

The age of biota in old islands: updating the dating for New Caledonia biodiversity?

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New Caledonia is an island biologically very rich and diverse. It was long considered as a "Gondwanan refuge" harboring many old species and diversifications the origin of which can be traced back to vicariance with Australia 80 My ago. Both the rise of molecular and geological studies independently suggested a history of long Eocene submersion in discordance with this previous "Gondwanan refuge" paradigm. The time is ripe now for a meta-analysis of molecular datings which accumulated in the last decade. We thus conducted such an analysis which brought interesting and clear results concerning the origin of New Caledonian biota. In a general perspective, these results question both the traditional views about the origin of biota in old islands and the datings based on poorly informed molecular inferences.

The *Fauna of New Zealand* series: 30 years, 70 contributions, and 10,000 pages

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On 23 December 1982 the first 3 contributions in the *Fauna of New Zealand* monograph series were published. Their publication was preceded by 20 years of specimen collecting by the systematics group of Entomology Division, DSIR (founded in 1963 by Society Fellow Dr Willy Kuschel): this collecting was needed to provide better representation of groups in the N.Z. Arthropod Collection (NZAC) for the monographic revisions that were envisaged. The series has now published some 10,400 pages in the 70 contributions, with about 17,100 illustrations. Information is available on about 1700 genera and 5000 species of our terrestrial invertebrates, ranging from detailed cataloguing information to full descriptions. In the series 4 new families, 141 new genera, and 828 species have been described. Especially in the days preceding online publication, it provided a publication outlet for New Zealand and overseas researchers that might otherwise not be published. In 1997, the first pages for the series went online on the Landcare Research website (now fnz.landcareresearch.co.nz), so that abstracts, checklists of taxa, and introductory material became more accessible. In 2008 the Editorial Board allowed medium-resolution PDFs to be made available without cost so the information was freely available to all, and in 2010 simultaneous online publication commenced.

Tokoriro taxonomy: progress with an online resource for recognition of cave weta and other orthoptera

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Taxonomy and systematics of the New Zealand Rhabdophoridae are in disarray, yet this group of insects is diverse in New Zealand forests and relatively high profile. Possibly there are too many genera described (~17), but there are also species that await description. Many existing generic and specific descriptions are deficient and/or contradictory. To help expedite an improvement in this situation we have begun establishment of a web-based resource on tokoriro and other weta, assisted by funding from the Terrestrial and Freshwater Biodiversity Information System programme (TFBIS). This approach puts the cart before the horse in some respects, but we think that clarifying the existing situation with regards to recognition and taxonomy of tokoriro is a valuable first step in rectifying the situation. In parallel with development of the website, which is called the BetaWetaGeta, we are actively working on species discovery, testing and systematic revision using ecological, morphological and genetic data. Recently we demonstrated synonymy of three genera that represent the largest and most frequently encountered tokoriro, that represent many of the populations encountered in caves. *Pachyrhanna* subsumes *Gymnoplectron* and almost certainly *Turbottoplectron* too. Our emerging data reveals that what was true for these large and prominent species is true for the majority of the fauna that are small, cryptic and do not form aggregations in caves. We will present information on the developing web resource and on developments with tokoriro taxonomy. Draft pages of BetaWetaGeta are visible at <http://evolves.massey.ac.nz/Root/Text%20files/home.html> (or by clicking through Gallery&Links > A cave weta on the evolves.massey.ac.nz site). We welcome helpful feedback and ideas as well as contributions of information and images.

Invertebrate biodiversity; comparison and identification of Tokoriro (cave weta) taxa at three locations in the North Island, New Zealand

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Eligible for student prize

New Zealand cave weta or Tokoriro, are diverse. Understanding the full diversity and taxonomy of this family has been hampered by problems including synonyms, poor descriptions, lack of diagnostic characters, sexual dimorphism, poor characterization of juvenile stage, under sampling and a general deficiency in our knowledge of cave weta ecology. Our recent work using high density sampling has confirmed high levels of sympatric diversity among Tokoriro living in North Island forest systems. We routinely find 5-10 taxa per site. It is therefore not surprising that historically, attempts to describe this biodiversity have faltered when sampling has consisted of one or few individuals per location. We examined Tokoriro from three locations, Taranaki, Manawatu and Hawke's Bay. We started with two simplistic hypothesis: 1) Each taxon (judged by morpho-type and DNA) is unique to each of the three locations, 2) taxa are shared across all three locations. This approach helps in understanding how visible characters such as spine morphology and sub-genital plate shape of each specimen informs diagnosis of taxa and diversity. Comparison of DNA sequence data enabled us to match males with females and assess the relative difference between similar and dissimilar morphs. What we find is, not surprisingly, a mix of the two hypothesis where some morphological identical species are shared in two or more locations and some morphological species are unique to a location in the current sampling. DNA sequencing shows us how the different morphological units are related and whether the morphological characters are reliable as a tool for species diagnosis. This work supported by a scholarship from MSI supports a related TFBIS project to develop online weta identification and recording tools.

Towards a robust taxonomy of the *Irenimus* broad-nosed weevils (Coleoptera: Curculionidae)---Morphology, sequences and biogeography

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The broad-nosed weevil genus *Irenimus* is one of the larger genera of weevils in New Zealand. The genus is found throughout New Zealand, though they find their greatest diversity in the southern half of the South Island. They are found in forest-edge, shrubland and grassland habitats, with an altitudinal range that spans over 2000 m. A number of species are present in agricultural pastures, where they can attain high numbers and occasionally cause problems. A number of species are also susceptible to parasitism by parasitoid wasps introduced to control adventive weevil pest species. All these characteristics make the group of great economic, environmental and evolutionary interest; however research on the group is hindered by an outdated taxonomy and there being no modern tools for the identification of *Irenimus* species. My PhD seeks to remedy this by revising the genus using morphological and DNA sequence data. Initial indications are that the genus will be tractable; though there remain some challenging species groups.

Speciation and species delimitation in ground weta (*Hemiandrus*)

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Why does diversity vary among taxon groups and places? Some features of organisms make them more prone to speciation e.g. strong sexual selection; while other properties may open up new adaptive zones and prevent extinction. The genus *Hemiandrus* (ground weta) consists of approximately 40 species (most of which are undescribed) and is the most speciose of all New Zealand Anostostomatid genera. My research explores the question: why are there so many species of ground weta? Ground weta have various traits that indicate that they are or were subject to strong sexual selection such as nuptial gifts and female morphological adaptations for receiving nuptial gifts. Ground weta also have distributions of traits that suggest adaptive radiations, such as variation in ovipositor size and maternal care. My research uses molecular and morphometric tools to study the evolutionary relationships among *Hemiandrus* species and help delineate species boundaries. This data will be used to address questions about the role of selection in the speciation of *Hemiandrus*.

New perspectives on an Australasian mite (Acari: Mesostigmata; Laelapidae)Matthew Shaw ^{*1}¹ Canterbury Museum mshaw@canterburymuseum.com

Mites of the family Laelapidae have an extraordinary ecological range. While many Laelapidae are free-living predators in soil and leaf litter, others have forged many types of symbiotic relationships with birds, mammals, reptiles, insects, myriapods and arachnids. Phoretic and/or parasitic relationships are frequent within some groups. *Gymnolaelaps annectans* Womersley 1955 was described from shearwater burrows in Bass Strait, southern Australia. It was subsequently found in mainland Australia, Britain, Hawaii, the Azores, and New Zealand. Its initial genus placement and its subsequent transfer to the free-living genus *Pseudoparasitus*, was uncontroversial. This placement implied it was just another soil-based predator although having a curious habit of phoretically associating with nesting mammals and birds. Investigation of old museum specimens and nest habitats has uncovered two closely related species in Papua New Guinea and southern Australia. All three species have been placed together in a new genus, *Nidilaelaps* Shaw. A rather different interpretation of its biology and relationships is now necessary. The inferred relationships of all these species strongly suggest that this genus is an Australopapuan endemic. At least one species has spread to other landmasses secondarily, probably phoretically transported on synanthropic rodents.

Genital evolution and sexual conflict in the lichen tuft moths.

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Many animal species may be defined by the morphology of their male genitalia. Species almost identical in general morphology may still display a wide variation in male genital morphology. Therefore, genital evolution appears to be a rapid and divergent process. Theories explaining genital evolution include species isolation (lock and key hypothesis) and pleiotropy, however recent comparative and experimental research has proposed sexual selection to be the best explanation; one promising hypothesis involving the theory of sexual conflict. Sexual conflict may drive genital evolution through opposing selection on male and female reproductive strategies. Genital adaptations that allow males a competitive advantage may consequently reduce female fitness. Females may counter adapt to reduce the harm imposed by male adaptations, leading to an evolutionary arms race via sexually antagonistic co-evolution (SAC). Species within the genus *Izatha* (Lepidoptera: Oecophoridae) are candidates for exploring the occurrence of sexual conflict. Within this genus, males of some species have detachable spines (deciduous cornuti) which they eject into the female reproductive tract during their first mating; some have permanently attached sclerotised teeth on the phallus which cause damage; others lack these structures all together. Species within the genus *Glaucocharis* (Lepidoptera: Crambidae) also display variation of male genitalia and a number of fixed cornuti. To gain an insight into the evolution of these complex genitalic adaptations, morphological characteristics were mapped onto a molecular phylogenetic analysis of both genera. To further examine reproductive functionality and co-evolution, specific genitalic structures of male *Izatha* were compared with female *Izatha* structures that they make contact with during copulation.

Range shifts and adaptation to local conditions in a pair of parapatric weta

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The consequence of past climate change can be used to infer possible biological responses to current rapid global warming. Evidence of changes in species' distributions are common in phylogeographic studies world wide and can be understood in terms of both environmental limitations and species interactions. We infer past population history of a pair of parapatric tree weta species (*Hemideina* spp) where competitive exclusion interactions are thought to control their distributions, and the climate is likely to be responsible for determining the winner of these interactions. We also look for evidence of local adaptation by comparing growth rates under controlled conditions of individuals that have originated from high and low altitude locations. Although measures of genetic diversity support past changes in species' distributions predicted from their current parapatric range, we have also detected convergent evolution of local adaptation in growth rates. Although 'evolve' versus 'move' are frequently regarded as mutually exclusive alternative responses to climate change, we should perhaps accommodate both into our models. In these two insect species, both range shifts and local adaptation seem likely to result from current climate warming.

Invertebrate extinction risk listing

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Every three years a national process led by the Department of Conservation (DOC) lists plant, fungal and animal taxa according to the risk of extinction they face. The next review of the lists for terrestrial invertebrates is due to be carried out in 2013-14. The New Zealand threat Classification System will be briefly explained, the findings of the 2008-11 cycle of listings of terrestrial invertebrates will be reviewed, and information will be provided on information needed for the next review of the lists and how to contribute.

Department of Conservation's intent: Where will wētā be?

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The Department's outcome statement "New Zealanders gain environmental, social and economic benefits from healthy functioning ecosystems, from recreation opportunities, and from living our history" places society at the front of natural heritage conservation. Our five year statement of intent considers the context: "The resources available for conservation work are constrained by an ongoing tight fiscal environment and the inevitable effects of inflation. However, the value of conservation's contribution to 'brand New Zealand' is increasingly recognised. There is potential to draw on the increasing environmental awareness of consumers, businesses and communities to sustain and grow their contribution to conservation work". An ambitious programme of change includes centralising science and advisory roles followed by restructuring operational capacity and objectives (underway) while at the same time nationalising the process of choosing sites where ecosystems and species are to be conserved. This process reflects the dual goals to conserve a full range of ecosystems and secondly, persistence of nationally threatened species. In the medium term, strategic drivers include ongoing decline of native plants, animals and ecosystems, economic drivers and a requirement to deliver better public services. The priority then is to optimise species and ecosystems management to achieve better value for money. The results planned for include; increasing the number of species (including some invertebrates) actively managed through nationally prioritised prescriptions from 50 in 2011-2012 to 300 by mid 2016. A more challenging intent is to implement nationally prioritised ecosystem management for 400 ecosystem management units over the next 4 years. Native invertebrate assemblages are expected to benefit from reduction of pest plants and animals among ecosystems and new systems and tools for monitoring and reporting will include invertebrate indicators as well as population trend for threatened species.

Getting to grips with grasshoppers: syncopated speciation in central South Island *Sigaus*Edwina Dowle ¹, Mary Morgan Richards ¹, Steve Trewick ^{*1}¹ Ecology Group, Massey University, Private Bag 11-222 Palmerston North

Species concepts are hard to apply when individuals that look similar share genetic material. Species concepts and our understanding of speciation is becoming more complex as we move further away from typological approaches and allopatric models. New speciation models show there is not justification for assuming physical isolation as a prerequisite, and sympatry models now recognize locus specific gene flow and selection. Speciation with gene-flow requires that some traits of two entities (groups of individuals) be maintained through strong selection despite extensive genetic exchange. In South Island NZ, *Sigaus* alpine grasshoppers form a complex of species that appear to show several interesting evolutionary phenomenon in this regard. One is formed in Central Otago around the township of Alexandra, with the species *Sigaus australis* ranging over much of the lower/middle South Island, and completely encompassing the very localized and rare species, *Sigaus childi*. These species share some identical mitochondrial haplotypes, and microsatellite data reveal no population structure between them. In contrast morphological analysis shows little evidence of hybridization between the two species with individuals having one or other parental form regardless of their degree of genetic mixing. These observation are consistent with a model involving selection on distinct physical characteristics despite exchange of neutral genetic. Previous work on species complexes such as this have typically been data limited. Using a new technique called double-digest RAD-sequencing we have generated extensive SNP data that is allowing us to further test among alternative explanations (hybridization, incomplete lineage sorting, and speciation with geneflow) for the pattern we have seen in *Sigaus*.

Clasper function and morphology across a hybrid zone of stick insects.

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Male genitalia are unarguably one of the most morphologically diverse traits in the insect class. The function of fertilising female eggs and the genitalia's shape play an important role influencing whether a female will engage in copulation, or use his sperm to fertilise her offspring. A hybrid zone is the geographic area in which two species meet to form hybrid offspring. It is common for the offspring of hybridising species to have reduced fitness. Reinforcement theory predicts that prezygotic barriers will evolve to between hybridising groups so that there will be selection against hybridisation. In the far north of New Zealand the widely distributed stick insect species *C.hookeri* is replaced by an ecologically similar and undescribed species of *Clitarchus*. These species are differentiated on the basis of male and female genitalia. Male stick insects have a complex external genitalia system comprising of a clasper structure which holds onto the female during copulation. The aim of this research project is to utilise this natural hybrid zone of varying genitalia to uncover the importance of the male clasper. Across the *Clitarchus* hybrid zone, not only do male genitalia become more complex, female *Clitarchus* have a corresponding varying structure. The new species have a keel like structure where the male's clasper attaches to the female's subgenital plate. The apparent co-evolutionary correspondence in male and female genitalia provides an ideal system for looking at the functionality of the clasper. This has been achieved using a multidisciplinary approach involving behaviour, 2D and 3D morphometrics and genetics.

Weta affairs: An investigation into the possibility of hybridisation on Banks Peninsula

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Eligible for student prize

Recently, hybridisation has been increasingly recognised as contributing to the extinction of species; with the risk especially high for rare species hybridising with more common species. Such risks have raised concerns for the Banks Peninsula tree weta, *Hemideina ricta*, which is restricted to the eastern half of Banks Peninsula and in some areas lives in sympatry with the more widespread Canterbury species, *H. femorata*. The two species share similar morphology, mating behaviour, chromosome structure and no apparent distinguishing calls or pheromones. A previous genetics study found evidence of hybridisation between these species and a mating experiment determined that male *H. ricta* will respond to female *H. femorata* and *H. ricta* in a similar manner. However, for various reasons, both studies were limited. Therefore, in order to adequately assess the risk hybridisation poses to their continued conservation, a more detailed study was undertaken. With hybridisation between *H. ricta* and *H. femorata* previously hypothesized to be a rare event, I modelled likely sympatric zones in an attempt to optimize sampling efforts. While species distribution models have often focused on using environmental data to make predictions, it has been suggested that these models neglect important biotic interactions and the dispersal capabilities of the species under study. In the present study the resolution of much of the environmental data was deemed unsuitable for predicting the distribution of *H. ricta* and *H. femorata*. Therefore, spatial interpolation was used to model sympatric zones. Results from the subsequent sampling and genetic analysis confirm the presence of hybrids between *H. femorata* and *H. ricta*, and suggest introgression may have occurred. Despite this, hybridisation appears to be limited. In order to gain further information into what processes could be limiting hybridisation, plans are underway to observe mating behaviour between *H. femorata* and *H. ricta* as well as offspring survival.

Species identification and tools to study hybridisation of tree weta

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Eligible for student prize

The concept of species is central to the field of biology. Defining the line between species can be difficult, especially where hybridization occurs. Hybridization may or may not lead to introgression of alleles between species, which can have important implications for both understanding a species evolutionary history and the speciation process itself. It is also important for many conservation issues, as introgression of genetic material may swamp endangered species and threaten their genetic integrity, although in other cases it can lead to much needed increases in genetic diversity. Tree weta (genus *Hemideina*) have attracted interest both because of their close relationship to many endangered giant weta (*Deinacrida*), and also because two species are known to have multiple chromosomal races. So far, little is known about hybridization between species in this genus so the aim of this project is to look for introgression between two species pairs (*H. thoracica* & *H. crassidens*, and *H. thoracica* & *H. trewicki*). Both morphological characters that distinguish species, as well as genetic data are used to define species and look for potential hybridization and introgression.

Metabolic rate variation among New Zealand Orthoptera

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Metabolic rates determine an individual's rates of resource acquisition, assimilation, growth, survival, and reproduction. In insects and other ectotherms, the resting body temperature corresponds to ambient temperature and the rate of biochemical processes increase rapidly with increasing temperatures. Q_{10} is a quotient that reflects the capacity of change in metabolic rate relative to changes in temperature. Q_{10} can be considered a measure of organismal performance as well as an individual attribute. Globally, researchers are focusing on the likely and predicted responses of insects to climatic changes in temperature, water availability, elevated CO_2 levels, and their interaction. A good starting point will be gathering original data on physiological traits of individual species. New Zealand Orthoptera includes representatives of six families, dominated by Anostomatidae and Rhabdophoridae. In order to develop testable models about evolutionary drivers and likely responses to rapid anthropogenic climate change at the species level, we estimated variation in oxygen consumption (a proxy for metabolic rate). We targeted representatives of the genera *Hemideina*, *Deinacrida*, *Hemiandrus*, *Motuweta*, *Pachyrhamma*, *Talitropsis*, *Caedicia*, *Locusta*, and *Teleogryllus*. This is the first study to present data on the adult body mass for this set of Orthopteran. We aimed at measuring metabolic rate in representative New Zealand Orthopteran species to estimate the amount of extant variability; calculating Q_{10} for each individual to measure thermal sensitivity of metabolic rate; and comparing variation among species while inferring possible causes for it, after controlling for phylogeny. As expected, metabolic rate increased with body mass whereas mass-specific metabolic rate decreased with body mass. The Cook Strait Giant Weta (*Deinacrida rugosa*) presented the lowest mass-specific oxygen consumption while little cave weta of the Rhabdophoridae the highest.

Dancing on the Head of a Pin: Unraveling Nature One Mite at a Time

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Mites are among the smallest of terrestrial animals and on average so small as to appear insignificant to ecosystem function. Yet we know from agriculture, animal husbandry, and human health that mites can cause consequences that are far in excess of their physical size. Here I consider the roles of mites in a single stratum of two ecosystems, the rainforest phyloplane and the boreal forest organic soil, and show how even esoteric research on insignificant mites can yield results that are positive for human welfare.

Effects of a neonicotinoid insecticide on native and invasive ants

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Eligible for student prize

Sublethal doses of neonicotinoid insecticides have been reported to negatively affect insect populations. The native Southern ant *Monomorium antarcticum* co-occurs with and displays agonistic reactions towards the invasive Argentine ant *Linepithema humile*. Thus, neonicotinoids may diminish biotic resistance by native species towards invaders. We tested the hypothesis that sublethal doses of neonicotinoids facilitate the invasion of Argentine ants by impairing cognition, agonistic behaviour and fitness of the native Southern ant. Ant walking speed and the probability to find food sources were reduced as consequence of exposure to neonicotinoids in both species. Having sublethal contamination with neonicotinoids did not reduce survival probability of the native Southern ant, but increased survival probability of Argentine ants during aggressive interactions. There was no significant effect of neonicotinoids on final colony population density of both species or egg production of the Southern ant. However, contaminated colonies of Argentine ants had significantly diminished egg production to similar amounts to those observed by the Southern ant. The effects of sublethal doses of neonicotinoids on the native Southern ant have the potential to facilitate the invasion of Argentine ants. The reckless use of neonicotinoids in urban and agricultural areas could potentially alter the agonistic responses displayed by insects and act as a human mediated driver of invasion.

Sampling and replication in soil invertebrate research

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The selection of appropriate spatial scale when designing experiments is of crucial importance for soil fauna research, as many groups display spatial dependence and spatially structured diversity patterns at small and intermediate scales. From methodological point of view, estimation of spatial variability in community structure and abundance of soil fauna is essential. Spatial autocorrelation in soil fauna distribution violates the assumptions and affects the results of classical tests of significance and regression analysis in inferential statistics. This study investigates diversity patterns in communities of soil oribatid mites (Acari: Oribatida). The distribution patterns at the metacommunity level were analyzed as the decay in community similarity as a function of intersample distance. In all three sites community assemblages were spatially autocorrelated. The results suggest that Oribatida communities separated by distances as large as 60 m may not be spatially independent. Soil cores collected within such vicinity should not be used as independent examples of community response to environmental factors, and should not be treated as independent replicates in statistical analysis.

Alkaloid chemistry, not phylogeny, predicts insect herbivores associated with *Senecio* plant species in New ZealandMikey Willcox ¹, Stephen Hartley ^{*1}, Geoff Lane ², Mike Dodd ², Jon Sullivan ³¹ Victoria University of Wellington² AgResearch, Palmerston North³ Lincoln University

Senecio is a large genus of perennial herbs. Species within the genus typically produce a suite of pyrrolizidine alkaloids (PAs) which play a role in defence against specialist and generalist insect herbivores. Variability in insect host-plant specificity has led to different ways in which insects respond to PAs. Similarly, the variety of insects on *Senecio* may select for the synthesis of specialist PA derivatives, or maintain more generalist PAs. Previous research on some *Senecio* species has also shown differences between the PAs of species in their native and introduced ranges, perhaps as a response to changes in selection pressure. Here, we assessed intraspecific PA variation between New Zealand populations of six introduced and six native *Senecios* within the context of the enemy release hypotheses. Intraspecific variation in PAs was greater for native *Senecios* than for introduced ones. Interspecific variation in PAs across all 12 species correlated with the recorded presence of insects, but not with plant phylogeny. Insects that associate with novel invasive plants are better predicted by plant chemistry than plant phylogeny. Using PAs as a surrogate for shifting energy resources, this study provided some support for the enemy release and evolution of increased competitive ability hypotheses. Further research is required to elucidate the processes driving diversity patterns in PAs.

Host plant selection and local adaptation in a polyphagous herbivore, *Eucolaspis* Sharp (Coleoptera: Chrysomelidae)

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The range of host plants that a generalist herbivore can use depends on several factors. A generally accepted theory is that diet-breadth of generalists may depend on nutritional requirements as well as toxic compounds such as plant secondary metabolites. Some suggest that a generalist herbivore is made of several populations of locally specialized individuals. Phenotypic plasticity sustained within populations of herbivores enable radiation of individuals / populations into new ecological niches. Plant volatiles are known to shape such insect-host plant association in many insect groups. More pronounced association is widely documented in specialist herbivores, but little is known in generalist herbivores. We used a polyphagous native beetle from New Zealand, *Eucolaspis* (Chrysomelidae: Eumolpinae) to explore role of olfaction and other cues in locating host plants and local adaptation. Olfactory bioassays and feeding bioassays were conducted in the laboratory. Adult *Eucolaspis* beetles were attracted to fresh leaf / fruit volatiles from Rosaceae plants, apple and blackberry. Male and female beetles behaved similarly to olfactory and contact cues of host plants; however males spent more time to decide. An indication of evolutionary affiliation was observed in geographically isolated conspecific populations. It appears that local adaptation did involve fine scale olfactory capabilities for differentiation between closely related plant genera. However, other cues (gustatory and tactile) were shown to override olfactory cues in feeding preference. Blackberry and bushlawyer leaves were more palatable than apple leaves to both populations. We argue that plant volatiles play important role in host choice by *Eucolaspis* despite being a generalist.

The Life History of the Lepidopteran Seed Predator *Cryptasasma querula* and its Relationship with Potential Host Plants

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Eligible for student prize

Cryptasasma querula is a polyphagous obligate seed predator endemic to New Zealand. Related species (*Cryptasasma*) have attracted attention overseas because these lepidoptera can have significant effects on natural and economic seed populations. Field experiments investigating infection rates, host survivability (germination/establishment), advantages of seed dispersal (seeds were cleaned of flesh to simulate pigeon seed dispersal) and potential host suitability were conducted over a number of different sites in the North Island of New Zealand including transect and monthly surveys of host plant infections. Laboratory experiments investigated host suitability, host preferences, and life history in *Cryptasasma querula*. *C. querula* infection rates of tawa (*Beilschmiedia tawa*) reached over 90% for most sites surveyed. Seeds were shown to have reduced germination/establishment rates if they were infected with *C. querula* but some seeds were still able to establish despite damage. Seeds that were cleaned and taken away from the parental canopy to simulate dispersion still suffered drilling from *C. querula* yet many sites showed increased numbers of establishing seeds potentially due to seeds given time to germinate before they are attacked. Seeds of tarairi (*Beilschmiedia tarairi*) and oak (*Quercus spp.*) were utilized by *C. querula* in the field. Karaka (*Corynocarpus laevigatus*) and Miro (*Prumnopitys ferruginea*) suffered little damage to the endosperm from the seed predator and is likely not a host in nature. Miro and Hinau (*Elaeocarpus dentatus*) were shown in laboratory experiments to be inadequate hosts and Tarairi and Tawa were preferred hosts. *C. querula* has a high infection rate on *B. tawa* than expected ultimately having a strong impact on germination and establishment in the seeds. Coupled with reduced natural seed dispersers (kereru), there may be major consequences for tawa demography and regeneration.

An enemy of an enemy is a friend of mine: the tri-trophic interactions between a predator-parasite-host assemblage in New Zealand.

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Eligible for student prize

The Pūriri moth (*Aenetus virescens*) is New Zealand's largest endemic moth. During their 4-6 year larval stage, caterpillars' parasitise host trees by excavating a "7" shaped tunnel, feeding on living tissue at the entrance. Silk and frass webbing covers the tunnel entrance, perhaps concealing larvae from predators such as North Island Kaka (*Nestor meridionalis septentrionalis*), that predate Pūriri moth larvae by excavating bark and wood from trees. I hypothesise that Pūriri moth larvae select host trees based on wood density and that Kaka attack rate is correlated with parasite load. Furthermore, I hypothesise that host tree fitness is affected by both Pūriri moth parasitism and Kaka attacks. Preliminary results indicate Pūriri moth larvae preferentially select particular tree species and that Kaka visually locate tunnels excavated by the larvae. I propose a trade-off exists between the ability of Pūriri moth to parasitise host trees and protection host trees provide from predating Kaka. This tri-trophic system presents a unique and novel predator-parasite-host relationship whereby predators directly influence parasites and their hosts. Understanding the drivers and outcomes of this complex relationship will provide important missing elements in tri-trophic predator-parasite-host research.

We know what you ate last summer: Determining trophic position of endemic New Zealand dung beetles using N and C stable isotopes

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Eligible for student prize

Worldwide, dung beetles (Coleoptera: Scarabaeidae: Scarabaeinae) are recurrently linked to a number of critical ecological processes, yet in some regions the role of dung beetles has not been examined. The enigmatic nature of New Zealand's endemic dung beetle fauna, coupled with their high abundance in indigenous forests, presents an intriguing conundrum as to their role in current ecosystems. This is compounded by New Zealand's lack of native terrestrial mammals and the widespread use of mammal dung by dung beetles elsewhere. Stable isotope analysis is an excellent tool for investigating such anomalies, as it reveals trophic level and food resource use over extended periods. We used nitrogen stable isotope analysis to investigate the trophic position of four endemic New Zealand dung beetle species: *Saphobius edwardsi*, *S. inflatipes*, *S. squamulosus* and *Boreobius lescheni*. Additionally, nitrogen and carbon stable isotope analyses were used to determine if the dung beetle *S. edwardsi* will incorporate squid carrion into its diet, in the field. We found that on average, *Saphobius* species were more ¹⁵N enriched than detritivores, but were less enriched than predators. In contrast, *B. lescheni* was less ¹⁵N enriched than detritivores and omnivores. Nitrogen and carbon stable isotope ratios of *S. edwardsi* provided with squid carrion shifted significantly towards that of squid compared to controls. These findings suggest *Saphobius* species exploit higher quality food resources than *B. lescheni*. This possibly reflects the availability of nutrient rich resources such as dung or carrion in different habitats. Moreover, *S. edwardsi* appear to readily incorporate squid carrion into their diets, suggesting potential associations with marine-derived carrion.

Nutrient intake and character displacement in sympatric tree weta

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Sympatric occurrence of closely related species is expected to result from resource partitioning and a separation of ecological niches. However, distributions resulting in sympatry are not always at equilibrium. In this study, we examined diet and nutritional intake in two sympatric tree weta species, the Wellington and the Auckland tree weta (*Hemideina crassidens* and *H. thoracica* respectively). We first determined nutrient targets for these species in the lab, before analysing the crop contents of wild caught weta to determine nutrient intake during the late summer breeding season, as well as identifiable foods in the frass. We then considered whether nutrient assimilation was similar in these species. In addition, we examined longer term diet and intra and interspecific resource competition, using ¹²C /¹³C and ¹⁴N /¹⁵N stable isotopes. We found that tree weta diets largely overlap, and we could not detect strong interspecific differences between the species. In sympatric species, interspecific competition for non-substitutable resources such as carbohydrates and protein selects for character convergence. In this case, character displacement was not apparent, and we conclude that our evidence on resource partitioning supports similar ecological niches for these two species of tree weta, such that co-existence is likely to be short-term rather than long-term.

Convergent local adaptation in size and growth rate but not metabolic rate in a pair of parapatric Orthoptera species.

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Local adaptation is inferred for many morphological and physiological traits but determining the role of natural selection in shaping geographic variation relies on evidence such as provided by fitness estimates or transplantation experiments. In addition, habitat-specific convergent (or parallel) evolution provides a powerful means of testing adaptive hypotheses. Here we contrast size, growth rate and metabolic rate in a pair of Orthoptera species collected from high and low altitude locations and raised in identical environments. We find that two related insects (tree weta: *Hemideina crassidens* and *Hemideina thoracica*) have the same (convergent) pattern of larger adults and faster growth rates in populations from a high altitude location compared to conspecifics from low altitude. However, variation in metabolic rate was detected only between species and not among altitudes. The high and low altitude populations of each species were collected from the same location therefore selection pressures on the two species are likely to be similar or identical. Thus the independent evolution of larger adults and faster growth rate at high altitude suggests an adaptive role for both these traits in tree weta.

The parasitoid wasp *Nasonia vitripennis*: An emerging model system for genetics, molecular biology, and biocontrol research.

Dave Wheeler ^{*1}

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Nasonia vitripennis is a small (1-2 mm) wasp that parasitises several filth fly species that are important human and agricultural pests. *Nasonia* has become the lab rat of hymenoptera research, as it has several features that make it an excellent genetic system, including a short generation time, ease of rearing, RNA interference, and a well annotated and sequenced genome. The genome project has provided a wealth of polymorphisms that facilitate positional cloning of genes involved in species differences in behavior, morphology, and development. Advances in the genetics of this system also open a path for improvement of parasitoid insects as agents of pest control. The venom of *Nasonia* is also interesting from the perspective of identifying bioactive compounds that might be useful in the development of pharmaceuticals. To this end, we have used Next generation sequencing technologies to developed the flesh fly (*Sarcophaga bullata*) as an assay system to study venom function. In this talk I will introduce the *Nasonia* system, describe some interesting aspects of its biology and genome, as well as highlight some recent results from our venom research.

Aggressive floral mimicry in the orchid mantis (*Hymenopus coronatus*)

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Mimicry, a phenomenon where one organism benefits from a resemblance to another distantly related organism, is widespread with many varied manifestations. These similarities can occur between distantly related organisms, such as insects that appear to resemble plant parts, yet the function of these resemblances is rarely experimentally demonstrated. Here we provide the first evidence that floral mimicry may function as a predatory strategy in the praying mantis *Hymenopus coronatus*. The colour of *H. coronatus* is indistinguishable from sympatric flower colours when incorporated into hymenopteran visual models. We observed *H. coronatus* attracting wild pollinators at a rate greater than that of a local flower species, and observed direct predation of pollinating insects as they inspected the mantis. We also used artificial models of *H. coronatus* to explore additional aspects of its interactions with pollinators, experimentally assessing the interaction between prey visitation, colour and shape variation, and location with respect to native flowers. This is a unique predatory strategy in the animal kingdom that has not been shown to occur in any other species, and the orchid mantis appears ideal for further investigation of the sometimes blurry distinction between crypsis and mimicry.

Diet, Maturity and Male-Male Competition in Male Tree Weta

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Eligible for student prize

The Wellington tree weta (*Hemideina crassidens*) is a sexually dimorphic, polygynandrous species in which adult males fight for access to females, using their large mandibles. Males can mature at the eighth, ninth or tenth instar, and thus show large differences in head and mandible size. We hypothesised that male weta would use nutrient intake during development, and specifically the level of protein in their diet, as a cue for head size at maturity. We predicted that adult males on a high protein diet would mature at a later instar, than male weta raised on a low protein diet. In addition, if protein is a limiting factor in the wild, few males should make it to the tenth instar. We analysed morphological measurements in adult males that had been raised on high and low protein diets in the laboratory, and adult males caught from the wild. We found that the proportion of tenth instar males was greatest in the high protein group, and there were significant differences in overall head length as a proportion of body size between the three groups. Few tenth instar males were observed in the wild caught group. Intra-specific combat trials demonstrated that males with large heads won the greatest number of bouts, and that bouts between males with the most similar size heads were longer than those with very dissimilar size heads. We conclude that nutrient intake during development is an important determinant of final instar in adult males, and thus could potentially have an important influence on mating success in this species.

The effect of food availability on the costs and benefits of sexual cannibalism in the Springbok mantis, *Miomantis caffra*

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Eligible for student prize

Sexual conflict arises when behaviours ensuring one sex's optimal reproductive fitness impose fitness costs on the opposite sex. Sexual cannibalism is one such expression of this conflict and is one of the rare cases in which female behaviours impose costs on males. In order to better understand the costs and benefits of these behaviours for each sex, this project investigated the Springbok mantis, *Miomantis caffra*, in which this conflict seems to have intensified to unprecedented levels. Females were placed on high and low feeding regimes in order to examine the influence of adult feeding success on both fecundity and the rates of cannibalism in mating trials involving potential mating pairs. Contrary to expectation, although there was a positive correlation between female body condition and fecundity, poorly fed females did not cannibalise males more often than well fed females and there was little evidence to suggest that cannibalistic females would produce larger oothecae. One characteristic of this species that may help to explain these data is that aggressive females which never mated could still reproduce via parthenogenesis which occurred frequently in this study. Since oothecae produced asexually were not significantly smaller than those produced sexually, females were not strongly 'penalised' for not mating with males. The results of this study add to the growing literature on the adaptive significance of sexual cannibalism and praying mantid mating systems, demonstrating that facultative parthenogens have the potential to escalate sexual conflict to new heights.

Ministry for Primary Industries' Emerging Risks System

Heidy Kikillus¹, Melanie Newfield¹, Christine Reed^{*1}

¹ Ministry for Primary Industries

The identification of potential and emerging threats is an important component of the effective management of biosecurity risks. In response to the introduction of *Pseudomonas syringae pv. actinidiae* (Psa) into New Zealand, an independent review of import requirements and border processes recommended that New Zealand's Ministry for Primary Industries (MPI) "renew efforts to centralise the identification and management of emerging risks". Implementation of an "Emerging Risks System" (ERS) is a key deliverable of the MPI Management Action Plan that constitutes the response to the review. This project, implemented in August 2012, screens multiple information sources and identifies alerts relevant to New Zealand biosecurity. These alerts are then assessed by risk analysts and, if necessary, forwarded to Risk Managers within MPI so that appropriate management action can be implemented. The ERS also monitors the flow and uptake of information, with regular reporting which allows MPI to understand and assess its overall response to new risks. Since its inception, this proactive system has screened over 300 alerts, sent almost 50 alerts to risk analysts for further assessment, identified 13 potential issues to Risk Managers, and, ultimately, has resulted in the amendment of Import Health Standards for several imported commodities. Although currently operated manually, the Emerging Risks System will be transforming into a more automated system by mid-2013.

Developing an ecological risk based approach to manage phytosanitary pests risks on export logs from New Zealand

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New Zealand currently exports \$4.7 billion of wood products, including more than 12.7 million m³ Developing an ecological risk based approach to manage phytosanitary pests risks on export logs from New Zealand of logs. At present all logs are treated to eliminate infestation by phytosanitary pests, these treatments are specified by the import requirements of our trading partners. The most common treatment used at present is fumigation with methyl bromide, or in the case of China, phosphine is permitted on the basis of an experimental use permit. Research has begun to evaluate the necessity of such end point treatments and to assess the feasibility of replacing them with an ecologically based assessment of phytosanitary risk. The concept uses ecological information, e.g., pest phenology, habitat requirements, developmental biology, and dispersal capabilities, to determine if the potential pest pressure at a given time and place warrants the need for end point disinfestation treatments. This alternative approach to exporting commodities is often referred to as a systems approach. In essence a systems approach seeks to minimise risk across the entire supply chain as opposed to eliminating accumulated risk at the point of export. This talk outlines the concept of a systems approach and its application to the New Zealand export log trade. We will present an overview of key phytosanitary pests and outline our long term approach to removing end point treatments for wood exports. Removing endpoint treatments for wood exports, which will significantly reduce NZ's emissions of chemical fumigants, such as methyl bromide. This talk is supported by two complimentary poster presentations that discuss key aspects of this research programme: 1) A national pest trapping network, and 2) thermal development models of key quarantine species to predict adult phenology.

***Halyomorpha halys* (brown marmorated stink bug) a new threat from the USA**

Catherine Duthie ^{*1}

¹ Ministry for Primary Industries

Halyomorpha halys, or brown marmorated stink bug, is a species of stink bug native to China, Japan, Korea and Taiwan which has recently become invasive in the USA. It infests both cultivated and wild hosts and feeding damage results in economic loss and disruption of integrated pest management programmes. Additionally *H. halys* is a significant public nuisance in its aggregation phase. *Halyomorpha halys* is not present in New Zealand; however, there have been recent border and post-border interceptions. This analysis examined the biosecurity risk posed by *H. halys* entering New Zealand. The most likely pathways of entry were assessed. Also assessed were the economic, social and environmental impacts of establishment.

The Great White Butterfly Incursion Response: Progress on eradication of a new threat to many endemic and commercial Brassicas.

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The Great White Butterfly (*Pieris brassicae*) (GWB) was first found in Nelson on 14 May 2010 as caterpillars feeding on nasturtium. GWB is classified as an Unwanted Organism under the HSNO Act. Publicity from Ministry of Primary Industries (MPI), generated further records from within Nelson City but not beyond. By the end of 2011 GWB had been confirmed at 39 sites, all within 6 km of the Port but mostly within 2 km. The species was therefore considered established. Overseas records show that GWB caterpillars feed on a broad range of species but mostly within the cosmopolitan family Brassicaceae (cresses). As well as brassica species grown commercially as crops, including forage crops, there are 79 species of native cresses in New Zealand, 92% of which are endemic and 71% are classified as "Threatened" or "At Risk" with 18 species being "Nationally Critical". Many of our endemics are known hosts for the small white butterfly (*Pieris rapae*) and overseas records show an overlap in the host range between the two butterfly species. The arrival of the GWB represents a significant additional threat to many endemic cresses. MPI initiated an incursion response and considered three options, eradication, monitoring and do nothing. Overseas GWB is known to have migratory abilities and it was thought that the new population would expand rapidly into surrounding districts. The monitoring option was chosen involving mostly passive surveillance to assess the size and rate of spread of the GWB population with spot treatment of known sites. However, by spring 2012 the population was still within Nelson City. In November 2012 the MPI response transitioned into a joint agency eradication programme led by DOC with support from Vegetables New Zealand, MPI and Tasman District Council. The presentation will describe the eradication programme and the results from the 2012-2013 season.

Peri-urban mosquitoes (Diptera: culicidae) in the Concepción and adjacent coastal area of central Chile: some similarities and contrast with New Zealand.

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Chile, like NZ (& unlike Argentina or Australia) has a small known mosquito fauna and no indigenous mosquito-borne disease on the mainland. There has accordingly been only sporadic scientific interest in this field. Nevertheless and also as in NZ, there is a significant seasonal biting nuisance in some areas and there are some species present which transmit virus diseases elsewhere. There are also local species of unknown vector ability. We sampled mosquito species around Concepción and the adjacent south coastal region of central Chile, in similar latitudes and environment to parts of NZ, as part of a wider project. Adults were obtained using CO₂-baited light traps in built, wetland and remnant forest areas around Concepción city during February-March 2012. Weather information was obtained from on-site loggers and the Chilean Meteorological Service. Larvae were obtained by dipper from standing water and link-reared to obtain males for identification. Disease associations are reviewed from the literature for species in these samples and in collections of larvae made in late 2006. Some similarities with the situation in NZ and incipient concerns for human health and biosecurity are noted. It is interesting that NZ has higher reported levels of non-indigenous disease.

Strategy and serendipity: reflections on the search, release and establishment of a biocontrol agent for clover root weevil

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Chance frequently leads to unexpected discoveries in science, and astute researchers following good scientific practice can create the conditions to identify and benefit from serendipity. The classical biocontrol programme for the clover root weevil *Sitona lepidus* Gyllenhal (Coleoptera: Curculionidae) provides an example of this synergy. Little was known of the natural enemies of *S. lepidus* when it became an economically important pasture pest in New Zealand in the 1990s. We outline the approaches we adopted to undertake a classical biocontrol programme on limited resources, that has culminated in the widespread successful establishment of an Irish biotype of *Microctonus aethiopoidea* Loan (Hymenoptera: Braconidae) throughout the North Island and much of the South Island by 2013. The strategy adopted in this programme was based on the knowledge and expertise that New Zealand biocontrol practitioners had gained from prior introductions and the access to advice, resources and research facilities through international collaborations. The serendipity involved the unexpected discovery of the Irish biotype of *M. aethiopoidea*. This asexual semi-gregarious biotype has biological attributes that not only enable rapid establishment, population increase and dispersal, but also to remain reproductively isolated from the Moroccan biotype that provides control of *S. discoideus* Gyllenhal in New Zealand.

Preference-performance testing in the aphid parasitoid *Diaeretiella rapae*

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Eligible for student prize

Parasitoids make mating and oviposition decisions during foraging, and encounter trade-offs while making decisions to maximise fitness. The aim of this study was to test how the three aspects of the reproductive choice - (1) oviposition vs. mating choice, (2) mate selection and (3) host selection - affect the reproductive performance in a parasitic wasp, a cabbage aphid parasitoid *Diaeretiella rapae*. The reproductive output was quantified as the number of progeny produced and the progeny sex ratio. Protandry (the majority of males emerge before females) and haplodiploidy in *D. rapae* give females the opportunity to choose between ovipositing and mating when they first emerge. When the choice was given to female *D. rapae* in laboratory conditions, most of them preferred to spend time searching for mates and parasitise the hosts after mating, even though they were more likely to encountering hosts than potential mates. The females which chose to mate before oviposition eventually produced more female offspring. Female *D. rapae* are monandrous (mate only once). In mate choice experiment, the female *D. rapae* rejected the multiple-mated males, and preferred to mate with virgin males, which resulted in more female offspring. Females that mated with multiple-mated males became sperm depleted. When given hosts of various sizes, females preferred larger hosts to oviposit fertilised eggs even though the females had to spend more time and energy (stings) to parasitise them. The offspring that emerged from larger hosts developed quicker, larger in body size, lived longer and themselves produced more offspring than offspring produced from small host. Results of this study, therefore, suggest that parasitoids make their foraging decisions to maximise their reproductive performance.

Pulling the wings off wasps: determining the likely Eurasian origin of New Zealand populations of *Vespula vulgaris*

Evan Brenton-Rule¹, Monica Gruber¹, Phil Lester^{*1}

¹ Victoria University of Wellington

Eligible for student prize

The development of biological control options for invasive species requires knowledge of their native range. Here, we estimate the native range of New Zealand populations of the invasive common wasp *Vespula vulgaris*, which is one of our most serious biodiversity and conservation threats. We collected these wasps from New Zealand and from 23 countries across their native Eurasian range. We used mitochondrial DNA markers (cytochrome oxidase c subunit 1, and cytochrome b) to assess genetic variation among 100 wasp samples. No variation existed in sequences from New Zealand population, which were most genetically similar to samples from the UK and Belgium. In addition, we assayed the samples for the presence of *Nosema* spp., which are a genus of microsporidian pathogens associated with population regulation in other social insects. We observed *Nosema* infection in New Zealand at a similar rate to those in Europe. Our work has identified the likely origin of *V. vulgaris* and is an important first step in the examination of this native range for potential biological control agents. These population regulators could include microbial pathogens, which can have a major influence on social insect population dynamics. Given their effects on other social insects, pathogens such as *Nosema* spp. are good candidates for further study.

PCR gut analysis reveals that a common introduced spider (*Tenuiphantes tenuis*) is a potentially significant predator of Argentine stem weevil (*Listronotus bonariensis*)

Cor Vink *¹, John Kean ²

¹ Canterbury Museum, Christchurch

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PCR (polymerase chain reaction) analysis of gut contents can be used to determine what arthropods are feeding on in ecosystems as DNA from the food ingested by an arthropod will be present in the gut for a certain amount of time before digestion takes place. PCR gut analysis was conducted on specimens of the introduced spider *Tenuiphantes tenuis* collected from pasture in Canterbury, New Zealand. PCR primers were specifically designed to amplify a fragment of the mitochondrial gene cytochrome *c* oxidase subunit 1 (COI) from *Listronotus bonariensis* and revealed that this major pasture pest species is consumed in the field by *T. tenuis*. The field predation rate of *L. bonariensis* by *T. tenuis* was estimated from our PCR results together with published data on the degradation of DNA and the density of *T. tenuis* in Canterbury pastures. We found that *T. tenuis* is a potentially significant predator of *L. bonariensis* in New Zealand pastures.

A metagenomic survey of the invasive yellow crazy ant *Anoplolepis gracilipes* suggests candidates for population regulation

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Eligible for student prize

Invasive species often experience rapid increases in population size when introduced to a new range, followed by population stabilisation. However, declines of large populations of invasive species are occasionally observed, sometimes to the point of local extinction. Although the causes of these declines are difficult to ascertain, disease is often assumed. Our metagenomic study used Illumina GAIIX short-read sequencing to investigate endosymbiont diversity of the invasive yellow crazy ant *Anoplolepis gracilipes*. Although the prevalence of many bacterial groups did not differ among *A. gracilipes* populations, bacterial diversity varied among our samples. A population known to have low ant abundance also had the lowest number of matches to bacterial sequences (i.e., the lowest bacterial prevalence). Compared to other populations, this low abundance population also had more bacterial orders that are proposed to have beneficial relationships with ants, particularly involving antibiotic activity. This study has identified a range of bacteria that were previously unknown in *A. gracilipes*. Several of these are candidates for further research, which may shed light on the effects of endogenous parasites and symbionts on the population dynamics of the species.

In readiness for Fruit fly

David Voice ^{*1}

¹ Ministry for Primary Industries. Plant Health and Environment Laboratory.

This presentation discusses the technical capacity required to manage a fruit fly detection like the one experienced in Auckland on May 2012; where a single male Queensland fruit fly was discovered in a surveillance trap. The presentation outlines fruit fly identification and how trap catches might relate to a sustainable breeding population. Which fruit fly species are of most concern to New Zealand horticulture and what can we learn from fruit fly interception and incursion records?

Experimentally reducing the competitive ability of a dominant invader increases resource acquisition by resident species.

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Eligible for student prize

The invasive Argentine ant *Linepithema humile* often becomes the dominant species in its invaded range, frequently overpowering competitors. One of the factors conferring advantages to Argentine ants is the dynamic and effectiveness of their recruitment system. It allows them to quickly divert workers from depleted to newly discovered resources. We tested if the dominance of this invasive species can be broken, by confusing it with synthetic trail pheromone, reducing its competitive ability. We offered baits and applied pheromone in close proximity to study the effects on foraging success and behavioural interactions. By disrupting the trail following behaviour of Argentine ants, other resident ant species were able to significantly increase their foraging success. Differences in behavioural reactions of the invader and the competing ant species towards each other provide an explanation for differences in foraging success of the competing resident species. Our results suggest that the mechanism determining an increase in resource acquisition of resident ant species is a decrease in aggressive behaviour displayed by the Argentine ant, which is presumed to create an opportunity for other resident species to forage without being attacked. Reducing the competitive ability of an invader could have important applications for invasive species management and enable native species to reclaim native habitats.

The diet of two tree weta species: the natural and captive folivory preferences of *Hemideina crassidens* and *Hemideina thoracica*.

Robyn Dewhurst ^{*1}, Mary Morgan-Richards ¹, Steve Trewick ¹

¹ Ecology Group, IAE, Massey University

Tree weta are common and widespread in New Zealand but we know little about their ecology because they are nocturnal. Basic knowledge of tree weta diet was sought by examining wild diet using cuticle analysis of frass, and captive experiments with *Hemidiena crassidens* and *Hemideina thoracica*. This base line data should help improve our understanding of where tree weta fit into New Zealand forest ecosystems. In the present study I examined the natural (wild) diet of two tree weta species *Hemideina crassidens* and *H.thoracica* and some aspects of dietary preference. The frass of thirty-three wild tree weta indicated that tree weta do not eat at random when compared to the plant species available to them. Some common plants were never eaten by tree weta. It was of note that a favoured plant species present in the frass was an exotic legume, known to have a high nitrogen content. Weta in this study ate on average only two plant species in a single night, however they increased the number of plant species they ate over two nights. By limiting the number of plant species eaten in a single night, tree weta may be allowing themselves time to deal with toxic compounds in the plant. Additional research into tree weta use of natural resources and dietary requirements would help further our knowledge of tree weta ecology.

How to find a new moth family

George Gibbs ^{*1}

¹ Victoria University

In October 2009, Richard Glatz, an insect molecular biologist with the Waite Institute, Adelaide, collected a small moth which looked 'very unusual' to him and was fortuitously passed on to the Australian National Insect Collection at CSIRO, Canberra, where it was pronounced sufficiently different to become the target of a special field expedition. My involvement in a trip to Kangaroo Island in October 2012, and its outcome, will be discussed. The result is indeed a new family of primitive moths with some extraordinary features that place it close to the base of Lepidopteran phylogeny. The age of discovery is clearly not yet over—a little serendipity and a sharp eye can achieve results where perhaps a massive research grant and expeditionary force might not.

The role of pathogens in the decline of the invasive yellow crazy ant (*Anoplolepis gracilipes*) in Arnhem Land, Australia

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Eligible for student prize

The yellow crazy ant (*Anoplolepis gracilipes*) is a widespread invasive species which can have severe ecological impacts on native ant and invertebrate communities. In some areas of their invaded range, yellow crazy ant populations have been observed to fluctuate strongly. In Arnhem Land, Australia, populations of these ants fluctuate spatially and temporally and sometimes disappear altogether. The mechanisms responsible for such declines have yet to be investigated. Yellow crazy ant populations in Arnhem Land represent a unique opportunity to investigate mechanisms by which a globally significant invader declines. It is my hypothesis that microorganisms affect fitness of yellow crazy ants. In order to test this hypothesis, I will compare pathogen and bacterial endosymbiont load of ants from sites with declining and expanding populations, I will also evaluate the effects of these microorganisms on colony fitness. Initial findings suggest pathogens may affect egg production in queens. By identifying the mechanisms behind such population collapses, we may improve the management and control of invasive species.

The prevalence of three endosymbiotic bacteria in the invasive yellow crazy ant (*Anoplolepis gracilipes*)

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Eligible for student prize

Invasive ant species, such as the yellow crazy ants (*Anoplolepis gracilipes*), are a global issue causing both economic expense and ecological damage. We screened populations of yellow crazy ants for the presence of three known endosymbionts (*Wolbachia*, *Arsenophonus* and *Rhizobiales*) from four sites in the Pacific Islands and five in Australia. The same genotype of *Wolbachia* was found in all samples with a high prevalence. *Arsenophonus* was detected in six out of the nine populations with a maximum prevalence of 51% in Arnhem Land, Australia. *Rhizobiales* was found at a prevalence of less than 15%, and in only three sites. We suggest that the introduction of different strains of *Wolbachia* or *Arsenophonus* could form part of a management program in highly infected sites as individuals infected by different strains of these bacteria cannot reproduce.

Does buzz pollination have an effect on fruit and seed set of egg plant, *Solanum melongena*?

Shanika Jayasinghe *¹, Inoka Karunaratne ¹

¹ University of Peradeniya

Eligible for student prize

Buzz pollination and anther dehiscence are co-evolved adaptations. It is estimated that sixty percent of the angiosperms including *Solanum melongena*, with poricidal anthers are buzz pollinated by various species of wild and domesticated bees. Buzz pollination promotes fruit and seed set of *Solanum* species hence it is important economically and in plant propagation. We studied the species of bee visitors, the frequency of visits, and rates of fruit and seed set of *S. melongena* by buzz pollination in two sites in the Kandy District, Sri Lanka. The floral preferences of bees were studied in relation to the morphology and age of flowers and the life cycle of *S. melongena*. Handling time was recorded for two common buzzing bee species on *Solanum* flowers. Effectiveness of buzz pollination was determined by comparing open buds and buds covered with pollinator exclusion bags. Results suggest that the peak activity period of bees ranges from 0800hrSLST to 1100hrSLST, which was also the time when we found that stigma receptivity and pollen release were greatest. Handling time of the selected bee species indicates that bees spend more time at new flowers than at older flowers. Data from the pollinator exclusion experiment indicate that the fruit and seed set of *S. melongena* is significantly enhanced by buzz pollinating bees. The findings of this study suggest that in New Zealand, it is possible to use the bumble bees (*Bombus* sp.) as efficient buzz pollinators to enhance the production of crops belonging to plant families Solanaceae, Melastomataceae, Fabaceae, etc. including crops such as tomatoes, egg plants, blue berries and many other.

The ecological interactions between the New Zealand Giraffe weevil (Coeloptera: Brentidae) and associated mites

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Eligible for student prize

Many mite species hitchhike on other arthropods in order to disperse to a new food source or where they can successfully complete their life cycle. The relative load of mites on hosts can be affected by sexual selection. According to this theory male hosts, already bearing physiological costs of a sexually selected trait, are more likely to be infected with ecto-parasites. Thus the load, prevalence and incidence of ecto-parasites tend to be more skewed toward male hosts. The New Zealand endemic giraffe weevil (*Lasiornychus barbicornis*) displays incredible sexual dimorphism; a male rostrum makes up half its body length and is used as a weapon to fight with other males and defend females. An assemblage of mites has been found on the bodies of these weevils, and there appears to be at least 4 different mite morpho-types observed on an average weevil. It is of interest to determine whether these mites are parasitizing the weevils in order to survive and reproduce, or using the weevils as a vehicle of dispersion (phoresy). Using data collected over 3 years for a single wild population of giraffe weevils, we explore whether mite load corresponds to host sex, size, time of year, and eco-habitat the host was initially found. We also aim to determine if a high density of hosts at a given location correlates to a high incidence of mites. To determine whether these mites are specialised 'hitchhikers' or not, we will be examining the assemblage of mites found on different body parts of the host, other potential host insects and possible sources of where the mites come from. We will discuss the findings in relation to host and parasite interactions and the possible reasons why giraffe weevils are a suitable candidate for mite dispersion

The *Fauna of New Zealand*, 30 years of publication

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The *Fauna of New Zealand* is a widely acclaimed monograph series, publishing revisions and descriptions of the terrestrial invertebrate animals of New Zealand. Since it was established in 1982, about two contributions have been published each year. The main group covered in the 70 contributions published so far is insects (59), but the series also includes contributions on mites (5), spiders (3), amphipods (1), nematodes (1), and introduced slugs and snails (1).

Velvet worm diversity in New Zealand

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Eligible for student prize

Peripatus, of the phylum Onychophora, are soft bodied, velvety textured invertebrates that commonly inhabit decaying logs and leaf litter on the forest floor. In New Zealand there are two genera (*Peripatoides* and *Ooperipatellus*), currently comprising nine species. The larger, livebearing, genus, *Peripatoides*, is the main subject of this study. Sympatry has been documented among five of the seven species in this genus. All in the North Island, with the habitat of *Peripatoides sympatrica* overlapping with *P. aurorbis*, *P. suteri* and *P. morgani* separately, and *P. morgani* overlapping with *P. kawakaensis*. Such sympatry accompanied by multilocus genetic data showing no interbreeding provide compelling evidence of the species status of these taxa. However, given no known ecological difference among these taxa, prompts the the question of how such relationships might occur and be maintained. Modern models of sympatric speciation (the process through which new species evolve from an ancestral species occupying the same geographic region) predict that some traits/genes of the insipient taxa are under intense selection. This might involve niche differentiation, which could also arise when ecologically similar species that evolved in allopatry come into contact through range expansion. We are exploring these and other possible explanations for how these species are able to occupy the same habitats, whilst simultaneously testing their population genetic structure and reproductive isolation.

Using thermal development models to predict the phenology of key quarantine pests: applying an ecologically-based risk assessment approach to wood exports

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Before export, all New Zealand grown logs are treated to eliminate infestation by phytosanitary pests. These treatments are applied to comply with phytosanitary requirements of importing countries. Presently, treatments are applied irrespective of actual infestation risk, however we are conducting research to evaluate the necessity of such end point disinfestation treatments. We propose a new approach where phytosanitary treatments are only applied when ecologically-based assessments of phytosanitary risk indicate there is a quarantine risk. Using temperature-based phenological data for a range of pests, along with information on developmental biology, we plan to develop temperature development models that will be used to determine when pest species are present. This will enable the calculation of the time of year when adult pests are expected to be most active, therefore demanding an aggressive disinfestation strategy. In addition, models will also infer times of the year when phytosanitary treatments are not required because the risk of infestation is low. Incorporating ecological information, specific to each pest species of concern, as part of integrated phytosanitary practices allows for scientifically informed phytosanitary pest management. This approach will lead to reductions in use of chemical fumigants as well as guide the development of long-term, sustainable wood exporting practices.

Exotic Coleoptera and Lepidoptera are biosecurity threats to New Zealand pasture species

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The biosecurity threats to New Zealand's priority pasture species are not well understood. There is currently a lack of understanding of which exotic pests are a threat to New Zealand pasture species, what the likely impact of their establishment in New Zealand would be, and what the potential pathways of introduction are. As a starting point in addressing this knowledge gap, a modified 'hazard identification' methodology was used to create a list of some of the biosecurity hazards for New Zealand's priority pasture species. Likely pathways of entry into New Zealand were also identified. The hazards were grouped into high and low hazard groups according to their potential to establish in New Zealand and potential impact to the pastoral sector. The vast majority of the 'high' hazard pests are arthropods, particularly Coleoptera and Lepidoptera. This work was co-funded by the Ministry for Primary Industries and the pastoral sector organisations Beef+Lamb NZ, DairyNZ, with in-kind contributions from Deer Industry New Zealand and Dairy Companies Association of New Zealand.

Bronze bug gone walkabout - update from New Zealand

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In March 2012 *Thaumastocoris peregrinus* was discovered in a localised area of Auckland, during routine surveillance conducted by New Zealand's Ministry for Primary Industries and partners. This sap feeding bug causes leaf discoloration, or 'winter bronzing', and can lead to premature leaf drop and branch death. Hosts include over 30 species of eucalypts. To date the population appears to be confined to Auckland, but it is expected to spread rapidly. Following an initial outbreak in the Sydney area in 2001, this Australian insect appeared in South Africa and Argentina and quickly spread to several neighbouring countries. In 2011 it was also discovered in Italy. Thus, apart from the US, bronze bug has now been found in every major eucalypt growing region in the world. It is regarded as a pest both in Australia and overseas, where biological control efforts to protect urban and forestry trees are underway using the Australian egg parasitoid, *Cleruchoides noackae*. Research on the biology and ecology of this insect in New Zealand is underway at the University of Auckland (Dr. Greg Holwell and Dr. Toni Withers supervising M.Sc. student, Maria Roman), with results expected to assist longer term management efforts.

Creating a national phytosanitary pest trapping network to monitor export wood species

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New Zealand currently exports \$4.7 billion of wood products, including more than 12.7 million m³ of logs. At present all logs undergo mandatory treatment, at the request of our trading partner, to eliminate infestation by phytosanitary pests. We believe such endpoint treatments should not be mandatory and that an ecologically based assessment of phytosanitary risk can determine the need for treatment. The concept uses ecological information, e.g. pest phenology, habitat requirements, developmental biology, and dispersal capabilities, to determine if the potential pest pressure at a given time and place warrants the need for end point disinfestation treatments. A key aspect of this research is to quantify and validate the phytosanitary pest pressure within the landscape. Fundamental to ecology is the concept that population abundance is constrained by the availability of resources and the suitability of the local environmental conditions, particularly the composition and arrangement of habitat types and climatic variation. To quantify how such factors influence pest abundance, we will establish an experimental Quarantine Pest Trapping Network (QPTN) to produce a comprehensive seasonal pest pressure map. The aim is to establish a nationwide network of flight intercept traps to monitor the seasonal phenology of key quarantine species, *Hylastes ater*, *Hylurgus ligniperda*, *Arhopalus fesus*, *Prionoplus reticularis*, and *Sirex noctilio*. Traps will be placed to provide structured information on abundance by region, to identify times when the concept of pest free areas of production could be applied to the export of *Pinus radiata* logs from New Zealand. This poster is in support of a presentation that gives an overview of the research programme: Developing an ecological risk based approach to manage phytosanitary pests risks on export logs from New Zealand. Accompanied by a complimentary poster presentation: Thermal development models of key quarantine species to predict adult phenology.

The efficacy of squid-baited pitfall traps in collecting weta species in Aorangi Forest, Wairarapa, New Zealand- a preliminary study.

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Eligible for student prize

Pitfall traps are commonly used to sample active and surface-living invertebrates, though this technique could be not effective to study some target invertebrate species. The goal of this approach is to evaluate the efficacy of squid baits on sampling weta species as part of the PhD research: Top-down and bottom-up forces in forest invertebrate communities-implication for mammal control in New Zealand. Five pitfall sampling points were established on November 2012 and nine on February 2013 in Aorangi Forest. Four non-baited and three squid baited kill pitfall traps were set up around the center of each transect and were active one night during November and three night during February. Caught invertebrates were taken to the laboratory for later classification. The total number of weta caught in squid baited pitfall traps was 187 individuals, more than four times the number (46 individuals) caught in non-baited pitfall traps. The abundance of weta was particularly high in three-night active traps (February), 6.48 (± 2.63) individuals on average, compared with 0.8 (± 0.91) individuals on average in one-night active traps (November). Diptera and Araneae were almost always present in baited-traps. Our preliminary results show that squid-baited pitfall traps seem to be more effective than non-baited pitfall traps to catch weta species and one-night active traps is not enough to evaluate the weta diversity in Aorangi Forest.

Parthenogenetic vs. Sexual Reproduction in the New Zealand stick insect *Clitarchus hookeri*

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Eligible for student prize

Although parthenogenetic individuals have many advantages over their sexual counterparts, in nature sexual reproduction is still the predominant mode among animals. The New Zealand stick insect *Clitarchus hookeri* is capable of both parthenogenetic and sexual reproduction. All females are capable of parthenogenetic reproduction but parthenogenetic females are unable to return to full sexual reproduction. What prevents parthenogenetic females from returning to sexual reproduction? After the loss of sexual reproduction, changes in reproductive morphology has been known to occur. Describing and comparing the reproductive anatomy of parthenogenetic and sexual individuals will provide a better understanding on their reproductive morphology and process. It is possible that infection by the microbe *Wolbachia* is responsible for the presence of parthenogenesis in *C. hookeri*. DNA analysis of the stick insects will be used to test whether this microbe induced parthenogenesis. Parthenogenetic females do not utilize males' sperm in the reproduction process. Therefore it would be a disadvantage for a male to mate with parthenogenetic females over sexual females, as their genes are not passed on to the offspring. Are males able to distinguish between parthenogenetic and sexual individuals? Male mate choice experiments will provide a better understanding on whether males are able to distinguish between parthenogenetic and sexual females. Previous research has indicated that *C. hookeri* exhibits geographic parthenogenesis, where the asexual females occur at higher latitudes than their sexual counterparts. The presence of a sexual population in the wellington region is interesting as it is part of the main parthenogenetic clade. Extensive survey of the area will help create a better picture of what is happening on as it might represent an ancestral sexual population or an invasion of males from the north.

Armed Arachnids: Investigating male weaponry in a polymorphic native harvestman (Opiliones: Monoscutidae).

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Eligible for student prize

Exaggerated secondary sexual characteristics are common in animal groups where one sex competes for access to mates. Males of many invertebrate species are equipped with weaponry that is used in physical contests. Generally, larger weapons are associated with larger males (majors) who are more often successful in competitions for females. In some species, smaller and less well-armed males (minors) will avoid physical contests in favour of alternative strategies to achieve mating success. These alternative reproductive tactics (ARTs) are often associated with substantial differences in appearance and behaviour. Male polymorphism was recognised in some groups of New Zealand harvestmen more than 50 years ago but the nature of this intrasexual variation remains unknown. Males of a number of species in the genus *Pantopsalis* (Opiliones: Monoscutidae) exhibit dramatic morphological differences in the size and shape of the chelicerae which can constitute up to half of the total mass of the individual. These appendages are long and slender in some males while in others they are relatively short and broad. A third morph has been described that reportedly resembles the female, the chelicerae of which are much smaller than those of the armed males. Preliminary observations of a population of *Pantopsalis* sp. in and around two caves near Waitomo have confirmed the presence of the two armed male morphs. We hypothesise that (i) enlarged chelicerae are used in physical contests between males; (ii) fighting strategies differ between male morphs, and (iii) there is a relationship between body size, weapon size and the fighting tactic adopted. Using a combination of behavioural observations and allometric analyses we aim to answer some longstanding questions about one of New Zealand's most secretive and heavily armed invertebrates.

Good reason to be nasty to your sister: Aggression towards pathogen infected nest-mates in the honey bee, *Apis mellifera*Zak Murray ^{*1}, [Phil Lester](#) ¹¹ Victoria University of Wellington, PO Box 600, Wellington

Eligible for student prize

The honey bee (*Apis mellifera*) is an vital ecological and commercial pollinator, though is subject to population pressure from an array of pathogens and parasites. Potential pathogens implicated in colony collapse in North America include the two microsporidian gut parasites *Nosema apis* and *N. ceranae*. Bee keepers are dubious as to the presence of *Nosema ceranae* in New Zealand. We collected honey bees from hives in the North Island, especially around the supposed *Nosema ceranae* incursion site. DNA sequencing confirmed that the gut pathogen *Nosema ceranae* is established in NZ. The confirmed presence of this pathogen has implications for our export/import industry. Little information is available about how our bees respond to such pathogens. In the laboratory we infected honey bees with *Nosema* spores and observed the behaviour of pathogen-free siblings towards the infected bees. We observed that honey bees can recognize and are aggressive towards their *Nosema* infected siblings. The most extreme sibling aggression occurred towards more heavily infected bees. This behaviour represents a form of “social immunity” for bees to fight pathogens such as *Nosema* spp.

