

AWC Projects 2012

Theme: 2. **Biodiversity & Human Impacts**
Activity: A. Biodiversity knowledge & strategy for New Zealand

Investigator	Project	Stakeholders
Daugherty	<p>Conservation Genomics of Kiwis Team members: Dr Kristina Ramstad, Helen Taylor (PhD) This project describes conservation genomics of New Zealand's rarest kiwis, working in close collaboration with the Department of Conservation.</p>	
Daugherty	<p>Genomics of Tuatara Team Member: Dr Hilary Miller This project undertakes a genomic assessment of selected portions of the genome of tuatara, especially MHC and other functionally related components.</p>	
Nelson	<p>Sex determination and impacts of climate change on tuatara Team members: (Andrew Douglas (PhD student), Lindsay Mickelson (PhD student), Ilse Corkery (PhD student), Kristine Grayson (PDF), David Towns (DOC), Alison Cree (U. Otago), Nicola Mitchell (U. Western Australia), Darren Day (VUW)). This research project focuses on the thermal biology of tuatara and implications of climate change for sex determination and sex ratios of natural, translocated and recovering populations of tuatara. Studies include ecological investigations, incubation experiments, developmental staging, and niche modeling.</p>	<ul style="list-style-type: none"> • Iwi in general and specifically communities in areas we have on-going field work • Department of Conservation • Colleagues working in related fields and research students
Nelson	<p>Ecological relationships of NZ wildlife Team Members: (Ilse Corkery (PhD student), Anna Carter (PhD student), Alexei Drummond (AWC), Jo Hoare (DOC), James Russell (U. Auckland), Ben Bell (VUW), Stephen Hartley (VUW)). For this project, we are (a) investigating the ecological relationship between burrowing seabirds and tuatara, including whether tuatara gain thermal benefits from sharing a burrow with a seabird that could result in fitness advantages (Ilse Corkery); and (b) Investigating impacts of climate change on community interactions on Little Barrier Island, as part of the Model Ecosystem Strategic Initiative (Anna Carter).</p>	<ul style="list-style-type: none"> • Iwi in general and specifically communities in areas we have on-going field work • Department of Conservation • Colleagues working in related fields and research students
Waters	<p>Rafting communities in the West Wind Drift Team members: Dr Raisa Nikula, Dr Ceridwen Fraser, Chris Garden (PhD student), Jenny Trickey, Laura Bussolini (MSc students), Dr Kirsten Donald, Prof Hamish Spencer, Prof Jon Waters This Marsden-funded study uses molecular markers to investigate the role of kelp-rafting in promoting trans-oceanic gene flow and connectivity between otherwise isolated marine habitats. Our recent work has demonstrated such rafting-connectivity over vast geographic scales [http://news.sciencemag.org/sciencenow/2010/09/kelp-raft-carries-marine-stowawa.html]. We are now comparing levels of gene flow in kelp-dwelling (rafting) versus rock-dwelling (non-rafting) marine invertebrates.</p>	<ul style="list-style-type: none"> • Ecologists studying biodiversity and biogeographic connectivity (NZ and worldwide) • Invertebrate taxonomists and museum researchers • Oceanographic researchers (NZ and worldwide) • Local communities connected to coastal NZ (e.g. recent research was highlighted on front page of Otago Daily Times)
Waters	<p>An icier Ice Age: evolutionary impacts of climate change in the Southern Hemisphere Team members: Dr Ceridwen Fraser, Prof Hamish Spencer, Prof Jon Waters Our recent genetic analyses of bull-kelp indicate that Southern Hemisphere sea-ice may have been considerably more extensive during the Last Glacial Maximum than previously thought [http://www.reuters.com/article/idUSTRE51A2LL20090211]. We are now testing this hypothesis further by assessing signatures of postglacial recolonization across a variety of circum-subantarctic seaweed species.</p>	<ul style="list-style-type: none"> • Climate change researchers (NZ and worldwide) • Ecologists studying biodiversity and biogeographic connectivity (NZ and worldwide) • Subantarctic researchers
Drummond	<p>Genomics for Ecosystem Conservation Team Members: Alexei Drummond, Thomas Buckley, Richard Newcomb, Nicola Nelson, Craig Millar, Nigel French, Mark Stevens, James Russell, Matt Renner, DOC collaborators - Jo Hoare, Dave Towns & Iwi collaborators Modelled on an innovative international project in Tahiti and led by Alexei Drummond, this project undertakes a comprehensive analysis of the biological and physical components of a model New Zealand ecosystem, defining the niches of key species in the systems and the environmental variables key to their survival. Our primary study site is Hauturu/Little Barrier Island, one of New Zealand's most significant protected areas. As the project develops, selected other North Island sites will be</p>	<ul style="list-style-type: none"> • Iwi in general and specifically communities in areas we have on-going field work, Ngati Manuhiri • Department of Conservation • Auckland Council • Conservation management agencies internationally • Colleagues working in related fields and research students

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	<p>included following consultation with DoC and iwi. Over half of AWC investigators are working on this initiative. Key anticipated outcomes include AWC support for DoC in development of their Natural Heritage Management System, a comprehensive database and repository for environmental information, and baseline information to better assess impacts of introduced species.</p>	
Millar	<p>DNA barcoding the birds of New Zealand and the Antarctic Team members: Dr Craig Millar, Dr Howard Ross, Prof David Lambert, Prof Allan Baker, Ms Selina Patel. DNA barcoding is an attempt to identify species based on a short region of the mitochondrial genome. This system has the potential to revolutionize the study of biodiversity and systematics and has been successfully applied to a very large number of continental Northern Hemisphere avian species. However, the effectiveness of DNA barcoding to reliably identify Southern Hemisphere avian species that have evolved and speciated rapidly on islands remains to be established. We aim to test this system by creating a comprehensive DNA based identification system for the birds of New Zealand and the Antarctic. In addition the DNA database can be used to investigate a broad range of issues of importance to New Zealand, including improved conservation management, the rapid and effective surveillance of bird species being transported across our borders and the identification of the species involved in bird strikes on aircraft.</p>	<ul style="list-style-type: none"> • New Zealand Department of Conservation • New Zealand Civil Aviation Authority • Air New Zealand • National and international scientific community
Millar	<p>The moa genome: a targeted approach Team members: Dr Craig Millar, Prof David Lambert, Dr Leon Huynen, Dr Craig Smith, Ms Selina Patel The extinct moa of New Zealand is an iconic group that possessed many unique phenotypes. Some moa species were the largest birds ever to have lived, while others were relatively small. In addition moa are the only species of birds that had no wings. Using new technologies for sequencing ancient DNA, we will use a targeted approach to recover the moa genetic networks that controlled growth and forelimb development. We are isolating and sequencing these genetic networks using new DNA capture methods in combination with next-generation sequencing. This approach will allow us to identify any genes that contain potential functional variants that are responsible for the extreme size and winglessness seen in moa. In so doing we will gain a better understanding of genetic changes that have resulted in the evolution of these unique animals.</p>	<ul style="list-style-type: none"> • National and international scientific community
Newcomb	<p>The molecular basis of speciation in New Zealand endemic leafroller moths Team members: Jerome Albre (Postdoc), Leah Tooman (Research Associate), Bernd Steinwender (PhD student), Thomas Buckley (PI), Richard Newcomb (PI) How new species are formed is still a major question in evolutionary and conservation biology. We are studying a recently evolved complex of New Zealand endemic leafroller moths comprising the genera <i>Ctenopseustis</i> and <i>Planotortrix</i>, as much is known regarding their mating system such as their sex pheromones. Using this system we are asking what molecular changes are responsible for the evolution of new species and what is driving this process through focusing on the genetic basis of changes in sex pheromone biosynthesis in the female by desaturase genes and pheromone recognition in male antennae by pheromone receptors.</p>	<ul style="list-style-type: none"> • Scientific Community
Ritchie	<p>Multi-species Analysis to Coastal Marine Connectivity Team Members: Danielle Hannah, Heather Constable and Peter Ritchie The overall aim of this research is to determine patterns of regional connectivity in a range of New Zealand coastal marine organisms to define the geographic units of genetic diversity for protection and the dispersal processes that maintain this diversity. We are determining the genetic structure within populations of at least two coastal marine taxa using microsatellite markers, particularly focusing on organisms found in estuarine and soft substrate habitats and attempting to survey a full range of geographic locations around the New Zealand coastline. We aim to measure levels of connectivity among populations of the study organisms and the factors that are influencing these patterns, for example the life history traits of the organisms and the physical environment they encounter. We will compare the results of this study to previous studies and look for common patterns of connectivity, particularly</p>	

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	with regards to previously identified barriers to dispersal and biogeographic demarcations in order to make recommendations about how the observed patterns of connectivity can be used as part of a biodiversity management strategy. The project is in collaboration with Jonathan Gardner, James Bell and Joe Zuccarello at VUW, and funded by the Ministry of Fisheries Biodiversity Research Programme.	
Spencer	I am working with research fellow, Dr Martyn Kennedy, on the rate of evolution of slug formation in the endemic carnivorous semi-slug, <i>Schizoglossa</i> . Martyn and I are also looking at genetic variation within the world's only bioluminescent freshwater mollusc, the endemic limpet <i>Latia</i> . Dr Kirsten Donald is leading a study on the biogeography of the Australasian whelk genus <i>Cominella</i> , as well as the parasite fauna its New Zealand species harbour.	<ul style="list-style-type: none"> • DoC • Te Papa • National & international Scientific community • Amateur shell collectors & naturalists

Theme: 2. **Biodiversity & Human Impacts**
Activity: B. Genetic studies on human and wildlife health in a changing environment

Investigator	Project	Stakeholders
Ritchie	The Population Genetic Structure of New Zealand Blue Cod (<i>Parapercis colias</i>) Stocks Team members: Hayden Smith and Peter Ritchie Blue cod is endemic to New Zealand and is abundant throughout the coastal waters of New Zealand, supporting important commercial, recreational, and customary fisheries. As a result of sustained fishing pressure populations recently experienced a sharp decline in abundance. For example, the inner Marlborough Sounds have been closed since October 2008. The outstanding scientific question is whether blue cod are one large intermixing stock, or there are different genetic stocks in different part of the inshore New Zealand environment. We are developing new genetic markers for Blue Cod with the aim of determining the phylogeographic and population genetic structure of the New Zealand-wide stock. The development of microsatellite markers for Blue Cod is a collaboration with Craig Millar at the University of Auckland.	
Ross	Estimation of the relationships and dates of divergence among Australo-Papuan species of rats (Robins, J. H., P. A. McLenachan, M. J. Phillips, B. J. McComish, E. Matisoo-Smith, and H. A. Ross. 2010. Evolutionary relationships and divergence times among the native rats of Australia. BMC Evolutionary Biology 10:375.)	
Waters	Ancient DNA analysis of New Zealand sea-lions Team members: Catherine Collins (PhD Student), Dr Michael Knapp (Postdoc), Prof Lisa Matisoo-Smith, Prof Jon Waters Recent DNA studies of <i>Megadyptes</i> penguin subfossils from South Island have revealed unexpected prehistoric extinction and recolonization events [http://news.bbc.co.uk/2/hi/7735500.stm]. We hypothesise that similar extinction/replacement events may apply to other iconic coastal vertebrates, such as the New Zealand sea-lion <i>Phocartos hookeri</i> . By studying ancient DNA of such species, we hope to better understand the biological consequences of human settlement in coastal New Zealand.	<ul style="list-style-type: none"> • NZ archaeologists • Museum researchers • Dept of Conservation • Ngai Tahu
Buckley	Phylogeny of the stick insects Team members: Thomas Buckley We are building a data set of nuclear and mitochondrial genes from stick insects sampled around the world with an emphasis on the Australasian region. These data are being used to test the higher classification of the stick insects, perform studies of character evolution and understand the biogeography of this insect order. We are particularly interested in the evolution of stick insects on island systems in Australasia and processes of convergent evolution.	<ul style="list-style-type: none"> • Department of Conservation (Primary)
Matisoo-Smith	Ancient DNA of Pacific Tupuna Team members: Post Docs – Michael Knapp (AWC funded) and Ann Horsburgh; PhD students: Stefan Prost (AWC funded). Using techniques developed in Theme 1, Lisa and AWC post-doc Michael Knapp have been undertaking the ancient DNA analysis of a number of ancient Pacific Island populations (see below) in order to finally identify the genetic makeup and origins of ancient Pacific peoples. AWC PhD student, Stefan Prost, will incorporate these data with data from modern Pacific populations collected as part of the Genographic project (see below).	<ul style="list-style-type: none"> • The descendant communities in NZ and throughout the Pacific • National museums in the countries from which we obtain samples • Other researchers interested in the prehistory and settlement of the Pacific • General public

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	<p>Projects currently underway:</p> <ul style="list-style-type: none"> Wairau Bar, New Zealand-The origins of the first New Zealanders. In conjunction with Rangitane and colleagues from the University of Otago. Teouma, Vanuatu – origins of the earliest Lapita colonists in Remote Oceania. In conjunction with the Vanuatu National Museum and Art Gallery and colleagues from the University of Otago and the Australian National University. Watom, New Britain, PNG – genetic interaction in Near Oceanic Lapita population. In conjunction with the National Museum and Art Gallery of Papua New Guinea and colleagues from the University of Otago. Papua New Guinea South Coast - in conjunction with the National Museum and Art Gallery of Papua New Guinea and colleagues from Monash University. New Caledonia – Genetic Change through Time. In conjunction with colleagues from the New Caledonia Institute of Archaeology and the University of Paris. Chile – Identifying Polynesian contacts in South America. This is a Marsden project (Matisoo-Smith, Knapp and colleagues from Chile, Dr Andrea Seelenfreund and Jose Miguel Ramirez) focused on studying ancient DNA of Polynesian looking human remains from Isla Mocha, Chile. 	
Matisoo-Smith	<p>National Geographic's Genographic Project Team members: Post Docs – Michael Knapp (AWC funded), Ann Horsburgh and Andrew Clarke; PhD students: Stefan Prost (AWC funded), Karen Greig We are responsible for sampling the Pacific region as part of the Genographic project, which is sponsored by National Geographic, IBM and the Waitt Family Foundation. This involves collecting DNA samples and analyzing mtDNA and Y chromosome markers from communities across the Pacific. Current fieldwork includes work in New Guinea, Tokelau and French Polynesia. We are working with Dr John Mitchell, from LaTrobe University in Melbourne and Prof Pascal Murail, from the University of Bordeaux on this project. For more information on the Genographic project see: https://genographic.nationalgeographic.com</p>	<ul style="list-style-type: none"> Participating communities across the Pacific including NZ National Geographic Colleagues interested in human dispersals and Pacific prehistory
Matisoo-Smith	<p>Origins and genetic histories of New Zealand and Pacific plants and animals. Team members: Post Docs – Michael Knapp (AWC funded) and Ann Horsburgh; PhD students: Stefan Prost (AWC funded), Karen Greig We have numerous projects assessing the origins and genetic histories of New Zealand and Pacific plants and animals including: Paper Mulberry (Matisoo-Smith), Dogs (Matisoo-Smith & PhD student Karen Greig), Rats (Matisoo-Smith, Horsburgh, Greig), Pigs (Matisoo-Smith, Horsburgh and Knapp), Chickens (Matisoo-Smith & former AWC PhD student Alice Storey, now at Univ of New England, Armidale, NSW, Australia) and NZ Native Coastal Fauna (Knapp, Matisoo-Smith and AWC PI Jon Waters).</p>	<ul style="list-style-type: none"> Dept of Conservation and other conservation organisations working in the Pacific Pacific Island communities Colleagues working in a range of fields including archaeology, biogeography, evolution
Spencer	<p>Prof. Jon Waters, postdoc Dr Raisa Nikula and I are studying long-distance dispersal in the invertebrate community of bull-kelp holdfasts.</p>	<ul style="list-style-type: none"> National & international Scientific community DoC Amateur naturalists

Theme: 2. **Biodiversity & Human Impacts**
Activity: C. Genetic studies on human and wildlife health in a changing environment

Investigator	Project	Stakeholders
Matisoo-Smith	<p>Identifying disease in ancient Pacific populations Team members: Post Docs – Michael Knapp (AWC funded) and Ann Horsburgh; PhD students: Stefan Prost (AWC funded). We are working with colleagues from the University of Otago to look at genetic markers of gout in ancient populations, and with colleagues from New Caledonia and Paris investigating the identification of treponemal disease in a pre-contact Kanak sample.</p>	<ul style="list-style-type: none"> Pacific Island communities Researchers focused on Pacific health Pacific archaeologists and prehistorians
Nelson	<p>Wildlife disease ecology Team members: (Danielle Middleton (PhD student), Nigel French (AWC), Paul Rainey (AWC), Anne LaFlamme (AWC Affiliate), Kate McInnes (DOC), Laryssa Howe (Massey U.), Brett Gartrell (Massey U.)). We are investigating the microbial diversity of NZ wildlife, including transmission, molecular epidemiology and potential</p>	<ul style="list-style-type: none"> Iwi in general and specifically communities in areas we have on-going field work Department of Conservation Other captive holders and/or agencies protecting wildlife Colleagues working in related fields and

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	impact of pathogens on natural populations. Specific areas of research include the ecology of salmonella in NZ wildlife, and patterns of distribution, prevalence and genetic diversity of microbes in natural versus translocated populations.	research students
Nelson	<p>Kiwi ecology and genomics</p> <p>Team members: (Helen Taylor (PhD student), Kristina Ramstad (AWC PDF), Hugh Robertson (DOC), Fred Allendorf (AWC, VUW, U. Montana)).</p> <p>In this project we are investigating the ecology, effects of inbreeding and population viability of Little Spotted kiwi, including implications for conservation management</p>	<ul style="list-style-type: none"> • Iwi in general and specifically communities in areas we have on-going field work • Department of Conservation • Other captive holders and/or agencies protecting wildlife • Colleagues working in related fields and research students
Rainey	<p>Evolutionary emergence of infectious disease</p> <p>Team members: Paul Rainey, Steve Ritchie (AWC post doc), Yeserin Yildirim (AWC student), Nigel French, Craig Millar</p> <p>Infectious disease – of people, animals, and plants – is a fact of life. Despite impressive developments in medicine and disease control, infectious disease remains a significant cause of death. New Zealand, like all nations, has a history of established infections, but epidemics (and non-epidemics) of new and old infectious diseases continue to arise. The causes of disease persistence and outbreaks are not clear, but there is increasing recognition that much infectious disease emerges from non-pathogenic strains (commensals) influenced by complex ecological and evolutionary relationships between microbe, host and the environment (particularly environmental impacts wrought by humans). As an island nation NZ needs to understand how disease emerges and is maintained over a regional scale. Using population genetic / genomic approaches we are undertaking studies concerned with: (i), the causes of tetrodotoxin production in sea slugs from coastal waters of NZ; (ii), the origins and evolutionary dynamics of NZ-specific strains of <i>Staphylococcus aureus</i>; (iii), the genetic structure and biogeography of <i>Vibrio</i> and (iv) the origins and evolution of the kiwifruit pathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> (PSA) in NZ</p>	<ul style="list-style-type: none"> • Cawthron Institute • Auckland Regional Council • Zespri International Ltd, Plant & Food Research, Dnature, Seeka, Green Growers Association
Spencer	Prof. Sir Peter Gluckman, several overseas collaborators and I are writing about genetic conflict and human health. I am also working on a project looking at the eugenics movement in New Zealand.	<ul style="list-style-type: none"> • Medical research community • NZ & international historians
French	<p>Population genetics and source tracking of pathogens associated with drinking water at Department of Conservation campgrounds</p> <p>Team members: Nigel French, Paul Rainey, Nicky Nelson</p> <p>The aims of this study are to identify which animals, domestic and wildlife, are contributing to the loading of faecal pathogens in drinking water at DOC campgrounds, and the nature of associated human health risks. We are examining bacterial and protozoan populations present in drinking water at DOC campgrounds using both conventional isolation and metagenomics/Next Generation Sequencing approaches. The likely source of microbial and protozoan contamination of drinking water will be explored using evolutionary (coalescent-based) modelling techniques.</p>	<ul style="list-style-type: none"> • DoC • Ministry of Health
French	<p>Molecular epidemiology of campylobacteriosis in urban wild birds</p> <p>Team members: Nigel French</p> <p>Populations of wild birds in urban areas pose a potential risk to human health due to faecal contamination of the environment. In this study we consider the carriage of <i>Campylobacter jejuni</i> in sympatric urban populations of starlings and ducks. Using multilocus sequence typing of housekeeping genes and hypervariable genes we are exploring the population structure of <i>C. jejuni</i> in multiple host populations occupying the same geographical location to gain insight into inter and intra-species transmission, and associated human health risk.</p>	<ul style="list-style-type: none"> • DoC • MAF-Investigation and Diagnostic Centre • NZ Centre for Conservation Medicine