



Programme

Friday 29 November

5:00pm Arrival and registration
7pm Dinner

Saturday 30 November

8:00am Breakfast
9:00am Welcome

Session 1

Chair: Pete Ritchie

| | | |
|---------|----------------------|--|
| 9:15am | Victoria Twort | Giant weta genomics |
| 9:30am | Natalie Stewart | Determining the population structure of <i>Polyprion americanus</i> (Sea bass) and <i>Polyprion oxygeneios</i> (Hapuku) using microsatellite and mitochondrial DNA markers |
| 9:45am | Angela Parody-Merino | Godwit genomics and migration |
| 10:00am | Felix Vaux | Phylogenetics of three bumblebee RNA viruses |
| 10:15am | Lizzie Daly | <i>Placostylus</i> –old shells, new study |
| 10:30am | Morning tea | |

Session 2

Chair: Rob Cruickshank

| | | |
|---------|-----------------------------|---|
| 11:00am | Anna Seybold | Molecular adaptation mechanisms in the Antarctic nematode <i>Panagrolaimus davidi</i> |
| 11:15am | Mike Gemmell | Punctuated equilibria as an evolutionary mode in New Zealand Mollusca |
| 11:30am | Balam Jimenez Brito | Coastal marine connectivity of the grey mullet (<i>Mugil cephalus</i>) using microsatellite and mitochondrial DNA markers. |
| 11:45am | Iara S. Chapuis | Freshwater red algae: diversity of Batrachospermales in the Iberian Peninsula |
| 12:00pm | Sarah Wells | The role of islands in divergent evolution: driven by isolation and lack of gene flow? A case study in the tui, <i>Prothemadera novaeseelandiae</i> |
| 12:15pm | Lunch | |
| 1:15pm | Beach walk/explore QE2 park | |

Session 3

Chair: Mary Morgan-Richards

| | | |
|--------|-----------------|---|
| 2:30pm | Jorge Bresciano | Symbiotic bacteria resisting <i>Batrachochytrium dendrobatidis</i> in Ecuador: Implications for amphibian |
|--------|-----------------|---|

| | | |
|------------------|--|---|
| 2:45pm | Rachel van Heugten | ecology Insect Affairs: An investigation into possible hybridisation on Banks Peninsula |
| 3:00pm | Gemma Collins | Genetic variability of mites in the Ross Sea Region, Antarctica |
| 3:15pm | Ayla Van Loenen | Reconstructing the genetic legacy of Cook's Petrels (<i>Pterodroma cookii</i>) |
| 3:30pm | Afternoon tea | |
| Session 4 | Chair: Lara Shepherd | |
| 4:00pm | Steve Woods | Molecular identification of zooplankton for aquatic environmental monitoring |
| 4:15pm | Maren Preuss | Host switch in the red algae parasite <i>Pterocladophila hemisphaerica</i> |
| 4:30pm | Tarsha McKean | Tree weta hybrids |
| 4:45pm | Keith King | Phylogeography of the alpine weta (<i>Hemideina maori</i>) in relation to melanism and its physiology. |
| 5:00pm | Claire Gebbie | Population genetic structure of New Zealand blue cod (<i>Parapercis colias</i>) based on microsatellite DNA markers |
| 5:15pm | Annual North vs. South Island soccer match | |
| 7:00pm | Dinner | |
| 8:30pm | Quiz | |

Sunday 1 December

| | | |
|------------------|-----------------------|---|
| 8:00am | Breakfast | |
| Session 5 | Chair: Rod Hitchmough | |
| 9:15am | Rob Cruikshank | Spatial molecular ecology of epiphytic lichens |
| 9:30am | Bhargavi Yellapu | Population genetics of spiny rock lobster- <i>Panulirus ornatus</i> |
| 9:45am | Emily Koot | Sympatry and diversity among New Zealand velvet worms |
| 10:00am | Nathan Watson | DNA barcoding of New Zealand freshwater cyclopoid copepods |
| 10:15am | Morning tea | |
| Session 6 | Chair: Joe Zuccarello | |
| 10:45am | Mary Morgan-Richards | Cospeciation of birds and lice |
| 11:00am | Simon Hills | East Cape, marine biogeographic barrier or transition zone? |
| 11:15am | Lara Shepherd | Prion evolution |
| 11:30am | Start cleanup | |
| 12:00pm | Lunch | |
| 1:30pm | Departure | |

Abstracts

Symbiotic bacteria resisting *Batrachochytrium dendrobatidis* in Ecuador: Implications for amphibian ecology

Bresciano J.C.^{1*}, Salvador C.A.^{2,3}, Paz-y-Miño C.², Parody-Merino A.M.¹, Bosch J.⁴ & Woodhams D.C.^{5,6}

¹*Programa de Maestría en Biodiversidad de Areas Tropicales y su Conservación, Spain*; ²*Universidad de las Américas (UDLA). Quito, Ecuador*; ³*Universidad Técnica del Norte (UTN). Ibarra, Ecuador*; ⁴*Museo Nacional de Ciencias Naturales, Spain*; ⁵*University of Colorado, US*; ⁶*Smithsonian Tropical Research Institute, República de Panamá*
Email: ecobio@iscb.org

Amphibian populations are decreasing worldwide due to a variety of factors. In South America, the chytrid fungus *Batrachochytrium dendrobatidis* (*Bd*) is linked to many population declines. The pathogenic effect of *Bd* on amphibians can be inhibited by specific bacteria present on host skin. This symbiotic association allows some amphibians to resist development of the disease chytridiomycosis. Here we aimed (1) to determine if specific anti-*Bd* bacteria are present on amphibians in Ecuador and Southern Colombia, (2) to monitor anti-*Bd* bacteria across developmental stages in a focal amphibian, the Andean marsupial tree frog, *Gastrotheca riobambae*, that deposits larvae in aquatic habitats, and (3) to compare *Bd* presence and anti-*Bd* bacteria associated with host assemblages including 10 species at sites ranging in biogeography from Amazonian rainforest (450 masl) to Andes montane rainforest (3200 masl). We sampled and identified skin-associated bacteria of frogs in the field using swabs and a novel methodology of aerobic counting plates, and a combination of morphological, biochemical, and molecular identification techniques. The following anti-*Bd* bacteria were identified and found to be shared among several hosts at high-elevation sites: *Janthinobacterium lividum*, *Pseudomonas fluorescens*, and *Serratia* sp. No previously recognized anti-*Bd* bacteria were found in two low-elevation Amazonian sites and *Bd* was not detected in a limited preliminary sample. *Bd* was detected in *Gastrotheca* spp. In *G. riobambae*, recognized *Bd*-resistant bacteria start to be present at the metamorphic stage. Overall bacterial abundance was significantly higher post-metamorphosis. Further metagenomic studies are needed to evaluate the roles of host identity, life-history stage, and biogeography on the microbiota, and their function in disease resistance.

Freshwater red algae: diversity of Batrachospermales in the Iberian Peninsula

Iara S. Chapuis

Victoria University of Wellington

Email: iaraschapuis@gmail.com

The red algae (Rhodophyta) is an abundant and cosmopolitan group of algae, consisting of more than 6000 species world-wide. While mostly marine, one order (Batrachospermales) is restricted to fresh water. Most of diversity of Batrachospermales is included within the genus *Batrachospermum*, which has nine sections and one unclassified group. Currently, a Spanish national project (Iberian Flora of Continental Algae) is focused on freshwater red algal diversity in the Iberian Peninsula (Spain and Portugal), where very few systematic studies have been carried out. There is evidence, from local floras, of high diversity of freshwater red algae, compared to other European regions. The main objective of this study is to know the diversity of Batrachospermales and establish the phylogenetic relationships found within. We collected 56 samples between 2011 and 2013 in lotic environments. We analysed a set of morphological features and performed molecular analysis using RUBISCO large subunit (rbcL) gene sequence data. We show the first phylogeny with newly sequenced Iberian taxa of *Batrachospermum*. Five sections are represented in the Iberian territory, with high diversity within each section. In addition some new clades are found. These novel results suggest a new genus and new species within *Batrachospermum* and again emphasises how little we know of the diversity of these ecosystems.

Genetic variability of mites in the Ross Sea Region, Antarctica

Gemma Collins, Ian Hogg, Kristi Bennett, Nick Demetras

University of Waikato

Email: gec9@students.waikato.ac.nz

Antarctic mites have proven challenging to obtain mitochondrial cytochrome c oxidase subunit I (COI) sequences from. As an alternative, we obtained 28S rRNA nuclear gene region sequences for 19 *Nanorchestes antarcticus* and 7 *Stereotydeus* mites from within Miers Valley, Antarctica. We found high levels of sequence diversity suggesting the possibility of cryptic speciation in *N. antarcticus*. These preliminary results support the utility of the 28S rRNA gene as a useful genetic marker. Ultimately the COI gene region should be amplified for these challenging species, possibly through trialling newly designed primers or primer combinations. This will facilitate comparisons between *N. antarcticus* and other existing mites on the global Barcode of Life Datasystems (BOLD) database.

Spatial molecular ecology of epiphytic lichens

Robert H. Cruickshank, Hannah L. Buckley, Arash Rafat, and Johnathon Ridden

Lincoln University

Email: Robert.Cruickshank@lincoln.ac.nz

Lichen symbiosis is a complex ecological interaction based on a mutualistic relationship between a fungal and algal (and/or cyanobacterial) partner. In order to understand the factors affecting the geographical distribution of lichen partners, specimens of epiphytic lichens were collected from a number of sites across New Zealand. DNA sequences were obtained from the nuclear internal transcribed spacer (ITS) of the fungal and algal partners and used to construct genetic distance matrices and phylogenetic trees for each partner. These were compared with each other, and with the geographical distances between the sites where they were collected, in order to reveal the relative importance of phylogenetic and geographical factors for explaining current spatial patterns of association. Due to recent criticisms of the Mantel test in this context we used an alternative approach based on multivariate statistics. The results are complex and suggest that different factors may be important at different spatial scales.

***Placostylus* – old shells, new study**

Elizabeth Daly, Eddy Dowle, Mary Morgan-Richards, Steve Trewick
Massey University
Email: E.E.Daly@massey.ac.nz

New Zealand is home to three endemic species of the south-western Pacific landsnail genus *Placostylus*. All species are restricted to the Te Pahi district, northland and can be found on the mainland and offshore islands. All New Zealand species are considered threatened with many populations ranked Nationally Critical or Nationally Endangered. Subfossil shells have been collected from the region and some samples have been radiocarbon dated. Ages of fossils range from ~700 ybp to ~6000 ybp with one individual dated at >40,000 ybp. I plan to use geometric morphometric analysis to examine both fossil and extant populations. This approach uses multiple shell characters accurately and easily allowing differences within and among populations to be more easily elucidated. I am interested in the changes between and within populations through time to the present day and testing models of morphological evolution. Genetic analysis will use multi locus data from present day populations in conjunction with published mtDNA data to examine genetic diversity within and among species, as a recent study of the New Caledonian *Placostylus* has shown that mtDNA is not revealing the full picture of gene flow and structure within this group.

Population Genetic Structure of New Zealand Blue Cod (*Parapercis colias*) based on Microsatellite DNA markers

Claire Gebbie
Victoria University of Wellington
Email: gebbieclar@myvuw.ac.nz

Blue cod (*P. colias*) are an endemic species that are important to recreational and commercial fisheries in New Zealand. They are currently managed by the Ministry of Primary Industries as eight separate fishery stocks. Depletion of these stocks, particularly in the Marlborough Sounds region, calls for further investigation into population structure to provide basic units for conservation and management. A previous study investigated the phylogeographic structure of blue cod using control region sequence data. This indicated that mainland populations follow an isolation-by-distance pattern with the Chatham Islands as a genetically distinct population. With the use of next generation sequencing, eight microsatellite DNA markers have been developed and are being used to further determine the fine-scale population genetic structure of *P. colias*.

Punctuated Equilibria as an Evolutionary mode in New Zealand Mollusca

Michael Gemmell, Mary Morgan-Richards, Steve Trewick and Simon Hills
Massey University
Email: M.R.Gemmell@massey.ac.nz

The fossil record of New Zealand molluscs is an invaluable resource for exploring the process and patterns of evolution. Eldridge and Gould made use of similar fossil records to formulate their Punctuated Equilibria (PE) model. PE makes a direct link between geologically rapid morphological changes and speciation and provides testable predictions about evolution. This project looks to combine the latest morphometric techniques analysing extant and fossil molluscs with genetic analysis of extant species to test the mode of evolution. Genetic data will be obtained through next generation sequencing and analysed to provide information about population structure and infer molecular phylogenies. Morphometric analysis of modern and fossil shells using landmarks, procrustes superimposition and fourier analysis will provide information about the morphospace inhabited by the focal species.

Species in the genus *Amalda*, common near shore carnivorous neogastropod molluscs, will be one of the focal groups of this investigation. Using specimens collected from around New Zealand detailed population level analysis will be performed. Combining morphometric and genetic methods will provide information about the amount of variation within extant species. When compared with analysis of the fossil record some of the predictions of PE can be tested providing more detailed understanding of evolution and the role of cladogenesis in rapid morphological evolution. This will provide a framework on which to further interpret the fossil record and provide an insight into the evolution of New Zealand's biota.

Insect Affairs: An investigation into possible hybridisation on Banks Peninsula

Rachel van Heugten¹, Dr Marie Hale¹, Dr Roddy Hale², Mike Bowie²

¹University of Canterbury, ²Lincoln University
Email: rav17@uclive.ac.nz

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*. A previous genetics study found evidence of hybridisation between these two species. However, conclusions made by this study were likely limited by its small sample size. To further assess the risk hybridisation poses to the conservation of these species, a larger genetic study was undertaken. With hybridisation between *H. ricta* and *H. femorata* previously hypothesized to be a rare event, modelling of likely sympatric zones was undertaken to optimize the sampling effort. The results of genetic analysis on the resulting samples were consistent with the previous study, in that they suggest hybridisation does occur but is fairly rare. To help determine what processes are maintaining the distinction between the two species, the current study has expanded to incorporate observations of mating behaviour and egg hatching experiments. As with the genetic analyses, a limited mating behaviour study was previously attempted. This study concluded that male *H. ricta* will respond to female *H. femorata* and *H. ricta* in a similar manner. Preliminary results of the current study are consistent with this finding but there appears to be variation in how male *H. femorata* respond to female *H. ricta*.

East Cape, marine biogeographic barrier or transition zone?

Simon Hills
Massey University
Email: s.f.hills@massey.ac.nz

The East Cape of New Zealand an important region when assessing marine biogeography. It has traditionally been recognised as the boundary between the Auporian and Cookian bio-provinces, based on species composition differences in communities from the north-west verses communities from the south-east. However, examination of the population genetic structure of various marine species have provided mixed results regarding the East Cape as a barrier to gene flow. Important ecological transitions occur in the region, such as current regime and rock strata, but the effect of these on species and population structure remains unclear. Using marine molluscs I examine the species occurrence and the population genetics of select species to assess the biogeographic patterns seen at the community and population levels around the local area of the East Cape. Initial species occurrence results indicate that, with a few exceptions, there is little variation in the molluscan assemblage around the East Cape. Population genetics results, including a pilot study using ddRAD high-throughput sequencing indicates no barriers to gene flow in sampled species.

Coastal marine connectivity of the grey mullet (*Mugil cephalus*) using microsatellite and mitochondrial DNA markers.

Balam Jimenez Brito

Victoria University of Wellington

E-mail: Balam.Jimenez@vuw.ac.nz

Mugil cephalus is a cosmopolitan tropical, sub-tropical species world-wide distributed and in New Zealand it is typically found in the area GMU1. It is a euryhaline species and it can tolerate a wide range of dissolved oxygen levels; spawns at sea during the summer and its larvae move into harbours and estuaries. The vagility of *M. cephalus* is limited across open oceans and highly divergent mitochondrial DNA lineages have been reported at different locations all over the world; nowadays, it is not clear whether *M. cephalus* is a species complex or comprised of highly genetically structured populations. Moreover, grey mullet has a long history of supporting local fisheries since pre-European Māori and for management purposes grey mullet stock is considered as two sub-stocks (east coast and west coast). Also, it has been an increase amount of awareness about the sustainability of commercial fisheries because of high levels of exploitation and it is a growing concern about the effects of intensive land use on the coastal marine environment such as harbours and estuaries.

The aim of this research project is to determine the population genetic structure of *Mugil cephalus* in New Zealand waters. Use mitochondrial DNA sequencing to identify lineages; develop microsatellite DNA markers and use them to determine the level of genetic variation and differentiation within and among populations; and, compare the levels of variation and relatedness of a sample of juveniles taken in one season to the adult populations and estimate levels of reproductive success at a site.

Phylogeography of the alpine weta (*Hemideina maori*) in relation to melanism and its physiology.

Keith King

University of Otago

Email: keith.king.gev@gmail.com

A phylogeographic study of *Hemideina maori* was performed using mtDNA and nuclear sequences. Analysis of *cox1* from 23 sites around South Island found nine regions with mostly reciprocally monophyletic, deeply differentiated lineages. The results support an earlier model of either alpine radiation or localized refugia rather than a “beech gap” model or a model that allows for recent environmental changes (i.e global warming/predation). As seen in previous studies, *H. maori* formed a paraphyletic group in relation to *H. ricta*, the Banks Peninsula tree weta, suggesting a recent divergence of this species.

H. maori has melanic morphs that were collected from seven sites. The relationship among these individuals was examined with melanic weta not found to be reciprocally monophyletic, suggesting independent evolution of melanism in different regions. This suggests that there may be a selective advantage to melanism, potentially driven by local ecology or environmental factors that have yet to be determined.

Two such factors associated with melanism in other species (thermal melanism and decreased desiccation) were tested. Melanic individuals were found to both heat significantly quicker and lose significantly less cuticular water than non-melanic counterparts. The altitudinal distribution of *H. maori* morphs, however, suggests these traits may have a correlated or pleiotropic effect in *H. maori*, with these physiological characteristics secondary to, or consequences of, other unknown factors.

Sympatry and diversity among New Zealand Velvet Worms

Emily Koot, Steve Trewick
Massey University
Email: fast38_emily@hotmail.com

Peripatus, of the Phylum Onychophora, are soft bodied, velvety textured invertebrates that commonly inhabit decaying logs and leaf litter on the forest floor. Hutton (1876) described *Peripatoides novaezealandiae* on specimens (but no type) from three locations (Wellington, Nelson, Auckland), which he characterized as having 15 pairs of legs. Dendy (1894) later described *P. suteri* (Taranaki), as being distinguished by having 16 pairs of legs. In 1998, following initial analysis of allozyme data by Tait & Briscoe (1995), Trewick split *P. novaezealandiae* into five different lineages, citing genetic difference and lack of gene flow between these lineages in sympatry. Sympatry has been documented among five species in this genus in the North Island. Current data from allozymes and mtDNA sequence indicate little if any gene flow among lineages, even where they occur in microsympatry. Modern models of sympatric speciation predict that some traits/genes of insipient taxa are under intense selection so independent evolution could proceed despite some gene flow. Sympatric species could however also result 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 morphological differences.

Tree weta hybrids

Tarsha McKean, Steve Trewick, Mary Morgan-Richards
Massey University
Email: N.McKean@massey.ac.nz

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 confirm hybridisation between *H. thoracica* & *H. crassidens* where they exist in sympatry and 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 (cytogenetics, microsatellites, nuclear and mtDNA sequencing) are used to look for evidence of hybridization and introgression.

Cospeciation of birds and lice

Mary Morgan-Richards, Gaia O'hare, Juan Carlos Garcia Ramirez, Steve Trewick

Massey University

Email: M.Morgan-Richards@massey.ac.nz

When host populations are isolated they inflict isolation on all of their parasite species that are poor dispersers. As lice are generally transmitted vertically (from parents to chicks in the nest), one expects the evolution of these parasites to be influenced by their hosts. Cospeciation of hosts and parasites predicts a close match between the phylogeny of host and the phylogeny of parasite. We test this hypothesis using New Zealand birds (Rails) and chewing lice from the family Philopteridae. Phylogenetic relationships are inferred using mtDNA sequence (COI) data. Differences in both generation time and population size are likely to result in differences in the level of standing genetic diversity within bird and lice populations, but how this impacts on rate of molecular evolution is less clear.

Godwit genomics and migration

Parody-Merino, A.M., Prosdocimi, F., Battley, P.F., Fidler, A.

Cawthron Institute

Email: Angela.Merino@cawthron.org.nz

Bird migration is perhaps one of the most extraordinary behaviours observed in nature, and has intrigued humans for millennia. Bar-tailed godwits (*Limosa lapponica baueri*) are extraordinary avian migrants performing the longest recorded non-stop flight from Alaska to New Zealand across the Pacific

Ocean (11,690 km). They migrate back to Alaska via Asia, leaving New Zealand from early March to early April. This month-long departure span reflects a latitudinal gradient on the breeding grounds, with southern-breeders leaving earlier than northern breeders. Individual godwits, however, have proven remarkably consistent year-to-year in when they leave New Zealand on migration. The control of migration timing is believed to involve changes in daylength, but that in itself cannot explain how individual birds at given site maintain consistency different schedules, therefore, a significant genetic component may be implicated. My PhD will look for associations between migration departure times and genotypic (and epigenetic) variation in candidate genes. Currently, the genomic sequence of a female godwit is being assembled and annotated. Building on this resource I will; 1) analyse population structuring in N.Z. departing godwits using a putatively non-functional genetic variants (i.e. microsatellites); 2) look for association between individual migration departure times and sequence variation/genotype (and epigenetic variation) at a number of candidate genes. My PhD thesis aims to better understand and characterize underlying mechanisms linking inherited genetic/epigenetic variation and a quantifiable aspect of avian migration departure timing.

Host switch in the red algae parasite *Pterocladophila hemisphaerica*

Maren Preuss

Victoria University of Wellington

Email: preussmare@myvuw.ac.nz

Red algal parasites are common within in red algae and they are often closely related to their host. Red algal parasites can switch hosts and their development is unique. There are only three red algal parasites described in New Zealand and those are based on morphological characteristics. This study gives the first phylogenetic insight of the relationship from a red algae parasite to its host in New Zealand. The parasite *Pterocladophila hemisphaerica* is grouped taxonomically, based on morphology, in the order Gracilariales and parasitises *Pterocladia lucida* in the order Gelidiales. We used molecular marker to reveal the relationships of the parasite to its host, and if host switches might have occurred. Nuclear DNA (SSU rRNA, LSU rRNA), mitochondrial (COI) and plastid regions (rbcL-rbcS spacer) from the parasite were sequenced and phylogenetic analysis performed. The results suggest that mitochondrial, nuclear and chloroplast regions have different origin and reflect a complex evolutionary history. The nuclear genes suggest that the parasite *Pterocladophila hemisphaerica* is not grouped within in the Gelidiales. The mitochondrial marker groups the parasite with *Pterocladella*, another species in the order Gelidiales and the chloroplast marker are identical between parasite and host. The parasite *Pterocladophila hemisphaerica* probably evolved from a different red algae order and switched hosts from *Pterocladella* and later to *Pterocladia lucida*. Those results are the first genetic data, which show multiple host switching in red algae parasites as well as phylogenetic relationship in red algae parasites in New Zealand.

Molecular adaptation mechanisms in the Antarctic nematode *Panagrolaimus davidi*

Seybold A, Marshall CJ, Wharton DA, Dearden P.

Otago University

Email: seyan398@student.otago.ac.nz

The Antarctic nematode *Panagrolaimus davidi* tolerates desiccation and freezing and is the only animal known to survive intracellular ice formation. Although physiological mechanisms of this extreme adaptation are partly revealed, mechanisms on the molecular level remain largely unknown. Recent studies identified genes up-regulated during desiccation such as late embryogenesis abundant proteins, heat shock proteins, antioxidants and trehalose genes. Furthermore, the presence of ice-active proteins has been suggested by the observation of recrystallization inhibition and hexagonal ice crystal shape. To identify the genes involved in this extreme adaptation we are currently testing high throughput RNAi techniques, such as feeding and soaking. To investigate whether *P. davidi* is accessible to RNAi via feeding, the embryonic lethal genes Pd-rps-2 and Pd-dhc as well as the blister gene Pd-duox-42 were tested and the expression level was confirmed by quantitative PCR. While Pd-rps-2 treated samples showed a significant increased lethality compared to the control samples, there was no significant difference at the expression level. To investigate whether *P. davidi* is more accessible to RNAi via soaking, neurostimulants and desiccation supported soaking techniques are currently tested.

Prion evolution

Lara Shepherd, Alan Tennyson, Colin Miskelly, Sarah Jamieson, Susan Waugh

Museum of New Zealand Te Papa Tongarewa

Email: Lara.Shepherd@tepapa.govt.nz

Prions (*Pachyptila*) are small seabirds that are likely to be the most abundant birds in the Southern Oceans. Six species are currently recognized but there has been considerable past debate and confusion about their relationships and taxonomy. Prions came to the attention of the New Zealand public during a winter storm in 2011 when several hundred thousand prions were wrecked on the New Zealand mainland. This wreck largely comprised broad-billed prions and more birds were wrecked than the entire species estimate, highlighting the paucity of knowledge about this species.

Our aims are to resolve the relationships between the prion species and breeding colonies and to determine from which colonies the wrecked prions originate. Our initial DNA sequencing indicates some complex and unexpected relationships within prions.

Determining the population structure of *Polyprion americanus* (Sea bass) and *Polyprion oxygeneios* (Hapuku) using microsatellite and mitochondrial DNA markers

Natalie Stewart

Victoria University of Wellington

Email: Natalie.Stewart@vuw.ac.nz

Polyprion support both commercial and recreational fisheries throughout the Southern hemisphere, and although catches in South Western Australia are relatively low, *P.oxygeneios* is listed as an indicator species for the South Coast demersal fisheries. The genus *Polyprion* is currently represented by two species; *P.americanus*, which is widely distributed in both the Northern and Southern hemisphere, and *P.oxygeneios*, limited to the southern hemisphere. Recent data has suggested however that *Polyprion* are being overfished in Southern Australia and there is a need to understand their stock structure. The aim of my thesis research is to use microsatellite and mitochondrial DNA markers to determine the levels of genetic variation and differentiation of both *Polyprion spp.* in South Western Australia and compare them to samples collected from a number of sites in the Southern hemisphere, including New Zealand. I will be describing some preliminary results and compare them to genetic data that has previously been reported from New Zealand sites.

Giant Weta Genomics

Victoria Twort¹²³, Richard Newcomb²³⁴, Howard Ross²³, and Thomas Buckley¹²³

¹Landcare Research, ²University of Auckland, ³Allan Wilson Centre for Molecular Ecology and Evolution, ⁴The New Zealand Institute for Plant and Food Research Ltd

Email: TwortV@landcareresearch.co.nz

Giant Weta are among the largest extant insects on earth and are an iconic part of the New Zealand fauna. However, a number of these species are highly endangered, with 10 of the 11 species being subject to conservation efforts. The Poor Knights Giant Weta (*Deinacrida fallai*, Orthoptera) is one such species, and is restricted to a small offshore island. The genome of this species is large, with current estimates indicating that it is approximately 10 GB in size. We are using Illumina technology to sequence the genome of this endemic New Zealand insect. Our current draft assembly has been obtained from a mixture of paired-end libraries, with additional insert sizes and mate pair libraries currently being sequenced. RNA-seq data has also been obtained from various tissues, to aid genome annotation and candidate gene identification, with the aim of investigating various phenotypic characters, including those involved in reproduction and chemosensing. The draft genome along with comparative SNP and RNA-seq data will be used to investigate a range of evolutionary questions and conservation genetics issues in this and related weta species. The current state of the draft genome

and RNA-seq data will be discussed.

Reconstructing the Genetic Legacy of Cook's Petrels (*Pterodroma cookii*).

Ayla van Loenen, Tammy Steeves
University of Canterbury
Email: alv15@uclive.ac.nz

Cook's petrel (*Pterodroma cookii*) is a threatened, migratory seabird endemic to New Zealand. Cook's petrel previously bred throughout mainland New Zealand, but today it breeds exclusively at the northern and southern extremes of its historic distribution (Little Barrier Island and Codfish Island, respectively). Comparative studies have shown significant behavioural, morphological, and ecological differences between the two extant populations. Mitochondrial DNA (mtDNA) data suggests that they are genetically distinct. However, because mtDNA is maternally inherited, it solely reflects the evolutionary patterns of females. In addition, the genetic composition of extinct populations and the taxonomic status of the two extant populations remain unknown. Here, I provide an additional measure of genetic differentiation between the two extant Cook's petrel populations using biparentally inherited nuclear intron sequence data. I also investigated the genetic structure among extant and extinct populations of Cook's petrel by including mitochondrial and nuclear sequence data obtained from historic and ancient samples. The combined mitochondrial and nuclear data indicates significant genetic structure between the two extant populations. The genetic data from this study, combined with previous comparative studies, suggest that birds on Little Barrier Island and Codfish Island should be considered distinct sub-species: *P. cookii cookii* and *P. cookii orientalis*, respectively.

Phylogenetics of three bumblebee RNA viruses

Felix Vaux¹, Lena Wilfert²
¹ Massey University; ² University of Exeter
Email: F.Vaux@massey.ac.nz

Many pollinator species have undergone a global population decline over the last few decades and the frequency of colony collapse events is on the increase in bee livestock. The economic contribution of bees is valued conservatively at 100 billion USD, and a significant diversity of plants rely on the existence of both specific and generalist pollinators. Obviously therefore the decline is of serious concern but the root cause remains elusive.

RNA viruses are linked to the decline in many species but the evolutionary history of the diseases is poorly understood. We investigated the phylogenetic distribution of three viruses (ABPV, DWV, BQCV) among multiple hosts, and conducted a phylodynamic (phylogenetics applied to epidemiology) study of the transmission of ABPV between the buff-tailed bumblebee (*Bombus*

terrestris) and the western honeybee (*Apis mellifera*). We calculated the first evolutionary rate estimate for a pollinator RNA virus and found that ABPV has a fast evolutionary rate, equivalent to foot-and-mouth disease, in *B. terrestris*. We estimated that ABPV has been transmitted from *A. mellifera* to *B. terrestris* on multiple occasions between 96 and 141 years ago, with indicative data suggesting similar, recent transmission events in DWV and BQCV. Overall this implies recent disease emergence in most species, although the ultimate origin of the diseases requires further sampling. For conservation, mutational escape and the apparent absence of significant barriers to horizontal transmission are likely to make vaccines ineffective. An appropriate aim to tackle pollinator decline presently is to reduce opportunities for transmission between commercial and wild populations.

DNA Barcoding of New Zealand Freshwater Cyclopoid Copepods

Nathan Watson, Ian Hogg, Ian Duggan
University of Waikato
Email: watstar14@gmail.com

New Zealand freshwater cyclopoid copepods have been largely understudied and several of the species described from New Zealand have traditionally been identified as cosmopolitan. This is surprising given New Zealand's significant geographic isolation and wide variety of endemic fauna. Furthermore, the number of cyclopoid species described from New Zealand is remarkably low suggesting that diversity is likely to be underestimated. Here, we use variation in mitochondrial cytochrome c oxidase subunit 1 (COI) gene sequences (DNA barcodes) to assess the diversity of the New Zealand freshwater cyclopoid copepods (Crustacea). Specifically, we used recently developed clustering algorithms (e.g. BINs) and the 'barcode gap' to assess intraspecific and interspecific variation. Preliminary results suggest that DNA barcodes are useful for distinguishing between the currently described species of New Zealand cyclopoids with interspecific variation of the COI gene being significantly higher than intraspecific variation. Further, initial data suggest that there are at least two cryptic species of New Zealand cyclopoids, indistinguishable using traditional morphological characteristics.

The role of islands in divergent evolution: driven by isolation and lack of gene flow? A case study in the tui, *Prosthemadera novaeseelandiae*

Sarah Wells⁺, Weihong Ji⁺, James Dale⁺, and Dianne Gleeson^{*}
⁺ Massey University; ^{*} University of Canberra and Landcare Research
Email: S.J.Wells@massey.ac.nz

Islands play an important role in speciation and, accordingly, the majority of endemic species occur on islands. However, the traditional view of strict biogeographic separation with no gene flow occurring during species formation has been challenged, and divergent evolution is now also thought to

occur in the face of ongoing gene flow. In this study we investigate phylogeography and population genetics in the New Zealand tui, *Prosthemadera novaeseelandiae*, focussing on the genetic status of the remote populations of Raoul and Chatham Islands. Little is known of these populations, although the Chatham Island tui is purported to be a separate subspecies. Using mitochondrial DNA (mtDNA) sequencing and microsatellite genotyping my research investigates how differentiated these populations are from mainland populations, and whether there is ongoing migration that may (or may not) preclude their subspecies status. The mainland showed weak population structure that was not explained by isolation-by-distance, and exhibits no North-South divide; although significant differentiation in Maud and Tiritiri Matangi Islands was observed. Mainland genetic structure appears shallow and most populations have undergone a recent demographic expansion after the last glacial maximum. F-statistics and AMOVA indicate significant differentiation and structure between Raoul and Chatham Islands and the mainland populations. Preliminary results from STRUCTURE and IMA, however, appear in conflict and are discussed. Our findings provide the first genetic investigation into tui populations and will contribute towards understanding the role of islands in species formation. Additionally, this study will help to delimit management units for improved conservation of this unique Kiwi icon.

Molecular identification of zooplankton for aquatic environmental monitoring

Steve Woods¹, Ian Hogg¹, Jonathan Banks^{1,2}, Ian Duggan¹, Nathan Watson¹, Gemma Collins¹, Clare Beet¹

¹University of Waikato; ²Cawthron Institute

Email: steve.woods00@gmail.com

Zooplankton communities are commonly used to assess water quality. However, morphological assessment of zooplankton for environmental assessments requires a high level of taxonomic expertise and is time consuming. Here, our aim was to use DNA barcoding to expedite the routine monitoring of zooplankton communities. We are testing different gene regions (COI, 28S, ITS) to find a suitably short and easily amplified fragment that will reliably identify species using current next generation sequencing platforms. To date, reference libraries have been developed for New Zealand freshwater rotifers, copepods and cladocerans. We now aim to characterise aquatic communities using DNA from environmental samples with next-generation sequencing approaches such as the Illumina platform. This approach can then be used to rapidly assess zooplankton diversity in aquatic environments as well as to monitor water quality.

Population Genetics of Spiny Rock Lobster-*Panulirus ornatus*

Bhargavi Yellapu, Shane Lavery, Andrew Jeffs

University of Auckland

Email: byel849@aucklanduni.ac.nz

Panulirus ornatus is a highly valued tropical rock lobster, not only for its high demand in fisheries, but also for its opportunities for aquaculture. These lobsters endure a long oceanic larval phase, drifting in the open ocean for up to 6 months, which provides potential for large scale dispersal and high levels of gene flow between the populations. In this study nearly 300 samples have so far been acquired covering the entire species distribution to investigate the genetic diversity and connectivity among the populations. Mitochondrial control region and highly polymorphic microsatellite markers are being used to estimate the genetic diversity. Despite expectations of panmixia, analysis using MtDNA sequences (500bp) have shown significant population structure among the West Indian Ocean (WIO), East Indian Ocean (EIO) and Pacific Ocean (PO) samples (overall $F_{ST} = 0.11$, $p < 0.00001$). Tajima's D and Fu's F test values suggest population expansion. This information will be useful not only for a better theoretical understanding of the species' evolutionary history and current population demography, but also for practical use in fishery management. Further knowledge of genetically distinct populations provides valuable resources for assessing different traits within the species that can be cross-bred in the future.