

The blue-rinse moth with the secret inflatable hair-drier, the star-spangled can-opener and other wonders of the wainscot world

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New Zealand used to have an amazing radiation of Hadeninae (Lepidoptera: Noctuidae), beating anything the Australians have to offer by a trans-Tasman mile. Recent taxonomic shenanigans have resulted in New Zealand losing all its hadenines, but fortunately these have been replaced by exactly the same number of noctuines of the tribe Leucaniini. How many are there? In how many genera? What do their genitalia look like when squashed and mounted on slides? Why, oh why? All of these questions will be addressed, though not necessarily answered.

Patterns - and lack of patterns - in Thysanoptera host associations

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There is no direct correlation between the number of thrips species in an area and the number of available plant species, nor yet between the number of thrips species and the number of species in any given higher plant taxon with which those thrips are associated. Some plant taxa have a disproportionately large number of associated thrips species, yet other taxa are not exploited. Thrips species richness will be considered in relation to the relatively few plant species on which these insects are dependent.

Australasians behaving badly Up-Over: a downunder thrips killing an invasive New Zealand tree in California

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This is a story of novel interactions leading to unintended biocontrol. It is the result of human intercontinental trade between the South Pacific and North America. Ngaio, *Myoporum laetum*, is a New Zealand endemic small tree that was widely planted through coastal California in the 1950s to 1970s. It has naturalised and become an environmental weed in places. In 2005, an unidentified thrips was found on ngaio in Orange County, later described as *Klambothrips myopori*. The thrips has close relatives in Australia and is presumed to be of Australasian origin. Since 2005, *K. myopori* has undergone a dramatic, sustained population eruption that has killed off large numbers of ngaio. We provide a quantitative description on the impacts on *M. laetum* at several Southern California coastal sites. In just three years, *K. myopori* had reached almost every individual at the surveyed sites, killing 25–41% of plants, and partially defoliating most of the rest. Searches for *Klambothrips* in New Zealand to date have been unsuccessful, and are ongoing in Australia. If the species is not a New Zealand native, it may pose a biosecurity threat here. Regrettably, since its invasion of California, *K. myopori* has been accidentally transferred to Hawaii where it is now beginning to kill off individuals of the Hawaiian endemic naio, *Myoporum sandwicense*.

Lessons from the diet of a native pest, the grass grub beetle - host shift or host range expansion?

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Understanding the mechanisms underpinning the process of biological invasions is nowadays recognised as a challenge. The particular status of ‘pest’ and ‘invasive’ given to some native insects holds potential as an approach to unravel fundamental aspects of the biological invasion phenomenon. With more than 60 native insect species in New Zealand that have become prominent for the environmental and economic damage that they induce, there are many opportunities to investigate the characteristics that enable an organism to become invasive. One such opportunity is given by investigating the diet of the pest *Costelytra zealandica* (White) (Coleoptera: Scarabaeidae), also known as ‘grass grub’, and by clarifying the relationship between an emerging invasive phytophagous insect and the dietary component of a changing environment. In this study, we investigated the fitness response of different populations of *C. zealandica*, to several feeding treatments involving native and exotic host plants under different temperatures. The results of this experiment suggest that *C. zealandica*, occurring in exotic pastures, might have experienced a host-shift (loss of fitness on ancestral host) rather than a host-range expansion (ability to equally use both ancestral and new host). This statement is currently under further investigation, and subsequent results will also be presented. Ultimately, the combined results of this series of experiments, will increase understanding of biological invasions.

Eriophyoid mites on *Corymbia* spp. (Myrtaceae)

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Corymbia spp. are high priority species for hardwood timber plantation development in Australia. Eriophyoid mites can severely affect their growth. The eriophyoid mites on *Corymbia* spp., their relationships, biologies and damage were determined in field and laboratory studies in south-east Queensland, Australia. Seven eriophyoid species were found on *Corymbia citriodora*; that number of species is very rarely found on one host. In spring, *Acalox ptychocarpi* and *Acalox* sp. caused the initial damage on immature leaves. *Rhombacus* spp. moved to the damaged area and all species cohabited. Epidermal blisters formed and spot and patch type damage were observed. In mite feeding experiments, both spot and patch type damage were seen on inoculated potted and in-ground seedlings of the *C. citriodora* complex. The mites were active during the mild, subtropical winter but there were differences in population densities between localities. In the laboratory, *Rhombacus* spp. adults fed on undamaged, mature leaf discs, but *Acalox* spp. and immature stages of the other mites did not feed.

The role of bark beetles as vectors in the colonisation of windthrown timber by fungi

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Recent wind and snow storm events in New Zealand affecting plantation forests of *Pinus radiata* have raised questions regarding the colonisation of fallen trees by sapstain fungi. These fungi are known to be spread by a multitude of factors including wind, rain splash, harvesting processes, and insect vectoring. Apart from the ecological interest in these interactions between fungi, plants and insects, sapstain fungi are also economically important because their hyphae discolour the sapwood and reduce the overall quality of the timber. In New Zealand we know that snapped trees accumulate sapstain and insect attack faster than trees that topple but remain rooted, and that the most common stain fungus affecting these trees is *Diplodia pinea*. Manipulative experiments were established to examine seasonal and regional variation in sapstain attack following windthrow, and to investigate the importance of bark beetles as vectors. A range of methods were implemented to assess the effects of bark beetles. Experimental billet logs were caged to exclude beetles, and subsequently analyse fungal attack in comparison with identical logs left exposed to beetles. Also, individual beetles were analysed to determine what fungal species may be associated with them. Finally, a novel application of DNA melt peak analysis was developed to investigate the fungal communities on beetle vectors at both inter-specific and intra-specific levels.

Host range testing of xylem feeders by measuring real time feeding

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We investigated whether the Electrical Penetration Graph (EPG) technique could be used as a rapid method to determine the host-range of invasive xylem feeders. The New Zealand endemic xylem feeder *Carystoterpa fingens* (Hemiptera: Aphrophoridae) was studied as a model insect. Stylet penetration and real time feeding of adult *C. fingens* was monitored on EPG in the laboratory to assess whether 17 plant species belonging to 15 families were hosts. EPG waveforms indicating xylem ingestion were categorized based on their amplitude, frequency, voltage level, and electrical origin. Four plant species on which *C. fingens* spent less than 12% probing and less than 2.3% for xylem ingestion of the total recording time were ranked as non-host plants. Five additional EPG parameters (duration of xylem ingestion as a percentage of probing period, number of xylem ingestion events, length of the longest xylem ingestion event, duration from the beginning of the recording to the first probe, and the time between the first probe and the first xylem ingestion) were measured from the remaining 13 plant species. Plant species with the longest duration of xylem ingestion with the longest xylem ingestion events were deemed to be host plants. Host plant acceptance was also compared by the time taken to start probing and to reach the xylem. Accordingly 17 plant species were ranked from 'hosts' to 'non-hosts' of *C. fingens*.

A new tussock butterfly species (Nymphalidae: Satyrinae: Argyrophenga) for New Zealand?

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Over the last ten years large series of tussock butterflies (*Argyrophenga* spp.) were collected from throughout the South Island. It was noticed that specimens of *Argyrophenga antipodum* found in alpine areas of Central Otago differed in both morphology and behaviour to those found elsewhere. Using a combination of morphological, molecular, behavioural, and ecological information we are investigating the taxonomy of these butterflies, taking an integrated approach. DNA sequences from mitochondrial and nuclear genes were used to test the hypothesis that there is an additional fourth species of *Argyrophenga* present in Central Otago, which is distinct from the three named species; *A. antipodum*, *A. janitae* and *A. harrisi*.

Multigene phylogeny of Australian darkling beetles (Coleoptera: Tenebrionidae)

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Darkling beetles (Coleoptera: Tenebrionidae) are species rich and show a great diversity of morphology. Adaption to scavenging primarily on dead plant and fungal material has allowed them to better survive in arid habitats and it is thought this adaptation has led to their successful diversification. There are currently over 1600 known species of Australian tenebrionids in 216 genera in eight sub families. Relationships between almost 100 genera of darkling beetles were investigated using two mitochondrial (cytochrome oxidase 1 and partial large subunit, 16S) and nuclear (partial large subunit, 28S) genes. Separate and combined data analyses were performed under parsimony, maximum-likelihood and Bayesian methods. The utility of each of these genes for examining relationships differed for each gene and is discussed. We also assess the traditional morphology-based classification of tenebrionid families, sub families and tribes based on the results of the phylogenetic analyses.

Taxonomic triage: molecular tools complementing morphological description, a New Zealand case study

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Morphological analysis was once the only means of accomplishing the taxonomical description of new species and identifying those already described. Today, molecular tools are often complementary to classic morphological description. Indeed, DNA barcoding is now recognised as an additional character that can contribute to taxonomic descriptions and facilitate identification of morphologically cryptic species. In many cases, molecular tools are solicited after the morphological description of a species. However, there is also significant benefit from using these tools the other way around. One such circumstance is when a taxonomic description is based on the adult, 'trappable' life stage of a pest species, but is not available or extremely difficult to attain for the more sessile and, often more damaging juvenile stages. In New Zealand this situation exists for the larval stage of the native scarab *Costelytra zealandica* (White) (Coleoptera: Scarabaeidae), which is a significant pasture pest that occurs sympatrically with con-generic non-pest larvae. High morphological similarity makes it extremely difficult to study these larvae for ecological or pest management research without first having confirmed their species identity. We report on the use of molecular markers to separate morphologically indistinct larvae into their species groups, which can then be critically examined to try and correlate novel morphological features that distinguish them. In this presentation, we will demonstrate how we triaged morphological description with molecular tools to differentiate the larval stages of the pest *C. zealandica* from the non-pest species, *C. brunneum* (Broun).

Phylogeny of Australian *Saprinus* spp. Erichson (Coleoptera: Histeridae) - contrasting ecological, morphological and molecular data

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The genus *Saprinus* Erichson (Coleoptera: Histeridae) is a highly conspicuous taxon of predatory beetles often observed on mammalian carcasses throughout Australia. Recent studies in Richmond, NSW found that due to the relatively predictable presence of *Saprinus* spp. and other Sapriniinae at carrion throughout the year, these taxa may provide potential as indicators for estimating the post mortem interval. Their preference for feeding on dipteran maggots and pupae also makes them potentially important biological control agents. However, the identification and classification of many of the taxa within the subfamily of Sapriniinae based on morphology alone is difficult and remains unresolved. This is especially evident for the species currently identified as *Saprinus australis*, *S. cyaneus*, *S. pseudocyaneus* and their existing synonyms. We therefore utilised available information about morphology as well as molecular techniques in an attempt to clarify the identification and classification of the Australian *Saprinus* spp. This was achieved using fresh, field-collected, as well as dry museum specimens. Initial results utilising the mitochondrial cytochrome oxidase I (COI) and nuclear 18S rRNA genes have shown that the current classification of the genus *Saprinus*, based on morphology, is polyphyletic. Despite the previous synonymisation of *S. cyaneus* and *S. laetus* the current study has shown that they are, separate species. This study also shows that while *S. cyaneus* and *S. pseudocyaneus* have previously been differentiated morphologically, they are indistinguishable on the basis of COI and 18S genes. Further work on other *Saprinus* spp. and other genera in the Sapriniinae will attempt to further elucidate the identity and phylogeny of this important beetle subfamily.

Structure and function of 3-D photonic crystals in weevils (Coleoptera: Curculionidae)Ainsley Seago *¹¹ CSIRO Ecosystem Sciences, ANIC, GPO Box 1700, Canberra, 2601, ACT, Australia

Beetles display a remarkable diversity of colour patterns, including iridescent hues and ultraviolet reflectance. The iridescence of the weevil clades Eupholina, Pachyrrhynchini, Naupactini, and other brightly-coloured entimine species is unique among beetles: while other groups derive their colour from pigments or two-dimensional multilayer reflectors, the colours of entimine weevils are produced almost entirely by three-dimensional photonic crystals analogous to those found in mineral opal and titanium oxides. In this complex iridescence mechanism, a nanoscale three-dimensional lattice of chitin and air reflects certain wavelengths of light with constructive interference, producing vivid structural colours. In entimines, this lattice forms within the lumen of the scales during pupation, as an aggregation of small, variously-oriented crystalline domains. Using electron microscopy and short-angle X-ray scattering (SAXS), my collaborators and I have examined the lattice structure within the scale lumen of twelve weevil species selected to represent all major clades of the family Curculionidae. Here I present the first hypothesis for an evolutionary pathway by which these highly-ordered photonic structures could have arisen, and note ecological correlates which suggest a selection mechanism.

New Zealand's micro-caddisfly fauna: why so depauperate?

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Today's distributions of faunal groups reflect historic events — geological and evolutionary, as well as dispersals, extinctions and chance. To what extent is each of these responsible for the depauperate micro-caddisfly (Trichoptera, Hydroptilidae) fauna of New Zealand? This question is explored by comparison with the fauna, geology and geography of New Caledonia, Tasmania and mainland Australia.

The evolution of sticks; quantifying clasper morphology across a hybrid zone in the stick insect genus *Clitarchus*

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A hybrid zone is the geographic area where two species can meet and form offspring. It is common for the offspring of hybridising species to have reduced fitness. The theory of reinforcement predicts that prezygotic barriers will evolve between hybridising groups and there will be selection against hybridisation. In the Far North of New Zealand, the widely-distributed stick insect species *Clitarchus hookeri* is replaced by an ecologically similar and undescribed species of *Clitarchus*. These species are differentiated on the basis of male terminalia (specifically the claspers), egg morphology and mitochondrial DNA. Populations sampled between the two species show intermediate morphology. The aim of our research is to quantify the intra- and interspecific variation in clasper structure of *Clitarchus* populations across Northland. It is likely that variation in genital structures represents the differing abilities of males to control mating duration, and that those males with hybrid clasper phenotype suffer from a reduction in fitness. Quantification of clasper structure will provide a basis for addressing the questions: Does variation in morphology correspond to differences in mating behaviour? And does morphological variation reflect reproductive isolation? The research presented will cover the methods behind complex morphological quantification and demonstrate the relationship with speciation.

The curious case of New Zealand Coelostomidiidae

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The endemic fauna of New Zealand has always attracted much interest for their unique attributes, such as large size and flightlessness. But such attributes are just scratching the surface of an extremely complex system, as exemplified by the scale insect-honeydew system. In New Zealand, an endemic family of scale insects, Coelostomidiidae, comprises nine species that occupy a range of native ecosystems throughout the country. These scale insects produce copious amounts of carbohydrate-rich honeydew and influence several trophic levels in the food-web, as well as important ecosystem functions such as carbon cycling. Our research aims at understanding microbial and ecological aspects of this system. This paper reports on the bacterial symbionts that co-exist with endemic New Zealand scale insects. Using modern molecular microbiology techniques, we detected up to three novel insect bacteria and several other facultative bacteria associated with coelostomidids. Using fluorescence in situ hybridisation, dense clusters of Bacteroidetes bacteria interspersed with facultative Wolbachia were detected in *Coelostomidia wairoensis*. In addition we are investigating the coevolutionary relationships of these insects with their bacterial symbionts. Using modern molecular tools instead of traditional methods has allowed us to resolve some long standing mysteries, such as the phylogeny of New Zealand Coelostomidiidae. This work will provide the first insights into how microbial symbionts may contribute to the ecological success of New Zealand's scale insects.

Associating the life stages of Calocidae (Trichoptera) using genetic methods

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The morphological characters associated with specific life stages can provide important taxonomic information. In holometabolous insects the immature forms are greatly different to that of the adult and, in many species, associations of immature life stages are difficult to determine. This is true of many of the Trichoptera species. In the past, associating larval specimens of Trichoptera has required either rearing larvae into adulthood or collecting paratype male pupae. The former of these is time consuming. The latter relies on chance collecting of appropriate specimens. Both are often unproductive. Through analysing genetic data, rapid and accurate associations of life stages can be made. Using nuclear (EF1a and 28s) and mitochondrial (CO1) DNA fragments, we have been able to associate the larval life stages of 5 species in the family Calocidae.

Phylogeography of the trans-Tasman marine caddisflies (Trichoptera: Chathamidae)

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Marine insects are an oddity but New Zealand is host to a small family of caddisflies whose larvae are entirely marine. Five species are described in the Chathamidae, all from the New Zealand region. One species (*Philanisus plebeius*) has long been known to also live in Australian waters. This is the only example of a non-endemic New Zealand caddisfly. The origin of this trans-Tasman distribution has been debated with competing arguments for recent dispersal in one direction or the other. We report the results of the first phylogeographic study of marine caddisflies, which shows a lack of genetic variation in Australian *P. plebeius* but extensive and deep variation within New Zealand populations. We also confirm (with morphological and molecular evidence) the existence of a second 'New Zealand' marine caddisfly in Sydney Harbour, *Chathamia integripennis*.

Is host source location a factor in the presence of chewing lice on birds introduced to New Zealand?

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Many United Kingdom (UK) bird species were introduced to New Zealand in the mid-to-late 1800's. In the UK, these species host chewing-lice parasites (Insecta; Phthiraptera); however, some of these parasite species failed to establish in New Zealand (NZ) while their host species succeeded. Two explanations have been offered for this phenomenon: (1) the source hosts lacked infestation (missed the boat); (2) parasite taxa failed to survive on host taxa that established in NZ (lost overboard). To determine whether host source location is an explanation for why some parasite species missed the boat, this research focuses on UK geographic distributions of host (Passeriformes) and parasite (chewing-lice) species. New UK louse data were collected from an area where previous sampling is sparse, and combined with historic parasite records. Bayesian regression was used to analyse whether the probability of the number of parasitised hosts differed between six geographic regions. Hosts in northern UK regions were less likely to be infested than in other regions. Therefore, if hosts were sourced from regions with low louse prevalence, lice might have missed the boat and failed to establish in NZ. Furthermore, hosts were less likely to be infested with ischnoceran lice than amblyceran lice. These results highlight the need to account for variations in louse prevalence at source host locations and louse phylogeny when modelling the probability of louse presence on an exotic host population.

Of lice and Men(acanthus): supercoloniser or host-race complex?

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Menacanthus eurysternus (Burmeister, 1838), is the most widely distributed louse species being found on at least 176 host species throughout the Passeriformes. The cosmopolitan nature of *M. eurysternus* is all the more interesting given that mean number of host species sharing louse species for passerines is 1.9. *Menacanthus* species are not generally widespread with most species found on only a few host species. *M. eurysternus*, therefore, represents an interesting anomaly amongst lice. There are several hypotheses that may account for the pattern observed. *M. eurysternus* may represent: [1] a true multi-host species that has exploited an as yet unknown mechanism to move easily between different host species at a level that maintains high levels of gene-flow; [2] a species that was found on a group of European passerines, e.g. blackbirds, sparrows and starlings, which have been extensively introduced around the world and from which endemic passerine species have been recently colonised; [3] a morphologically conservative group which forms a cryptic species complex, e.g. '*M. eurysternus*' from some hosts in a given area may be genetically distinct from lice of other hosts or areas. We have collected *M. eurysternus* samples from New Zealand, Australia and England and from several common species of passerines. We have examined molecular markers (COI and EF1alpha) and they imply a complex level of genetic variation that suggests hidden diversity among the lice and some structures that match the phylogeny of host species.

Using stable isotopes to track nutrient flow through invertebrates at the marine-terrestrial interfaceDavid Hawke *¹, John Clark ¹¹ Christchurch Polytechnic Institute of Technology Box 540, Christchurch, New Zealand

Cross-boundary nutrient flows at the marine-terrestrial interface can profoundly influence recipient systems, but the routing of nutrients through invertebrates is poorly known. Stable isotopes provide a way of exploring the ecology of this interface, the ratio of $^{13}\text{C}/^{12}\text{C}$ and $^{15}\text{N}/^{14}\text{N}$ being higher in marine biota than in terrestrial biota. In this paper, we present three case studies which demonstrate the application of stable isotope technology. In the first, we explain why the newly-described mesostigmatic mite *Ayersacarus woodi* can be said to be a predator dependent on seabird guano carbon. In the second, we show that soil invertebrates found in a seabird colony mostly process terrestrial carbon, with only two taxa involved in routing marine carbon. Finally, we show that an undescribed mesostigmatic mite ectoparasitic on the larvae of the endemic sand scarab *Pericoptus truncatus* is not actually parasitic.

Mites from Procellaria burrows of the Antipodes Islands

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The mite fauna of Antipodes Island is poorly known. However, the seabird burrow soil there supports a diverse mite fauna. Burrow soil samples taken at arm's length from five grey petrel and five white-chinned petrels were extracted with a Tullgren funnel. Holothyrids were absent; ticks were represented by *Ixodes uriae* and *I. auritulus*; mesostigmata by *Ayersacarus*, *Davacarus*, *Leptolaelaps* and a new genus close to *Leptolaelaps* and *Austrocheles*; and two species of uropodid. The most common mite was a small oribatid; at least three other non-ptychoid oribatid and a large pthiracaroid species were present. Parasitengonids were absent; with prostigmata represented by a stigmaeid. Astigmata were represented by a new genus of terrestrial Algophagidae. It bears a regressed axillary organ, the epigynum is fused to coxal apodeme II and it probably feeds in soil interstitia. This taxonomic work is essential to permit the study of the nutrient flow at the marine/terrestrial interface using stable isotopes.

Picky learning: understanding the specific conditions under which the kleptoparasitic spider *Argyroides antipodius* learns

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In animals with a limited number of neurons, learning is heavily constrained. Such animals will most likely demonstrate learning when it is most advantageous, such as when variation between generations is large but variation within generations is low. *Argyroides antipodius* is a kleptoparasite that steals food from other, larger spiders and will opportunistically attack spiderlings. As *A. antipodius* can exploit a number of host species, *A. antipodius* needs to adjust its stealing behaviour to the idiosyncrasies of each host species in order to be successful. Previous work has shown that *A. antipodius* is capable of learning, as males can learn to be winners and losers in competition for females. This study tested whether *A. antipodius* was able also to learn to modify its foraging behaviours. The results showed that *A. antipodius* was able to modify its foraging behaviours, but that males seemed more apt at learning than females. These results are discussed with respect to behavioural plasticity within the sub-family *Argyrodinae*, and in the more general context of learning in invertebrates.

When substrate matters; drivers of assemblages and interspecific relationships in tussock grasslands spiders

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Vegetation, which has flippantly been referred to as “only substrate” by some arachnologists, is known to determine arthropod diversity and composition in various ecosystems. Here we present the first study that investigates the effects of the physical and botanical characteristics of native tussock vegetation on spider assemblages. We address two questions: (1) What are the effects of the physical characteristics and species composition of vegetation on spider communities? (2) What are the associations between spider assemblages and plant communities? We found that although there was a positive relationship between plant and spider diversity, the effects of tussock cover varied depending on the spider families or species. Overall, the physical structure and species composition of the vegetation had a similar effect on spider assemblages, with approximately the same number of taxa affected by either characteristic. Gradients in vegetation were matched to gradients in spider communities, whose diversity and composition varied. Species of the family Orsolobidae were associated with wetland vegetation, and Linyphiidae (money spiders) species with shrubs. After confirmation of relationships by individual variables, it was concluded that environmental factors, such as soil moisture, may affect plant composition and structure in tussock ecosystems, which in turn determine spider assemblages. Lycosidae (wolf spiders), as a group, and two species of this family were consistently affected by vegetation. These taxa deserve further research as they can provide information on plant structure and potentially be used as indicators of ecological processes in tussock grasslands and become valuable for monitoring environmental changes in conservation management.

Introduced Vespidae: patterns of invasion and attempts at control

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More than 30 vespid species have been introduced around the world, but the seven most invasive species are all eusocial. Most introduced Vespidae only occur in one or two countries, but some areas have become geographic hotspots of invasion; Hawaii (15 species), North America (8 species), New Zealand (5 species), Australia (4 species) and South America (4 species). Two invasive species, *Vespula vulgaris* and *V. germanica* have become particularly widespread and abundant with a range of impacts on biodiversity and ecosystem function. Other successful invasive species include several *Polistes* spp., which affect local biodiversity through direct predation or competition for food or space. Toxic baiting has been the most successful control strategy against invasive vespids to date. Several attempts at biological control using parasitoids have not successfully reduced invasive wasp populations, although the biocontrol agent has only established in one case. The social structure of colonies and their high reproductive efficiency has facilitated invasion by these species, but it also means management at the population level will be difficult. This emphasises the need to prevent such invasions from occurring in the first place.

Behavioural and population genetic divergence of an invasive ant in a novel environment

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Invasive species may undergo rapid evolutionary changes in their new environment. The introduced unicolonial yellow crazy ant *Anoplolepis gracilipes* exhibits considerable variation in abundance throughout its current distribution in the tropical monsoonal savanna of Australia's Northern Territory, where it was first detected in the 1980's. First, we aimed to determine if *A. gracilipes* variation in abundance was associated with behavioural and genetic differentiation. Second, we investigated if population divergence of *A. gracilipes* has occurred since introduction. *Anoplolepis gracilipes* abundances were assessed at 13 sites throughout the region. We used microsatellite molecular markers to determine population genetic structure at these 13 sites and a further seven sites. Behavioural differentiation was assayed using aggression trials and analysed together with genetic data. Although we found considerable variation in abundance we found no correlation between abundance and population genetic differentiation. Our analyses suggest that *A. gracilipes* in Arnhem Land are genetically and behaviourally a single supercolony, and resulted from a single introduction. The population is not homogeneous, however, as aggression varied over both genetic and geographic distance, and we found a positive relationship between genetic and geographic distance. The genetic and behavioural differentiation we observed is suggestive of incipient genetic and behavioral divergence, which may be expected when an invasive species enters in a new environment.

The catastrophic collapse of Argentine ant populations in New Zealand

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The Argentine ant (*Linepithema humile*) is a widespread invasive species and is thought to exert great pressure on native communities. In their introduced range they are well known to displace resident ant species where they occur. First detected in Auckland in 1990, this invasive has since spread widely around New Zealand, with the date and location of the first observed infestations recorded. However, like many invasive organisms, little research has investigated their long-term persistence. We surveyed 150 sites throughout the known distribution range of Argentine ants within the country and recorded the presence of these and other ant species. Argentine ant populations were found to have collapsed at many sites across this range. A survival analysis indicated that the time to collapse was significantly influenced by temperature and rainfall. Climate change may delay the time to population collapse in some areas, but enhance collapse in others. Ant species richness was significantly reduced at currently invaded sites compared to formerly invaded; however, resident ant communities appeared to recover after the collapse of Argentine ant incursions. In Auckland, formerly invaded communities were indistinguishable from those that had never been invaded. This study demonstrates the widespread collapse of an invasive species and the recovery of resident communities, suggesting that the Argentine ant, though devastating elsewhere, may not be a long-term threat to New Zealand's ant communities.

Does New Zealand have a hope against invasive ants?

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Ants have proved very successful at invading New Zealand in recent times. Excellent progress in the Pacific by the Ministry of Agriculture shows that careful management of pre-border risks can dramatically reduce ant interception rates. Despite this, some invidious species such as black crazy ant *Paratrechina longicornis*, tropical fire ant *Solenopsis geminata* and red imported fire ant *Solenopsis invicta* have breached our borders and formal surveillance systems, triggering expensive incursion responses. Current surveillance methods, such as those used in the annual National Invasive Ant Surveillance programme, may not be sufficient or practical with increasing trade projections. Fortunately post-border ant incursions, such as red imported fire ant, have been discovered by the public early enough to enable successful eradication, but this is less than ideal. How can we further improve our game against this onslaught? Perhaps, identification and use of ant female sex pheromones will create new opportunities for detection with much greater efficiency than other sampling systems, as has happened for Lepidoptera and a number of other insects at landscape scale. Other useful approaches in the shorter-term, could include a study of past examples of ant eradication programmes. So far, we have examined 52 ant eradication programmes in seven countries in order to identify critical factors leading to the success or failure against 11 species. About half of these programmes have declared eradication (22), or are likely to have been successful (4). Most programmes have lasted under seven years, but a few required longer, illustrating the need for long-term commitment in order to prevail against ants.

The biogeography of ant invasions and its implications for biosecurity

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A longstanding goal in the study of biological invasions is to predict why some species are successful invaders while others are not. To understand this process, we need detailed information on the pool of species with the opportunity to become established. Interception data from ants detected in quarantine is a great source of information on anthropogenic modes of dispersal in ants. Moreover, interception records provide unparalleled biogeographic and taxonomic perspectives on the species pool from which invaders are derived. In my talk, I will discuss general biogeographic and taxonomic patterns of ant invasions and highlight the value of using interception data as a monitoring tool. I will also discuss the importance of research on native populations of introduced species to gain a better understanding of the mechanisms of success in biological invasions.

Role of fitness trade-offs and dispersal in persistence of generalists across a wetland predator-permanence gradient

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Mechanisms that allow populations of generalists to persist and disperse across a range of heterogeneous habitats despite experiencing variable selection pressures are important in lentic habitats. Invertebrates in temporary habitats must develop quickly and disperse, or have wide environmental tolerances. Conversely, those in permanent habitats must avoid vertebrate predators (e.g., fish). These diverse conditions result in life-history trade-offs that influence fitness and population dynamics. In addition, gene flow and recruitment between spatially separated habitats are influenced by terrestrial dispersal between permanent and temporary habitats and resulting meta-population dynamics. We predict that (1) terrestrially dispersing generalists have bet-hedging behaviors and oviposit in both habitat types to maximize reproductive potential, and that (2) distance between habitat types and spatial arrangement of ponds influences the extent and persistence of generalists. Population dynamics of *Xanthocnemis zealandica* and *Sigara arguta* are being examined through field surveys, microsatellite analyses and mesocosm experiments with generalists in Canterbury alpine lake-pond complexes. Results will enhance understanding of how life-history trade-offs and dispersal interact to maximize aquatic generalist fitness with implications for population, community and evolutionary responses to global changes.

Exploratory study of *Macrosiphum hellebore*'s vectoring capability of Helleborus Net Necrosis Virus

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Helleborus are rhizomatous herbaceous perennial plants cultivated for their flower structure blossoming from late winter through to early spring. *Macrosiphum hellebore* Theobald & Walton is a monophagous species found in association with Helleborus, recently being identified in Australia in 2009. In 2009 a Carlavirus, Helleborus Net Necrosis Virus (HeNNV) or more commonly referred to as 'Black Death,' tested positive in Helleborus species within the United States. Symptomatic plants exhibit black streaking of the veins on leaf blades and a blackening of the stems with heavily infected plants perishing within a single season. The first incursion of HeNNV in Australia was positively confirmed in 2010. Although *M. hellebore* is a monophagous species the insect's ability to acquire and transmit HeNNV has yet to be proven. A transmission experiment under laboratory conditions, will be conducted by exposing groups of *M. hellebore* adults to infected and then uninfected Helleborus plants. Exploratory studies will also be conducted to investigate *M. hellebores* through a range of experiments to further understand this insect through parameters such as, developmental time, temperature's effect on development time, fecundity as well as, artificial rearing techniques. The purpose of this experiment is to determine if *M. hellebore* is capable of vectoring HeNNV and to a lesser extent CMV under laboratory conditions. Through conducting these experiments a possible target for vector control could be identified, enabling a means to stop HeNNV spreading throughout Helleborus species.

Response of the bird cherry-oat aphid (*Rhopalosiphum padi*) to climate changeKyla Finlay ^{*1}, Jo Luck ¹¹ DPI, BioSciences Research Division, 621 Burwood Highway, Knoxfield, Victoria, 3180, Australia

Global climate change threatens world food production not only via direct effects on plant growth but also by alterations to pest and pathogen prevalence and distribution. Complex relationships between host plant, pest, pathogen and environment create uncertainty particularly involving pathogens vectored by an insect pest. We attempt to improve the understanding of the effects of climate change on such systems via a detailed review of one crop-vector-pathogen system. The bird cherry-oat aphid, *Rhopalosiphum padi*, is a global pest of cereals and vector of yellow dwarf viruses that cause significant crop losses in cereals. *Rhopalosiphum padi* exhibits both sexual and parthenogenetic reproduction, alternating between crops and other host plants. In Australia, where only parthenogenesis occurs, due to the absence of the primary host, the aphid continuously cycles from grasses to cereals allowing for continuous virus acquisition and transmission. We have reviewed the potential impact of future climate projections (increasing temperatures, elevated CO₂, altered weather patterns) on *R. padi* population dynamics, persistence and abundance and the timing, rate and extent of dispersal and migration events. We also looked at the interaction between vector, virus, crop and environment, all of which are critical to the development and behaviour of the vector and its ability to transmit the virus. We identify a number of knowledge gaps that currently limit efforts to determine how this pathosystem will function in a future climate.

Understanding range shifts: using current and historical data to model the invasive redlegged earth mite, *Halotydeus destructor*

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The niche of an invasive species is often conserved during invasion, although there are numerous examples of species distributions expanding via range-shifts beyond expected climatic boundaries of their invasive range. *Halotydeus destructor* is an important agricultural pest in Australia and has been the focus of extensive surveys that suggest this species has expanded its invasive range inland to hotter and drier environments. We compiled comprehensive distribution datasets for *H. destructor*, representing the native range in South Africa, its invasive range in Australia in the 1960s (40 years post-introduction), and its current range in Australia. Using MAXENT, we built correlative models and reciprocally projected them between South Africa and Australia, and investigated post-invasion range expansion with historical and current models. We used model exploration tools to examine the climate similarity between native and invasive ranges, and subsequently examined climatic variables that limit distributions. The invasive niche of *H. destructor* transgresses the native niche and the species has expanded in Australia beyond what is predicted from the native South African distribution. Our models support the notion that *H. destructor* has undergone a more recent range shift into hotter and drier inland areas since establishing a stable distribution in the 1960s. Our models demonstrate that invasion is an ongoing dynamic process, and that once a species has reached an established range it may still expand at a later stage. The models generate hypotheses about adaptive shifts in *H. destructor*, and may aid future climate change predictions.

Hot bugs or hot trees? Responses of eucalypt feeding insects to climate change

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The ecological effects of climate change are frequently studied from a plant perspective that focuses on crop systems or Northern Hemisphere plant communities. However, climate-driven changes in plant properties, such as leaf carbon and soluble protein concentrations, can also be expected to have significant flow-on effects for herbivorous insects and all other trophic levels. In Australia, Eucalyptus dominates natural forests and woodlands, and also plantation forestry, yet eucalypt responses to climate change are only now beginning to be assessed. As with most plants, increasing temperature and CO₂ are expected to have opposing effects on eucalypt foliar C:N ratios. This will affect the balance between the nutritive value of leaves, which is naturally low, and levels of secondary plant metabolites that drive leaf defensive chemistry. It is not clear how simultaneous increases in CO₂ and temperature will interact to affect plant quality, or how plant-mediated effects will interact with direct effects of climate changes to influence insect development. Here we assess both plant-mediated and direct effects of simultaneous increases in CO₂ and temperature on eucalypt herbivores development by comparing the responses of insects reared directly under altered climates to those of insect reared under ambient conditions on leaves grown under altered climates. When fed leaves grown under elevated CO₂, larvae consumed more and took longer to develop. However, this was partially mitigated by direct and also indirect effects of increasing temperature. Based on these observations we discuss the mechanism by which predicted future climate change may affect insect communities in Eucalyptus ecosystems.

Biological control in a changing world: How climate affects host-parasitoid dynamicsCecilia Romo *¹¹ School of Biological Sciences, University of Canterbury, Private Bag 4800, Christchurch 8140, NZ

Climate change is expected to affect the abundance, distribution and availability of predators that are important for maintaining pest suppression. Moreover, higher temperatures and increased climatic variability are expected to induce differential responses from predators and their prey, with different trophic levels responding differently. Using manipulative lab experiments and field observations, we examined the differential response of a model host-parasitoid system to two climate variables: temperature and drought. The mechanisms affecting predator-prey dynamics were first examined using controlled lab experiments incorporating both climatic drivers. We examined parasitoid fitness, longevity, and development rates and found that parasitoids responded differently when exposed to each climatic variable in isolation compared to the interaction of both variables at once. Although temperature and drought both showed positive effects on parasitoids in their ability to control aphid populations, these drivers, when expressed in concert, had an antagonistic effect, highlighting the importance of studying the interactions between various climate change drivers rather than just their singular effects. Additionally, field results showed that temperature had a positive effect on aphids, parasitoids, and higher-level hyperparasitoids. Although temperature positively affected aphid and parasitoid abundance, hyperparasitism rates also increased, partly offsetting the benefit to parasitoids, which suggests that higher levels may impede predictions of predator-prey interactions. Overall, in the absence and presence of predators, both temperature and drought had a positive effect on pest abundance, suggesting that predicting future pest outbreaks will be difficult.

DNA barcoding: A tool to identify exotic wood-boring beetle larvae of the family Bostrichidae

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The beetle family Bostrichidae contains economically important timber pests. These include powder post beetles and auger beetles, which are regularly detected as larvae boring into imported wooden items at the border and post border. In this presentation we will discuss the processes followed to establish a reference library of Bostrichidae DNA barcodes at the Plant Health and Environment Laboratory (PHEL), Ministry of Agriculture and Forestry, New Zealand. The current identification method for wood-boring beetle larvae relies on morphological characters and dichotomous keys that are not easy to use and require specialist diagnostic skills to interpret. In addition, rearing immature stages to adults is often necessary for identification. This is problematic in a biosecurity context, as rapid identification is crucial to enable appropriate risk management. Recent advances in DNA barcoding methodologies have revolutionized the classical taxonomic process by allowing rapid identification, and barcoding is gaining prominence as a reliable diagnostic tool for species level identification. Very few barcodes for economically important species of the Bostrichidae family are available in on-line sequence databases. This limits the use of DNA barcoding as a routine diagnostic method for wood-boring beetle interceptions. This study validated approximately 30 frequently intercepted species of Bostrichidae from different geographical regions in order to establish a reference barcode library for this family. This study also trialled several DNA extraction methods, and we will show that this is a key component to obtaining reliable, high quality DNA barcodes. The utility of barcoding Bostrichidae species for rapid species identification will be discussed.

Northern Australian Quarantine Strategy: Pre-Border Surveillance in the Far North

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The Northern Australia Quarantine Strategy (NAQS) has been conducting quarantine surveillance in Australia's north for the last 20 odd years. Established in its current form in 1989, NAQS came into being as a response to an unusual set of quarantine risks posed by the proximity of countries to the north with different plant and animal health statuses. Annual monsoon winds along with traditional trading and visitation rights increase the likelihood of incursions of quarantine significance. NAQS conducts surveillance on the coast from Cairns to Broome, the islands of the Torres Strait and countries to our near north, where staff monitor for new incursions of animal and plant diseases, along with weeds and insect pests. Entomology in NAQS covers the areas of plant health, veterinary entomology as well as entomological risk posed by illegal foreign fishing vessels (IFFVs). Here we give an overview of NAQS surveillance activities and report on detections of exotic species over the years and present case studies on recent entomological detections of quarantine concern. We present data on the NAQS fruit fly monitoring network and the regular incursions of exotic fruit fly species into the Torres Strait as well as the response activities undertaken.

Pieris brassicae (L.) Large white butterfly in Nelson

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The new to New Zealand large white butterfly, *Pieris brassicae*, was first reported to MAF in May 2010. The colourful larvae were found feeding on Nasturtium in a home garden in Nelson. On the wing, the adults can be difficult to differentiate from the long established small white butterfly *Pieris rapae* (L). The presentation outlines some differences between the two species, its distribution, and discusses the likely impact that *P. brassicae* is likely to have should it become widely established in New Zealand. This presentation will also outline what monitoring and control measures have been put in place by MAF, including response to public notices and media articles.

Comparison of the efficacy and longevity of two types of dichlorvos strips (DDVP) proposed for use in New Zealand fruit fly surveillance traps

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The New Zealand Fruit Fly surveillance programme was initiated by Ministry of Agriculture and Forestry (MAF) in the mid 1970's to provide assurance of country freedom from economically important fruit flies, and early warning of fruit fly incursions to facilitate eradication. Approximately 7500 Lynfield traps are set up and maintained from September to June of each year. Should any fruit fly arrive, there is a reliance on dichlorvos-2,2-dichlorovinyl dimethyl phosphate, (DDVP) insecticide strips to kill any flies that are attracted into the traps by male pheromone lure attractants. A blue DDVP strip manufactured in the United Kingdom specifically for New Zealand has been in use for over 15 years. More recently, MAF was advised byASUREQuality, who are contracted to service the surveillance grid, that the strips currently in use were not able to be sourced because of a manufacturing plant failure. However, an alternative larger yellow DDVP strip with similar specifications would be available in approximately four months. Moreover, this strip is being currently used in other countries. Nevertheless, as an interim measure, a second smaller yellow DDVP strip with different specifications was supplied as a prompt suitable replacement before stocks of existing DDVP strips became critically low. MAF's Plant Health and Environment Laboratory conducted experiments to test both the smaller and larger alternative yellow strips. House fly bioassays and Gas Chromatographic (GC) destructive testing methods were used to measure the efficacy and longevity of alternative strips. Trials were undertaken at two sites, Auckland and Christchurch. The combined results of fly bioassays and GC testing at weeks 2, 4, 6, 8 will be discussed.

Hitching a ride to Australia

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Pests that are associated with specific commodities are relatively easily managed by biosecurity agencies. Unfortunately, many high risk organisms are not restricted to well defined pathways and these hitchhiker pests can present significant inspection, detection and treatment challenges for biosecurity agencies. Two recent cases that were dealt with by the Australian Quarantine and Inspection Service (AQIS) are discussed, highlighting some of the responses undertaken to manage hitchhiker organisms. These were the detections of egg masses of the saturniid moth (*Hylesia nigricans*) on vehicles imported from Argentina, and burnt pine longicorn beetles (*Arhopalus ferus*) on the cruise ship 'Queen Elizabeth'.

Bamboo Moth and Other 'Hairy Caterpillars' Reported Through MAF's Public Enquiry Surveillance Programme

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The New Zealand Ministry of Agriculture and Forestry provides an Exotic Pest and Disease Emergency Hotline service to members of the public allowing them to report any unusual insect or plant disease. This autumn a high number of 'hairy caterpillars' were reported from the Auckland area. With pertinent questions it was possible to rule out high profile exotics such as the recently eradicated painted apple moth, *Teia anartoides* and gypsy moth, *Lymantria dispar* (Lepidoptera: Lymantriidae). The caller descriptions were all recognisable as the recently established bamboo moth, *Artona martini* (Lepidoptera: Zygaenidae). *Artona martini* was first recorded in Northland in 1996 and has slowly been extending its distribution. In its native Asian range *A. martini* is known to have occasional outbreaks, and this is what appears to have happened during the Auckland summer of 2010-2011. These 'hairy caterpillar' enquires provided an opportunity to give callers positive reinforcement for taking the time to report and assisted in promoting awareness of other exotic Lepidoptera not yet established in New Zealand. The Auckland bamboo moth observations are summarised with a comparison of other types of enquires received during the same period.

Above- and below-ground herbivore interactions: what do they mean for weed biocontrol outcome?

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The effects of below-ground herbivory on plant population dynamics and on plant communities are becoming increasingly recognised in recent years. For a long time root feeders were hardly used in classical weed biocontrol because they are difficult to work with, yet they have similar-to-better establishment rates than above-ground herbivores and more of them appear to contribute to target weed suppression than above-ground herbivores. Root feeders used in biocontrol are usually used in combination with above-ground biocontrol agents. It is therefore important to tease apart the effects of the above- and below-ground interactions and their effect on the biocontrol outcome. We studied paired above- and below-ground interactions between the three biocontrol agents introduced to New Zealand for the biocontrol of nodding thistle, *Carduus nutans*. We used cages in a garden experiment to quantify the effects of individual and paired agent species. We then manipulated the results in a matrix model to investigate the potential effect on the growth rate of the target weed population. We conclude that competitive above-ground interactions between the two seed predator agents limit the potentially more effective of the two, and that there was evidence that the crown-root feeder negatively affect the above-ground gall-forming agent. Population models indicated that no combination of the three agents was sufficient to bring nodding thistle populations in New Zealand to decline.

Classical biological control of *Cirsium arvense*: lessons from the past

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Cirsium arvense (L.) Scop. is a perennial herb indigenous to Eurasia that is now present throughout temperate regions of the world where it is considered one of the worst weeds of pastoral and agricultural systems. Classical biological control has been attempted in both North America (NA) and New Zealand (NZ). However, nearly 50 years after the first agent releases there are no indications of successful control. We retrospectively evaluate *C. arvense* as a target weed, critique the agents selected for release, and contrast the different situations in NA and NZ. The failure of the programme in NA is attributed to non-target impacts, and the fact that some agents either failed to establish, or had no impact on the weed. In contrast, there is a unique situation in NZ, where there are no related native thistles (Cardueae), and thus little chance of non-target impacts. In the past, the same agents that were released in NA were subsequently released in NZ, without considering whether or not these were the best choices. Thus, the past failure in NZ might be due to the previous lack of a NZ-specific approach to biocontrol of thistles in general and *C. arvense* in particular. A new approach taking into consideration the absence of native Cardueae has resulted in the release of agents more likely to be effective, and has potentially set NZ on track towards successful biological control of *C. arvense*, and other thistles.

Impact of the heather beetle (*Lochmaea suturalis*), a biocontrol agent for heather (*Calluna vulgaris*), in New Zealand

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The heather beetle (*Lochmaea suturalis*) was released into Tongariro National Park, North Island, New Zealand, as a biocontrol agent for heather (*Calluna vulgaris*) in 1996. Populations have slowly established and started to damage or kill heather. Heather was planted in Tongariro National Park in 1912 to re-create UK grouse moors, but the grouse failed to establish and heather quickly became an invasive weed. It has now infested more than 50 000 ha of the North Island's Central Plateau including Tongariro National Park and the adjacent Waiouru Military Training Area. Between 2007 and February 2011 beetle populations have grown exponentially at three release sites and severely damaged or killed approximately 100 ha of heather. Prior to successful biocontrol, the herbicide Pasture Kleen® (2,4-D ester) was applied aerially to manage heather within the Waiouru Military Training Area. Impact assessment plots were set up in 2008 to compare and contrast herbicide application with biocontrol for the control of heather and the associated responses of native and exotic plant species. After two years heather cover has reduced by 90% after herbicide application, by 99% after heather beetle attack, and by 99.9% following a combination of methods. Herbicide application resulted in significant non-target damage to native shrubs and herbaceous plants, and the exotic grass *Agrostis capillaris* is invading plots following a combination of control methods. It is too early to determine the relative impact of each method on grass invasion. No non-target impacts were found as a result of beetle feeding and there is early evidence that native shrub recovery is occurring following biocontrol.

Successfully eliminating parasitic gregarines from *Neolema ogloblini* (Coleoptera: Chrysomelidae) - a biocontrol agent for *Tradescantia fluminensis* (Commelinaceae)

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Tradescantia fluminensis (Comelinaceae) was introduced into New Zealand (NZ) as a house plant, but is now a serious under-storey weed of indigenous forest. Surveys for potential biocontrol agents in SE Brazil, starting in 2005, identified a rich natural enemy biota including herbivorous insects and plant pathogens. Routine screening of the first insect agent to be host range tested, the leaf beetle *Neolema ogloblini* (Chrysomelidae), revealed high levels of a gregarine (sporozoan protozoan) gut parasite. This appeared to reduce beetle fecundity, longevity and general vigour, potentially compromising its biocontrol efficacy. Depending on the host specificity of the gregarine, it could also threaten NZ fauna. In NZ biocontrol agents can only be released from containment if they are shown to be free from unwanted associated organisms. We report on two years of increasingly intensive attempts to obtain a gregarine-free population of *N. ogloblini* including use of highly hygienic field collection methods in Brazil to get clean material at source, surface sterilisation of eggs, use of cages with HEPA-filtered air in containment, and attempts to improve our gregarine detection methods by gut dissection and DNA probes (both of which proved less easy, and more expensive than anticipated). In December 2010 we finally released *N. ogloblini* from containment after showing we had three consecutive generations of beetles tested negative for gregarines. Success was achieved by repeated sub-culturing. Firstly, eggs were collected as hygienically as possible from single female beetles (each having been paired with a single male). Then each larva was reared in solitary containment but with poor hygiene to ensure that any low level of gregarine infection would be expressed sufficient to minimise the risk of getting false negatives in subsequent testing. All lines testing positive were eliminated. Final crossing of lines before release from containment was carried out in an attempt to restore lost heterozygosity and overcome any inbreeding depression or adaptation to laboratory conditions.

How will predicted climate change affect weed biocontrol in New Zealand?

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By 2090, New Zealand (NZ) is predicted to be around 2°C warmer, on average, than in 1990. Rainfall is expected to increase in the west and decline in the east, and extreme weather events may be more common. We report on a recent assessment of the potential effects of these predicted climate changes on weed biocontrol systems in NZ. We conclude that “sleeper weeds” are likely to become problems under future climate change scenarios, and pre-emptive action could be taken, particularly if biocontrol has already been successful overseas. Existing weeds are likely to expand or shrink their geographic ranges under predicted climate change, but we consider that existing biocontrol agents will mostly track the changing distributions of their host plants. Exceptions could occur with existing weed biocontrol systems being affected positively or negatively. For example, the released biocontrol agents for *Pilosella officinarum* do not do well in summer droughts in NZ, so the increased rainfall predicted for inland South Island areas might improve biocontrol of this weed. Conversely, increases in flooding may decrease the effectiveness of biocontrol of alligator weed. Other issues of potential concern include losses of synchrony between weeds and their biocontrol agents, changes in host plant nutrition, and possible increases in non-target effects, but almost all are speculative as we lack data. However, recent studies show that suppression of ragwort by flea beetle, *Longitarsus jacobaeae*, is likely to fail when mean annual rainfall exceeds 1670mm. A preliminary GIS analysis showed increased annual rainfall could cause ragwort biocontrol to fail in some western regions, while suppression of ragwort through biocontrol could be attained in parts of North Island as rainfall decreases.

Community implementation of biological control of weeds across south-eastern Australia

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Encouraging community participation can be an effective way to speed up the delivery of weed biological control programs. A program aimed at engaging farmers, community groups, schools, and government agencies was implemented across four States in south eastern Australia. Eight different invertebrates and two plant pathogens were released at hundreds of sites infested by the Weeds of National Significance blackberry, gorse, salvinia, boneseed, bridal creeper, and bitou bush, and the highly invasive weeds English broom and cape broom. The program recognised the benefits of researchers engaging with existing weed management, land management, and community networks to (i) facilitate the release, establishment and assessment of biological control agents, (ii) ensure biological control is integrated with local and regional weed management strategies, and (iii) promote biological control in the community. Many participants in the program are now able to identify weed infestations suitable for biological control, rear or collect their own agents, conduct releases, and implement an appropriate monitoring program. However there were also limitations in delivering a program to a diverse mix of scientists, land management officers, teachers, volunteers, and school children. An important consideration is the ability to deliver and support biological control efforts within relatively short funding cycles. Despite these challenges, a large, coordinated biological control program, with a carefully planned engagement strategy can reduce duplication of effort across jurisdictions, deliver a sound return on investment, and provide a strong basis for future collaboration.

Searching for the signal of competition in plant-mediated interactions among coexisting gall insects on broad-leaved paperbark

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The central prediction of competition theory is that a reciprocal struggle for resources should manifest itself among coexisting species under conditions of increasing functional similarity (e.g. similar feeding niche), density and spatio-temporal overlap. We investigated whether such a struggle was evident in a community of phytophagous gall insects on *Melaleuca quinquenervia* meeting these conditions. Specifically, we examined plant-mediated interactions among three species galling vegetative tips with varying degrees of temporal overlap. The abundance of early gallers (*Sphaerococcus ferrugineus* and *Fergusonina turneri*) did not influence resource availability for the late galler (*Lophodiplosis indentata*), suggesting the absence of temporally separated exploitative competition. However the abundance of *S. ferrugineus* was positively correlated with the abundance of *L. indentata*, which suggests facilitation. Examination of the reciprocal impacts of the late galler on early gallers paradoxically revealed that though galling by *L. indentata* may be reducing the resource availability for early gallers, the abundance of *L. indentata* was positively influenced by the abundance of early gallers (an effect that is stronger for *S. ferrugineus* than for *F. turneri*) suggesting facilitation. The strong influence of site on the interactions among the different cecidogenic species indicated that any role for competition/facilitation may be spatially constrained. We discuss the implications of our findings within the broader context of competition theory, and the in terms of the implications for the use of these species as biological control agents for *M. quinquenervia*.

Predicting parasitism of weed biocontrol agents

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We conducted a nationwide survey of parasitism of weed biocontrol agents in New Zealand (NZ) and found that 19, mostly native, parasitoid species attack 10 weed biocontrol agent species. Fifteen of these parasitoid species were confined to five agents that possessed “ecological analogues”, defined as a native NZ insect that belongs to the same superfamily as the agent and occupies a similar niche on the target weed. Parasitoid species richness in NZ was positively correlated to richness in the area of origin. However, only agents with ecological analogues contributed significantly to this pattern. Our results support Lawton’s (1985) hypothesis that, to find enemy-free space, selected agents should “feed in a way that is different” and “be taxonomically distinct” from native herbivores in the introduced range. A review of NZ weed biocontrol programmes indicated that parasitism is significantly associated with the failure of agents to suppress weed populations. Although our conclusions are based on an unavoidably limited data set, we conclude that biocontrol agents that escape attack from parasitoids are more likely to suppress weed populations and should be less likely to have significant indirect non-target effects in food webs. Biocontrol practitioners can reduce the chance of weed biocontrol agents attracting species-rich parasitoid faunas after introduction by i) selecting agents that have species-poor parasitoid faunas in their area of origin, and/or ii) avoiding agents that have ‘ecological analogues’ awaiting them in the introduced range.

Climate change, invasive species and impact on productive and indigenous ecosystems: where might we end up?

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Increasing globalisation combined with climate change is intensifying the threat caused by invasive insect species to biodiversity, environment, economic activity, as well as human and animal health. While a small number of iconic insect invaders capture attention, there are many hundreds that could cause immeasurable impact in any country. Judging which species that have potential to establish and cause significant impact is not easy. While direct impacts of new alien insect incursions may be obvious, indirect effects that can cascade through an ecosystem may not be considered. How can we be better prepared? Internationally, biosecurity agencies recognise the threat and are focused on providing the strategies and policies for efficient prevention and mitigation. Large international research programmes such as PRATIQUE, a European FP7 Framework Program, the Centre of Research Cooperation for National Plant Biosecurity in Australia and the Better Border Biosecurity programme in New Zealand have been funded to deliver the science and tools badly needed by decision makers to diminish the impact of new incursions. Climate change, however, has not featured strongly in these initiatives. Given the potential impacts of invasive insects and the need for greater preparedness, integrative approaches that include a range of modelling methods to project species distribution and impact under climate change, are particularly important.

Predicting insect responses to climate change

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The effects of climate change on insects are normally predicted through correlative distribution modelling but other approaches can provide additional data. In particular physiological and evolutionary information can inform likely distribution shifts and also indicate the vulnerability of different insect groups. In this talk I will cover some of the approaches that can be used and illustrate them with recent data from *Drosophila* species collected by our group.

Odonata of the Pacific islands - a contemporary story for enthusiastic treasure hunters

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Odonata fauna of the Pacific islands is largely inconsistently studied. Marginal island groups, like Hawaii, Papua New Guinea and New Zealand are the most thoroughly investigated with research started in mid-eighteen century. Studies on Odonata of New Caledonia and island of the Fijian archipelago began around the same time, but there were large gaps during decades with no information. Other island groups, like Samoa, Solomon Islands, Vanuatu, Tonga, French Polynesia, Cook Islands, Wallis & Futuna, Tuvalu, Niue, Easter Islands and the whole Micronesia are poorly known in terms of their Odonata fauna. They have been either: a) overviewed for the whole region with little attention to regional studies, b) investigated more than 80 years ago, c) included in research performed for neighbouring regions, or d) not investigated at all. Pacific islands in the present study were investigated as one large geographic unit. A database was initiated to harbour everything compiled so far from literature, museum specimens and recent field studies. It provides the most updated information about Odonata species distribution, flying periods and habitat preferences over this enormous region. Total of 7,903 entries collected so far comprise roughly about 60% of the expected data. The information will be then included in a large scale GIS based spatial analysis, which will elucidate priority areas for future studies on Odonata from regions that have never been studied or are difficult to access. Here the first data are reported with habitat models prepared for the New Zealand species. Some advantages and drawbacks of this method are considered during the model testing and discussed in details as well.

Taxonomic illustration in the digital ageRudi Schnitzler *¹

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Insects are the most diverse group of organisms on earth with almost 1 million described species. They come in a remarkable array of sizes, colors, shapes, and textures. Taxonomists use the complexity of insect morphology not only as the primary means of identification, but also for inferring evolutionary relationships. Accurate illustration of characters is critically important in describing insect diversity, especially for new species that are regularly being discovered. Equally important are high quality illustrations that are fit for publication. This presentation will cover computer-assisted techniques of scientific illustrations using Adobe Illustrator® and Adobe Photoshop® for the production of high resolution character drawings. A brief introduction of techniques for the preparation of full characteristic colour illustrations of insects will also be given. While the focus of this presentation will be on taxonomic illustration of insects the methods described in the presentation are equally transferable to other organisms.

MicroCT imaging of insects

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In order to gather, manage and disseminate biodiversity information in a meaningful time frame, there is an urgent need to develop and utilise new methodologies for capturing and digitising a wide range of information. Critical among these are technologies for capturing and managing morphological information that might match some of the advances made in genomic technology. MicroCT imaging is examined as a potentially powerful tool in insect systematics and morphology, which could have utility in research, teaching and training, digital dissemination of biodiversity data, and ultimately in a variety of accelerated phenomics platforms. Examples of high-resolution CT scans are presented. Potential uses, advantages and drawbacks of this technology are discussed, along with the time, computing and storage implications of acquiring and rendering insects with MicroCT.

Remote Microscopy: A success story in plant biosecurity

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Diagnostics is a critical first step in determining the significance of suspected biosecurity threats posed by emergency plant pests and other invasive pests and pathogens. Remote Microscopy (RM) allows entomologists to interact in real time to identify pests and pathogens, viewing live high quality images via the internet in order to act, particularly in quarantine settings. The RM network has now expanded to include Thailand, Vietnam, Lao PDR, Malaysia, Indonesia, East Timor, Papua New Guinea, New Zealand and Australia with over 60 locations actively participating in identifications and using RM to educate and train each other. With the release of the new Padil (www.padil.gov.au) has come the Remote Microscope Diagnostics (RMD) portal. This dynamic, adaptable, secure, Padil image and information integrated, freely available service facilitates the "Taxonomic Triage" process, from user to diagnosis and appropriate action. The RMD portal will also include delivery of the microscope feed itself, thus eliminating many of the troublesome IT security issues that have plagued RM users in the past. The RMD portal allows users to upload information, GPS coordinates, images and video for action by a "Triage Officer" who will either identify the pest or utilize the extensive pool of taxonomic expertise found throughout the RM network and greater entomological community in Australia, New Zealand and South East Asia. The RMD portal will also allow the formation of "Triage Organisations" for application to specific lab groups or quarantine bodies, which will allow user group driven application and extensive domestic and international application. The dynamic design of the RMD portal and the extensive pool of expertise available has enhanced the diagnostic capacity of regional entomological communities in the form of identifications and the taxonomic triage process as well as in the realms of taxonomic training and the delivery of online training packages.

New approaches for collaborative key design and development: What Bug Is That? and IdentifyLife

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The Taxonomic Research and Information Hub (TRIN) recently funded the collaborative development of web-based keys to all 640 Australian Insect families, found at the website What Bug Is That? <http://anic.ento.csiro.au/insectfamilies/>. Most of these keys are deployed as Lucid interactive keys using the server-side player application; a minority are HTML dichotomous keys and other formats. The Lucid server-side player allows the keys to be deployed effectively over the web and enables easy updating of content. Each family treatment includes a fact sheet, and wherever available, images. The site acts as a clearing-house for order and family-level keys, offering links to multiple web based resources in this domain. Many of the keys originated as publications in CD format, the TRIN collaborative model has allowed them to be accessed for free, and has been able to increase the scope of keys to the entire fauna. IdentifyLife (<http://www.identifylife.org/>) is a new project that has developed a collaborative web-based environment for building and maintaining identification keys and the descriptive data underpinning them. With funding from the Atlas of Living Australia and the Encyclopedia of Life, IdentifyLife seeks to:

- bring together into one resource - Keys Central - a wide range of identification tools to help people throughout the world identify living organisms.
- create a collaboration space - My IdentifyLife - where the world's community of experts and enthusiasts can collaboratively manage community-agreed character lists for groups of organisms, identification keys and descriptive information for all the world's organisms.
- build an ambitious key - the Key to All Life - capable of handling identifications for all the world's living organisms.

Existing systems for handling descriptive data, such as Lucid and DELTA, are mostly desktop software and have limited capability in a connected (web) world. IdentifyLife brings advantages in the collaborative management of data, the ability to share resources between projects, and the opportunity for creating super-projects by combining descriptive data from a variety of sources to address new questions and challenges.

PaDIL - A Virtual Diagnostic tool to assist in plant pest diagnostics

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Fundamental to minimising the risks of pests crossing national or internal borders is to be able to rapidly diagnose them accurately and efficiently. Activities aimed at lowering risks, such as surveillance, or managing plant pests need to know what species they are dealing with. Added to the complexity of this task are two factors: first, the majority of pests encountered are not local, hence diagnosticians often require a world-wide knowledge of the pests; and second, there is a worldwide decline in the availability of diagnosticians and taxonomists for plant pests. To begin to address these issues, PaDIL (<http://www.padil.gov.au>), a Virtual Diagnostic tool was developed to harvest reference specimens from recognised Museums and Herbaria around the world with the view to building a Virtual Pests collection. PaDIL provides high quality, colour, diagnostic and symptom images (almost 40,000 images) and basic information for almost 2000 recognised plant pests species (ie. taxonomy, distribution, hosts etc). The interactive software allows users to Navigate and Explore the datasets and allows the user to create their own views/outputs to the results returned to their queries. PaDIL is freely accessible, requires no software downloads and the images are free to use under the Creative Commons License for non commercial use. The primary target audience of PaDIL is plant biosecurity diagnosticians with some level of experience; however, the image-based website can be easily used by specialists and non-technical users. PaDIL is an example of transitioning taxonomy from a Museum-based resource into an Information-based resource.

Australasian contributions to systematic entomology: a decade of Zootaxa

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The entomological contributions by Australasian systematists over the last decade were analysed using Zootaxa as an example. Zootaxa was chosen because it is the largest journal in entomology/zoology. After a review of the growth and success of Zootaxa over the last ten years, the contributions from Australasian systematic entomologists were compared with those of other countries. Critical issues in disseminating entomological information in general (such as data archiving and financial stability) will be discussed.

The online Australian Faunal Directory, a vital biodiversity resource

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Spawned by the Australian Biological Resources Study's traditionally published Zoological Catalogue of Australia, the online Australian Faunal Directory (AFD) is being brought up-to-date to include all species names recorded for the Australian Fauna. The AFD will become the baseline names list for the Atlas of Living Australia (ALA) and over the last 18 months, mainly with support from the ALA, some 40–50 compilers have been adding missing taxa and data through our novel online (off-site) editing facility. Over this period addition of about 5,000 names has raised to around 90,000 the number of valid species we list, and some 5,000 entries have been modified. The contents of the AFD vary, depending on the taxa compiled and the compiler, with some entries rich in detail and illustrated. A snap shot is presented of the variety of information available in this resource.

Publish - or perish? What has paper to do with it?

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Scientific publication - that is, the dissemination of our research in all possible forms - has always involved ink on paper. When papers were 'read' or 'communicated' at learned societies such as the meeting at which Darwin's and Wallace's papers were presented to the Linnean, the proceedings were reported and published in the Society's journal. Dissemination to the fellows (rather few of whom attended meetings) and to the interested public was through reprints and combined volumes of papers were deposited in selected national and international repositories. Ever since, society publishing has been a major force in sustaining specialist journals to promote and disseminate their fields of endeavour. Specialisation and expanding research in traditional and new fields has led to ever increasing numbers of journals, with more pages allocated to each. And all-the-while publication has become more commercial including as a source of revenue raising for societies, with professionals in many roles previously undertaken by volunteers. Commercialism raises questions concerning why we continue to disseminate on (costly, mailed) paper when all processing to dissemination is totally electronic. Fewer society members want to store paper copy, libraries purchase bundled e-journals and even editors and advisory boards prefer e-access. Reprints are available by pdf, and 'early view' of accepted manuscripts also is electronic. Paper will perish - the move away is inexorable, whether we like it or not. Perhaps only in taxonomy, constrained by a code, will paper copies persist but changes are happening here too, exemplified by Zootaxa.

Antipodean contributions to the dissemination of entomological information.

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Australia and New Zealand have for several years been punching above their weight in developing effective methods of disseminating information about insects. The tyranny of distance - our low population and lack of extensive libraries - have probably stimulated this. Electronic resources such as LucID, Zootaxa, PaDIL, the ABRS faunal web site, and the TRIN initiative are major elements in the revolution in how we communicate about our science. This introductory talk to the symposium will explore where we have come from, and consider where we might be going - emphasising the importance of retaining scholarship in scientific communication rather than the currently popular but undisciplined social networks.

The ongoing biological consequences of climate change: lessons from and for ectotherms

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Climate change is proceeding apace, with forecasts now routinely including consideration of a +4°C world, when previously, dangerous levels had been set at +2°C. Moreover, concern is mounting that changes to water availability may have as significant a consequence as changes in temperature, especially for areas that are water-limited. Documentation of biological responses to these changes and forecasts for their continuation are well-developed for temperature effects in some, especially north temperate, areas. However, for elsewhere current and likely future biological responses are less clearly understood and especially outcomes as a consequence of interactions with other environmental change drivers. Moreover, how animals will respond to changes in water availability is also less obvious than how plants might do so, with interactions among abiotic and biotic drivers remaining relatively under-investigated. Given the significance of ectotherms in global ecosystems, understanding how they are responding to climate change, how they might continue to do so, and how these responses and efforts to mitigate them might be detected, are among biology's greatest modern challenges. Here I explore these challenges using examples from our recent research and from similar studies undertaken by other groups.

Making the most of intelligence information and expert judgments for biosecurity

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Biosecurity deals with predicting, finding, identifying and treating pests and diseases on traded commodities. The task becomes more difficult as the volume and diversity of trade increases, exacerbated by the changing distributions of species and the effects of climate change. These conditions create an imperative to improve the efficiency with which agencies search for pests and treat potential exposure pathways. ACERA has been working with DAFF to develop better ways of gathering biosecurity information, to assist it to make better strategic investments in quarantine and biosecurity. The tools include foresight activities, intelligence gathering software and social network analysis. Each tool is outlined briefly, and the presentation describes how they can be used together to improve biosecurity effectiveness.

Mating versus oviposition in *Diaeretiella rapae* (Hymenoptera: Aphidiidae)

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Reproductive fitness of a haplo-diploid parasitoid depends on its mating and oviposition success. Oviposition by virgin females produces all-male offspring, while mated females produce both male and female depending upon the environmental condition. Whether oviposition occurs before or after mating, may affect the reproductive fitness of parasitoid, as unmated females may lose fitness by producing more males than required. This study assessed mating vs. oviposition preference in *Diaeretiella rapae*, a solitary endoparasitoid of cabbage aphid (*Brevicoryne brassicae*), and its importance in reproductive fitness gain. In *D. rapae* females emerge after males, and can choose whether to mate or to oviposit first. About a two-thirds of *D. rapae* females preferred to mate before oviposition in a mating/oviposition choice test. The females who oviposited first, parasitised only 10% of the aphids available in the arena before mating. The mean number of aphid nymphs parasitised, and the parasitism rate per unit time were significantly greater when oviposition occurred after mating, compared to the oviposition before mating. Mated females of *D. rapae* self-superparasitised their host aphids with fertilised eggs which resulted in a highly female-biased sex ratio of the offspring.

Intraspecific host choice and suitability in the solitary koinobiont parasitoid *Eadya paropsidis* Huddleston & Short (Hymenoptera: Braconidae): Bigger hosts are not necessarily better

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Although host stage selection in koinobiont endoparasitoids is frequently measured, the mechanisms that underlie parasitoid oviposition preferences are often overlooked. Here, we determine the preferred host stage of the braconid wasp *Eadya paropsidis* when attacking the leaf beetle *Paropsisterna* (= *Chrysophtharta*) *agricola* Chapuis (Coleoptera: Chrysomelidae) in the field and laboratory, and examine how behavioural and developmental interactions may be mediating host stage preferences and parasitoid reproductive fitness. In field choice tests, *E. paropsidis* parasitised significantly more small hosts than large, and in laboratory tests, deposited 30% more eggs into first instars than any other instar. Parasitism doubled the probability of premature host death across all instars, though the host's internal ability to kill a developing parasitoid larva did not vary with host instar. Multiple ovipositor insertions by the wasp reduced the chances of the host beetle surviving parasitism by 2.5 fold for every additional insertion, but did not significantly increase host mortality. Oviposition took twice as long and attempts were only half as successful with large hosts compared to small. Larger hosts were over three times more likely to tail flick and 27 times more likely to walk away from the attacking parasitoid than small hosts. Parasitoid larval weights were higher for those individuals originating from first instar hosts with parasitoid development taking significantly longer from first instars. We found no fitness advantage for *E. paropsidis* in attacking larger hosts, and apart from a taking slightly longer to develop from first instars, small hosts offered the best potential for the parasitoid to maximise fitness via increased body size and reduced host handling time.

Sneaking versus fighting: Alternative reproductive tactics in the New Zealand giraffe weevil (*Lasiornychus barbicornis*)

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Males of many animal species possess enlarged body structures that are used as weapons during contests with male conspecifics. Generally males with the largest weapon or body size have the competitive advantage during these contests. In some species where there is high natural size variation, smaller males have evolved alternative behaviours that do not rely on the use of weaponry to gain access to females for copulation. Males of the New Zealand giraffe weevil (*Lasiornychus barbicornis*) have an elongated rostrum which is used as a weapon to fight other males for access to females for reproduction. However, due to extreme size variation in this species where there can be a six-fold difference in body length of adult males, it is expected that smaller males will be less successful at defending females than larger males, and will therefore adopt alternative behaviours during mate searching and copulation. I will discuss the results from a series of focal animal observations conducted in January and February 2011 which revealed sneaking behaviours conducted by the smallest males. Alternatively males would defend females by guarding them both pre- and post-copulation, and use aggressive behaviours to fend off other male intruders. I will discuss the probability in relation to body size of sneaking or fighting to secure access to females, and explore the factors that affect these conditional behaviours.

Gumleaf skeletonizer (GLS) and Desire: field testing the New Zealand sex pheromone lure system during a recent outbreak of GLS (*Uraba lugens*) in south-west Western Australia

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In December 2009 and January 2010 an outbreak of *Uraba lugens* the gumleaf skeletonizer (GLS) affecting jarrah, *Eucalyptus marginata*, became apparent in southwest of Western Australia. By the end of January 2011 the outbreak severely affected more than 250,000 hectares of jarrah forest. The current status of this outbreak is outlined in comparison with the past outbreak in 1982-1988. In addition we tested a commercially produced pheromone lure for use in a standard delta trap system as a method for assaying populations of GLS. We report here a preliminary field trial of the New Zealand Desire® GLS pheromone lure and trap system and compare trap results with larval populations determined from branch clip samples. We found that the GLS lure is highly specific for GLS in jarrah forest in southwest Western Australia. The trap and GLS lure system are effective for monitoring both outbreak and basal populations of GLS in jarrah forest with an open understory. However in locations with thick understory that exceed trap height, effectiveness is impaired.

Scent of the New Zealand honeydew beech forest and the attraction of introduced *Vespula* wasps

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The introduction of social *Vespula* wasps to New Zealand has been disastrous for many of the native ecosystems. This is particularly true in the black beech forests (*Nothofagus* spp.) of the South Island, where these wasps are able to reach very high population densities due to the abundance of honeydew produced by native scale insects (*Ultracoelostoma* spp.) that feed on the phloem of black beech trees. There is a very characteristic aroma associated with honeydew in beech forests that we hypothesized is attractive to wasps. Volatile collections were taken of trees with honeydew present on the trunk in the field using portable solid phase microextraction (SPME), and analysed with a gas chromatograph-mass spectrometer. Five aromatic compounds were found in the headspace and were shown to elicit an antennal response from workers of both *V. vulgaris* and *V. germanica* using an electroantennogram. Field trapping tests using these five compounds both individually, and in blends, provided conclusive evidence of wasp attraction to only a portion of the treatments tested.

Parasitoids use chemical footprints to 'sniff out' present and future hosts

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Parasitoids are extremely important agents in the biological control of herbivorous insects. Thus, the behavioural mechanisms and chemical cues that parasitoids use to locate their hosts have been well studied since the 1930s. Nevertheless, little attention has been paid to chemical footprints that host insects leave behind on the substrate while moving over leaf surfaces. The mechanisms of how these chemicals may serve as host searching cues (kairomones) for parasitoids was explored. We compared two tritrophic systems involving the larval parasitoid *Cotesia marginiventris* (Braconidae) and the egg parasitoid *Trissolcus basalis* (Scelionidae). Bioassays confirmed that both species exploit chemical footprints from caterpillars and adult bugs, respectively, and that in the latter case, footprints of female bugs carrying eggs were more attractive than those of males. Chemical and behavioural experiments showed that in both hosts, kairomones consisted of a range of cuticular hydrocarbons with n-nonadecane playing a key role in host sex recognition by *T. basalis*. Using mutant plants with alterations in their epicuticular wax compositions, we furthermore demonstrated that the physicochemical property of the leaf plays a role in the perception of insect footprints by parasitoids. We speculate that the host finding efficiency of natural enemies may also depend on the epicuticular wax chemistry of crop plants.

Conservation vs. Restoration: the battle of the Chathams coxella weevil

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The coxella weevil, *Hadramphus spinipennis*, is a large, flightless weevil endemic to the Chatham Islands, New Zealand. It is specific to the plant host *Aciphylla dieffenbachii*, which only grows on exposed coastal areas, and its distribution is limited to two islands: Mangere and Rangatira. Although both islands were once heavily grazed and farmed, they were turned over as conservation land, and the Department of Conservation started an intensive reforestation program. This study aims to investigate the possible detrimental effects of reforestation on the distribution of *A. dieffenbachii*, and indirectly, the weevil populations and their genetic diversity. An original survey conducted in 1996 of *H. spinipennis* and *A. dieffenbachii* populations on Mangere and Rangatira was repeated in 2010 and 2011 to provide information regarding the conservation status of the weevil. Current distributions of *H. spinipennis* and *A. dieffenbachii* were recorded and tissue samples of 15 weevils from each island were collected for DNA analyses: the mitochondrial gene, CO1, and the nuclear gene, ITSII. Although a decline in *A. dieffenbachii* distribution was found, the weevil population was found to be breeding and surviving on Rangatira. In Mangere, there was a slight decline in the distribution of the plant. Overall, CO1 showed little genetic variation whereas some variation was found in ITS2. It appears that reforestation may constrain weevil populations and alternative plans may be needed to protect the species. However, the lack of genetic variation between the two island populations suggests that management plans may have to consider them as one population.

Te Paki: a spider hotspot revealed

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The Te Paki Ecological District is recognised as a hotspot of national significance for several broad taxa, including vascular plants and molluscs. Many other, less numerous, taxa present in the district also show significant levels of morphological and molecular divergence from species and populations elsewhere in the country. This deep phylogeographic rift is assumed to be the consequence of repeated isolation and connection of the Te Paki district with the rest of the North Island during the Pleistocene ice age. Two invertebrate pitfall trapping studies conducted over two years and encompassing 16 sites in three habitat types has revealed that the phylogeographic rift also applies to the spider fauna. Together with previously known endemics, a number of undescribed species of spider not recorded elsewhere were found. Te Paki endemic spiders are, in many cases, closely related to spiders of the Three Kings Islands to the north, and those of the northern North Island to the south. There is also evidence of taxonomic imbalance in the Te Paki spider fauna. For example, the diversity of some families (e.g. Hahniidae) is very high compared with other parts of the mainland. Although the diversity of spiders in general does not appear high compared to other parts of the country, the number of endemic species and their likely threat status indicates that the Te Paki Ecological District is a spider hotspot. The spider fauna of the Te Paki Ecological District is therefore in urgent need of further research.

Surveillance for introduced invertebrates on Barrow Island, Western Australia

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Entomologists at Curtin University have been coordinating the Barrow Island Invertebrate Baseline Survey for Chevron Australia Pty Ltd since 2005. This has resulted in a comprehensive reference collection of over 2,000 terrestrial invertebrate species for Barrow Island. Barrow Island is a Class A Nature Reserve and is protected under Federal and State Environmental Legislation; it represents a unique blend of conservation and industry. Chevron Australia has been operating Australia's largest onshore oilfield on Barrow Island for more than fifty years. As a result of Chevron's operational control and a lack of public access, Barrow Island has retained its mammalian fauna and has, to date, not introduced any vertebrate pests on the island. As a result of a targeted invertebrate survey only 20 synanthropic invertebrate species have been collected from the island. In 2009, Chevron Australia and the Gorgon Joint Venture Participants received Ministerial approval to build a gas processing plant on the island. One of the main conditions of Ministerial approval was that no invasive species is to be introduced to the island as a result of the gas plant and pipeline construction process. This resulted in the Gorgon Project funding an extensive quarantine and monitoring programme for all of its contractors and an on-island surveillance programme for non-indigenous vertebrates, invertebrates and plants. A group of statisticians and biologists at Queensland University of Technology were commissioned to design an Integrated Surveillance System (ISS) for plant, vertebrates and invertebrates. This was based on risk maps of areas of vulnerability of introductions coupled with the footprint of efficacy of the various sampling methods for catching any of five chosen exemplar invasive species. This presentation will outline progress as Chevron uses this ISS to monitor invertebrates on the island. The Gorgon Project is operated by an Australian subsidiary of Chevron and is a joint venture of the Australian subsidiaries of Chevron (approximately 47%), ExxonMobil (25%) and Shell (25%), Osaka Gas (1.25%), Tokyo Gas (1%) and Chubu Electric Power (0.417%)

Conservation of New Zealand's rarest tree weta (*Hemideina ricta*)

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The Banks Peninsula tree weta (*Hemideina ricta*) is the rarest of the seven tree weta species in New Zealand and is restricted to the eastern part of Banks Peninsula. Habitat destruction and predation by introduced mammals are likely threats to this species. We worked with landowners to monitor weta using artificial refuges called weta motels. Ten weta motels were placed at each site and left for at least 3-4 months before checking. Canterbury tree weta *H. femorata* and *H. ricta* distributions on eastern Banks Peninsula appear to be relatively unchanged from the 1990s, with *H. ricta* generally found at higher altitudes than the *H. femorata*. Weta were quick to occupy weta motels - after nine days 10% of motels at Ellangowan Reserve were occupied by *H. ricta* and occupation increased to 28% after 44 days. As many as seven weta were found in a single motel. 64% of motels with open canopy cover and low sub-canopy density contained *H. ricta* indicating that weta do not require dense bush. Landowner advocacy for weta conservation was achieved through the use of brochures and meetings.

Using next-generation sequencing for food web analyses; a detective story involving endemic landsnails and earthworms

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The study of food webs is of major importance in ecology; however, feeding is sometimes difficult to observe or quantify for species that are rare, very small, aquatic or nocturnal. The assessment of such species' diet often relies on the study of prey remains (e.g., arthropod cuticle) in predator gut contents or faeces. However, this method often lacks precision at the species level, and is not applicable for soft-bodied prey such as snails, slugs, earthworms, etc. The development of molecular techniques targeting prey DNA remaining in the guts and faeces predators appears to be a good alternative. As it is based on DNA barcoding, this approach is both very precise in terms of species identification and applicable to soft-bodied prey. We used next-generation sequencing (454-pyrosequencing) to analyse the diet of *Powelliphanta augusta*, an endangered carnivorous landsnail endemic to New Zealand that was suspected to feed mainly on earthworms. This technique is capable of sequencing many thousands of DNA fragments simultaneously from mixed samples, which allows molecular identification of all prey species in a single faecal sample. Although earthworm tissue was not detectable in snail faeces, earthworm DNA was still present in sufficient quantity for molecular tools to detect and analyse it. Based on faecal samples collected from 40 landsnails, our results provide a complete map of the earthworm-based diet of *P. augusta*. These results are helping to ensure that snails translocated to new areas have access to an appropriate range of prey species, enhancing their likelihood of survival.

From Rumble to Raoul. A biodiversity expedition to the Kermadec Islands, May 2011

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The Kermadecs are a sub-tropical volcanic island arc 800-1000kms north of Tauranga, New Zealand. The group comprises sea mounts, stacks, rocks and forested islands and is the most remote reserve area managed by the Department of Conservation. This will be a pictorial presentation of a biodiversity expedition organised by the Auckland Museum which sailed on the research vessel RV Braveheart in May 2011. The aim was to visit each island along the Kermadec rise, culminating with Raoul and near islets. Landfall was attempted on as many locations as possible where invertebrate and plant collections were made, while dive surveys documented the marine life. Some of the islands are no larger than 100 metres in radius with bluffs, volcanic calderas and no fresh water. Entomological collecting on the Kermadecs has been irregular, with most specimens dating to a 1908 expedition and the majority from Raoul Island. Several of the Islands have not been collected from and some taxa may require new descriptions.

Invertebrate functional biodiversity in plantation forests

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Plantation forests in New Zealand are dominated by fast growing exotic conifers (predominantly *Pinus radiata*) that are largely grown in even aged monospecific stands. Recent studies have shown that *P. radiata* stands can provide habitat for many native invertebrates, plants and birds, including threatened species. In New Zealand, forest managers are particularly keen to quantify the ecosystem services that are provided by plantation forests. This interest has been largely stimulated by the recent development of carbon markets and trading in carbon credits. Forest managers are keen to 'monetarise' other environmental services from forests, such as the provision of clean water, erosion control, and biodiversity conservation. However, presently, little is known of the functional role of invertebrate biodiversity in New Zealand's plantation forests. I provide a brief overview of what we know about the composition of invertebrate biodiversity in plantation forests and then report on two ongoing long-term studies that are investigating invertebrate functional biodiversity; 1) quantifying the role of wood borers and bark beetles in the decomposition of dead wood in plantations, and 2) the importance of understorey native plant species in exotic plantation stands as habitat for deadwood feeding and litter feeding invertebrates.

Indirect control of the invasive yellow crazy ant through biological control of its mutualist scale insect on Christmas Island

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The invasion of the yellow crazy ant (*Anoplolepis gracilipes*) on Christmas Island, Indian Ocean, threatens the conservation value of its unique island rainforest by triggering an ecosystem “meltdown”. Mutualism with introduced honeydew-producing scale insects, especially the lac scale, *Tachardina aurantiaca* (Hemiptera: Kerriidae), appears key to the ant’s success. Although initial suppression of the crazy ant using toxic bait has been successful, repeated use of toxic chemicals in maintenance management in remote natural areas has proved difficult to sustain. Development of biological control programs on islands, and of invasive scale insects in particular, have proved especially successful. Biological control of *T. aurantiaca* may provide a self-sustaining system to indirectly control crazy ants by denying them resources provided by these honeydew-secreting mutualists. Initial on-island research on feasibility is promising: (i) *T. aurantiaca* does not appear to be controlled by natural enemies. Widespread surveys across island rainforest have detected a single primary parasitoid species, *Marietta* sp. (Hymenoptera: Aphelinidae), a primary/secondary parasitoid that attacks only a small percentage of male lac scale and does not appear to provide effective control of *T. aurantiaca*. Nevertheless, potential hyperparasitism by *Marietta* sp. must be taken into consideration during agent selection. (ii) Further intensive surveys have detected no native or endemic scale insect species which should minimize the potential for non-target effects of parasitoid introduction for *T. aurantiaca*. The search for effective natural enemies of *T. aurantiaca* in Southeast Asia, its putative area of origin, has begun.

Identifying generalist predators of polyphagous pest species for potential use in conservation biological control in viticulture

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Biological control is often based on prey-specific predators or parasitoids. They can reduce the pest species' populations, ideally, without impacting on non-target fauna. In contrast, conservation biological control (CBC) enhances existing ecosystem services through habitat manipulation to improve survival, fecundity, longevity and searching activity of predators or parasitoids. Because CBC manipulates the existing environment and its species interactions there is an opportunity to use polyphagous natural enemies as well as prey-specific ones. By identifying a successful generalist predator that preys upon multiple pest species already present in the vineyards, the negative implications of chemical pesticides could be removed and biodiversity enhanced. Vineyards usually have a dearth of biodiversity compared to other environments in the same 30-50° latitudes. The European earwig (*Forficula auricularia*), the European harvestmen (*Phalangium opilio*), and the whirligig mite (*Anystis baccarum*) are generalists that have been identified as the chief predators of the lightbrown apple moth (*Epiphyas postvittana*), the predominant invertebrate pest in New Zealand's largest wine-producing region, Marlborough. The relationship between these predators, *E. postvittana* and another pest of growing concern, citrophilus mealybug (*Pseudococcus calceolariae*), was examined. The prey and foraging substrate preferences of these three predators is used to distinguish which are suitable for further investigation for managing vineyard pests through CBC. Outcomes from this study can be transferred to other agricultural and horticultural practices using vineyards as a model system because both of the key pests studied here are harmful in a wide range of crops.

Vegetation effect on invertebrate abundance in Australian vineyards

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Vegetation diversity has long been known to enhance natural pest control at both the local and landscape level. However little is known about the characteristics of this vegetation that promote/shelter more natural enemies and suppress pests. To consider vegetation characteristics we compared the impact of grasslands and treed areas as well as within-crop vegetation on natural enemy abundance in Australian vineyards in a replicated design. Pitfall and yellow sticky traps sampling occurred throughout the grape growing season in 2010-2011, starting from bud bursting stage of vines and continuing through until harvest. A range of natural enemies and other invertebrates were sampled in vineyards which were then sorted to family level to analyze groups affected by adjacent vegetation. The outcome of these surveys will be presented and results compared to similar trials carried out in northern Europe.

Floral resource provision for insect communities: the effect on multi-trophic interactions in agricultural systems

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The addition of floral resources to agroecosystems to improve biological control may enhance the third trophic level (i.e. the pests' natural enemies), but also provide a resource that benefits the second trophic level (i.e. the target pest). However, it is currently unknown if the presence of a pest parasitoid mediated by floral resources, results in increased crop yields or reduced crop damage. We manipulated insect communities by providing *Phacelia tanacetifolia* and *Fagopyrum esculentum* to investigate if these two floral resources mediated a trophic cascade effect. Using field cages we studied if the presence of these flower species affected parasitism by *Diadegma semiclausum* on the diamond back moth (DBM) *Plutella xylostella*, a major pest of cruciferous crops. The resultant effect measured was seed yield of pak choi (*Brassica chinensis* var. *parachinensis*). Our results showed that floral resource availability did not significantly increase the number of parasitoids. We also found that parasitoids reduced DBM populations by up to 68%, compared to the DBM control, irrespective of floral resource availability. Furthermore, the mediating effect of floral resources on the insect community resulted in no significant effect on seed yield. Combining all our results, we conclude that the likelihood of a trophic cascade occurring, mediated by the provision of floral resource remains unclear.

The arrival in Australia of *Hippodamia variegata*: consequences for insect communities and pest management

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This paper explores the effects arising from the recent arrival in Australia of the ladybird beetle, *Hippodamia variegata* (Goeze) (Coleoptera: Coccinellidae). Monthly surveys of various habitats on vegetable farms in the Central West of New South Wales, Australia showed it to have become an important numerical component of the natural enemy fauna and the most common coccinellid. Predator densities in non-crop habitats were relatively high in the period leading up to brassica crop planting and may be an important source of natural enemies. A mark-capture technique study showed that adult *H. variegata* move into crops from the adjacent non-crop habitats. In-crop sampling demonstrated that marked predators were recovered even at the farthest point of the crop transect, 100m from the non-crop vegetation, though catch declined with distance from the field margin, showing biological is likely to be influenced by edge effects. A second experiment investigated repopulation of an insecticide sprayed field over time and further demonstrated the significance of non-crop habitats as source habitat. DNA gut analysis of field collected predators was carried out to examine the diet of *H. variegata* and a second common predator, the brown lacewing, *Micromus tasmaniae*. Both were generalist predators of the primary brassica pests: *P. xylostella*, *B. brassicae* and *P. rapae* but intraguild predation was common; highly asymmetrical and in favour of *H. variegata* consuming the lacewing.

Attract and reward: combining chemical ecology and habitat manipulation to enhance biological control in field crops

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Plants produce natural enemy-attracting semiochemicals known as herbivore-induced plant volatiles (HIPVs) in response to herbivore damage. Synthetic HIPVs deployed in crops have potential to enhance biological control of pests by recruiting natural enemies but these could starve unless well timed to coincide with host/prey availability. Combining the use of nectar and pollen producing plants with synthetic HIPVs offers scope to improve nutrition for parasitoids and predators. This project aimed to test the potential for such an 'attract and reward' strategy. Field experiments tested methyl salicylate, methyl anthranilate, methyl jasmonate, benzaldehyde, cis-3-hexenyl acetate, cis-hexen-1-ol at 0.5, 1.0, 2.0%, mixed with Synertrol® (v/v) and buckwheat (*Fagopyrum esculentum* Moench) as the reward. Synergistic 'attract and reward' effects were demonstrated in broccoli with Scelionidae being increased in MeSA treatments with reward. 'Attract' and 'reward' alone increased catches of several beneficial hymenoptera and predators in grapevines and sweetcorn as well as broccoli. In sweet-corn, increases in natural enemy numbers were complemented by effects at the first and second trophic level with plant damage and pest densities reduced. Laboratory studies indicate that synthetic HIPV application has a short effect on plant head space but longer term effects (ca 6 days) are brought about by triggering endogenous production of HIPVS by treated plants.

The role of refuges in the resistance management of *Helicoverpa* moths and the implications of this to IPM in cotton

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Bt cotton has transformed cotton growing in Australia by drastically reducing the amount of insecticides used on cotton crops. Nevertheless it could lose its efficacy if the target pest, *Helicoverpa* spp, developed resistance to Bt toxins. In order to delay resistance, growers are required to plant refuges to ensure a supply of moths not subjected to Bt selection pressure. The rationale is that moths emerging from refuges will mate with any resistant moths emerging from Bt cotton, thereby diluting their resistant genes. Currently, growers must ensure that 10% of the area planted in Bt cotton is planted as a conventional cotton refuge. However, if they use pigeon pea as the refuge crop they need only plant 5% of the area to refuge. This is because pigeon pea is thought to be twice as affective at producing moths as cotton. In this study the efficacy of different types of refuges over the last two seasons was compared. The results suggest that while pigeon pea can attract high egg lays, its attractiveness is very variable and high egg lays do not necessarily result in a high number of moths. In addition, changes in the survivorship of larvae over the season modified the productivity of refuges. The results are discussed in respect to the efficacy of refuges and the implication of this to Integrated Pest Management in cotton.

Biodiversity and biological control of arthropods

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“Even as a single hair casts a shadow does a weed steal profit from a harvest”. This saying from farmers in the USA in the last century represents the most extreme view that no non-crop biodiversity can be tolerated in the farm environment. Although this opinion is probably rare today, conducting appropriate research on farmland biodiversity and achieving adoption of the protocols by farmers remains the challenge. This presentation will outline the science behind some recent achievements in enhancing pest biocontrol on farmland and explore how successful ‘outreach’ can be achieved.

A comprehensive study of the commercial insectary industry in Australia

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The purpose of this study was to investigate the status of Australia's commercial insectary industry. The target population consisted of nine insectary company owners (including a previous company owner and a very small scale owner who does not mass rear). Semi-structured face -to- face and telephone interviews were conducted in 2011. There are only seven commercial insectaries in Australia that produce 29 species of biological control agents. Four other species of biological control agents are available but not on a commercial scale. Set-up cost is a major barrier to establish a new insectary. After 2000 only one new insectary has been established. Australian insectaries supply agents mainly to the horticulture industry. Most of the insectary companies produce only one or three biological control agents and are focused mainly on one crop. One biological control agent, the predatory mite *Phytoseiulus persimilis*, is the leading biological control agent in the Australian market. Producers do not record how many hectares of crop area receive mass produced biological control agents in Australia. Approximately 4500 farmers and other consumers use biological control agents and this translates to about \$3-5 million dollars gross in sales per year. All producers reported that insecticide resistance is the main reason that growers switch from a conventional chemical-focused to an integrated pest management strategy. Producers recommended increasing public awareness of IPM. They also support introducing new government legislation to reduce the use of chemical pesticides and believe this will help the commercial insectary industry to expand in Australia.

Impact of *Polistes chinensis* on invertebrates in kiwifruit orchards

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Polistes chinensis nests were introduced to kiwifruit orchards as a proxy for a biological control agent aimed at controlling pest leafroller species. The aim was to monitor the impact of this generalist predator on other species in the kiwifruit orchard habitat. The nests were introduced to 5 organic orchards and 5 IPM orchards, as the invertebrate assemblages in orchards under these two different management systems had been found to differ significantly. The nests were monitored for their growth and survival, and prey items were collected from the wasps for identification. PCR analysis of the CO1 gene of the prey items revealed the wasps were consuming a similar range of prey to those found in studies of other New Zealand or overseas habitats. Prey items were primarily Lepidoptera, including the pest *Epiphyas postvittana*, but also included some predatory species. The populations of 50 non-target species were also monitored in the orchards in an attempt to detect population impacts from the wasps. The results may have implications for the use of generalist predators and parasitoids as augmentative biological control agents, or the encouragement of these species in conservation biological control programmes.

Entomopathogenic fungi of Papua New Guinea oil palm pest, *Zophiuma butawengi* (Hemiptera: Lophopidae), and potential for biological control

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Oil palm *Elaeis guineensis* Jacq. is an important cash crop in Papua New Guinea. Production is currently under threat from Finschhafen Disorder caused by the planthopper *Zophiuma butawengi*, a native pest of coconut palms. The need for an environmentally friendly strategy to manage *Z. butawengi* is vital since the industry is committed to sustainable palm oil production. One option is the development of a biological control agent using entomopathogenic organisms that could be applied in response to outbreaks of the pest, thereby reducing the impact of *Z. butawengi*. Field collections were conducted in February 2010 during the wet monsoon season from five localities in PNG where populations of *Z. butawengi* were monitored. From these, three entomopathogens were identified from mycosed *Z. butawengi* cadavers; *Metarhizium flavoviride* var. *minus*, *Paecilomyces lilacinus* and *Hirsutella citriformis*. This is the first record of identified entomopathogenic fungi of *Z. butawengi*. In laboratory-based bioassays, the entomopathogens were tested on *Z. butawengi* nymphs. Although there was no significant difference between treatments ($P = 0.709$), the fungal treatments killed insects more rapidly than the controls ($P < 0.001$). *M. flavoviride* var. *minus* killed insects most rapidly, followed by *H. citriformis* and *P. lilacinus*. *M. flavoviride* var. *minus* showed promise as a candidate for further development as a biological control agent for *Z. butawengi*.

Parasitoids of *Zophiuma butawengi* (Heller) (Hemiptera: Lophopidae), the cause of Finschhafen disorder of oil palm in Papua New Guinea

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A study was initiated to investigate Finschhafen Disorder (FD) in which yellowing and dieback of coconut and oil palm frond leaflets occurs. The investigations confirmed the association of *Zophiuma butawengi* (Heller) (Hemiptera: Lophopidae) with FD. Unlike most yellows-type diseases associated with Hemiptera, results showed that FD is caused by a direct feeding effect on palms by *Z. butawengi* rather than transmission of a pathogen. This finding means that a threshold-based management strategy through biological control (BC) using parasitic wasps could be realised. An exploration for parasitoids was conducted in West New Britain (WNB) and mainland Papua New Guinea (PNG). Egg parasitoids belonging to the families Mymaridae and Encyrtidae were recovered from *Z. butawengi*. The mymarid has been identified as *Parastethynium maxwelli* (Girault) and represents the first host record for this genus, whilst the encyrtid has been identified as a new species of *Ooencyrtus* near *minor* (Perkins). The biology and a redescription of *P. maxwelli* has been completed while the biology and description of the new species of *Ooencyrtus* has been submitted for publication. Both parasitoid species were recovered from WNB and mainland PNG. No mymarids were recovered from mainland PNG, hence there is potential for classical BC for mainland PNG.

When density matters: development of teneral Argentine stem weevils under crowded conditions

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The introduced Argentine stem weevil (*Listronotus bonariensis*) causes damage to New Zealand pasture grass species. Field population studies have suggested that weevil population fluctuations can apparently be determined by the extent of weevil crowding where high populations have been found to lay low numbers of eggs per capita and vice versa. The objective of this study was to test if the development rate of teneral *L. bonariensis* changes with weevil density and whether there are any physiological consequences for the females. This study was part of a larger programme to determine the effects of confinement and crowding on teneral and gravid weevils. Two weevil densities (15 (low) and 45 (high)) were kept in plastic containers for either 11 or 21 days. Weevils were fed ryegrass proportional to the density and in sufficient quantity to off-set any suggestion that food supply was in any way a limiting factor for development or oviposition. Results showed that females at high density had significantly more oöcyte resorption β -carotene crystals in their pedicels after 11 days. This indicates egg production had stopped, suggesting oviposition rates sharply decreased. By 21 days, the females kept at both densities showed increased crystal inclusions. At 11 days, male weevils under the high density treatment had significantly lower levels of maturity than those at low density although this difference was no longer significant after 21 days. Overall for the females, crowding did not affect wing muscle or ovarian development. For the males, there was no effect on wing muscle development.

Impacts of ant-black scale mutualism on the biological control of red scale

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As part of my studies on the biological control of red scale (*Aonidiella aurantii*) in orange orchards on the central coast of New South Wales, I evaluated the impact of *Anonychomyrma itinerans* on five parasitoids and four predators of red scale and four predators of black scale (*Saissetia oleae*). *An. itinerans* is the most common ant associated with black scale and other soft scales on citrus in this region. Detrimental impacts of ants on natural enemies of red scale have been widely recognised for several decades, but never quantified in Australia where the scale is the most important citrus pest. A preliminary experiment in autumn 2010 indicated that high activity of *An. itinerans* markedly reduced levels of parasitism by *Aphytis chrysomphali*, *Ap. lingnanensis*, *Comperiella bifasciata*, *Encarsia citrina*, and *E. perniciosi*, and predation by *Orcus australasiae*, *Halmus chalybeus*, *Rhyzobius hirtellus* and *R. lophanthae*. In a comprehensive experiment involving use of polybutene bands to exclude *An. itinerans* from red scale and black scale-infested tree canopies from July 2010 to June 2011, it was confirmed that the ant significantly reduced the incidence of *H. chalybeus*, *R. hirtellus* and *R. lophanthae* and predation by these species on red scale. In contrast, the incidence of *O. australasiae* and predation by it on red scale was not affected. Incidence of the scale-eating caterpillar, *Mataeomera dubia*, a predator of black scale, was not affected. Parasitism of red scale by the *Encarsia* species was also significantly reduced. Asphyxiation by honeydew produced by black scale led to collapse of its populations on banded trees within four months of the trees being banded because *An. itinerans* was absent.

Optimising methods for collecting beneficial Hymenoptera in orchards

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Insects are monitored in agricultural systems for the purposes of detecting pest or beneficial species. The methods by which pest species are caught have had much time devoted to them and as a result a large number of traps, particularly pheromone based, targeting specific pests have been developed. Beneficial species have not been the subject of nearly as much testing; consequently, far less is known about the most effective methods of generalised monitoring of beneficials. I monitored four groups of beneficial Hymenoptera during February 2009 in three organic apple orchards in the Hawkes Bay, New Zealand. Each hymenopteran group was assessed for their attraction to trap type, trap colour, preservative type and their distribution within the orchard with regards to the shelterbelt. I found yellow sticky traps to be the most effective trap type overall for sampling the order Hymenoptera, and the two parasitoids *Anagrus* sp. (Mymaridae) and *Aphelinus mali* (Aphelinidae). White pan traps were most effective at sampling Halictidae (Apoidea). Sodium benzoate was a more effective preservative in pan traps than propylene glycol. Most Hymenoptera were found to be more abundant within the orchards than at the shelterbelt, excepting the Halictidae. In order to effectively sample particular beneficial species, prior testing should be done in order to find the most effective trap types and colours. Monitoring these beneficials in organic environments is important, so that their potential effectiveness in controlling pests can be gauged.

Management tools for *Frankliniella occidentalis* in hydroponic lettuce - mites might work. Is biocontrol spreading its wings in Australia?

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In Europe and other parts of the world, there is no doubting the utility of biological control agents when used within a greenhouse production system. In Australia, biological control is becoming widely used as a very successful management tool in many styles of greenhouses and in many different crops. Australian growers are now enjoying a supply of a broad range of biological controls and can now often target the pest with different organisms that attack either different life stages or different areas of the host plant. In a Horticulture Australia Ltd project, a combination of predatory mites *Transiulus montdorensis* and *Geolaelaps aculeifer* were tested for control of *Frankliniella occidentalis*, western flower thrips, on hydroponic lettuce. Using two very different strategies the two organisms affected numbers of the pest in indoor and outdoor trials. Results from this work and similar examples of other complementary systems will be discussed.

Parasitoid family planning: How can we help?

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Initiatives to increase biological control efficacy by sowing flowering plants for use by parasitoid wasps are based on the assumption that parasitoid reproduction is limited by floral resources such as nectar and pollen. Depending on the parasitoid and plant species involved, feeding on a floral resource has potential to extend the parasitoid female's lifespan, and sometimes also to increase the lifetime complement of eggs she has available for oviposition. The first of these potential benefits can only arise if, without the floral resource, the female will reach the end of her lifespan before she lays all of her eggs (time limitation), and the second can only arise if she is destined to run out of eggs before she reaches the end of her lifespan (egg limitation). The question of whether parasitoid females should be expected to be predominantly time limited, or predominantly egg limited, has long been debated because models both of parasitoid reproductive behaviour and of parasitoid-host population dynamics can produce widely differing predictions depending on which of these two potential limitations is assumed to be most important. From a biological control perspective, it is interesting that field studies of parasitoid ecology have generally been of limited assistance in resolving the debate. This apparently weak connection between field studies and modeling to advance ecological theory is noteworthy, partly because the scarcity of empirically derived insights about the reproductive constraints experienced by parasitoids suggests a requirement for ongoing careful scrutiny of the assumption that floral resource availability is a critical limitation. Our presentation outlines some reasons why it has proved difficult to obtain clear insights about the relative importance of egg and time limitation from empirical studies, then evaluates several seasons of field data on oviposition by *Microctonus hyperodae* (Hymenoptera: Braconidae), a biological control agent of a pest of pasture grasses, *Listronotus bonariensis* (Coleoptera: Curculionidae). It discusses the data both in the context of recent theoretical advances in understanding constraints to parasitoid reproduction, and with a view to increasing biological control efficacy.

Impact of climate change on biological control in New Zealand

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By 2090, New Zealand's climate is predicted to average around 2°C warmer than in 1990. Rainfall is expected to increase in the west and decline in the east, and extreme weather events will increase in frequency. Some cropping systems will move southward and their biocontrol systems will move with them, with little change in composition and impact. But others will face challenges. Case studies of five biocontrol systems showed: 1) Ragwort suppression by ragwort flea beetle will be less in areas of western regions, but larger areas in northern North Island will attain suppression; 2) The viability of current IPM systems to control tomato fruitworm over much of the North Island may be compromised; 3) The overall effectiveness of the woolly apple aphid IPM programme is predicted to be maintained, but with increasing importance of an insecticide application in spring; 4) The current success of lucerne weevil biocontrol may be compromised as New Zealand's climate approaches that of South Australia, where the biocontrol agent is ineffective; 5) Continuing biocontrol suppression of the Argentine stem weevil may rely on local adaptation of its parasitoid which exhibits some genetic variation. New Zealand can ensure biocontrol continues as a mainstream pest management tool by identifying and addressing risks in existing IPM systems, providing refuge habitats, taking pre-emptive action against "sleeper pests", introducing new genetic lines for biocontrol agents founded by few individuals, and maintaining border biosecurity and surveillance to defend against the increased risk that the frequent subtropical "door knockers" become permanently established.

How New Zealand pasture ecosystems provide unique opportunities for biocontrol and ecological experimentation

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This contribution discusses the biological control impact of three beaoned parasitoid wasps (*Microctonus aethioides* Loan (Moroccan strain), *Microctonus aethioides* Loan (Irish strain) and *Microctonus hyperodae* Loan) on the broad-acre exotic forage pests, the lucerne weevil (*Sitona discoideus* Gyllenhal), the clover root weevil (*Sitona lepidus* Gyllenhal) and the Argentine stem weevil (*Listronotus bonariensis* (Kuschel)) respectively. Observed repeated success of these biocontrol releases was unexpected, given that the historical frequency of efficacious releases has been c. one in ten. The mechanisms for this result are considered. It is noted that the exotic invasive weevil species themselves reached spectacular population densities compared to those found in their centres of origin. These high population levels are usually attributed to the lack of biodiversity in New Zealand forage production systems, including few natural enemies and an abundance of unfilled niches. As an extension of this, it is therefore proposed that the parasitoid wasp species, via an abundance of hosts and again, a lack of biotic resistance, have similarly reached very high levels of parasitism again far beyond those noted in their original ecosystems. These simplified New Zealand ecosystems, where there is little plant diversity and very simplified host-parasitoid interactions, offer great opportunity for the advancement of understanding of parasitoid-host interactions. Such consideration includes complex density-dependent effects in the presence of sometime maladapted relict behaviours. In some circumstances has been possible to manipulate weevil population densities to determine the presence of damage thresholds, thereby demonstrating useful biological pest suppression. Insights thus gained have the ability to develop ecological theory applicable to more complex ecosystems elsewhere.

The Economics of Nature - findings from the TEEB study

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The UNEP hosted study into The Economics of Ecosystems and Biodiversity (TEEB) set out to make an economic case for the conservation of, and investment in, Nature. Since its publication in 2010, some countries are moving forward on recommendations to value their Natural Capital. This presentation highlights some of the key recommendations from the TEEB studies, some examples of the application of the economics of nature from around the world, and a glimpse of how business and policy makers are starting to apply these concepts to their decision making.

The deader the better: invertebrate communities of decaying timber in a sea of hostile terrain

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Saproxyllic invertebrates are dependent on deadwood to complete their life-cycle. They play key roles in important ecosystem processes such as decomposition and nutrient cycling. Forest loss has been recognised as a critical agent of species decline and saproxyllic organisms are a key group affected by the large scale conversion of native forests to agricultural uses, which has occurred in the past. Exotic plantation forests provide important alternate habitat for a range of native species, however little is known about New Zealand's saproxyllic fauna. A chronosequence approach was used to sample invertebrate communities of different aged decomposing *Pinus radiata*. Deadwood age was determined using thinning information from forestry companies and is accurate to 1 month. We found that rarefied richness of orders and species was higher in older deadwood. The community structure also differed significantly with age of deadwood and certain orders and species preferred deadwood of a specific age. This suggests a succession of species due to changes in resource quality and abiotic conditions. These changes may in part be due to facilitation, where the action of colonising species affects future colonisation and species richness pattern. We discuss the results of a related study showing how the proportion of native habitat in the landscape influences saproxyllic beetle communities and subsequent decomposition of *P. radiata*. The importance of the proportion of native habitat was tested using saproxyllic communities sampled in passive flight intercept traps and actual colonisation of experimental log billets of both native timber and pine. This experiment was replicated across native forest to pine habitat gradients in landscapes that differed in their degree of native forest fragmentation.

Wildfire or mosaic fires? Impacts on beetles in South-West Australia

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In March 2003 an intense wildfire burnt approximately 20,000 ha of southern jarrah forest and heathland plains, near the south coast of Western Australia. The rapid southward spread of the fire was largely halted at the northern boundary of London forest block, patchily prescribed burnt in the spring of 2002. In 2004 a study was established to compare fire impacts on the beetle (Coleoptera) species representing roughly 20% of invertebrate richness. My PhD tested standardized metrics for monitoring changes in beetle biodiversity using a protocol which: 1) collected an inventory of 460 morphospecies over six years; 2) determined spatial autocorrelation effects of pitfall-trapping, with lower beetle richness in single forest patches; 3) compared fire impacts on the distinctiveness of the beetle fauna of the litter microhabitat; 4) used pitfall-trapped sites to compare the complementarity of beetles in these fire regimes; and 5) quantified the productivity of beetle trophic guilds. Total study richness is partitioned amongst 232 common beetle species and 228 singleton or rare species, of which 105 only occurred in patchily, mosaic burnt sites, while 68 species were exclusive to wildfire burnt sites. This ratio of complementarity within the rare beetle fauna reinforces the need to use mosaic fire at landscape scales to establish heterogeneity of post-fire ages at a fine-grained scale within individual forest and vegetation patches in southern Western Australia.

Using trait-based theory for predicting functional losses in dung beetle communities: Do species matter?

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Anthropogenically created habitat edges have pervasive impacts on the distribution and persistence of invertebrate species in forest ecosystems. The response of species to edge effects can be highly dependent on variability of species traits (response traits), which may in turn co-vary with traits that are important in ecosystem functioning (effect traits). Therefore, non-random loss of species, due to traits conferring higher susceptibility to extinction, may also result in the loss of functionally important species across a habitat edge gradient. In tropical ecosystems, dung beetles (Coleoptera: Scarabaeinae) are one of the most functionally important taxonomic groups providing critical ecosystem services such as nutrient cycling and secondary seed dispersal. However, there have been no studies which have quantified the effects of habitat edges on dung beetle abundance, species richness, species traits, or ecosystem function in forest remnants. We compared dung beetle community structure at forest edges, both protected and unprotected from intense livestock grazing in a severely-fragmented montane forest landscape surrounding the Ngel Nyaki forest reserve in Nigeria. This study has found significant effects of livestock exclusion on edge response functions in dung beetle abundance, species distributions and dung removal rates. Furthermore, results suggest that relative abundances of dung beetle species and provision of associated ecosystem functions are strongly determined by trait differentiation among these species. This study exemplifies the importance of measuring response and effect traits of species for predicting community and ecosystem responses to disturbances in intensively managed anthropogenic landscapes.

Influence of land-use on dung-associated interaction webs in an Afrotropical forest

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Use of land surrounding forest reserves can have profound effects on the structure of the adjacent forest communities, influencing the non-trophic interactions among invertebrates. These interactions, in turn, provide information about competitive effects within the community that are not provided by food web studies. Field studies of competitive interactions permit quantification of the complexity and connectedness of natural communities. Many factors can affect the structure and functioning of an interaction web and the organisms present in an ecosystem. Until now, there have been no empirical studies quantifying competitive interaction web structure in the dung community, and its potential responses to change in land use. To test for potential impacts of agricultural practices, such as cattle grazing and fire, on interaction web structure, we measured competitive interactions in dung-associated communities at Ngel Nyaki forest, Nigeria. Results show that protecting the forest edges by fencing off adjacent grassland has a positive impact on invertebrate abundance and diversity in these areas, and this has ramifications on competition in the dung community. These results underscore the vital need of understanding how non-trophic interactions are influenced by anthropogenic activity, and provide insight into how best to manage Afrotropical forest reserves.

Weevil diversity in a podocarp-hardwood forest fragment in Canterbury, New Zealand

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Ahuriri Scenic Reserve is a 7 ha podocarp-hardwood forest fragment on the Port Hills of Canterbury, New Zealand. Pitfall trapping was carried out over a year from August 2007 to September 2008. Weevil specimens were removed and identified. Overall, weevil numbers showed significant seasonality, with over 75% being collected over the summer months of November to March. However some species, particularly *Abantiadinus nodipennis* and *Xenanthribus hirsutus* were less affected by season than others. Diversity was high, with 30 species representing 26 genera being collected. The majority of these species are rare however, with 75% of specimens representing only six species. This research shows the need for more taxonomic research into weevils with five undescribed species, including three of the five most common species, being found in the reserve. The data set resulting from this project will enable models to be built to determine the influence of vegetation type on weevil presence, and provide a foundation for future research on the community phylogenetics and ecology of weevils in Canterbury scenic reserves.

Spatial analysis of a gall midge (Diptera: Cecidomyiidae) and its associated parasitic wasps (Hymenoptera) on *Hebe stricta*

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Climate change and landscape fragmentation are two major threats for global terrestrial biodiversity. In particular, habitat size, habitat quality and isolation are influenced by climate change and landscape fragmentation. Within the concept of meta-population biology, the survival of species in fragmented landscapes is mainly due to these three environmental factors. To cope with rising temperatures, stenotherm species such as mobile insects may migrate to higher and therefore cooler regions. However, at increasing altitudes, habitat quality can change or the host plant might still be restricted to lower altitudes. While these spatial and temporal "bottlenecks" are already a problem for monophagous insects, species of higher trophic levels are even more vulnerable to these spatial shifts. For example, parasitic wasps have to rely on both the respective host insect and its host plant. This project investigates whether changes in population dynamics along an altitudinal gradient will result in increased species requirements of habitat quality and habitat size in a tritrophic system. Within the Tongariro National Park, spatial distribution of broad-leaved Koromiko clusters (mainly *Hebe stricta*), habitat quality and the abundance of bud galls caused by a hitherto undescribed gall midge (Diptera: Cecidomyiidae), were mapped on a local scale along a mountain stream in two consecutive years (2010 & 2011). Hymenoptera were reared from galls collected in 2011. First findings of the spatial pattern of parasitic wasps associated with the gall midge are presented.

Spatial patterning of invasive mice and indigenous weta in an alpine ecosystem

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A high proportion of New Zealand's endemic animals and plants live above the tree line in the alpine zone. These alpine ecosystems are a significant part of New Zealand's internationally recognised distinctive natural heritage. They have been less modified by humans compared with most of mainland New Zealand, although introduced mammals are present, including omnivorous house mice. We measured the year-round activity of mice in an alpine cirque in Fiordland National Park using inked footprint tracking tunnels. A complex of wētā (Orthoptera) were tracked at the same time. We found mice were active above 1060 metres throughout all seasons including between June and November, a period dominated by snow cover. Two Hemiandrus species wētā and one Raphidophorid species appeared to be spatially disassociated with mice in cooler seasons. This pattern broke down in summer when mouse density based on tracking varied locally across altitudes of 1040–1160 metres. These are only preliminary data, but they suggest the potential for conservation management actions in the future to mitigate putative impacts of pest animals on celebrated alpine invertebrates and other components of upland ecosystems.

Effects of land cover on parasitism of the red admiral, *Bassaris gonerilla* (Lepidoptera: Nymphalidae)

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The red admiral, one of New Zealand's few butterflies, feeds exclusively on nettles, primarily tree nettle, *Urtica ferox*. According to previous studies, two introduced parasitoids, the Australian ichneumonid *Echthromorpha intricatoria* and the European pteromalid *Pteromalus puparum*, can be responsible for remarkably high rates of parasitism. There are also concerns that admiral populations appear to be declining. Because both introduced parasitoids are apparently primarily associated with Lepidoptera occurring in agricultural and other non-forest areas, we hypothesised that admiral parasitism is affected by the vegetation surrounding nettle patches. We tested this by investigating pupal parasitism of admirals in eight study areas with different land cover across Banks Peninsula. In each study area we collected pupae from nettles that were either adjacent to agricultural land or mainly surrounded by native forest. This enabled us to test both the effects of land cover in the wider landscape context and the effects of the local vegetation around nettles. The overall parasitism rate was ca. 75%, however, parasitism varied considerably among sites, and reached 100% at several sites. Parasitism was not consistently related to the amount of non-forest in the wider landscape, and both parasitoids penetrated areas with high forest cover. However, pupae from forest sites, where nettles were entirely surrounded by forest, had considerably lower or no parasitism. This suggests that the vegetation directly surrounding nettle patches influences parasitism, although these findings could also be related to density dependence effects because admirals were generally rarer inside forest than at forest edge sites nearby.

Managing for the persistence of saproxylic beetles in Tasmanian production forest

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Coarse woody debris (CWD) and the saproxylic biota that facilitate its decomposition are increasingly recognised by conservation biologists as important functional components of forest ecosystems. Impending successive tree harvest rotations and pressures for shorter rotations and harvesting of logging residue for power generation threaten CWD availability in Tasmania and, as a consequence, the persistence of saproxylic biota and the forest processes they facilitate. Our study uses a landscape genetics approach to find out how much, what type and what spatial distribution of CWD is needed to retain and maintain necessary levels of functional and structural connectivity for saproxylic beetles in different managed forest contexts in Tasmania. The study contributes to a larger, collaborative, multi-taxon and multidisciplinary approach to understanding landscape-level forest management impacts and opportunities, by Forestry Tasmania and University of Tasmania. We introduce the larger collaborative project and present preliminary findings from the study, focussing on saproxylic tenebrionid beetle *Coripera deplanata*.

Do remnants of native vegetation on farmland provide a refuge for native mosquito species or a source to maintain introduced invasives?

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Land development for farming has created new ecological scenarios for many nuisance and disease organisms as well as for native diversity. The Manawatu rural floodplain was formerly extensive swamp and coastal forest, now converted to livestock farming & fodder cropping with only small fragments of native land cover remaining. This report investigates the occurrence of native and exotic mosquitoes on farmland and in remnants of native vegetation in the lower floodplain area as a basis to consider future climate and land use scenarios for nuisance and potential disease vector species. Adult mosquitoes were sampled at 2-week intervals Jan-April at three farm locations in 2008-10, and in 2010 also in three remnant forest and three wetland locations. CO₂-baited light traps were set out late afternoon-dawn, using 12 traps/night on a rotating schedule to a total of 420 trap-nights. Breeding habitats were identified by standardized dipping for larvae in available water bodies. Data were analysed with regard to species counts, meteorological measures and habitat type. The size and shape of remnant native areas and degree of native character was also considered. Two introduced species, and a common native species were present at all locations. Three further native species were found in forest sites. An expectation that one or both of two other native species might be found at wetland sites was not supported. Seasonal dynamics and the response of one species to severe drought, as occurred in 2008, and the possible role of native remnants in maintaining populations of native and introduced species are examined.

Inducible Bt tolerance in *Helicoverpa armigera* (Lepidoptera: Noctuidae) and its effects on egg production and subsequent parasitism by *Trichogramma pretiosum* (Hymenoptera: Trichogrammatidae)

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Toxin extracted from the soil bacterium *Bacillus thuringiensis* (Bt) has been widely used to control pest insects, particularly lepidopteran larvae. The widespread use of Bt toxin has led to development of Bt resistance in many pest species. Recently, we have shown that Bt tolerance of *Helicoverpa armigera* (cotton bollworm) can be induced by exposure to sub-lethal Bt toxin concentrations, and that this induced tolerance is not apparently related to changes in gene sequences. Although the mechanism of this mode of tolerance is still unclear, it is associated with developmental penalties and elevated immune processes (such as melanisation) in Bt tolerant larvae. In addition, inducible Bt tolerance is mainly maternally transmitted. This has led us to speculate that there may be changes in the immune status of eggs laid by tolerant female moths. In this study, we have investigated the effect of induced Bt tolerance on the eggs of *H. armigera* and on egg-parasitism by *Trichogramma pretiosum*, a biocontrol agent of *H. armigera*. In addition to the effecting the size of eggs, the sex ratio of emergent offspring were also affected. We hope to investigate further differences at the molecular level by utilising deep sequencing to detect expression of many immune genes in *H. armigera* eggs and qPCR of targetted immune genes in fertilized eggs.

Management of apple weevil in Australian olive groves

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Apple weevil is cited as the second major insect pest of Australian olives by growers in Western Australia and South Australia. Apple weevil affects tree survival, especially in establishing groves, and reduces tree vigour and yield in mature groves. Research on the biology and management of apple weevil showed that weevils are most abundant in early summer, but breeding is delayed until late summer. Control strategies are required at both times - to protect trees from attack and, with later control, to try to significantly reduce the breeding potential of weevils. Effective trunk and foliar applied treatments of olive trees with both synthetic insecticide and products suitable for organic groves can be recommended to growers. With appropriate timing of intervention options, growers may be able to reduce the need for action against this pest. Such strategies would have application in other agricultural situations where apple weevil is a pest.

Aceria tosichella and its role in the transmission of wheat streak mosaic virus in AustraliaAdam Miller *¹¹ The University of Melbourne, 15 Nicholson street, Warrnambool, VIC 3280, Australia

The wheat curl mite (WCM), *Aceria tosichella* Keifer, is a polyphagous eriophyoid mite, and the primary vector of wheat streak mosaic virus (WSMV) and five other viral pathogens in cereals. Using molecular markers and a series of laboratory experiments we found *A. tosichella* in Australia to consist of two genetically distinct lineages, which have broad overlapping distributions and differ in their ability to transmit WSMV under controlled conditions. This pattern of transmission also appears to be apparent in the field whereby a strong association between WSMV detection and a single WCM lineage has been detected. Using molecular markers we recently investigated the genetic structure of the Australian viruliferous WCM lineage. We assessed genetic differentiation of 16 WCM populations using 9 microsatellite markers. Strong evidence for extensive gene flow and low genetic structuring throughout Australia was evident, with an exception of Western Australian and far north Queensland populations that appear to be genetically isolated. The data also indicate genetic patterns consistent with an arrhenotokous parthenogenetic mode of reproduction. Implications of these findings are discussed with reference to the management of WCM and associated cereal pathogens in Australia and overseas.

Effect of larval predators *Thanasimus dubius* (Coleoptera: Cleridae), reared on an improved diet, against the southern pine beetle *Dendroctonus frontalis* (Coleoptera: Curculionidae)

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The clerid *Thanasimus dubius* is a predator of bark beetles that occurs in North America and Australia and could play an important role on bark beetle dynamics. The southern pine beetle, *Dendroctonus frontalis* (Coleoptera: Scolytidae) (SPB), is a major pest of pines throughout the southeastern United States. Evaluations of *T. dubius* against SPB have been limited by rearing methods. We first present an improvement of the rearing system that has previously developed a meridic artificial diet to feed larval *T. dubius*. Increasing feeding time interval and using preservatives such as sorbic acid could help to enhance the efficiency of the rearing system. We evaluated the effects on predator performance of: (i) adding sorbic acid at different concentrations (0, 0.1 and 0.2%) in the larval diet; and (ii) increasing the feeding time intervals (2-3 vs. 5 days). Sorbic acid in the diet reduced female fecundity (by 20-40%), but did not affect adult *T. dubius* size or longevity. However, using this preservative had no effect on the overall efficiency of the rearing system. Refreshing the larval diet every five days did improve the efficiency. In a second part, we conducted an experimental test where newly hatched *T. dubius* larvae were released at four densities (0, 50, 100, and 200 per log) on pine logs infested by SPB. The release of larval *T. dubius* resulted in a significant and negative effect on the SPB ratio of increase, but the initial SPB attack density also had an effect on SPB ratio of increase.

The changing nature of IPM in outdoor vegetables in New Zealand

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IPM programmes for outdoor vegetables have previously been successfully developed and implemented for processing tomatoes and vegetable brassicas in New Zealand. The success of these programmes was based on background research on developing cost-effective monitoring tools, successful classical biological control (CBC) programmes, registration of new selective insecticides, plus industry 'buy-in' of IRM and IPM strategies. However, these and other developing IPM programmes have recently come under threat from 1) new pest incursions including currant-lettuce aphid and tomato-potato psyllid, and 2) increasing insecticide resistance in key pests, for example diamondback moth and potato tuber moth. Underpinning research on biological control agents (BCAs) has switched from CBC programmes, previously focussing on introduction of specialist parasitic hymenoptera, to maximising the impacts of existing BCAs, in particular the generalist, foliage-dwelling predators such as brown lacewing and small hover fly. ERMA is reassessing a number of insecticides, with endosulfan now de-registered and a range of organo-phosphate products under review. The potential loss of broad-spectrum insecticide classes, combined with the fact that many key insect pests are now resistant to pyrethroids, provides a unique opportunity to emphasise the use of compatible controls, namely BCAs and selective insecticides. A real challenge is to maintain the activity of new valuable insecticide classes while managing pests that are already resistant to other insecticides. Other challenges include the development of IPM programmes for the large number of 'small' crops, disruptions to IPM stability by new pest incursions, plus the lack of intensive on-the-job training that is required for IPM implementation.

Food preferences, toxic bait preferences, and the toxicity of the baits for Argentine ants (*Linepithema humile*) and Darwin's ant (*Doleromyrma darwiniana*)

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By investigating the temporal variation in toxic bait preference in Argentine and Darwin's ants, we can provide better control options because we can identify with more accuracy when ants will be foraging for one food type over another. Improving our understanding is also fundamental as we can improve future bait formulations, bait application and timing, and increase levels of bait uptake. I studied the food preferences, toxic bait preferences, and the toxicity of the baits for Argentine ants (*Linepithema humile*) and Darwin's ant (*Doleromyrma darwiniana*). Food preferences varied between species and within species considerably throughout the year, although Darwin's ant consistently favoured foods higher in carbohydrates. Despite differences in carbohydrate and protein preferences the preference for individual toxic baits showed little temporal variation. Bait preference, however, did not correlate to toxicity. The success of a toxic bait is its ability to kill an entire ant colony. Xstinguish and Extermanant baits produced the highest mortality rate. Other commercially available toxic baits had little effect on workers or queens. The efficacy of even highly toxic baits was influenced by the degree of hunger with the ants. I discuss the implications of these results for the control of invasive ants.

Efficacy and safety of APITHOR™ for the control of adult small hive beetles in bee hivesGarry Levot *¹¹ NSW Primary Industries, Elizabeth Macarthur Agricultural Institute, Menangle, NSW 2568, Australia

Small hive beetle was detected in Australia in 2004 and following a survey was deemed to be non-eradicable. Since then it has spread along the eastern seaboard and been transported inland. Small hive beetle larvae can spoil honey, cause bees to abscond and destroy hives. The research into the insecticidal control of small hive beetles described in this paper culminated in the development of an insecticidal refuge trap comprising a fipronil-treated corrugated card held between two specially designed plastic shells. The device has been commercialised under the tradename APITHOR by Ensystem Pty. Ltd. and is being manufactured in Thailand. Safety and residue trials with APITHOR™ showed no significant differences in key indicators of hive health (frames of bees, area of brood and weight of honey produced) between 'control' and APITHOR™ treated hives. There was no evidence of any adverse effects on the bees. Moreover, no fipronil (or toxic metabolites) were detected in any honey produced while APITHOR™ was in place. Efficacy trials comparing 'control' with APITHOR™ treated hives demonstrated that APITHOR™ is highly effective in reducing adult beetle numbers.

Systematics and phylogeny of the plant bug genus *Felisacus* Distant, 1904 (Heteroptera: Miridae: Bryocorinae)

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The genus *Felisacus* (Heteroptera: Miridae: Bryocorinae) is revised. It is mainly a tropical and subtropical genus, inhabiting mostly Oriental and Australasian regions, and comprises 26 described species. The genus has been treated as a part of the tribe Dicyphini and subtribe Monaloniina based on similar pretarsal structure (Schuh, 1976). However, it shows strong differences in many other sets of characters. At this point in time, the material from different museums is sorted and 39 species within *Felisacus* are distinguished, using characters in external view and male and female genitalia. One new species with highly autapomorphic characters in external structure and male genitalia will be attributed to a new monotypic genus. A phylogenetic analysis for 50 terminal taxa and over 100 morphological characters using parsimony was carried out using TNT to support the relationships of the genus with other bryocorine genera and relationships of species within the genus. The analysis shows that the group of species comprising *Felisacus* and the new genus is monophyletic with high Bremer support. Additionally, phylogeny neither proved close relationships of *Felisacus* with other Monaloniina genera, nor provided strong evidences for sister group from other Bryocorinae subtribes or tribes. On this basis of very distinct morphological structure and absence of close relationships with other groups, the new tribe Felisacini, comprising the genus *Felisacus* and a new genus, is proposed.

Preparation of the Fulgoromorpha (Hemiptera) for the Australian Faunal DirectoryMurray Fletcher *¹¹ Orange Agricultural Institute, Forest Road, Orange, NSW 2800, Australia

Current work updating the checklists of names of planthoppers for the Australian Faunal Directory (AFD) has required examination of all original publications and this has revealed numerous errors and anomalies between currently accepted nomenclature and what was originally published. In addition, erroneous Australian records of species have been published by early taxonomists studying material from major collecting expeditions to the Southern Hemisphere. Such errors are usually perpetuated by subsequent authors who clearly did not check the original publication, or misinterpreted what it contains. Returning to these original publications has removed some of these errors from being repeated in the AFD. In addition to nomenclatural issues, there are sometimes discrepancies between the sex, date of collection and even the locality of type material as originally published and the label data of specimens which can be identified as comprising the type series. It is normal practice to exclude specimens from the type series when their label data do not match the original published data. However, the Code (Art. 72.4.1.1) allows unpublished evidence to be used, in conjunction with published evidence, to determine what specimens constitute the type series. Otherwise, we are in danger of excluding valuable specimens which were clearly used in creating the original description. In this presentation, I will look at some of the issues revealed in the planthopper families Flatidae, Nogodinidae and Ricaniidae during the revision of the AFD.

Systematics and diversity of native pest beetles, *Eucolaspis*, in New Zealand

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Eucolaspis Sharp 1886 is native to New Zealand comprising many endemic species. Although 15 species have been described, taxonomy remains unresolved with poor descriptions and inconsistency among treatments. These beetles feed on various introduced and native plants. Economic damage in orchards is usually attributed to the species *E. brunnea* (Fabricius 1792), but several taxa might be involved. We undertook an integrated taxonomic study of the genus, with special interest on the populations infesting organic apple orchards in Hawke's Bay, New Zealand. Beetles from several locations and host plants in New Zealand were used for our study. We also examined extensive museum collections including type specimens, which afforded valuable information about morphological variation, host plant use and spatial distribution. Morphometric analysis of museum samples suggested just two morphotype groups, but most of the named species were spread across both. DNA was extracted from representative individuals of all the fresh samples, and a short mitochondrial DNA Cytochrome c oxidase 1 region was sequenced. This revealed three distinct genetic lineages, which were found consistent with morphometric analysis. Two of the genetic lineages occur in beetles living in sympatry, but these are separated by greater genetic distances than each is from a third lineage. Our data provide the opportunity to decipher the extent of morphological variation within species and thus the actual number of extant species which has been variously interpreted as 5 and 15. Furthermore these data allow us to determine how many species and populations are implicated in infestation of exotic crops.

Developing a benchmark invertebrate group for biodiversity modelling: phylogenetics and databasing of the dung beetle (Scarabaeidae) genus *Lepanus*

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Biodiversity modelling methods such as Generalised Dissimilarity Modelling (GDM) are increasingly incorporating phylogenetic as well as species distribution data to more effectively model biodiversity. Developing and testing these methods rely on the existence of benchmark groups for which the taxonomy, phylogenetic relationships and distributional databasing are complete. Few groups of Australian organisms are so well known and at present no invertebrate examples are available. A native dung beetle genus *Lepanus* Balthasar which consists of 24 described species and 22 undescribed provisional species seemed like an ideal candidate for biodiversity modelling due to its distribution, having both widespread species and narrow range endemics. Almost 5,500 specimens were databased, providing complete distributional records for all pinned specimens at the Australian National Insect Collection and Queensland Museum. The examination of material for databasing prompted a revision of morphological diversity in the group and lead to the recognition of a further 34 undescribed species. *Lepanus* species are most reliably characterised by the distinctive shape of the pygidium. Based on this as a primary character, the species can be divided up into 12 assemblages. There are variations within the groupings and some groupings are more homogeneous than others, but pygidium structure provides a hypothesis to investigate genetic relationships within the genus. Phylogenetic analysis of species with both COI and 28S sequence data was performed on 27 *Lepanus* spp. (131 specimens) representing 10 of the 12 species assemblages. Species assemblages were generally well supported including monophyletic clades for species assemblages 1, 4, 5, 8 and 11. Associations between all species in assemblages 3 and 12 currently remain unsupported due to limited resolution of the tree; however clades containing multiple species in both complexes are supported. The only relationship which is supported that does not correspond to species assemblage is that of CYP3 and CYP5 (Assemblages 6 & 9), however assemblage 6 is only represented by a single specimen. Further taxon or gene sampling is likely to resolve these relationships.

Conservation through DNA: Unravelling the past of the weevil genus *Hadramphus*Emily Fountain *¹¹ Lincoln University, PO Box 84, Lincoln, 7647, NZ

New Zealand is home to many endemic invertebrates that have experienced range and population declines over the past 150 years with the arrival of humans, pest species and habitat modification. The weevil genus, *Hadramphus*, is a key example of endemic invertebrates in New Zealand in which every species is listed as endangered. Advances in molecular biology allow the use of old, even ancient specimens to answer important scientific questions. This research may provide valuable information about the evolutionary past of *Hadramphus*, such as the changes in genetic variation over the last century, and their current population viability. Non-destructive extraction methods were used to extract DNA from specimens of *H. tuberculatus*, *H. stilbocarpae*, *H. spinipennis* and *H. pittsopori* ranging from 1890-1995. Primers were designed to amplify short fragments of the CO1 mitochondrial gene (60bp, 100bp and 150 bp). Sequences were aligned and compared to CO1 sequences obtained from modern samples. Preliminary results suggest variation between modern and historic samples; however, testing will be undertaken to determine if this variation is a result of heterochrony. Currently, we are using next generation sequencing (454) to find single nucleotide polymorphisms for population genetic studies using both historic and modern samples of *Hadramphus*. This will allow for the calculation of the change in effective population size over time and the mapping of the loss of species' genetic diversity.

A survey of indigenous gall forming invertebrates in New Zealand

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New Zealand's indigenous gall forming invertebrates are represented in Acari, four insect orders: Coleoptera, Diptera, Hemiptera and Lepidoptera, and Nematoda. The number of gall inducing species are as follows: · Acari- Tarsonemidae (4 undescribed), Tenuipalidae (1), Eriophyoidea (57 + about 20 undescribed); · Coleoptera- Brentidae (1), Curculionidae (4 + 1 undescribed); · Diptera-Agromyzidae (1), Fergusoninidae (1), Tephritidae (2), Cecidomyiidae (7+ up to 150 undescribed); · Hemiptera-Aleyrodidae (2), Coccidae (5), Diaspididae (4 though *Poliaspis media* may be a species complex), Eriococcidae (13), Psylloidea (12 +>8); · Lepidoptera-Carposinidae (1), Gelechiidae (1), Gracillariidae (1), Oecophoridae (2), Thyrididae (1), Tortricidae (1); · Nematoda-Neotylenchidae (1). The galls induced by Coleoptera and Lepidoptera are relatively simple, mainly swollen stem tissue with a chamber. Many scale Coccoidea galls are shallow hollows/pits in leaves or deeper pocket galls in leaves or stems. Others involve leaf edge rolls or folds, or blisters. In the Acari, Tarsonemidae induce leaf edge roll galls (3) or shoot stunting, while the tenuipalid induces a large stem gall. Diverse and complex galls are induced by Eriophyidae with erineae, pocket galls and 'bud/callous' galls being common. The nematode *Fergusobia pohutukawa* Davies (Neotylenchidae) and its mutualistic fly, *Fergusonina metrosiderosi* Taylor (Fergusoninidae) induce basal stem galls in *Metrosideros excelsa* (Myrtaceae). The agromyzid and one tephritid induce stem galls while the other tephritid larva lives in a bud gall. The Cecidomyiidae induce a wide variety of galls of varying complexity. Some plants, such as *Coprosma* species may have up to five kinds of galls present.

Update on taxonomic revision of New Zealand Austrosimulium (Diptera: Simuliidae)

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Our focus is an essentially complete taxonomic revision of larvae, pupae, and adults of New Zealand Austrosimulium. Some 19 species are now recognized. Austrosimulium, established by André Tonnoir (1925), is a small segregate of simuliids in Australia, New Zealand, and some outlying islands. It was Edwards (1931) who noted the relationship to a simuliid of South America, now recognized as the monotypic Paraustrosimulium. This latter genus is aberrant in some aspects, but there are convincing apomorphies shared with one segregate included in Austrosimulium, and molecular work by Moulton (2003) also strongly substantiates this relationship. Dumbleton's (1973) species groupings are strongly supported by cladistic analysis of morphological characters, and hence are maintained. Furthermore the groupings are extremely well supported by molecular analysis, albeit with minor variance. While the genus as a whole has Gondwanan connections, the major lack of divergence in the 16S ribosomal DNA indicates that the New Zealand Austrosimulium are of relatively recent origin. We suggest the genus arrived from Australia at some point following the Oligocene Epoch (25 mya), in keeping with recent evidence for major inundation of New Zealand at that time. This is congruent with biogeographical patterns reported for other elements of NZ's flora and fauna. The CO1 mitochondrial DNA has good divergence for some species groups; however, it is very poor for the great majority of terminal taxa, even though there is good morphological divergence. This further suggests speciation in Austrosimulium is recent. We comment about dispersal during lowered sea levels during the last glacial maximum.

Recent advances in IPM in greenhouses in Australia and New Zealand

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In the last decade there has been a significant increase globally in the extent of covered cropping. Greenhouses (and similar structures) offer increased protection from climate variability, opportunities for efficient water use, and opportunities for reduced pesticide inputs through the use of biological control. The use of biological control in covered crops has increased markedly in some European countries in recent years, often driven by a combination of public pressure for low residue produce, grower concern about pesticide resistance and government incentives. Over 150 biological control species are now commercially available around the world and more than 50,000 ha of greenhouses use biological control. In Australasia, the uptake of biological control in covered crops has been slow, in part because of the unique challenges that growers face here. In both countries, biosecurity regulations restrict the import of new biological control agents and only approximately 25 insect species are currently commercially available for biological control in Australasia. In addition, in New Zealand the establishment of a new pest species (the tomato potato psyllid) has severely disrupted existing IPM programmes. Recent advances and set-backs in Australasian IPM will be discussed, and future prospects examined.

Key lessons from Australia inform the development of arable IPM in NZ

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In 2002 entomologists from IPM Technologies Pty Ltd and a group of collaborating farmers and their agronomists started developing integrated pest management (IPM) strategies for wheat, barley and canola crops in Victoria, Australia. The farmers underwent a change in practice from a routine broad-spectrum spray programme to an IPM approach aimed at maximising the use of beneficial predators whilst minimising pesticide use. The collaborative and participatory approach taken was a key factor contributing for this shift in pest management. This paper demonstrates how the same processes and methods used to develop and implement IPM strategies for broad-acre cropping in Victoria, Australia, were then used to guide and inform development of similar strategies in arable farms in Canterbury, New Zealand. Six crops of autumn-sown wheat managed under IPM were compared with six adjacent crops grown under the participating farmers' current pest management practices in demonstration trials in Canterbury during the 2008-09 and 2009-10 seasons. Farmer training with a focus on monitoring and beneficial predator identification was carried out. IPM adoption at these farms was very high after these participatory trials. The strategies developed, the participatory approach adopted, and the outcomes as experienced in the New Zealand setting are discussed.

IPM for potato crops: lessons from Australia

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An IPM strategy has been developed for Australian potato production and is available for Australian growers. Biological and cultural controls are the key elements and insecticide applications on potatoes are rare for those using the IPM strategy. These biological and cultural controls are described. The prospect of potato psyllid arriving in Australia from New Zealand has the potential to destroy the current methods of controlling potato pests. To prevent such an event occurring we are working on possible IPM compatible control measures for potato psyllid and this work is being done in New Zealand with colleagues from Plant and Food Research. The results of this project have potential for New Zealand potato growers to change to using an IPM strategy modelled on the Australian version.

Towards developing an IPM programme for potatoes in New Zealand; the role of natural enemies

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Recent initiatives to develop IPM for potato crops focussed mainly on controlling aphid pests as virus vectors and managing potato tuber moth (PTM) in the warmer regions of New Zealand. Research on PTM focussed on movement of moths, both as a crop monitoring tool, but also for resistance management. Proposals included a classical biological control (CBC) project for PTM, to assess *Orgilus lepidus* either to complement or replace the existing parasitoid, *Cotesia subandinus*. In 2008, we reported high levels of resistance in PTM populations from the Pukekohe and Waikato regions to pyrethroid and organo-phosphate insecticides, giving impetus to improving biological control and developing IPM tools, particularly for PTM. However, the arrival of tomato-potato psyllid (TPP) relegated prospects of CBC for other potato pests to a low priority compared with urgently required management tools for TPP. Research on CBC was redirected to assess existing biological control agents (BCAs) and their impact on pests, initially in the Pukekohe region. To date, two years of weekly monitoring and spring and summer field trials show that there are existing BCAs that give substantial control of all pests in potatoes. In particular, brown lacewing, small hover fly (*Melanostoma fasciatum*) and spiders can control aphids, exposed caterpillar pests and TPP for 8 months of the year. However, two summer generations of TPP from January to April cause major crop losses. Lower populations of TPP in cooler regions provide an opportunity for naturally occurring BCAs to give longer-lasting control of TPP. Laboratory choice and no-choice studies indicate that all life-stages of the common predators, brown lacewing, small hover fly, 11-spotted ladybird and nabids are capable of consuming all life stages, and that they consume large numbers of TPP. The potato industry urgently requires sound insecticide resistance management (IRM) strategies, compatible insecticides for managing resistance, selective insecticides for maximising BCAs, plus other robust IPM tools for sustainable production of potatoes, particularly for the longer (warmer) growing regions.

The tomato potato psyllid: lessons from New Zealand for Australia

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The exotic insect pest, tomato potato psyllid (TPP, *Bactericera cockerelli* (Sulc)) was first discovered in Auckland greenhouses and volunteer potatoes in 2006 and has spread rapidly throughout the North Island and into the South Island. To date the TPP has not been found in Australia, but is considered a high plant pest risk. In New Zealand the arrival of the TPP has significantly reduced the use of IPM in greenhouse crops and outdoor tomato and potato crops. In Australia, IPM practices are commonly used for the control of pests such as aphids and the potato tuber moth. The arrival of the TPP would severely impede the use of these practices. Australian researchers aim to gain a better understanding of the TPP/*Candidatus Liberibacter solanacearum* complex in New Zealand to enable development of a number of tools to combat an incursion into Australia. Australian researchers are anticipating an incursion by the TPP and have therefore developed collaborative research projects and an exchange of ideas with New Zealand researchers. New Zealand research to date includes: use of and mode of action of insecticides, national monitoring, diagnostic protocols and techniques, biological control, insect/pathogen/plant interactions, transmission, temperature effects on development and biology, alternative vectors and use of alternative host plant species, especially overwintering hosts. Australian research has involved preparation of diagnostic protocols for TPP and testing the effectiveness of different TPP surveillance techniques. Australia can gain valuable insights from New Zealand research, in particular: the developmental requirements of TPP life stages alternative plant, especially overwintering, hosts of the TPP and *Ca. L. solanacearum*; and the potential impacts of a diverse Australian psyllid fauna and its associated natural enemies.

Strategic trans-Tasman collaborations enhance arable and vegetable IPM in Australia and New Zealand

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The considerable similarities in pest and beneficial arthropod complexes in Australian and New Zealand arable and vegetable crop systems represent large opportunities for co-development of IPM Strategies in a range of crops between these two countries. This paper examines how strategic trans-Tasman collaborations can enhance arable and vegetable Integrated Pest Management (IPM) in Australia and New Zealand and serves as an introduction to and overview of a series of symposium papers on the same subject. To place the subject in perspective, the major arable and vegetable sectors (hectares, \$\$ returns) are reviewed for Australia and New Zealand to establish the relative importance of each crop in each country and to indicate where research collaborations might be worthwhile. Successful historic research collaborations that have contributed to the development of IPM in Australia and New Zealand are reviewed and commonalities identified. The paper summarises some current initiatives where collaboration between Australia and New Zealand researchers has proved beneficial to the development of arable and/or vegetable IPM in either country. It identifies current and potential sources of funding to drive research collaborations between Australia and New Zealand in the future and examines which aspects of IPM would be especially worthwhile to pursue in Trans-Tasman collaborations (e.g. biosecurity threats, classical biological control, diagnostics for pests and diseases, registration of pesticides).

Something old, something New - Australian spiders in New Zealand

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It should come as no surprise to learn that the majority of non-endemic spiders in New Zealand are shared with Australia, but the relationships between the Australian and New Zealand faunas are deeper and older than that. In this talk we take a look at the historical relationships between the spider faunas of Australia and New Zealand, recently arrived Australian species and the potential for establishment by others.

Flies regifted? Did Australia give New Zealand its horse flies (Saptia Diptera: Tabanidae)

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Horse flies are notorious for their feeding behaviour and transmission of disease in both humans and livestock, but also have a beneficial and underestimated role in pollination. The tabanid genus *Saptia* has an exclusively austral distribution, occurring in Australasia, New Zealand, and South America. Contemporary molecular techniques are combined with traditional morphological methods to create the first robust phylogenetic hypothesis for *Saptia*. We analysed a 5KB concatenated matrix of CAD, PGD, AATS, 28s, COI and COII DNA sequences, and 30 morphological characters. Results suggest that *Saptia* and its five included subgenera are monophyletic, however new subgenera will be required for a small subset of species. Divergence time estimation using the molecular data calibrated with fossils suggests that the New Zealand *Saptia* evolved in situ from a Gondwanan ancestor, rather than being colonized by long distance dispersal after the Oligocene drowning.

Systematics and biogeography of the Gondwanan Orthocladiinae (Diptera: Chironomidae)

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Restrictions to effective dispersal and gene flow caused by the fragmentation of ancient supercontinents are considered to have driven diversification and speciation on disjunct landmasses globally. Investigating the role these processes have played in the development of diversity within and among taxa is crucial to understanding the origins and evolution of regional biotas. Within the chironomid subfamily Orthocladiinae (Diptera: Chironomidae), a group of genera that are distributed across the austral continents (Australia, New Zealand, South America) have been proposed to represent a relict Gondwanan clade. We used a molecular approach to resolve relationships among taxa and infer the relative roles that vicariance and dispersal may have played in the evolution of this group. Continental biotas did not form monophyletic groups, in accordance with expectations given existing morphological evidence. Patterns of phylogenetic relationships among taxa did not accord with expected patterns based on the geological sequence of break-up of the Gondwanan supercontinent. Likewise, divergence time estimates largely post-dated continental fragmentation and implied instead that several transoceanic dispersal events may have occurred post-vicariance. Passive dispersal of gravid female chironomid adults is the most likely mechanism for transoceanic movement, potentially facilitated by West Wind Drift or anti-cyclone fronts. Taken together, these data suggest that a more complex relationship between both vicariance and dispersal may explain the evolution of this group. The sampling regime we implemented here was the most intensive yet performed for austral members of the Orthocladiinae and unsurprisingly revealed several novel taxa that will require formal description.

Hopping across the ditch: The New Zealand Orthoptera

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The New Zealand orthopteran fauna is an eclectic mix dominated by the Anostomatidae (weta) and Rhaphidophoridae (cave crickets). The native Acrididae comprise mostly montane grasshoppers species (~13) in endemic genera, two endemic species of the Australian genus *Phaulacridium*, and the ubiquitous migratory locust. Other families have even less representation: Gryllidae (a few species allied to/shared with Australian fauna), Tetigoniidae (a few species allied to or shared with Australian fauna), one gryllotalpid, and a recently established gryllacridid (*Pterapotrechus*). The Anostomatidae and Rhaphidophoridae are speciose and, except for one dubious case, are represented by endemic genera. Species in these two groups occur throughout New Zealand in a wide range of habitats. They comprise in Australia a similar or possibly smaller number of species than in New Zealand, whereas the Australian Tettigoniidae, Gryllidae and Gryllacrididae and Acrididae include some 1000, 715, 125 and 700 species respectively. Here we report ongoing analysis of phylogenetic signature from examples in the three most speciose NZ families, Anostomatidae, Rhaphidophoridae and Acrididae, which reveal a complex mixture of relationships with Australian taxa.

Biodiversity, biogeography and evolutionary history of giant springtails from Australia, New Zealand and New Caledonia

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The Uchidanurinae are amongst the most spectacular of all Collembola. These springtails are unusual as most possess brightly coloured digitations (epidermal spine-like projections) on their dorsal and lateral surfaces and are among the largest springtails recorded world-wide. The subfamily is undoubtedly ancient – possibly of Gondwanan origin – but, despite being of considerable biogeographic and phylogenetic importance, evolutionary relationships among members of the subfamily remain unstudied. Compounding this problem, out of the morphological characters that are particularly important in the separation of new species of Uchidanurinae (i) the extent of development of abdominal lobes or digitations, (ii) pigmentation, and (iii) colour pattern, only the former character is phylogenetically informative, assuming that, within genera, development cannot regress or reduce. Conversely, pigmentation and colour pattern variation are morphological characters that cannot be reliably used for phylogenetic analysis in Collembola. Owing to difficulties associated with establishing the evolutionary significance of morphological differences among members of the Neanuridae, and the lack of phylogenetically informative morphological characters within Uchidanurinae, a molecular approach to resolving species relationships as well as biogeographic hypotheses for the subfamily is essential. The subfamily Uchidanurinae – the ‘giant’ springtails – consists of eight highly endemic genera in India, Vietnam and Malaysia, Micronesia, New Caledonia, eastern Australia, and New Zealand. Here we reconstruct phylogenetic relationships based on COI and 28S sequence data. Accordingly, these data were used to test biogeographic hypotheses relating to processes that promote biological diversification, and hence, speciation with a focus on levels of divergence among species from Australia, New Zealand and New Caledonia. Our data clearly indicates that there are several new species from all three regions and mitochondrial DNA calibration of speciation events throughout Australasia.

The rise and fall of Zealandia: biogeographic implications for entomology

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Zealandia parted company with the Australian portion of Gondwanaland over 80 mya. Zealandia was a relatively small continent size about half as large as present-day Australia. Presently, less than 10% of this landmass is above water with most of that in New Zealand and New Caledonia. In a much younger time frame the New Zealand landscape has been substantially remodelled by tectonics forces at the Pacific/Asustralia plate boundary. We will trace the fate of this continent and summarise the geological history for this area and the "sister" Australian region. We will consider the implications of changes in land area, topography and climate on interpretations about invertebrate biogeography.

Australia: sistership or mothership to the NZ invertebrate fauna Opening remarks on testing biogeographic hypotheses

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Australia and New Zealand are spatial sisters that originate from the same geological mother- Gondwana. The tectonic history of the region has become increasingly well known since the widespread acceptance of continental drift in the 1970's. However, biogeography often shows signs of having not progressed far, despite the introduction of increasingly sophisticated tools, primarily in the realm of population genetics and molecular phylogenetics. One general problem is a tendency to assume, without good evidence, a correlation between isolation of land areas and isolation of biological populations. For Australia and New Zealand, continental breakup does provide one plausible mechanism for the sundering of extant lineages, however, demonstrating this to be the case is far from easy. NZ and Australian invertebrate faunas may be sister, through that old vicariance process, but equally, one could be the daughter of the other. It is challenging and possibly impossible to obtain the data necessary to distinguish these alternatives given that sampling is largely dependent on the living representatives of lineages. Extinction, range-change and long distance dispersal and establishment are known components of evolution that mean any simplistic and generalised biogeographic "solution" would be naive.

What can insects, especially Chironomidae, tell us about austral ecological and biogeographic history?

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Entomologists have been in the vanguard of southern hemisphere biogeographers. Views on origins of the austral biota have swung from endemic austral, to northern invasion, back to gondwanan vicariant, to dispersals from mixed sources. New Zealand insects have been claimed to represent gondwanan relicts dating to separation of Zelandia from Antarctica, and linked phylogenetically more to southern America than to neighbouring Australia. In perhaps the most extreme contrasting view, NZ diversity derives from neo-radiations with all extant biota derived by dispersal since the surmised Oligocene 'drowning' that eliminated all terrestrial biota. With increasing availability of phylogenetic estimates for a range of well-sampled austral insects, and with dating and tempo derived from increasingly sophisticated models of molecular evolution, we can re-assess these earlier views. Amongst the biogeographically-significant insects are the austral Chironomidae midges studied half a century ago (Brundin, 1966). With a good Cretaceous amber fossil record, and earlier wing compression fossils, a chronogram can now be presented for the tempo of the evolution of the 'Brundin taxa'. No NZ taxa are sister to Australians but to South Americans as Brundin argued. However dates for NZ nodes are too young for Gondwanan fragmentation (Cranston et al, 2010) but some straddle and pre-date the Oligocene. Northern hemisphere branches are very old (Pangean) or young - by colonisation from the south. Other Chironomidae represented in NZ are congruent but include sisters to Australians (recent dispersal, both ways). Other insects (and arthropods) challenge Oligocene drowning - an NZ biota persisted, at least in Nelson. Dating and placement of fossils is critical.

Better management of cotton refuges within the best management practices framework

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The implementation of genetically modified *Bacillus thuringiensis* (Bt) cotton has reduced the use of chemicals by suppressing *Helicoverpa armigera* and *H. punctigera* pest populations. This results in selection for resistance to Bt since pests tolerant to Bt survive and convey their resistant genes to the next generation. To maintain susceptibility to Bt in pest populations, refuges of unsprayed non-Bt cotton are planted with Bt cotton so that susceptible populations dilute any acquired resistance, preventing Bt cotton from becoming ineffective at controlling pest populations. Planting an unsprayed crop carrying high numbers of invertebrates and with a low yield potential can appear counterintuitive to growers. Therefore, quantifying and improving the efficacy of refuges is necessary to maintain industry support. Disease, predator and parasitoid populations increase with increasing densities of *Helicoverpa* larvae and could cause excessive mortality as larvae numbers increase. Consequently larger numbers of larvae may result in fewer moths. Part of the research will identify if there is a point at which the density of *Helicoverpa* in the crop causes the population to crash, and whether this point varies between refuge types. Though still in its infancy, the project will determine the best management strategy for refuges in cotton to ensure maximal output of Bt susceptible moths. From the practical perspective, the information gained will enable growers to be confident that they are getting the best biological benefit from their refuges via the most cost-effective means. From a biological perspective, the project will examine the interguild effects of high herbivore numbers.

Insecticides susceptibility in *Culex vishnui* Theobald in paddy field in Sekinchan, Selangor, Malaysia

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Culex vishnui is one of the primary vectors of Japanese encephalitis in Southeast Asia. The susceptibility of *Culex vishnui* larvae collected from paddy field in Sekinchan, Selangor, Malaysia, was studied against malathion, temephos and permethrin. The study sites were selected on the basis of contrasting agricultural practices and use of insecticides. Larval bioassays were carried out in accordance to the WHO standard procedures. Larvae of *Culex vishnui* were also tested against diagnostic dosage of malathion (0.125 mg/L) and temephos (0.002 mg/L). *Culex vishnui* larvae were resistant against diagnostic dosage of malathion and temephos with 24 hour post-treatment mortality (%) of 10.67 ± 1.15 and 0, respectively. In addition, permethrin exhibited significant lower LC₅₀ value (0.048 ± 0.003 mg/L) against *Culex vishnui*, in comparison to temephos (0.074 ± 0.003 mg/L) and malathion (0.227 ± 0.007 mg/L) ($p < 0.05$), indicating that *Culex vishnui* was still susceptible to permethrin which can be used to control *Culex vishnui* in the paddy field.

The circadian activity pattern of carrion flies in Malaysia

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Whether a corpse has been colonised by flies close to the time of death or a delayed oviposition might have occurred is an important question in determining the post mortem interval (PMI). The circadian activity and the oviposition behaviour of blowflies are some of the important factors. Two studies were conducted to investigate the circadian activity of blowflies by exposing euthanised monkeys to see if blowflies visited and oviposited on the carrion over three consecutive days. The first study was commenced at daytime (1130h) while the second study was commenced at nighttime (2200h). Both studies were monitored hourly for the first three days. The first study showed that flies were able to visit the fresh carrion within 30 minutes after it was placed outdoor in the day time. The second study showed no fly activity throughout the night until sunrise, indicating that the oviposition of blowflies was delayed. The result was further confirmed by observation on fly activity for another two consecutive days. Both studies showed that flies began visiting monkey carcasses about half an hour after sunrise (mean 29.25 ± 1.49 minutes) and actively laid eggs on the carcasses throughout the day until sunset. No flies were observed visiting the carcasses from approximately less than 10 minutes after sunset (mean 5.80 ± 0.68 minutes). No fly activity was observed throughout the night. Both studies confirmed that flies are inactive at night. Based on these results, presumably a victim killed after sunset would not be colonised by flies before the next sunrise. This may lead to a considerable discrepancy between the estimated PMI and the actual time of death.

Forensic entomological study on monkey carcasses submerged in river in tropical rain forest in Malaysia

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This forensic entomological study was conducted to estimate the post mortem interval (PMI) of monkey carcasses submerged in river in a forested area located in Ulu Gombak, Selangor, Malaysia. Monkeys were used as a model for human decomposition. Initially, monkeys were euthanized and the study protocol was approved by IMR's Unit of Animal Care and Use Committee. After death was confirmed, the carcasses were immediately clothed to simulate human cadavers. The carcasses were kept in metal cages and submerged in the river with water temperature of about 20°C. The carcasses were monitored daily until no more larvae and body remains were observed. The decomposition of carcasses underwent 5 stages, namely fresh (3 days), bloating (4 days), decay (1 - 2 days), advanced decay (1 - 2 days) and remains (10 - 12 days onward). No fly activity was observed on the first day. From Day-2 (fresh) to Day-11 (advanced decay), adult flies belonging to Calliphoridae, Muscidae, Sarcophagidae, Lauxaxiidae and Dolichopodidae were observed visiting the carcasses. However, no adult flies visited the carcasses at the remains stage from Day-10 to Day-12 onwards. No maggots were recovered from the carcasses in the first 5 days. On Day-6 (bloating), 2nd instar maggots of *Chrysomya pinguis* (Walker) were recovered. On Day-8 (decay), 3rd instar maggots of *Hemipyrelia* (Townsend) sp. and Sarcophagid were recovered, while on Day-11 (remains), 3rd instar maggots of *Ophyra* (Robineau-Desvoidy) sp. were recovered. This study indicated that PMI was delayed by 4 days on carcasses submerged in flowing river.

How to assess the risk posed to the New Zealand native flora by an invasive defoliator

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We assessed the risk posed to the New Zealand native flora by the Australian invasive defoliator, *Uraba lugens*, the Gum Leaf Skeletoniser. We tested native flora within the Myrtaceae, using host testing methods of larval feeding assays, adult laboratory and field cage oviposition assays, and a field survey. Two distinct mechanisms that could result in gum leaf skeletoniser impacting on native New Zealand plants was discovered: development of self-sustaining populations on native species, and/or temporary spill-over of solitary larvae. *Metrosideros umbellata* (southern rata) was the native plant ranked the highest risk yet still an unlikely host, all other plants were highly improbable to develop self-sustaining populations. Temporary spill-over feeding by larvae according to distance from infested host tree is highly likely on a number of native plant species but this will be more likely in urban areas, and mixed tree plantings. We continue to investigate rapid and novel methods of assessing risk from invasive insects as a part of Better Border Biosecurity research.

Ips Grandicollis (Eichhoff) (Coleoptera: Scolytidae) - a bark beetle on a mission.

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Sirex wood wasp, *Sirex noctilio* Fabricius (Hymenoptera: Siricidae), has been managed effectively by the nematode *Beddingia siricidicola* (Beddingidae) until the recent, unprecedented occurrence of the exotic bark beetle, *Ips grandicollis* (Eichhoff) (Coleoptera: Scolytidae). The bark beetle is disrupting the Sirex biocontrol programme by attacking trap trees primed for nematode introduction. Hence, we monitored trap trees for *I. grandicollis* in five states of Australia where pine trees are grown commercially in order to quantify the magnitude of threat facing Sirex biological control. In this poster, we map the geographical regions where suppression of *I. grandicollis* is urgently required and in addition, summarise factors that may favour distribution and spread of the bark beetle in Australia.

Comparing the fitness of woolly apple aphid *Eriosoma lanigerum* populations: evidence of different biotypes in Australia?

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The woolly apple aphid (WAA), *Eriosoma lanigerum* Hausmann, is a major pest of apple orchards that is known to have a high economic impact on apple production in Australasia but also worldwide. Since its arrival in Australia two centuries ago, WAA populations have established in various locations that are geographically isolated. Because of their isolation, these populations could represent separate biotypes that have different biological features and adaptation to different environments. To determine whether each population could represent a different biotype, we measured, under controlled conditions, the fitness parameters of two WAA populations collected in New South Wales (Albury) and Victoria (Stanley). Both populations were reared on potted apple trees in glasshouses and further compared in laboratory trials (22°C; 16 L: 8D). The average fecundity, size (body length) and developmental time of apterous virginoparae on excised stems of apple trees (*Malus domestica* cv. Granny Smith) were estimated for each population. Similarly, we evaluated the survival rate, size, and developmental time of newly born nymphs. Results indicated that the Albury population presented distinct features compared to the Stanley population. Overall, this suggests that there could be different biotypes of this pest insect in Australia. This is in agreement with previous work that has indicated a difference in feeding behaviour for the Albury population relative to another population (from Batlow, NSW). We discuss the importance of the existence of different WAA biotypes in Australia on the development of future management strategies.

Interactions among introduced ant species in the Auckland region

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For any given species, distribution in space and time may be determined by a number of factors, both biotic and abiotic. At the local scale, an interplay of both biotic and abiotic conditions are likely to play a role in the ability of a species to persist in an area. Our understanding of these questions can be greatly improved through the use of model taxa. One such model taxon is ants, due to their high abundance and diversity, and the importance of local scale environmental conditions in regulating their daily activities such as foraging. This work aims to investigate patterns in the distribution and abundance of introduced ant species in the Auckland region, and to model the relationship between the environment and these distribution patterns. This has implications for our ability to better predict and manage invasions of exotic ant species into New Zealand. An increasing number of ant species are being dispersed worldwide by human transport and travel, several of these have severe impacts in their introduced range. Their ability to colonise new areas has been shown to depend on both climatic suitability and the biotic resistance of the existing ant fauna, both native and introduced. The ant fauna of New Zealand is relatively impoverished, with 11 native and approximately 30 introduced species, and more species continuing to arrive. This low number of native species, and the increased likelihood of further introductions, makes this question of particular interest to New Zealand.

Negative occurrence patterns of two native ant species (*Monomorium antarcticum* and *Prolasius advenus*) within beech forests

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What are the factors that influence species distributions and abundances? *Monomorium antarcticum* and *Prolasius advenus* are native, generalist and ubiquitous ant species in New Zealand. Our study examines the spatial distribution of these species, as well as disentangling the mechanisms determining patterns. Two 1 km² sites were sampled; one in South Island (Nelson Lakes) and one in the North Island (Kaitoke Regional Park). Results indicate that these species present negative co-occurrence patterns. In beech forests *Prolasius* is very abundant and seem to exclude *Monomorium*, as this ant is only found in grassy areas or forest edges. However, some *Prolasius* nests can be found in open areas. Observations in the laboratory highlighted behavioral mechanisms that could explain these patterns. *Prolasius* is dominant over *Monomorium*, spraying acid and biting them, indicating that *Prolasius* may be an aggressive-key species in the ant community. Overall our results suggest that competition may play an important role in determining the ant mosaic in New Zealand beech forests.

A new attempt to introduce the lacy-winged seed fly to Australia for biological control of boneseed

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Mesoclanis magnipalpis Bezzi (lacy-winged seed fly or LWSF) is a tephritid fly whose larvae live and pupate in the flowers and developing fruit of shrubs of the southern African genus *Chrysanthemoides* Tourn. ex Medik. LWSF is approved for use in Australia as a biological control agent for *Chrysanthemoides monilifera* (L.) T. Norl. *C. monilifera* comprises six subspecies of which ssp. *monilifera* (L.) T. Norl. (boneseed) is a serious weed in Australia and ssp. *pisifera* (L.) T. Norl. is restricted to South Africa. LWSF utilises both of these as hosts. From 1998 to 2005 four attempts were made to establish LWSF on boneseed in Australia. These attempts were made with LWSF collected from *C. m.* ssp. *pisifera*. However LWSF was not recovered except in the boneseed flowering/fruiting season of release, even though LWSF from those introductions readily oviposited on boneseed, and boneseed sustained development from egg to adult. A further introduction was attempted in 2009 with LWSF collected only from boneseed. This attempt to introduce the LWSF to Australia appears to have failed. Possible reasons for failure include, (i) successive flowering of different *Chrysanthemoides* subspecies is required for LWSF population survival, or (ii) LWSF collected from *C. m.* ssp. *pisifera* (pre-2009 importations) represented a biotype of LWSF whose life cycle was not synchronised with boneseed flowering. If (ii) is true then the failure of the most recent introduction might be due to releasing too few LWSF, or the release being too late in the boneseed flowering season.

Intimacies and intricacies of rearing the Queensland fruit fly larval parasitoid, *Diachasmimorpha tryoni* (Cameron) (Hymenoptera: Braconidae)

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Research into the use of parasitoid wasps (Hymenoptera: Braconidae) to control the Queensland fruit fly *Bactrocera tryoni* (Froggatt) (Diptera: Tephritidae) is gaining momentum. The parasitoids are harmless to human health, self dispersing and, if properly implemented are a good control option. Hawaii, Mexico and Australia have successfully introduced non-native parasitoid wasps to control various fruit fly species. Native Australian species have been overlooked in their native environment. Rearing *B. tryoni* on an artificial diet is a well established technique but establishing a colony of the larval parasitoid, *Diachasmimorpha tryoni* (Cameron) from wild material is challenging. The complexity lies in enticing the parasitoids to mate, search and oviposit into hosts larvae contained within an artificial diet. Mating is pivotal to produce female offspring in these haplodiploid parasitoids. In this study, mating was encouraged by segregating male and female parasitoids from the time of eclosion until females reached their optimal mating period.

Reducing the size of the parasitoid enclosure forced the parasitoids to walk over the artificial diet, eliminating the necessity for long range cues, which under field conditions are provided by the infested fruit. Thus, the parasitoids were only required to use short-range cues produced by larval feeding to locate the larvae for oviposition. Oviposition into larvae contained within an artificial diet and increasing parasitism rates over subsequent generations demonstrated the parasitoid culture adapting to laboratory rearing conditions. This is encouraging and suggests that large numbers can be readily reared under Australian conditions for use in augmentative release programs.

Biological control of root-feeding scarabs: an experience in cooperation between New Zealand and Mexico

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Soil pests have represented one of the major challenges of crop production, yet a literature review on insect-plant interaction over the past two decades suggests that less than 2% of research has been applied to root feeding insects due to the difficulty of studying them in their subterranean environment. In the Michoacan state, Mexico, the immature stages of several species of Phyllophaga (Coleoptera: Melolonthidae) cause significant losses in maize production. With the goal of finding alternatives to chemical control of this pest, and to improve maize production and environmental quality, a team of researchers from INIFAP and AgResearch, developed a participatory research programme in collaboration with local farmers. The programme resulted in correct taxonomic identification of the most important pest species, the isolation of native strains of entomopathogenic fungi (*Beauveria bassiana* and *Metarhizium anisopliae*), their mass reproduction, evaluation and selection of highly pathogenic strains in laboratory and field tests. An IPM system was developed using plant tolerance through genetic improvement of native corn varieties and application of entomopathogenic fungi. In addition, training courses for farmers, technicians and researchers were held. The programme provided a foundation for new research and technology transfer projects, and the construction of the first biofactory for bioinsecticide production in Michoacan.

Unexpected genetic variation in an endemic ground beetle: the molecular surprise of *Megadromus guerinii* (Coleoptera: Carabidae)

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Megadromus guerinii Chaudoir 1865, an endemic carabid beetle found only on Banks Peninsula (Canterbury, New Zealand), is a forest specialist considered common and panmictic throughout its range. Recent data collected from the mitochondrial gene, cytochrome c oxidase subunit 1 (CO1), however, suggest that *M. guerinii* may not form a single panmictic population, or even represent a single species. Preliminary sequence data have identified two genetically distinct populations found in different areas of the peninsula. Specimens of *M. guerinii* were collected from various localities and reserves in the Banks Peninsula area to provide a sound geographic representation. Currently, work is being undertaken to both expand the CO1 dataset and to obtain sequences from nuclear genes. GIS software will be used, along with genetic data, to provide a higher resolution and more in-depth picture of the patterns of genetic diversity across the peninsula. The aim of this study is twofold: (1) to gain a greater biogeographic understanding of a range-restricted, but locally abundant, species and (2) to solve the molecular mystery of *Megadromus guerinii*.

Diversity and phylogeny of Australian chelonine wasps (Hymenoptera: Braconidae); parasitoids of lepidopteran eggs

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The Cheloninae is a diverse subfamily of braconid wasps which has a global distribution. There are about 1,300 described species but only 42 are recorded in four genera for Australia, virtually all of which are from the eastern coastal margin. Chelonines are egg/larval parasitoids of Lepidoptera and they can be easily distinguished from other braconids by the presence of a metasoma carapace, where the first three tergites are fused into a dorsal plate. Species vary in the number of antennal segments as well as having putatively diagnostic colour patterns, particularly for the genus *Phanerotomella*. This study aims to assess the taxonomic diversity of the subfamily for Australia and the phylogeny of genera and species groups using sequence data and morphology, in addition to documenting their host associations and biogeographic pattern across the continent. Here we present our preliminary findings on diagnosing species boundaries using the CO1 gene and morphology to indicate levels of species diversity at specific localities.

Exploring phylogeographic congruence in a continental island systemJulia Goldberg ^{*1}, Steve Trewick ¹¹ Institute of Natural Resources, Massey University, Private Bag 11222, Palmerston North 4442, NZ

A prediction in phylogeographic studies is that patterns of lineage diversity and timing will be similar within the same landscape under the assumption that these lineages have responded to past environmental changes (biotic and abiotic) in comparable ways. Eight invertebrate taxa from four different orders were included in this study of mainland New Zealand and Chatham Islands lineages, to explore their response to past geophysical events. These comprised two orthopteran genera: one an endemic forest-dwelling genus of cave weta (Rhaphidophoridae, *Talitropsis*) and the other a grasshopper (Acrididae, *Phaulacridium*) that inhabits open grassland; four genera of Coleoptera including carabid beetles (*Mecodema*), stag beetles (*Geodorcus*), weevils (*Hadramphus*) and click beetles (*Amychus*); the widespread earwig *Anisolabis* (Dermaptera) that is common on beaches in New Zealand and the Chatham Islands, and an endemic and widespread cockroach genus *Celatoblatta* (Blattodea). Mitochondrial DNA was used to reconstruct phylogeographic hypotheses for comparison among samples. Strikingly, despite a maximum age of ~4 million years for the Chathams there is no concordance among the examined taxa. They varied in the extent of genetic divergence and partitioning between Chatham and mainland populations with some Chatham lineages represented by island endemism and others by haplotype sharing with the mainland. These diverse patterns suggest that combinations of intrinsic (taxon ecology) and extrinsic (extinction and dispersal) factors can result in apparently very different biogeographic outcomes.

Beta Weta Geta: Rhabdophoridae taxonomy in New Zealand

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Rhabdophoridae are a diverse group in New Zealand with 18 genera in the subfamily Macropathinae. All genera are endemic and many have just a single species described (monotypic) although there are many undescribed species in collections. Combining genetic data (DNA sequence of the mitochondrial gene COI) with morphological information has contributed to a revision of the large-cave dwelling species. This work resulted in the synonymy of the genera *Pachyrhamma* and *Gymnoplectron* and tentatively *Turbottoplectron*. Characters used to distinguish *Turbottoplectron* are unreliable. We are continuing to assess the validity of the generic groups using multigene DNA phylogenetics and morphology, and work at the population level to determine species status of the small forest species of cave weta. Many of the smaller species of New Zealand Rhabdophoridae are poorly known and similar problems in the delimitation of generic boundaries probably exist with *Neonetus* and *Isoplectron* as is seen in the large cave genera. The project is developing tools for identifying New Zealand Rhabdophoridae genera and species; this involves identifying morphological traits that are diagnostic for genera and species, revising descriptions, and providing easily used guides for identification of adults and juveniles. Molecular phylogenetics and population genetics are being used to help understand the relationships among genera and species. Identification tools will be developed as an online resource that people can use to identify Rhabdophoridae.

Parasitic wasps of the Proctotrupoidea, Platygastroidea and Ceraphronoidea in New Zealand: review and analysis

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Moist cool-temperate forests virtually covered >90% of the New Zealand landscape prior to human colonization, and still represent the largest land area of natural habitat today. Sweep and pan trap samples for Hymenoptera in these forests are overwhelmingly dominated by individuals of Proctotrupoidea (49%) and Platygastroidea (16%), followed by Ichneumonoidea (11%), Chalcidoidea (10%), Vespoidea (8%), Ceraphronoidea (5%), Cynipoidea (<1%) and Chrysidoidea (<1%). Despite this abundance of individuals and the ease with which many are collected, there are only 105 named species of which at least 9 are introduced. The first species to be described were miscellaneous diapriids sent to P. Cameron and F. Smith in England in the late 19th century. This pattern of scattered alpha taxonomy has continued with three exceptions: the Ambositrinae (Diapriidae) were covered in a monograph by Naumann (1988); the endemic family Maamingidae with two species was treated by Early et al. (2001), and the genus *Archaeoteleia* (Scelionidae) was revised by Early et al. (2007). Here we present an overview of the three superfamilies based on published records combined with our collective experience of specimens in collections and from our field collection activity from the late 1970s to the present.

Imaging of whole insect drawers for virtual management and curation of the Australian National Insect Collection

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The Australian National Insect Collection (ANIC) is actively developing tools to deliver biodiversity informatics online, and accelerate collection management and delivery. One of these initiatives involves the use of ultra high-resolution imaging of whole insect drawers using SatScan™ by SmartDrive Ltd for upload to the web. This poster outlines examples and use-cases of whole-drawer imaging for virtual management and curation of Australia's largest entomology collection, reviews observed technical and functional limitations of the system, and describes the imaging workflow that is being developed for managing the whole drawer images.

Technology and collaboration helping improve eucalypt plantation pest surveillance in Western Australia

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The majority of Eucalyptus globulus plantations in Western Australia are managed by the private sector. Currently, most companies have no formalised pest and disease surveillance programs for their plantation estates. When pest or disease problems are encountered, there is no coordinated operational approach amongst the companies. This often leads to poor pest management outcomes. The poster will present how an industry formed collaborative group, the Industry Pest Management Group (IPMG), is addressing the shortfalls in forest pest surveillance and management. A program encouraging increased collaboration amongst stakeholder companies and the implementation of "new" technologies has been devised that includes; (1) development of plantation health recording software for mobile devices, (2) development of a regional database of pest and disease records and control actions, (3) development of a website to access industry specific pest and disease information, (4) a regional surveillance program conducted collaboratively amongst all the stake holders. It is hoped that this approach to plantation forest surveillance will allow companies to better devise strategies such as, integrated pest management (IPM) or area wide management (AWM), in a coordinated and regional fashion rather than acting in isolation.

Burnt pine longicorn surveillance in eastern Australia

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Arhopalus fesus (Mulsant) or Burnt pine longicorn (BPL) beetle, a native of Europe, became widely established in New Zealand in the 1970's. In recent years, BPL has been repeatedly intercepted in increasing numbers on container vessels, navy vessels and cruise ships arriving at eastern Australian ports from New Zealand. BPL is absent from Australia but if it were to become established it is likely to be a high-impact pest species. A joint New South Wales Department of Primary Industries and Australian Quarantine and Inspection Service surveillance operation was initiated in Sydney in February 2010 after a container vessel from New Zealand arrived with high numbers of BPL on-board. As a result, ten traps were deployed for two months in Sydney ports. Surveillance recommenced in early 2011, with twenty five traps deployed in Sydney, Newcastle and Wollongong ports for three months. Traps used beetle-specific attractants derived from pine tree volatiles and were monitored fortnightly with the attractants being replenished monthly. A limited number of traps were also deployed around Brisbane and Melbourne ports. The capture of two BPL beetles during the surveillance demonstrated that the traps were effective. In addition, another species already present in Australia, *Arhopalus syriacus* (Reitter), was trapped five times. As a bonus to the trapping operation a wide range of species were also recorded as by-catch with bark beetles particularly well represented. Even though no exotic bark beetles were collected, the genera represented did include those known to have exotic species currently absent from Australia.

Going beyond world's best practice - Barrow Island quarantine management system

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Chevron Australia has operated an oilfield on Barrow Island, a Class A Nature Reserve located 88 kilometres north-west of Onslow, for more than 45 years. The island is an important refuge for many rare and threatened species, some of which are endemic to the island and the surrounding waters. Understanding and managing this biodiversity is central to Chevron Australia's broader environmental stewardship and ensuring the integrity of Barrow Island against the risk of introduced (non-indigenous) species. In response to this risk, Chevron Australia has developed a comprehensive risk-based quarantine management system aimed at protecting Barrow Island and its surrounding waters. The Barrow Island Quarantine Terrestrial and Marine Quarantine Management System (QMS) is an interrelated set of more than 300 procedures, specifications, checklists and guidelines. Considered by the Western Australian Environmental Protection Authority as 'likely to be world's best practice', the QMS is likely establishing a new global standard. It is scalable and can be replicated in other regions of the world and focuses on all possible introduction pathways to limit or prevent the introducing non-indigenous species to environmentally sensitive areas. The overarching aim of the QMS is to facilitate the construction and operation of a gas processing facility on Barrow Island while simultaneously protecting the conservation values of the island. The specific objectives of the QMS are to: 1) Prevent the introduction of non-indigenous species 2) Detect non-indigenous species 3) Control and eradicate detected non-indigenous species 4) Mitigate adverse impacts of any control and eradication of non-indigenous species. Scientific knowledge from technical experts, in conjunction with input from the wider community, has been significant in identifying and addressing all aspects of potential risk. Importantly, the QMS is a responsive system that can readily react and adapt to changes in worldwide quarantine risk. The QMS enables industry to co-exist with and protect an environmentally sensitive ecosystem while facilitating the construction of Australia's largest single resource project. The Gorgon Project is operated by an Australian subsidiary of Chevron and is a joint venture of the Australian subsidiaries of Chevron (approximately 47%), ExxonMobil (25 %) and Shell (25 %), Osaka Gas (1.25 %), Tokyo Gas (1 %) and Chubu Electric Power (0.417 %).

Forestry-induced disturbances and biodiversity: an examination of population structures and gene flow among saproxylic beetles

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Saproxylic beetles drive carbon and nutrient recycling in forest ecosystems but their dependence on dead wood makes them vulnerable to forestry-induced reductions in wood through harvesting and removal for fuelwood. Sustainable forest practices that maintain biodiversity need to manage coarse woody debris (CWD) so that it continues to be available for saproxylic biota. A landscape genetics approach in Tasmania's southern wet *Eucalyptus obliqua* forests will provide information about the scale of dispersal of several saproxylic species, one of which is listed as threatened. Analysis of the genetic variation and population structure of each species across the landscape will reveal dispersal abilities of three species within different levels of disturbance in the surrounding landscape. Dispersal ability is influenced by the physiological capabilities, life histories and mobility of the dispersing species. These are unknown for most Tasmanian beetle species including those in this research. Distances and degree of connectivity between populations further influence dispersal ability. Forestry practices modify connectivity and may increase heterogeneity in a forest landscape where mature forest is replaced with regrowth forest with a smaller diameter cwd resource. Dispersal ability will guide recommendations for long term management to generate ongoing suitable diameter CWD at a spatial scale that ensures habitat continuity and connectivity for populations of saproxylic beetles in southern Tasmanian forests. This research complements concurrent projects investigating responses of plant and bird species to disturbance in a forest landscape. The research will contribute to a broader understanding of forest ecology and landscape processes and assist forest planners.

