categorised into searching and courtship. Long-range signals convey species- and sex-specific information during searching, while short-range signals provide information specific to individuals during courtship. Studies have shown that cuticular hydrocarbons (CHCs) can be used for mate recognition in addition to protecting insects from desiccation. In Psylloidea, four exotic psyllid species are known to rely on semiochemicals for long-range mate attraction. Psyllid research has focused on long-range mate attraction and largely ignored the potential use of CHCs as mate recognition cues. This study investigated whether CHCs of *Aacanthocnema dobsoni* have semiochemical activity for long- and short-range communication prior to mating. Using a solid sampler for solvent-less injection of whole psyllids and gas chromatography and mass spectrometry (GC-MS), we found quantitative sex- and age-related differences in CHC profiles. Males had higher proportions of 2-MeC$_{28}$, 11, 15-diMeC$_{29}$ and *n*-C$_{33}$ alkanes while females had higher proportions of 5-MeC$_{27}$, 3-MeC$_{27}$, 5, 15-diMeC$_{27}$, *n*-C$_{29}$ and *n*-C$_{30}$ alkanes. In males and females, 84 and 68% of composite CHCs varied significantly with age, respectively. Y-tube olfactometer bioassays provided no evidence that males or females responded to odours emanating from groups of conspecifics of the opposite sex. Tests of male and female psyllids for attraction to branchlets previously occupied by conspecifics showed no evidence of attraction to possible semiochemical residues. Our contact chemoreception bioassay showed that males were indifferent to freshly killed individuals of either sex with or without (removed using solvent) CHCs. It is known that *A. dobsoni* utilises substrate–borne vibrations (SBVs) for communication. Consequently, our results indicate that SBVs are likely to be more important than semiochemicals for long-range mate attraction. Furthermore, CHCs are unlikely to mediate short-range mate recognition or provide mate assessment cues.

# The need for a field based method to detect resistance in green mirid *Creontiades dilutes* (Stål) (Miridae: Hemiptera) from Australian cotton

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With the introduction of Transgenic Bollgard® II cotton Australian populations of green mirid *Creontiades dilutes* have required targeted insecticidal control, which may select for insecticide resistance. Mirids are very fragile and easily damaged but testing them against insecticides is not particularly difficult and laboratory based bioassay methods for *C. dilutes* have been successfully developed by the authors. Our ultimate concern with mirids remains the difficulty of establishing suspect resistant insects into culture and maintaining them prior to resistance testing. Mirids do not travel well because they are very fragile and in our experience most will die in transit. Those that do establish into culture will be slow and time consuming to breed and resistance may revert before it can be diagnosed. Consequently we consider mirids are a species that will benefit from molecular based testing but any molecular based result must be verified against biochemical and/or bioassay methods for confirmation. To that end, we intend to develop a field based bioassay as a more practical solution for detection of resistance in *C. dilutes*

# Morphology, phylogeny and microflora of the New Zealand psyllids (Hemiptera: Psylloidea)

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The importance of psyllids (Hemiptera: Psylloidea) has increased in recent years due to their capability to act as vectors for disease-causing bacteria of plants. The taxonomy and biodiversity of New Zealand psyllids remains poorly developed, and few resources are available for their DNA based identification. Also, little is known about the patterns of bacterial populations carried by Australasian psyllids. Therefore, extrapolating what is known of the pathogen-transmission associated with the exotic pests *Bactericera cockerelli* and *Diaphorina citri*, to situations beyond these as may arise in the future, is still not possible. This study aims to go some way to redressing this. Using New Zealand and Australian field-collected specimens, morphological identification has remained an essential tool since there are almost no DNA markers available for identification by non-specialists, and certainly no relevant reference data for New Zealand. Key to this was availability of the material and expertise of entomological collections and museums in New Zealand and Australia, especially when a formal description was not available. Subsequent molecular phylogenetic analysis of these specimens revealed they were mostly well separated, and fell into the species clades to which they had been attributed; interesting geographical differences were also apparent, as was the suggestion of new previously undescribed species. While this indicates that the development of simple diagnostic markers will be achievable for most species, some species from the same host plants are not as yet clearly separated and additional loci are being analysed. For a selected set of taxa, including some trans-Tasman species, initial 16S amplicon metabarcoding (MiSeq, Illumina) data shows the microflora composition within the same species to be similar, with variations following the geographical distribution. Plans to develop this analysis further are currently underway to make better sense of these associations.

# Ant-plant interaction: re-establishment of myrmecochory in bauxite mining restoration

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Alcoa of Australia Limited (Alcoa) operates open-cut bauxite mines in the Western Australian northern jarrah forest and refines the ore in refineries on the Swan Coastal (sand) plain. The residue is stored in engineered facilities termed residue storage areas. Restoration of plant communities occurs at both sites. Re-establishment of ecosystem processes is one of the ultimate goals of ecosystem restoration, and plant-animal interactions are recognized as a vital component. Myrmecochory, seed dispersal by ants, is an ecologically significant mutualism in dry sclerophyll Australian ecosystems. This study investigates the effect of rehabilitation age on the composition of the ant fauna, seed dispersal rate and seed dispersal distance along comparable restoration chronosequences. At each site there were three replicates from 20 (BMA only), 10, 5, 2 year old revegetation, and adjacent remnants (undisturbed). Elaiosome bearing *Acacia extensa* seeds (mean weight 13.4 mg) were offered to ants for 3 hrs and the fate of the seed (dispersed or elaiosome theft) recorded. Ant species richness was lower in the residue storage area (RSA) than bauxite mined areas (BMA). As restoration progresses, ant species richness increases in BMA but remains similar across RSA sites. During 1,528 seed removals, 14 species from four sub-families were observed, and a further eight species sampled feeding on the elisosome but not dispersing seed. *Rhytidoponera metallica* F.Smith was the most common disperser (87% of observations) while *Iridomyrmex purpureus* (F.Smith) had the highest mean dispersal distance (18.2 m) and the highest recorded dispersal distance (40.5 m). Seed removal rate in BMA declined as time since planting increased and was relatively similar between 20-year old sites (11%) and remnant sites (13%) indicating this ecosystem process may be returning to pre-disturbance levels. No seed dispersals were observed at the RSA, despite dispersal events in adjacent remnants, and may be a contributing factor to limited recruitment of plants in the RMA.

# Cousin Itt and dumpy: two new species of gall-inducing scale insect from Western Australia

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Australia is home to the highest diversity of gall-inducing scale insects in the world, including the most species-rich genus, *Apiomorpha*. *Apiomorpha* is restricted to hosts of the plant genus *Eucalyptus* and, previously, only two species have been described from the widespread but species-poor subgenus *E.* subgen. *Eudesmia*. Recently, two undescribed species of *Apiomorpha* feeding on eudesmids have been found in Western Australia: one from the Great Victoria Desert resembles the described species *A. pomaphora* but is found on a different host, and another on *E. jucunda* in which the galls of adult females are reminiscent of the TV character Cousin Itt. The aim of this study was to delineate and describe the new species, to test the species-group assignments of the two previously described species, and to assess the evolutionary relationships and host use of all four eudesmid-feeding *Apiomorpha* species.

# Systematics of Australian Hadeninae (Lepidoptera: Noctuidae)

*Mitchell, A.*

Australian Museum, 6 College Street, Sydney, NSW 2010

Noctuoidea is the most diverse superfamily of Lepidoptera globally, and the second most speciose superfamily in Australia with some 1,300 described species. It is also one of the most abundant insect taxa, especially in the open seasonal habitats covering much of Australia, and contains many pests, however the Australian fauna remains poorly known. The Checklist of Australian Lepidoptera (Edwards, 1996) still uses the 100 year old highly artificial Hampsonian classification system for noctuids, because too little is known about most Australian taxa to place them in the emerging modern classification of the family. Furthermore, many species are listed without valid generic names, because of the uncertainty about their relationships. Our current work is starting to address these problems. Analysis of DNA sequence data from seven nuclear genes is starting to shed light on the higher-level relationships within the family, with a particular emphasis on tracing the origins of the “pest clade” (sensu Mitchell. et al. 2005) of higher noctuids. We are also performing basic revisionary taxonomy of a number of noctuid genera, including the “southern endemic” element of the Australian Hadeninae, using an integrative approach. The Checklist contains 18 species in this group, with the majority placed in two “no available genus” groups. Alpine and arid zones in particular appear to harbour still unexplored noctuid diversity. Of the taxa examined to date, our analyses show that no more than half of the Australian species have been described.

# Electric Ants in Australia – is this the end?

*Morton, G.*

Coordinator of the National Electric Ant Eradication Program

Electric Ants (*Wasmannia auropunctata*) were first detected in Cairns in 2006 and the National Electric Ant Eradication Program has been conducting a campaign against this highly invasive pest ever since. This presentation will discuss the current situation and where the program is heading in the future.

# Quarantine significance of the disharmonic thrips fauna of Norfolk Island

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The thrips fauna of Norfolk Island was surveyed over a period of 24 months, from December 2012 to December 2014. A total of 66 species of Thysanoptera were found, of which 20% are considered endemics. Most of these endemics are fungus feeders, with only two species feeding on live plants. In contrast, most of the adventive thrips are phytophagous, although leaf-feeding Phlaeothripinae are conspicuously absent. However, many of the adventive species are recorded only from single samples or single individuals. Given the intense sampling effort by several entomologists, this suggests that, for thrips, there is a lack of correlation between introduction and establishment. This lack of correlation is difficult to incorporate into standard Pest Risk Analyses.

# Role of olfactory cues in host finding in the parasitoid *Diachasmimorpha kraussii*

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*Diachasmimorpha kraussii* (Fullaway) (Hymenoptera: Braconidae) is a polyphagous, koinobiont endoparasitoid of *Bactrocera* fruit flies and it has been used as a classical biological control agent against these flies. Previous research has demonstrated that the fly uses a range of environmental stimuli in their host-location foraging behaviour. The aim of the current study is to improve our understanding of how *D. krausii* finds its hosts, and more explicitly how olfactory cues may reinforce successful host finding. Y-tube olfactometer studies were used as a behavioural assay to investigate the influence of the female wasp's innate responses to fruit odours (nectarines) with larval host (*Bactrocera tryoni*) and non-host (*Drosophila melanogaster*) in female parasitoids. Naïve wasps showed significant positive responses to both un-infested and *B. tryoni* infested nectarines, and had a clear preference toward fruit infested with *B. tryoni* versus fruit infested with *D. melanogaster*. There were no significant difference in the preference to uninfested fruits and nectarines infested by *Drosophila*. Previously published studies have shown that *D. krausii* did not orientate differently to hosts infested with physiologically suitable or non-suitable *Bactrocera* species, but the poor wasp response to *D. melanogaster* infested fruit in this study does demonstrate that the wasp can recognises '*Bactrocera'* derived odours over those of other 'non-*Bactrocera'* frugivorous larvae.

# Asian Gypsy Moth risk on maritime vessel – an overview of the Department of Agriculture's border management strategy

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Asian gypsy moths (*Lymantria* spp., Lepidoptera: Erebidae; AGM) are polyphagous forest defoliators that pose a serious biosecurity threat for Australia. If AGM established, their larvae could cause severe damage to forestry production, street and parkland trees and native forests. The urticating hairs of AGM larvae are also known to affect human health. AGM egg masses are frequently intercepted on maritime vessels by Australian biosecurity activities, and maritime vessels departing ports in the Russian Far East between July and September have been subject to quarantine measures for AGM for some decades. The Department of Agriculture recently reviewed biosecurity measures for AGM and responded to the changing trade pathways from Asia in a proactive and unique manner. Here, the department's work on AGM risk management is described in detail, including use of geospatial intelligence for biosecurity risk assessment of a trade pathway, evaluation of egg hatch potential relative to vessel voyage history and profiling of maritime vessel risk based on egg diapause. Opportunities for the department to manage AGM risk into the future are also discussed.

# Looking for a weevil in a haystack — the hunt for the name and status of a potential pest weevil in Australasia (Coleoptera: Curculionidae)

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The so-called Gold-Dust Weevil, currently referred to as *Hypomeces squamosus*, is a pest of a wide range of agricultural crops throughout South-East Asia. It is not known to occur in Australia, and is one of a suite of species targeted by surveillance activities conducted by Australian quarantine authorities. It is a variable species and has been described under several names in the literature, but its taxonomy has never been investigated. The discovery in a CSIRO insect collection of a freshly hatched male, apparently collected in Kakadu National Park in 1995, prompted us to investigate the taxonomy of this weevil by morphological and molecular methods, in order to determine the origin of the Kakadu specimen and the name and status of the taxon it represents. The results of our research to date indicate that the "Gold-Dust Weevil" comprises a complex of closely similar species, that the Kakadu specimen is not conspecific with those occurring in South-East Asia and that a female, possibly of the same species, was collected by Captain Phillip Parker King back in about 1820 either along the Northern Territory coast or in Kupang, West Timor. This female was validly described in 1826 by WS Macleay, as *Cenchroma obscura*, but its name was subsequently forgotten in the scientific literature. Recent surveillance in and around the locality of the Kakadu specimen did not yield any further specimens, and 25 years of surveillance undertaken by NAQS have failed to detect the presence of this weevil anywhere in northern Australia. Investigations are ongoing to establish the status of *Hypomeces obscurus* in Australasia and its precise range and taxonomic boundaries. This case demonstrates the importance of maintaining continual vigilance and pest surveillance along Australia's borders and of carefully assessing the taxonomic status even of apparently well-known pest weevils.

# *Helicoverpa* spp. moth behaviour: Just what does emerge?

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*Helicoverpa punctigera* and *Helicoverpa armigera* are lepidopteran pests of many broad acre crops. They are highly mobile, existing across broad-acre landscapes where the composition of crops are constantly changing, yet little is known about how they respond to these landscapes dynamics.

We collected moths, eggs and pupae from plants, pheromone traps, and emergence traps and pupae digging, respectively, across multiple years in *Bt* cotton and sorghum at multiple spatial scales including fields and landscapes (20 km diameter) across the Darling Downs, QLD. We link these results to provide insights into 1) male mating success as a function of landscape structure, and 2) *Helicoverpa* spp. productivity. We show that the two species respond differently to spatial and temporal factors; *H. armigera* oviposition and number of male moths respond to the percentage of *Bt* cotton at 2 km radius while *H. punctigera* oviposition behaviour is influenced by the amount of fallow at 1km radius from the field.

# Quantitative changes in sex pheromone release of laboratory reared *Bactrocera tryoni* males

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Domestication and mass rearing of insects involves adaptation processes that modify life history parameters and behaviour. While beneficial in the adaptive context of a mass-rearing environment, such changes may be deleterious if insects need to later respond adaptively in other contexts. In the Sterile Insect Technique (SIT), large numbers of insects are reared, sterilised and released in field, where released males must compete for copulations with females of pest populations. SIT is an important tool for management of the Queensland fruit fly, *Bactrocera tryoni* (Diptera: Tephritidae) (‘Q-fly’). Although mass-reared flies are subject to rigorous quality control, many aspects of their chemical ecology remain unknown. In Q-fly, males rely on pheromones to attract mates, and so domestication-related changes in pheromones have potential to greatly diminish efficacy of SIT. We investigated the effects of domestication on pheromones produced by male Q-flies from each of three regions, Cairns, Brisbane, and Sydney. At each region, we assessed volatiles emitted by males during sexual calling in an old colony (>25 generations) and a new colony (<5 generations). The Q-fly sex pheromone is a mixture of six aliphatic amides. We did not find any evidence of differences in the blend of pheromone released by males from old and new colonies, and also found no evidence of differences between regions. However, at each region males from old colonies released more pheromone than males from new colonies. To investigate whether these results reflect differences in pheromone production, we compared rectal gland contents of flies from old and new Brisbane colonies. Matching the results of headspace analysis, rectal glands contained more pheromone in the old colony than in the new colony. We suggest that changes in the pheromone production are an adaptive response to rearing conditions in which males should overcome a chemically noisy environment to be sexually successful.

# Ecological symptoms of broad-acre landscapes and implications for biodiversity and biocontrol

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While broad-acre monoculture systems offer advantages in terms of management and economies of scale, the associated simplification of the landscape strongly influences the type of functional communities that can be supported.

The two main aspects of broad-acre monoculture production simplify the landscape in different ways: the broad-acre scale of fields increases the average patch size in the landscape (i.e. reduced configurational heterogeneity), which reduces the diversity of ecotones, increases fragmentation and disrupts dispersal, and monocultures reduce the diversity of land cover types (i.e. reduced compositional heterogeneity).Such simplified landscapes lead to biotic homogenization and tend to be dominated by generalist species (the so called 'winners') with wide dispersal abilities and long activity periods, whereas more-sedentary species, specialist species and species with more seasonal habits (the so called losers) are at threat in these systems. Such biotic homogenization may have important implications for the long terms sustainability of these systems. Additionally, ecosystem service providers such as pollinators and natural enemies, in such simplified habitats, can be easily disconnected from either the hosts and prey or the habitats on which they rely to provide their services.

# Paradoxes in Ecdysteroid-related gene conservation and loss

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The conserved role of the moult-promoting ecdysteroid hormones in arthropod development contrasts with wide variation in the life histories they regulate. Examples of developmental differences include the persistent adult moulting of lower insects as against the terminal pupal-adult moults of more derived insect orders and the drastic morphological contrast between the young of hemimetabolites (nymphs) and holometabolites (larvae). Differences in spatial and temporal patterns of ecdysteroid synthesis and degradation, molecular composition of ecdysteroid titre and signalling pathways downstream of ecdysteroid synthesis may help explain insect developmental divergence, but these have not been thoroughly investigated in non-model insect species. We have investigated the complement of ecdysteroid-associated genes in a broad range of moulting animal (Ecdysozoa) genomes and transcriptomes, including those recently released from the 1K Insect Transcriptome Evolution and 5K Insect Genome projects, to determine whether differences in their copy number or sequence can shed light on developmental variation within Ecdysozoa. Unexpectedly, we found evidence for losses within Insecta of ecdysteroid-related genes which are well conserved on a wider evolutionary scale. For example, *neverland* (cholesterol 7-desaturase), present in fish, birds, nematodes and most arthropods, seems to have been lost in beetles. Even more strikingly, the phylogeny of *DHCR24* (3β-hydroxysterol-Δ24-reductase), conserved not only in numerous animal phyla but also in plants, suggests multiple independent losses of this gene within Insecta. In contrast, a single copy of each ecdysteroidogenic cytochrome P450 gene, which lack clear orthologs outside Arthropoda, appears to be present in almost all insect species. Using a combination of RNAi, CRISPR and *in situ* RNA hybridisation, we will explore the potential functional consequences of an exception to one-to-one ecdysteroid-related cytochrome P450 conservation, namely multiple duplications in the *Drosophila* (vinegar fly) genus *Cyp307a* gene family, and the apparent losses of *neverland* and *DHCR24* in certain insect taxa.

# Colonisation of canola by diamondback moth, *Plutella xylostella*, in southern Australia: where are they coming from?

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The diamondback moth, *Plutella xylostella*, is the principal pest of Brassica vegetables and a periodic but damaging pest of winter canola grown in temperate southern regions of Australia. Many aspects of the ecology of diamondback moth in canola agro-ecosystems are little understood, despite the dramatic expansion in global canola production over the last two decades. The origins of populations that seasonally re-colonise canola in southern Australia are unknown but have important implications for the ability to forecast the risk of outbreaks and design appropriate insecticide resistance management strategies. Previous genetic studies using microsatellite markers have found no evidence of population structure in diamondback moth across its vast Australian range, suggesting a high level of gene flow, however migration routes have not been established. Next generation sequencing methods are able to generate molecular markers at higher resolutions than previously available for population genetic studies. Here, we combine genetic and field-based approaches to investigate the patterns of regional movement and gene flow in diamondback moth in canola-growing regions of southern Australia. We assess the utility of high throughput sequencing methods to generate new information about population structure in Australian diamondback moth, by restriction-site-associated sequencing (RADSeq) of nine populations collected from three Australian states. Regional networks of traps and sentinel fields are used to determine the timing of invasion of canola. A bioclimatic model (CLIMEX) and field surveys are being used determine the potential for local over-summering of diamondback moth in canola regions. The results will be collectively used to identify likely sources of seasonal invasion of canola and the implications for management.

# A brief history of traps: how to detect exotic mosquito-borne viruses without going mad

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Australia is threatened by several exotic diseases carried by mosquitoes, including dengue, chikungunya, Japanese encephalitis and Rift Valley fever. I have been involved in the surveillance and control of these pathogens since 1994, and have been especially motivated by the need to develop improved mosquito-borne virus surveillance systems (ie., a better mozzie trap). I will discuss my journey through a shedscape of mosquito traps as I have sought to make arbovirus surveillance safer, cheaper, and cleverer. This has involved eliminating logistical bottlenecks along the way, including the use of sentinel animals, the need for powered traps and batteries, the processing of thousands of mosquitoes, and potentially the requirement of carbon dioxide. Ultimately, we hope to utilise these traps as an efficient and inexpensive way to monitor for exotic mosquito-borne pathogens.

# Volatiles as an indicator of host-plant quality: response of light brown apple moth to healthy and fungus-infected grapes

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A three-way interaction among plant, herbivorous insect, and the phytopathogenic fungus is mediated by chemical cues emitted as volatile organic compounds. Herbivorous insects use sensory cues to choose their host plants for feeding and/or oviposition by assessing the host quality. Fungi induce variations in the chemistry of the plant. The induced variation can modify the volatile profile of the plant that could be recognized by the olfactory receptors of herbivorous insect as either an attractant or a deterrent. We hypothesized that herbivorous insect uses olfactory cues to assess the health status of potential host plant. To test this, we determined the host choice and oviposition behaviour of an Australian native moth, *Epiphyas postvittana*, towards uninfected berries of *Vitis vinifera*, as against that of the berries infected with a phytopathogenic fungus, *Botrytis cinerea*. We found that the volatiles emitted from *B. cinerea*-infected berries elicited deterrent behaviour in *E. postvittana* and in consequences they laid fewer number of eggs on infected berries. Alcohols such as ethanol, 3-methyle-1-butanol, and 2-phenylethanol were found abundant in the *B. cinerea*-infected berries. In oviposition bioassays with synthetic compounds, ethanol and 3-methyl-1-butanol confirmed the essential function of olfactory cues in this process.

# Prospects for slug control using pathogenic protozoa and RNA interference

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Current chemical control methods for pest molluscs in the Australian grains industry using carbamate, metaldehyde or iron EDTA complexes in baits are of relatively low efficacy and the first two are of increasing environmental concern.

Potential RNA interference (RNAi) targets were identified from the grey field slug (*D. reticulatum)* transcriptome. Target sequences were expressed in *E.coli* and improved extraction and purification methods enabled efficient production of double stranded (ds)RNA. dsRNA was very stable, both on leaf surfaces and in model baits containing potato, maize, tapioca or rice flours but not the flour of wheat (*Triticum* species). dsRNA degradation in a range of grain growing soils was demonstrated. dsRNA ingested by slugs or injected into the haemocoel, either naked or complexed with cationic polymers did not show lethal phenotypes. Injection of dsRNA into the albumen of developing eggs, has likewise proved unsuccessful. qPCR failed to show transcript knockdown of vacuolar ATPase by RNAi. Feeding or injection fluorescently labelled siRNA into the albumen of developing eggs has shown that siRNAs do reach the digestive gland. Work is ongoing to ascertain whether *D. reticulatum* has the capacity for cell to cell spread of RNAi.

An alternate strategy is to infect slugs with pathogenic protozoa such as *Tetrahymena rostrata.* We have shown that an undescribed *Tetrahymena* is widespread in pest molluscs across the eastern and southern states. *T. rostrata* itself appears to have a limited distribution but, where present, is capable of transovarial transmission with the subsequent death of a high proportion of developing embryos adding to direct mortality in adult slugs and a reduction in the number and viability of eggs laid. *T. rostrata* can be induced to produce cysts from which the infective form can emerge when conditions are optimal. We are exploring the potential to incorporate these cysts into field baits with the aim of generating both direct effects on the ingesting animals and field epizootics.

# Wing pattern evolution in jaw moths (Lepidoptera: Micropterigidae)

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Wing patterns in the order Lepidoptera are important taxonomic characters that serve various ecological functions and have long been studied by evolutionary and developmental biologists. However, the homologies between pattern elements in different moth families and superfamilies families are still not known. To address this fundamental gap in our current knowledge, I examined the relationship between wing pattern and wing venation in the Micropterigidae, or “jaw moths”: the most basal extant family of Lepidoptera, which occurs disproportionately in the Australasian region. My examination of multiple species within the two principal genera of this family, Micropterix (Palearctic) and Sabatinca (Australasian), shows that wing veins – specifically, the points where veins terminate at the costal margin of the wing – consistently predict the location of wing pattern elements. However, the color of these wing pattern elements varies between the two genera: the dark areas traditionally called “fasciae” in Micropterix correspond to light interfascial areas in Sabatinca, and vice-versa. It therefore appears that venation constrains the contrast borders between wing pattern elements, but not the color of these elements. My findings regarding the relationship between wing venation and wing pattern suggest that future efforts to designate homologous wing pattern elements in Lepidoptera should focus on the location of each pattern element, not the extent to which pattern elements are pigmented.

# Monitoring sugarcane moth borers in South East Asia – Keeping Australia safe

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Research on exotic sugarcane moth borers includes pre-border, border and post border activities. Pre-border research and surveillance programs study the biology, abundance and management of major moth borers in their respective regions. This work also includes selection of resistant varieties to use as candidates in case of incursion into Australia and to bolster breeding programs in country of occurrence. Border activities involve effective quarantine measures at all ports and entry points into Australia, while post-border activities include the deploying of inspection and surveillance programs in Northern Australia and the Torres Straits. Species of *Chilo*, *Scirpophaga* and *Sesamia* are widely distributed in South East Asia. Incursion Management Plans have been developed with detailed information on the biology, economic impact and management of all recorded species. A key aspect of any biosecurity program is proper identification of target threats. DNA barcoding work highlighted frequent mismatches between field and DNA identification of borer samples. Both *Chilo sacchariphagus* and *Chilo infuscatellus* samples showed deeply divergent mtDNA lineages among sites sampled, while specimens identified as *Scirpophaga excerptalis* in the field fell into three separate clusters. *Sesamia inferens* is a major sugarcane pest in Thailand but rarely attacks cane crops in Indonesia, and it is not clear whether it is one or a complex of species. Further work is needed to review the taxonomy of moth borers in South East Asia and develop reliable diagnostic methodologies to ensure better preparedness for potential incursion.

# Invasive flammable exotic grasses: increasing detrimental impacts on Australia’s invertebrate biodiversity

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More than 160 exotic grass species (most from Africa and the Americas) are naturalised in Australia following deliberate or accidental introductions. Besides intentional introduction as food crops, some of these species were introduced to enrich pastures for grazing, by supplementing or displacing unpalatable indigenous grasses and understory plants, and to control erosion and provide cover (e.g. bind sand dunes and saline soils). More than 30 of these naturalized species now have detrimental impacts on farmlands and in Australian ecosystems. Promoted by natural and accidentally-lit fires, and fire regimes aimed to reduce fuel loads, several exotic grasses are increasingly invading grasslands, wetlands, woodlands and rainforests, and having an impact on indigenous plant species and natural systems. Increases in frequency, scale and seasons for deliberate burns results in a positive-feedback loop (i.e. grass-fire cycle) that exacerbates the abundance and impacts of exotic grass species. Collectively these invasions are having significant transformational impacts on entire plant communities, and subsequent cascading impacts on native herbivorous invertebrate species reliant on these communities, and other higher order trophic interactions. The most seriously affected invertebrate fauna are likely to be those with poor mobility or with winter stages of dormancy, those that cannot avoid being burnt by sheltering underground or in the understory, and those with a high fidelity to certain native host plant species. Sustainable management solutions are in urgent need for some of these grasses. Following recent successes in managing invasive grasses with classical biological control overseas (i.e. using specialist agents to mitigate impacts), we suggest that similar efforts be undertaken for invasive grasses that cause substantial environmental impacts but provide little or no benefits in Australia. Such sustainable approaches may reduce impacts by these grasses on native ecosystems, enhance persistence of indigenous plant species and conservation of Australian invertebrate biodiversity.

# Emergence of a native *Coptocercus* species in the jarrah (*Eucalyptus marginata*) forest of Western Australia subject to drought

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The Southwest of Western Australia (SWWA) is currently experiencing a decline in rainfall, with higher temperatures leading to increased frequency of drought. Borers (Cerambycidae) favour drought conditions and successfully colonise water stressed trees. A sawn (50 cm length by 13-16 cm diameter) log experiment was conducted over the summer of 2014-15 to determine the type and extent of damage caused by borers in the jarrah forest. As the logs dried out over the summer, they were infested by a species of *Coptocercus* Hope (Cerambycidae), a little known borer not previously described in this forest. Damage occurred to 50% of the outer sapwood from borer larval feeding in sawn logs. Emergence of adults commenced approximately 8 months after logs were sawn and continued for a further 3 months and increased with temperature. The average density of borers was 15 per log with densities reaching 55. The main features of these borers are an enlarged tibia and longitudinal creamy yellow stripes on the elytra with a yellow ovule shaped marking at the apex of each elytra. The high densities of borers in fallen logs may be related to their small size compared to the size of *Phoracantha semipunctata* where, much lower densities of borers were found in a previous study in the jarrah forest. The successful infestation by *Coptocercus* may indicate that these borers have the potential to cause outbreaks in the future if increased droughts occur in this forest ecosystem as projected by climate change models.

# A systematic revision of the Macropsinae (Hemiptera: Cicadellidae) leafhoppers of Australia

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The currently described Macropsinae of Australia comprise 45 species in 9 genera with at least half placed in the "holdall" genus *Macropsis* Lewis. The three main objectives of this revision were to 1) determine whether the two largest genera in the subfamily, *Macropsis* and *Oncopsis*, mostly known from the Northern Hemisphere and containing four exotic plant disease vectors, are represented in Australia; 2) to revise which genera occur in Australia and 3) infer relationships between Australian and overseas genera. Morphological and molecular characteristics were examined and analysed separately in this study. Both external and internal (male genitalia) morphological characteristics were captured in a character matrix with 121 characters, representing 180 taxa and analysed using Maximum Parsimony methods. Partial mitochondrial Cytochrome Oxidase I (549 basepairs) and nuclear 28S (663 basepairs) gene sequences were analysed for over 60 specimens, representing 40 taxa from Australia and overseas. DNA sequences of individual and combined genes were analysed using Neighbour Joining, Maximum Parsimony and Bayesian Inference methods. Following results from overall analyses, a total of twelve macropsine genera are now recognised in Australia (including three new undescribed genera and one new generic record). The phylogenetic trees revealed a distinct clade of uniquely Australian genera and 21 of the described "*Macropsis*" species of Australia were placed in other (described or newly described) genera. There appear to be no species matching *Macropsis* (*Macropsis*) or *Oncopsis*, amongst Australian species tested. One described Australian species belongs to *Macropsis* (*Parapediopsis*). However, *Macropsis* was not consistently recovered in any of the phylogenetic trees and the genus and its subgenera require revision. None of the Australian taxa examined appear to belong to *Oncopsis*. This revision uncovered over 86 undescribed species, almost twice as many as described and corroborates claims that the Macropsinae fauna of Australia is indeed unique, rich and diverse.

# Binomial sequential sampling plan for the cabbage aphid *Brevicoryne brassicae* L. (Hemiptera: Aphididae) on canola and implications for remedial action

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Characterization of spatial distribution patterns of pests in large-scale agricultural fields is important, because these patterns affect the sampling effort needed to accurately estimate their population density. We conducted experimental releases of alate cabbage aphids (*Brevicoryne brassicae* L.) into centres of small plots of canola (*Brassica napus* L.), and their gradual spread over a seven week period was characterized. The small plot experiment demonstrated gradient effects from plot centres and a non-random vertical distribution, with initial colonization occurring on the abaxial side of lower canopy leaves and, later, highest numbers of cabbage aphids found on racemes. We also conducted large-scale assessment of cabbage aphid infestations in five commercial canola fields, using visual inspection and sweep net sampling. These large-scale assessments showed strong edge effects, and cabbage aphid distribution was more effectively modelled by visual inspection using logistic (i.e. presence/absence) regression than ordinary (i.e. cabbage aphid counts) regression and/or Spatial Analysis by Distance Indices (SADIE). Using a resampling validation approach of empirical data, binary sequential sampling plans were developed for the action thresholds of the proportion of canola plants infested with cabbage aphids at 0.1, 0.2 and 0.3 and minimum sample number of 10, 50 and 100. Based on the study findings, an optimised inspection approach is proposed to focus monitoring efforts on canola plants within 20 m from field edges with particular attention to the abaxial side of lower-canopy leaves for early detection and focus on the racemes for advanced cabbage aphid infestations. It is anticipated that these sampling protocols may provide the option of targeting insecticide application to field edges where strong edge effects exist.

# Ant fauna (Hymenoptera: Formicidae) of Socotra Island (Yemen) with description of three new species

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Socotra islands lying among three biogeographic regions, the Afrotropical, the Oriental and the Palearctic regions, consequently, it shares faunal elements from the three regions in addition to unique endemic fauna. The ant fauna of Socotra Island was studied, listed and keyed. In total, there are 26 species belonging to 10 genera and four subfamilies were collected from the island of which 10 (38%) are successful invasive species and Four species are endemic (15%), *Monomorium nimihil* Collingwood, 2004, *Syllophopsis abdeldayemi* sp. n., *Monomorium alghazaly* sp.n. and *Tetramorium socotricum* sp. n. Two genera were recorded for the first time from the Island Hypoponera Santschi, 1938 and *Syllophopsis* Santschi, 1915. Three species were recorded for the first time *Monomorium atomum* Forel, 1902, *Tetramorium* pauper Forel, 1907 and *Hypoponera punctatissima* (Roger, 1859). The human impact on the island introduced many famous invasive ants including *Tapinoma melanocephalum* (Fabricius, 1793), *Cardiocondyla emeryi* Forel, 1881, *Monomorium exiguum* Forel, 1894, *Monomorium pharaonis* (Linnaeus, 1758), *Pheidole teneriffana* Forel, 1893, *Tetramorium lanuginosum* Mayr, 1870, *Tetramorium simillimum* (Smith, 1851), *Tetramorium caldarium* (Roger, 1857), *Trichomyrmex destructor* (Jerdon, 1851), *Trichomyrmex mayri* (Forel, 1902).

# Probing our borders: exotic mosquito detections at first ports of entry

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International conveyances and the cargo they carry have long been associated with the global spread of exotic mosquitoes. The Commonwealth Department of Agriculture conducts vector monitoring activities at international air and sea ports around Australia to protect against the introduction of exotic mosquitoes through international pathways. Isolated detections of exotic mosquitoes at international ports are not uncommon, particularly at seaports in northern Australia. During the period 2009–2013 there were 18 detections through vector monitoring, of which 17 occurred at seaports. However, since the start of 2014 there has been an unprecedented increase in the number of exotic mosquito detections, particularly Dengue mosquito (*Aedes aegypti*), at international airports across Australia. Over the period January 2014 – May 2015 there were 38 detections, of which 36 occurred at airports. Response activities, including knockdown and residual harbourage treatments, were conducted in partnership with the state/territory health jurisdictions and prevented the local establishment of exotic mosquitoes. The increase in the number of detections at international airports also led to the implementation of additional border measures, including enhanced insecticide testing of risk aircraft and on-arrival retreatment of risk aircraft holds. While pathway analysis is still ongoing, these detections highlight the importance of having effective surveillance activities in place for the early detection and response of exotic mosquitoes entering Australia.

# Pestpoint: connecting field diagnosis to the lab for better biosecurity

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Pestpoint software enables field observers to connect with entomologists and other specialists via mobile devices to get help with identifying pests and to discuss management options. The software records standard collection information, along with camera and field digital microscope images. The information is delivered to secure, private networks where images can be discussed online until an appropriate level of diagnosis is achieved. Pestpoint is now being used in the field by the grain storage industry, commercial crop consultants and quarantine organisations within Southeast Asia. Diagnostic support is provided by government entomologists/pathologists as well as colleagues. The simple interface encourages field workers to take images and submit them to networks, thereby exposing more field observations to biosecurity scrutiny. It is envisaged that Pestpoint will increase the chance of detecting significant biosecurity threats and contribute databased evidence on general surveillance activity that will support Australia's plant health status.

# Selectivity of new generation insecticides on silverleaf whitefly parasitoid *Eretmocerus hayati* (Hymenoptera: Aphelinidae)

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The silverleaf whitefly (SLW), *Bemisia tabaci* biotype B (Hompotera: Aleyrodidae) is a widespread and difficult pest to control in Australia. The exotic parasitoid *Eretmocerus hayati,* imported for SLW biological control in Australia, was reported as an efficient parasitoid for SLW control in vegetable production systems. Integrate the parasitoid into SLW management programs it is important to know which insecticides are compatible with parasitoids.

The toxicity of four insecticides, chlorantraniliprole (Coragen®), indoxacarb (Avatar®), cyantraniliprole (Benevia®) and acetamiprid (Intruder™), applied with three adjuvants, were tested on the adult, larval and pupal stages of *E. hayati* under laboratory conditions. The treatments were applied as direct spray by using an automated Potter-tower sprayer.

Chlorantraniliprole, applied at the three rates, is less toxic to *E. hayati* adults, larvae and pupae. Cyantraniliprole is slightly toxic to all stages of *E. hayati* at the proposed label rate, and did not cause adverse effect on adult emergence. Indoxacarb displayed low mortality to *E. hayati* adults at label rates. The higher rate (1.3g ai/ L) caused high adult mortality (95%) but had no adverse effect on larval or pupal development of the parasitoid. Acetamiprid caused high acute mortality on *E. hayati* adult and had adverse effect on larval and pupal development. The three spray adjuvants (Hasten®, Agral® and Incide®) did not cause any significant mortality to *E hayati* adults.

Based on the International Organisation for Biological and Integrated Control (IOBC) classification chlorantraniliprole and three adjuvants were classified as harmless (rating 1), indoxacarb and cyantraniliprole as slightly harmful (rating 2) and acetamiprid as harmful (rating 4). Coragen®, Benevia® and Avatar® can be considered for IPM programs in crops where *E. hayati* is used for SLW control.

# Host and range expansion by a native psyllid [*Ctenarytaina bipartita* (Hemiptera: Aphalaridae)] as a consequence of revegetation: mechanisms and implications

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*Ctenarytaina bipartita* Burckhardt *et al*. is a recently described species of free-living psyllid first recorded from Victoria on artificially planted Bog gum (*Eucalyptus kitsoniana*). Bog gum has a restricted distribution in Victoria and is listed as rare. Host records for *C. bipartita* from Tasmania are from Manna gum (*E. viminalis*) which is widely distributed in south-eastern Australia. We quantified the performance of the Bog gum-Victorian metapopulation of *C. bipartita* on two genotypes of *E. kitsoniana* and three of *E. viminalis*. We also tested female preference for the odour of their natal host and settling on two non-hosts. Female *C. bipartita* exhibited host-associated plasticity in wing and proctiger length. Larger psyllids arose from a genotype of *E. kitsoniana*. Fecundity varied significantly among hosts and was highest on a genotype of *E. viminalis*. Hosts did not differ significantly in free amino acids (FAAs) but did differ in concentrations of essential amino acids (EAAs). However, nymphs did not differ significantly in EAAs. Fecundity was not related to total FAAs, availability of EAAs or concentrations of EAAs but was related to concentrations of four non-EAAs. Mean fecundity per host was also positively related to the relative abundance of galloyl groups (associated with hydrolysable tannins). Females did not prefer the odour of natal hosts and settled on non-hosts as frequently as they settled on a host. Leaf age was more important to settling than eucalypt. Planting *E. kitsoniana* in new habitats has expanded the range of Bog gum-Victorian *C. bipartita* and will provide a bridge for the colonisation of *E. viminalis*. Host expansion by Victorian *C. bipartita* is not constrained by nutritional quality and is likely to induce morphological and genetic divergence. Population genetics, host preference and the willingness of the Manna gum-Tasmanian and the Bog gum-Victorian metapopulations to mate will determine whether host-races exist.

# Development of an artificial diet for the large cabbage moth, *Crocidolomia pavonana* F.

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Large cabbage moth, *Crocidolomia pavonana* F. is one of the most damaging crucifer specialists attacking *Brassica* crops, but little is known about what affects its feeding choices. A suitable laboratory diet is necessary in order to study the influence of plant compounds on larval feeding. By assessing feeding preference, survival and development of *C. pavonana* on different kinds of wheat germ-based diets it was determined that neonates preferred diet that incorporated powdered cabbage. Neonate survival (82%) and completion of development (80%) was greater on diet containing cabbage than on other diets; on diet containing wheat grass or spinach powder 17% and 0% of treated larvae respectively were alive after 7 days. In behavioural experiments, 96% of the neonates located diet when it contained cabbage leaf powder while only 8% located it when it did not. More than twice the number of feeding marks were recorded on paper discs soaked on diet with cabbage than on diet without cabbage (43 vs 18). The results suggest that cabbage contains feeding cues/stimulants that are used by larvae of *C. pavonana*. Further study will assess the importance of glucosinolates and their isothiocyanate hydrolysis products in stimulating feeding behaviours of *C. pavonana* as these compounds are known to mediate other insect-plant interactions in the Brassicaceae.

# Using Stable Isotopes to determine movement and spatial mixing of *Helicoverpa spp.* populations within Australian cotton producing landscapes of varying complexity

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Transgenic (Bt) cotton has provided major benefits for the Australian cotton industry (e.g. control of *Helicoverpa* & reduced pesticide use), but the possibility of Bt resistance in these insects continues to be a major threat, as the industry now heavily relies upon this technology, making up over 97% of the crop. A Bt Resistance Management Plan has consequently been developed, and central to that is the use of mandatory refuge crops to provide susceptible moths to help delay the evolution of Bt resistance. However, our understanding of the degree of movement / spatial mixing of moths from different origins (Bt cotton, refuges, and other sources outside the cotton production system) within and between regions, is very limited. Such knowledge is critical to an effective RMP. Our current research uses stable isotope signatures, as indicators of plant host origins, to assess the importance of local landscape design in determining the structure of *Helicoverpa* populations. We have been working within two contrasting cotton production systems in southern Qld over the past three summer growing seasons: Darling Downs representing a complex agricultural landscape and St George representing a simpler one. The results show that moths from non-structured refuges (not specifically planted as a refuge) can constitute major proportions of populations at landscape scale, within both simple and complex agricultural systems. Moths generated within local cropping systems per se may therefore not be good indicators of the propensity for resistance evolution.

# Australian jumping plant lice and lerp insects (Hemiptera: Psylloidea): species richness, phylogenetics, host specificity and invasives

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Jumping plant lice and lerp insects or ‘psyllids’ (Hemiptera: Psylloidea) have undergone spectacular radiations on certain plant families in Australia. They generally show a high level of host specificity, where psyllid families are associated with certain plant taxa, often with congruence at the generic level, and many species are associated with single, or closely related plant species.

The Australian psyllid fauna currently comprise a little over 400 described species with major radiations of spondyliaspidine Aphalaridae host specific to the Myrtaceae, a diverse assemblage of Triozidae on the Casuarinaceae, Myrtaceae and Scrophulariaceae, and of Psyllidae on multiple hosts including Loranthaceae, Mimosaceae, Proteaceae and Sapindaceae. A new molecular phylogeny of the Australian Psylloidea depicts a high degree of genetic structure associated with their respective host taxa. Additionally, many new species, perhaps 200, remain to be described, including a major radiation of *Acizzia* from the Fabaceae, and a number of poorly represented psylloid families from unrecorded Australian host associations.

A number of psyllids are emerging as economic horticultural or forest pests. Some 30 species of Australian psyllids are now recorded as exotics in other countries, either through deliberate introduction as biocontrol agents, accidental introductions on ornamentals and in forestry or aerial long distance dispersers. Other exotic species are considered serious risks to Australian horticulture.

Ongoing studies aim to describe new species of Australian psyllids from novel plant taxa, further resolve the co-phylogeny of the Australian fauna and their hosts and provide information for biodiversity, conservation and biosecurity.

# The influence of light on insect behaviour and evolution: tracking transitions in photic niche with photoreceptive opsin genes.

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The role that light plays in influencing an animal's behaviour is contentious. In some cases it appears that the magnitude of light is the most important cue for temporally distinct behaviour, whereas in other instances it is clear that changes in the colour of light (photon wavelength) cues activity patterns. While for animals inhabiting aphotic environments there are no light derived cues and activity is often arrhythmic or cyclical in a protracted manner (not at a circadian scale). So is it an animal's quiver of photoreceptive opsins (visual & non-visual) that determines daily activity patterns and drives evolutionary diversification within a particular niche, or does the animal's behaviour drive selection and precede genetic change, as predicted by niche construction theory? Recent advances in high-throughput sequencing technology permit unrivalled opportunities to explore and connect the evolution of opsin proteins to various factors that have had critical influence on the evolutionary success of many animal forms; namely vision, circadian rhythm and social organisation. Opsin proteins arose in an ancient metazoan common ancestor and are therefore (*a*) conserved from a functional perspective and (*b*) highly useful for phylogenetic tracking over geological timescales. Here I briefly canvas two case studies that have used opsin genes to track insect transitions into novel photic environments, wherein the organisms have exhibited remarkable adaptive radiations. The first is a transition from diurnal to nocturnal foraging in social sweat bees from the genus *Megalopta* (Halictidae: Augochorini), common throughout neotropical lowland forests. The second is a transition from surface to subterranean water bodies by dytiscid diving beetles (Dytiscidae: Bidessini, Hydroporini) within isolated calcrete aquifers of the Western Australian arid zone. Nocturnal bees exemplify the creation an ecological space temporally freed of competitors and predators, while the subterranean beetles present a unique comparative system for understanding the regressive evolution of vision.

# Virus infected plants will improve host suitability for the aphid vector under future increased $CO_2$ concentration

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Since the beginning of the industrial revolution, atmospheric carbon dioxide ($CO_2$) concentration has increased significantly and is projected to double by the year 2100 to about 800 µmol mol$^{-1.}$ While the effects of elevated $CO_2$ ($eCO_2$) on plant physiology, yield and quality are well documented, less is known about the impacts on pests and diseases. Insect pests and plant diseases negatively impact food production by lowering yields and reducing quality, as well as raising input costs. In this study we have investigated the effects of $eCO_2$ (650 µmol mol$^{-1}$) on the interactions between wheat and the bird cherry-oat aphid (*Rhopalosiphum padi*), a vector of *Barley yellow dwarf virus* (BYDV). We found that changes in wheat biochemistry caused by $eCO_2$ reduced *R. padi* fecundity, lowering progeny production on noninfected plants by a third compared to plants under ambient $CO_2$ ($aCO_2$). By contrast, aphid progeny production on BYDV-infected plants was not affected by $eCO_2$. Electrical penetration graph recordings showed aphid feeding (phloem ingestion) on noninfected plants increased under $eCO_2$ compared to ambient conditions. No changes to aphid feeding were observed on BYDV-infected plants, irrespective of $CO_2$ treatment. Under $eCO_2$, wheat had lower nutritional quality (leaf N concentration) for aphids in noninfected plants but not in BYDV-infected plants. With BYDV infection, aphid performance and phloem ingestion remained unaffected despite $CO_2$ treatments. Given that BYDV infected plants under $eCO_2$ promoted greater aphid fecundity and had leaves with lower C:N ratios that are more attractive for feeding, aphids will be more likely to acquire and spread BYDV, and hence BYDV is likely to become a greater threat to wheat production in the future.

# Diversity of thrips (Thysanoptera) galls and thrips diversity

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Of the known 6,000 thrips species about 250 of these are known to induce galls on plants, a highly derived trait among thrips. The galls are presumed to result from direct feeding not oviposition as is common in other gall inducing arthropods. As in other parts of the world, most gall-inducing thrips in Australia are found in the Phlaeothripidae family, although one Thripidae species has been described from Brisbane that induces a double folded leaf, like an envelope, and this structure seems to provide protection from invasion by kleptoparasitic thrips (species that are known not to kill the gall inducers but drive out the original inhabitants and usurp the gall for their own breeding colony) as well as a few predatory thrips. Thrips galls provide a sheltered habitat for the gall inducer and sometimes also for inquilines - thrips species that move into the gall after it is formed and live as ‘guests’ of the inducer species.

The Phlaeothripidae species that induce discrete galls on the phyllodes of many *Acacia* species in arid Australia have been extensively studied, and despite their structural diversity, most of these are now considered members of one genus, *Kladothrips*.

Examples of the diverse thrips’ gall types observed from arid areas of Australia are given, as well as examples from the subtropical and tropical regions of Queensland.

# Modification of plant-induced responses by a galling insect affects the field distribution pattern of a subsequent herbivore

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An insect herbivore that functions as an ecosystem engineer can shape the herbivore community by altering plant morphology and providing novel habitats for subsequent herbivores. Its colonization could also induce changes in plant physiology, but how such modification can influence the field colonization pattern of subsequent herbivores is not clear. We explored plant physiological mechanisms by which an initial colonization by an ecosystem engineer, the rosette gall-midge (*Rhopalomyia solidaginis*), influences the spatial pattern of a subsequent colonization of a beetle (*Microrhopala vittata*) on the tall goldenrod (*Solidago altissima*).

In the field, beetles colonized almost exclusively on plants with rosette galls and exhibited a clumped distribution among them, suggesting a possible advantage for aggregating on the galled plants. We found that beetles remained longer on galled plants with previous beetle damage than that without beetle damage. No effect of beetle damage was found on plants without a gall. Similar interactions between galler-infestation and beetle damage were found in beetle's feeding choice, plant diterpene and serine protease inhibitor production and volatile organic compound (VOC) emission. These induction patterns indicated that the gall-midge can alter how plants respond to the beetle damage, and that gall presence coupled with beetle damage improves leaf palatability for the beetle. Finally, we found reciprocal effects of beetles on gall-midge performance to be neutral to positive, suggesting that the observed field association of the two herbivores could be formed by plant-mediated facilitation. Our study suggests that an ecosystem engineer could have significant impact on herbivore community not only by changing plant morphology and quality, but also by modifying plant induced-responses to subsequent herbivores.

# Dim-light foraging bees: construction of a new photic niche

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Foraging activity of bees is typically associated with visits to flowering plants during diurnal periods with ample sunlight. However a variety of bee lineages have phase-shifted their foraging to periods of dim-light. The majority of such behaviour occurs during crepuscular periods (sunset-astronomical twilight & astronomical twilight-sunrise) and may extend beyond these bounds surrounding full-moon phases, whereas a select few taxa are truly nocturnal and can consistently navigate in ambient starlight alone. There are documented occurrences of dim-light foraging in five of the nine bee families - *per* Michener: Andrenidae, Apidae, Colletidae, Halictidae, Megachilidae. Dim-light foraging can be either facultative or obligate, however it is only the obligate lineages that exhibit convergent external morphological specialisations, including: enlarged eyes (ocelli and ommatidia of compound eyes); relatively larger body size (*cf*. diurnal relatives); and wing dimensions typical of smaller species. It is the lack of external morphological specializations in facultative dim-light foraging bees that support the concept of *niche construction* – wherein behavioural change precedes genetic modifications, and actively drive this entry into a new photic niche. Such behaviourally driven theories extend beyond standard evolutionary theory, because the behaviour biases selection in a non-random manner and changes gene frequencies from one generation to the next. In this sense, it is the behaviour that creates new environments that could not otherwise occur; which is the flip side of standard views of evolution wherein a change of environment is believed to drive natural selection, to inturn affect gene frequencies. The world's largest and most ecologically successful radiation of dim-light foraging bees occur within the neotropical sweat bees, specifically the genus *Megalopta* (Augochlorini). *Megalopta* exhibit novel visual neuroanatomical specialisations and also develop small social colonies, which make them particularly well suited to evolutionary ecological studies that link caste-specific social behaviours to environmental cues, such as light.

# Assessing the threats and strategic responses to exotic mosquitoes

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Mosquito-borne disease management in Australia faces numerous challenges. Threats posed by endemic mosquito-borne pathogens, such as Ross River virus (RRV), may increase with a changing climate, but exotic mosquitoes and pathogens are an emerging threat. Local authorities must develop regionally specific surveillance and response programs to identify and respond to exotic mosquito incursions. The Asian tiger mosquito, *Aedes albopictus*, poses the greatest risk to temperate regions of Australia due to its peri- urban ecology and proven ability to transmit exotic pathogens, including dengue and chikungunya viruses. The mosquito is widespread in neighbouring countries, has been detected at international ports and, given the increasing frequency of flights from regions where this mosquito is abundant, it is probable that this species will be introduced in the future. When this occurs, what is the likelihood that it becomes established and could it render temperate regions of Australia to increased outbreaks of arboviral disease? Recent laboratory studies have confirmed that *Ae. albopictus* could survive as eggs under climatic conditions typical of a Sydney winter before proliferating in the summer months. Despite the endemic mosquito, *Aedes notoscriptus*, sharing the same ecological niche as *Ae. albopictus*, cohabitation studies demonstrated that interspecific competition would not limit the spread of *Ae. albopictus*. Critically, vector competence experiments have demonstrated the ability of *Ae. albopictus* to transmit endemic pathogens and, given their propensity to bite humans, could contribute to human-mosquito-human outbreaks of RRV in urban areas of NSW, exploiting the niche unoccupied by enzootic vectors that currently limit transmission to the metropolitan fringe. Local authorities need to develop a multiagency strategic approach to surveillance concomitant with strategic incursion responses beyond existing mosquito-borne disease surveillance programs to reduce the pest and public health threats associated with exotic mosquitoes.

# *Trichogramma* parasitoids for control of Lepidopteran borers in Taiwan: species distribution, life history traits, and *Wolbachia* infections

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*Trichogramma*, polyphagous endoparasitoids of lepidopteran eggs, are used against a variety of crop pests throughout the world including those of sugarcane and corn in southeastern Asia. Their ability to be easily and economically reared on factitious hosts and their wide host range has contributed to their widespread use in pest control. A key component in evaluating the feasibility of using a given biocontrol agent is to evaluate its likely impact under field conditions: the overall aim of this study is to select strains for eventual release in crop areas for control of lepidopteran borer pests of sugarcane and corn. To this end, we identified common *Trichogramma* species emerging from corn borer egg masses throughout southwestern Taiwan, compared their distribution, life history characteristics, assessed their thermal limits and identified the *Wolbachia* infection status of collected *Trichogramma* parasitoids. *Trichogramma ostriniae* was the most commonly-collected species on corn, with occasional detection of *T. chilonis* and an unidentified species designated as *T.* sp. *y.* Though the sex ratio varied widely between sites, *Wolbachia* infection was detected around sites in all species. *Wolbachia* –infected *T. ostriniae* were most tolerant to high temperature stress. *Trichogramma chilonis* had lowest fecundity of the three species tested, and a *Wolbachia*-infected *T. ostriniae* strain had lower fecundity than an uninfected strain. Given the limited availability of distribution and historical data for *Trichogramma* species in Taiwan, the current study provides a baseline for future work, and also highlights the importance of accurately identifying species when establishing colonies of natural enemies for biocontrol.

# Insects as food and feed in Australia: purpose and scale

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Publicity regarding the use of insects as human food in Australia seems to concentrate on people dining on whole insects in a western culinary context. This masks some of the important questions that need to be considered if we are serious about using insects as food. In Australia, the use of insects in non-traditional dining is probably a fairly minor issue because it involves a relatively small proportion of Australians. More important issues are traditional Aboriginal insect foods, the use of insect derived products as food supplements, and the use of insects as animal feed. In addition, promoting the use of insects as food and feed in Australia's near northern neighbours has important potential health, nutrition and fauna conservation benefits. One of the important practical factors influencing the successful use of insects as food or feed is the scale of production. Insect production for use at the household, village or local community levels has its benefits at the local level, but do we need to consider factory level production systems if we want to see national or global success? Some possible scenarios are presented for the future adoption of insects as food and feed in Australia.

## Effect of raspberry ketone supplements on mating performance of Queensland fruit fly, *Bactrocera tryoni*

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Raspberry ketone (RK) is highly attractive to sexually mature, but not immature, males of many *Bactrocera* species, and acts as a metabolic enhancer in a wide diversity of animals, including Queensland fruit fly (Q-fly). Related compounds have been found to promote sexual success when fed to sexually mature male Q-flies. Effects on immature males are unknown. We considered the possibility that, as a metabolic enhancer, RK might accelerate sexual maturation in Q-flies with a view to use as a pre-release treatment for Sterile Insect Technique (SIT) programs. Recently emerged adult Q-fly males (0-24 hrs old) were exposed to RK-treated food for 48 hours. Four doses of RK (1.25, 2.5, 3.75 and 5 %) along with 0 control were tested with two types of food; sugar alone, and sugar mixed with yeast hydrolysate (3:1). By mixing RK with food, we were able to treat sexually immature males that otherwise would not feed on RK. Mating trials were conducted every day from 4 days after emergence until 10 days and then at 5-day intervals until 30 days. For mating trials, each tested male fly was transferred to an individual 1-L clear plastic cage and paired with a 12–17 day-old protein-fed virgin female. Twenty males of each diet treatment and each RK dose were tested at each age. Separately, effects of RK on longevity were tested in individual cages (70 mL, solitary) and in group cages (1 L, containing 5 flies). All RK doses resulted in significantly increased mating success at early ages for the flies that were provided yeast, but no effects were found for flies that were provided only sugar as food. There was no evidence that RK affected longevity at any of the doses tested. We conclude that RK shows potential as a pre-release supplement for SIT.

# First occurrence of the *Monomorium setuliferum* species group (Hymenoptera: Formicidae) from the Arabian Peninsula, with description of a new species

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The new myrmicine ant *Monomorium sharafi* sp. n. is described from worker castes collected in Rawdhat Khorim nature preserve at Riyadh, Kingdome of Saudi Arabia. The new species is a member of the Afrotropical *M. setuliferum* species group and with closest resemblance to *M. havilandi* Forel, 1910, from South Africa. It is the first member of the *setuliferum* species group to be recorded from the Arabian Peninsula and outside the Afrotropical region. Differential diagnosis between *sharafi* sp. n. and *havilandi* is presented.

# Molecular species identification in biosecurity: a case study of an *Aedes aegypti* interception in Melbourne, Australia

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Routine surveillance is conducted at international ports around Victoria for exotic mosquitoes such as *Aedes aegypti* and *Aedes albopicta*. These mosquitoes pose a biosecurity risk due to their ability to transmit non-endemic diseases of considerable public health significance such as dengue, chikungunya, and yellow fever. Surveillance traps capture adult mosquitoes, and their eggs and larvae, however only adults and larvae are used for morphological species identification. In January 2015 eggs were found in one of the surveillance traps located at the Melbourne International Airport, following an interception of an *Aedes aegypti* adult mosquito. Species identification of eggs is hindered by the time required for eggs to hatch and develop into a form usable for species determination. Subsequent delays in identification can impact the appropriate treatment for the port. An alternative to morphological identification is DNA barcoding, a molecular approach that uses a short DNA sequence to determine species. In order to barcode the eggs and identify the species, DNA was extracted and the 5’ end of the mitochondrial Cytochrome Oxidase I (COI) gene was amplified and sequenced. The sequence was compared with reference specimens on the online Barcode of Life Database (BOLD), returning a species identification result of *Aedes aegypti*, with a 100% identity match. The barcoding process took two days, after which the airport area was treated to prevent the establishment of any *Aedes aegypti* mosquitoes. The use of DNA barcoding during this exotic mosquito detection helped to dramatically reduce interception response time and confirmed the usefulness of the technique in mosquito surveillance programs.

# Syco-killers: lethal mate competition in fighting fig wasps

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In many fig wasp species, armoured wingless males engage in lethal fights for access to females inside fig fruits, which act as discrete mating patches. Kin selection generally opposes killing brothers, because their reproductive success provides indirect genetic benefits (inclusive fitness). However, siblicide may be avoided if a) brothers do not occur in the same figs, or b) males avoid fighting brothers. Alternatively, siblicide may occur because c) intense mate competition between brothers at the local scale overcomes kin selection effects, or d) males do not recognise kin. A fig may also contain wasps from other closely related species and it is not known if males also fight with these individuals.

We used nine microsatellite loci in the first genetic analysis of fighting behaviour in fig wasps. We assigned species and sibling identities to males and tested alternative fighting scenarios for three *Sycoscapter* wasp species (Chalcidoidea: Pteromalidae: Sycoryctinae) in 58 figs of *Ficus rubiginosa*. About 60% of figs contained males from more than one *Sycoscapter* species and, while 80% of fights were between conspecifics, a surprising 20% were between heterospecific males. Within species, few figs contained brothers, suggesting that females typically lay one son per fig. Overall, most males do not compete with brothers and all fights observed were between unrelated males.

We also analysed genetically all male and female *Sycoscapter* wasps from a complementary (co-sampled) set of 55 figs. This analysis revealed that individual adult female wasps typically lay eggs in several figs, but only a few eggs (1-10) per fig. Moreover, the typical clutch laid by a female in a given fig comprises one son plus two daughters, generating female-biased sex ratios overall. Our study illustrates the value of molecular markers for uncovering details of insect reproductive strategies in the field.

# Honey bee nutritional requirements and foraging behaviours change when infected with the gut parasite *Nosema ceranae*

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The European honey bee, *Apis mellifera*, is an economically important generalist pollinator responsible for increasing agricultural outputs and maintaining plant communities. Infection by a microsporidian gut parasite, *Nosema ceranae*, increases the energetic demand of infected *A. mellifera* individuals. We manipulated pollen availability and quality in the diet of infected honey bees to determine whether pollen plays a role in resilience against *N. ceranae*. Bees were fed 5µl of 1:1 w:v sucrose either with or without $1 \times 10^5$ *N. ceranae* spores, caged in groups within growth chambers, provided with sucrose solution, and given access to either redgum (*Corymbia calophylla*), whitegum (*Eucalyptus wandoo*), or no pollen. After 19 days, 50.5% of infected bees with access to the more protein-rich redgum pollen remained alive compared to 38.9% of the whitegum-fed bees and 39.4% of the sucrose-only group. In contrast, non-inoculated groups experienced 61.4%, 57.9% and 59.0% survival for redgum, whitegum and sucrose-fed groups, respectively. Groups offered pollen did not differ in the amounts they consumed. To provide insight into how different *N. ceranae* infection influences foraging choices, we examined the pollen foraging characteristics of hives with different levels of natural infection. We observed a decline in pollen foraging in hives with higher infection levels ($p = 0.006$). Our results suggest that pollen quality plays a role in the health of bees infected with *N. ceranae*, though infected hives do not increase pollen collection to combat disease. Our work indicates high-protein pollen may aid in the treatment of *N. ceranae* and highlights a need for further study in how disease may affect floral preferences and pollination abilities of *A. mellifera*.

# Expecting the unexpected – the tale of *Cryptolestes cornutus* (Coleoptera:Laemophloeidae)

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*Cryptolestes* flat bark beetles are well known as stored product pests. This is a group that has made the jump from their natural hosts into dried foods and stored grains. *C. cornutus* was described in 1989 by the United States Department of Agriculture with specimens collected from dried chillies entering the US border from Thailand. Surveillance by the Northern Australia Quarantine Strategy has revealed this beetle at three locations in Western Australia. The circumstances raise some intriguing questions. We tell the tale of its discovery in Australia and explore why it is here.

# Molecular and morphological variation between a commonly widespread and a newly described *Plutella* species in Australia

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Diamondback moth, *Plutella xylostella* L. (Lepidoptera; Plutellidae) is one of the most destructive pests of Brassica crops, with widespread resistance to chemical controls and damage and control costs estimated to be US$ 4-5 billion annually.

In Australia the genus *Plutella* was represented by a single introduced species, *P. xylostella* until the description by Landry and Hebert (2013) of a native taxon, *P. australiana*, which they identified using cytochrome oxidase 1 (CO1) gene sequence and morphology of genitalia to describe *P. australiana* based on specimens caught in light traps. However, no data is available on the life history or possible pest status of this species.

Our study has collected adults (from light traps) and larvae (from crops) from around Australia and examined the specimens using both mitochondrial and nuclear marker genes and genitalia morphometric analysis. We are conducting life history and mating studies in the laboratory using iso-female lines of both species.

# Susceptibility of the silverleaf whitefly parasitoid *eretmocerus hayati* to insecticides used in cotton

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An important natural enemy of Silverleaf whitefly is the wasp *Eretmocerus hayati*. It is however susceptible to insecticides applied to cotton to control whitefly and other pest insects. We studied the toxicity of five insecticides that are registered for pest management in cotton by testing direct exposure and residues. The products we tested included; cyantraniliprole, sulfoxaflor, flonicamid, clothianidin and fipronil. We tested the effect of direct exposure and then residue at 1, 2 and 8 days after application. For cyantraniliprole and sulfoxaflor direct exposure was more toxic than residues. For the other products there was no difference between direct exposure and residue. Direct exposure of flonicamid was significantly less toxic than the other insecticides. Clothianidin residue was significantly more toxic than the residue of the other insecticides. Overall clothianidin was the most toxic insecticide followed by sulfoxaflor, fipronil, cyantraniliprole and flonicamid was the least harmful.

# Land use influences mosquito communities and disease risk on remote tropical islands: a case study using a novel sampling technique

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Land use changes, such as deforestation and urbanization can influence interactions between vectors, hosts and pathogens. The consequences may result in the appearance and rise of mosquito-borne diseases, especially in remote tropical regions.  Tropical regions can be hotspots for the emergence of diseases due to the high biological diversity, and complex species interactions. Furthermore, frontier areas are often haphazardly surveyed as a result of inadequate or expensive sampling techniques, which limit early detection and medical intervention. We  trialed a novel sampling technique of non-powered traps and a $CO_2$ attractant derived from yeast and sugar to explore how land use influences mosquito communities on four remote, tropical islands in the Australian Torres Strait. Using this technique we collected > 11,000 mosquitoes from urban and sylvan (natural vegetation) habitats. We found that human land use significantly affected mosquito communities in this region. Mosquito abundances and diversity were higher in sylvan habitats compared to urban areas, resulting in significantly different community compositions between the two habitats. An important outcome of our study was determining that there were greater numbers of disease-vectoring species associated with human habitations. . Based on these findings we believe our novel sampling technique is an adequate and realistic tool for assessing mosquito communities in remote tropical regions. The continual development of inexpensive, unpowered and readily transportable trapping methods is vital to the surveillance of mosquito-borne diseases and healthy human communities in the world's remote tropical regions.

# Seasonal prevalence and role of minor vectors in malaria transmission in coastal and forest areas in southwestern Nigeria

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Malaria remains the major burden to human health in Nigeria and the mosquitoes primarily responsible for the disease transmission include *Anopheles gambiae* Giles, Anopheles arabiensis Patton, *Anopheles funestus* Giles. Apart from these major vectors, other species often regarded as minor or secondary vectors include *An. nili* (Theobald), *An. moucheti* Evans, *An. coustani* Laveran complex, *An. leesoni* Evans and *An. rivulorum* Leeson. Due to complexity of malaria vectorial systems in Africa, with different species involved in transmission in different bio-geographical zones, there is the need for the acquisition of further knowledge to improve the control of the disease. In the present study, we investigate the role played by these minor or secondary vectors in the malaria transmission intensity in the forest and coastal areas of Nigeria. In total, 4,332 female anophelines belonging to seven different species were collected. Major vectors including *An. gambiae* Giles, *An. arabiensis* Patton, *An. funestus* Giles and *An. melas* represented ~98% of the total anopheline fauna identified. The remaining 2% was composed of *An. nili* (Theobald), and *An. moucheti* Evans, *An. coustani* Laveran complex, and *An. leesoni* Evans. There was no significant difference in seasonal density of the minor vectors in the areas (P=0.6969), however *An. leesoni* Evans occurred more in the dry season. Circumsporozoite (CSP) infection status as determined by Enzyme Linked Immunosorbent Assay (ELISA) showed that the mean infection rate of minor vectors (0.82%) was significantly (P=0.7652) lower than that of major vectors (2.36%). *Plasmodium falciparum* infection was high and repeatedly found in *An. moucheti*, indicating its contributory role to the total malaria transmission especially in the forest area. This study provides information germane to the understanding of the potential role played by the identified Anopheles mosquitoes in malaria transmission.

# One step ahead: parasitoids disperse farther and form larger populations than their fig wasp hosts

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The structure of populations across landscapes influences the dynamics of their interspecific interactions. Understanding the geographic structure of populations can thus shed light on the potential for coevolution and adaptive responses of interacting species. Parasitism is an important aspect of insect ecology in natural and agricultural settings, and also represents a significant force in the evolution of plant – insect interactions. However, there have been few comparisons of population structure in an insect host and its parasitoid. We used microsatellite markers to analyse the population genetic structure of *P. imperialis* sp. 1 (Hymenoptera: Agaonidae), a pollinating wasp of *Ficus rubiginosa* (Moraceae), and its main parasitoid, *Sycoscapter* sp. A (Hymenoptera: Pteromalidae), in eastern Australia. Matched sampling was conducted at several sites in two regions separated by up to 2000 km. We found that pollinators occupying the two regions represent distinct populations, but there was limited genetic structure in the parasitoid across the sampled range. We observed weak patterns of isolation by distance for each species, suggesting that both pollinator and parasitoid are capable of long-distance dispersal. The contrasting geographic structure of host and parasitoid populations could have varying influences on the scale and direction of evolution in each species. Incongruent structure of host and parasitoid populations highlight the potential for geographic mosaics in an ecologically important and evolutionarily significant system, supporting the significance of their role in the coevolution of interspecific interactions. Furthermore, we provide the first report on the population structure of a non-pollinating fig wasp species.

# The brown marmorated stink bug, *Halyomorpha halys* (Heteroptera: Pentatomidae); diagnostic features and similar Australian species

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The brown marmorated stink bug, *Halyomorpha halys* (Heteroptera: Pentatomidae) is an exotic agricultural pest which is being increasingly intercepted at Australia's borders. This poster will aid in the identification of this and some similar Australian insects.

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# Screening of sugarcane cultivars to assess the incidence against *Chilo infuscatellus* (Pyralidae, Lepidoptera)

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Research was conducted to screen out the fifteen sugarcane cultivars with an objective to assess the varietal response against the *Chilo infuscatellus.* The experiment was designed in a randomized complete block designed (RCBD) with three replication. It is evident from the results that the US-394 showed maximum pest infestation (21.90%) while NSG-555 and (21.60%) showed significantly different from other varieties BL-4, US-162, US-394, L-116 and CP-77-400. The variety US-718 showed minimum infestation (15.49%) after US-133 and US-676 with (15.59) and (16.46%). The variety CPF-237 showed (17.81%) which significantly different from US-312, US-1491, US-824 and CPF-246 respectively. The Host Plant Susceptible indices (HPSIs) showed that CPF-237 showed maximum HPSIs (13%) and proved susceptible whereas all the other varieties showed equal response each with 11% HPSIs. The variety US-718 showed minimum HPSIs (10%). It concluded that most of the varieties of sugarcane showed equal response towards population of *Chilo infuscatellus* except CPF-237 that showed maximum HPSIs (13%).

# An epiphytic ant-plant and the structure of arboreal ant communities

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Epiphytes play an important role in structuring arboreal ant communities. They can provide physical niches (typically nesting sites) and nutrients in the form of nectar and hemipteran honeydew, resources that usually increase ant species diversity. Ant-plant mutualisms are a common feature of tropical forests worldwide. Ant-plants provide ants with nesting space and occasionally food rewards. In return the ants provide the plant with protection from herbivores and/or provision the plant with nutrients. To date, little work has examined what role epiphytic ant-plants play in structuring arboreal ant communities. The ant-plant *Myrmecodia beccarii* (Rubiaceae), endemic to northern Queensland, is an epiphyte found in *Melaleuca* woodland and mangrove forest. It is inhabited by the ant *Philidris cordata* (Dolichoderinae) which provisions it with nutrients. We used carbohydrate and protein lures to survey the arboreal ant fauna of *Melaleuca* woodlands with populations of *M. beccarii*. We found that the distribution of territorially dominant ants did not overlap, rather they were arranged in discrete clusters – what is commonly referred to as an 'ant mosaic'. This mosaic is a result of competition between the two dominant arboreal ant species: the green tree ant *Oecophylla smaragdina* (Formicinae) and *P. cordata*. We suggest that the ant-plant *M. beccarii* plays a role in structuring these communities by providing *P. cordata* with nesting space, a limiting resource for this species. Our findings highlight the importance of mutualistic insect-plant interactions in the structuring of insect communities.

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