

AWC Projects 2014/2015

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

Investigator	Project	Stakeholders
Drummond/ Nelson	<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</p> <p>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 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>	<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
Gemmell	<p>Molecular ecology for the conservation and management of NZ threatened species Team members: Neil Gemmell, Amy Osborne, Monika Zavodna, Catherine Gruber, Ian Jamieson,</p> <p>We are developing new knowledge about the population level relationships of variety of endemic/native terrestrial and marine species e.g. sea lions, fur seals, whio</p>	<ul style="list-style-type: none"> DoC
Gemmell	<p>A pigs tale - a replicated experiment in evolution Team members: Neil Gemmell, Peter Visscher, Marcel Medrano (PhD student)</p> <p>When the first Europeans colonized Australia, New Zealand and the islands in the southern Pacific Ocean, they often carried with them a variety of livestock species. In these new homelands small numbers of animals, notably pigs, goats, cattle and sheep, were released or managed to escape into the wild. A few of them survived and established stable populations over time. Descending from formerly domesticated stock, over multiple generations the phenotypic appearance of these animals has altered such that many features of these feral pigs now resemble those of wild boar, e.g. their coat color, coat texture and body shape. Presumably these adaptations were driven by the survival requirements in the wild where the animals needed to forage and survive in a relatively hostile environment, albeit relatively safe from predation and diseases. As the release or escape of domestic pigs into the wild occurred several times at different places, we have the rare opportunity to explore the process of feral adaptation in what are effectively a series of natural replicates. These natural experiments, coupled with new genomic tools, including the full genomic sequence of the pig and a commercially available DNA chip (SNP-chip) assay, provides an opportunity for us to look at how selection has shaped the genomes of these animals to turn what was a domesticated animal back towards its wild form. What we particularly wish to know is whether the same genes or genetic pathways are involved in the adaptation seen in each isolated population of feral pigs, or whether there were multiple genetic mechanisms that effectively lead to the same phenotype. In addition, through comparison to genetic data from domesticated pig breeds we also hope to find clues as to whether the genetic variants that led to the feral phenotypes we now observe in these populations already existed in the feral pigs' forebears or if new mutations occurred that enables adaptation to the harsher environments in which these animals found themselves transplanted.</p>	
Gemmell and Johnson	<p>Molecular ecological research for the management of NZ fisheries species Team members: Neil Gemmell, Tom McCowan (PhD student), Chris Hepburn, Sheri Johnson, Jane Symonds, Peter Ritchie</p> <p>We are developing new knowledge about the population level relationships of variety of species of fisheries importance e.g. paua, crayfish, hapuku, salmon</p>	<ul style="list-style-type: none"> Ministry of Primary Industry Various stakeholder groups including the Pāua Industry Council

Investigator	Project	Stakeholders
Gemmell and Rosengrave	<p>The genetic basis of cryptic female choice</p> <p>Team members: Neil Gemmell, Patrice Rosengrave, Bob Montgomerie (Queen's), Cornelia Geßner (PhD student).</p> <p>In many species females can control fertilisation after mating via behavioural, morphological, and physiological mechanisms – a process called cryptic female choice (CFC). While undoubtedly widespread, it is generally unknown, if and how CFC might be exerted in external fertilisers, where eggs and sperm are shed simultaneously into the surrounding water. Recently we demonstrated that Chinook salmon ovarian fluid, a viscous substance released with eggs during spawning, differentially alters male sperm function in a female-dependent fashion, and thus that females appear to exert cryptic control of male reproductive success. The rationale for this CFC is unknown, but ovarian-fluid-mediated sperm selection may promote favoured genetic combinations that enhance offspring quality. Using state-of-the-art computer-assisted sperm analysis, competitive fertilisation trials, and genetic-marker-based parentage assignment we are seeking to determine if the observed differential sperm function has any impact on male fertilisation success and if so whether there is a genetic basis for the observed CFC.</p>	
Jamieson	Comparing changes in genetic diversity between neutral and functional (MHC, TLRs) DNA markers in bottlenecked and in hybridized populations.	<ul style="list-style-type: none"> Dept. of Conservation and conservation biologists in general
Jamieson	Using immunity genes to identify immunocompetent parakeets, kakapo and saddlebacks.	<ul style="list-style-type: none"> Dept. of Conservation, Regional Councils, conservation biologists and zoos worldwide
Jamieson	Detecting inbreeding depression and its consequences on population viability in the highly inbred Chatham Island Black Robin.	<ul style="list-style-type: none"> Dept. of Conservation
Millar	<p>DNA barcoding the birds of New Zealand and the Antarctic</p> <p>Team members: Dr Craig Millar, Dr Howard Ross, Prof David Lambert, Prof Allan Baker, Ms Selina Patel.</p> <p>DNA barcoding is an attempt to identify species based on a short region of the 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 bird species. However, the effectiveness of DNA barcoding to reliably identify Southern Hemisphere bird 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"> Department of Conservation New Zealand Civil Aviation Authority Air New Zealand, contracts that involved the identification of the species and sex of birds involved in birdstrike on aircraft. National and international scientific community Local and national museums Iwi
Millar	<p>The moa genome: a targeted approach</p> <p>Team members: Dr Craig Millar, Prof David Lambert, Dr Leon Huynen, Dr Craig Smith, Ms Selina Patel</p> <p>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. The project will be of interest to both scientists and the New Zealand public.</p>	<ul style="list-style-type: none"> National and international scientific community Local and national museums Iwi The New Zealand public
Nelson	<p>Conservation Genomics of Kiwis</p> <p>Team members: Dr Kristina Ramstad, Helen Taylor (PhD)</p> <p>This project describes conservation genomics of New Zealand's rarest kiwis, working in close collaboration with the Department of Conservation.</p>	<ul style="list-style-type: none"> Dept of Conservation
Nelson	<p>Sex determination and impacts of climate change on tuatara</p> <p>Team members: Lindsay Mickelson (PhD student), Stephanie Price (PhD Student), Anna Carter (PhD student), David Towns (DOC), Alison Cree (U. Otago), Nicola Mitchell (U. Western Australia).</p> <p>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,</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

Investigator	Project	Stakeholders
	and niche modelling.	
Nelson	<p>Ecological relationships of NZ wildlife Team Members: Anna Carter (PhD student), Alexei Drummond (AWC), Jo Hoare (DOC), James Russell (U. Auckland), Stephen Hartley (VUW)). For this project we are 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
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 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.</p>	<ul style="list-style-type: none"> • Ministry of Primary Industries
Russell	<p>Phylogeography of rats originating from Europe in the New Zealand region Team Members: James Russell, Rachel Fewster, Judith Robins This project investigates the mtDNA haplotype diversity <i>Rattus rattus</i> and <i>R. norvegicus</i>, two species of invasive rats which arrived with Europeans. This project complements (and completes) work already published on the phylogeography of <i>R. exulans</i> and <i>Mus domesticus</i> in New Zealand. Through engagement with a wide range of stake holders (DOC, Regional councils, Animal Health Board, community groups, museum collections) samples of these rat species have been collected from around New Zealand over the past ten years. These samples will be used to complete the phylogeography of these species across New Zealand and its offshore islands and surrounding outlying island groups in the Pacific. Results will be used to make inference on the invasion pathways and secondary contacts of invasive rats in the New Zealand region, and may shed light on eradication units for landscape rat management</p>	<ul style="list-style-type: none"> • Department of Conservation • Regional Councils • Animal Health Board • Community Groups • Museums • Conservation Biologists
Spencer	<p>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>. This work is of interest in understanding how major quickly differences in body plans can evolve. 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.</p>	<ul style="list-style-type: none"> • DoC, because it will increase our knowledge of NZ's molluscan fauna • Te Papa, Amateur shell collectors & naturalists, because it will improve our molluscan taxonomy • Evolutionary biologists, because it will shed light on fundamental long-standing questions about the evolution of novelty
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</p>	<ul style="list-style-type: none"> • Ecologists studying biodiversity and biogeographic connectivity (NZ and worldwide) • Invertebrate taxonomists and museum researchers

Investigator	Project	Stakeholders
	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.	<ul style="list-style-type: none"> • 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</p> <p>Team members: Dr Ceridwen Fraser, Prof Hamish Spencer, Prof Jon Waters</p> <p>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

Theme: 2. Biodiversity & Human Impacts
Activity: B. Tracing the origins and histories of the peoples and biota of New Zealand and the Pacific

Investigator	Project	Stakeholders
Buckley	<p>Phylogeny of the stick insects</p> <p>Team members: Thomas Buckley</p> <p>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.</p>	<ul style="list-style-type: none"> • Department of Conservation (Primary)
Gemmell	<p>New tools to detect, monitor and predict the spread of marine bioinvasive species</p> <p>Team members: Neil Gemmell, Sharyn Goldstien, Joanne Povey, with assistance from NIWA and the Cawthron Institute</p> <p>Recent bio-invasions of NZ waters by several noxious species have highlighted the vulnerability of our aquatic ecosystems and the productive sectors that rely on them. Managing the spread and impact of marine invasives is problematical because of inadequate knowledge and tools for positively distinguishing invasive species from natives or each other, their point(s) of origin, the vector(s) of transmission, and the pattern of spread once established. We are developing new tools and knowledge to help identify the sources and pathways of dispersal of new marine incursive species, such as the club tunicate, <i>Styela clava</i></p>	<ul style="list-style-type: none"> • MPI, BiosecurityNZ
Gray	<p>The phylogeography of Oceanic languages</p> <p>Team members: Remco Bouckaert, Simon Greenhill (ANU)</p> <p>In this project we will develop novel phylogeographic models to analyse the dispersal of Austronesian languages in the Pacific.</p>	<ul style="list-style-type: none"> • Pacific Island communities • Pacific archaeologists, linguists and prehistorians • General public
Matisoo-Smith	<p>Ancient DNA of Pacific Tupuna</p> <p>Team members: Post Docs –Darnell Kennedy and Ann Horsburgh; PhD student: Anna Gosling.</p> <p>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).</p> <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 	<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

Investigator	Project	Stakeholders
	<p>Otago.</p> <ul style="list-style-type: none"> 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 – Ann Horsburgh and Andrew Clarke; former PhD student: Stefan Prost, Olga Kardailsky. 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 sampling the New Zealand population – Africa to Aotearoa. We are working with Dr John Mitchell, from LaTrobe University in Melbourne and Stephen Wilcox WEHI Melbourne. For more information on the Genographic project see: https://genographic.nationalgeographic.com I have also begun collaboration with other Genographic research groups addressing human migrations in the Middle East and North Africa – Neolithic expansions etc</p>	<ul style="list-style-type: none"> Participating communities across the Pacific including NZ National Geographic Colleagues interested in human dispersals and Pacific prehistory Researchers interested in ancient human migrations, Neolithic expansions and the origins of specific culture groups and civilizations in the Near East.
Matisoo-Smith	<p>Origins and genetic histories of New Zealand and Pacific plants and animals. Team members: Post Docs – Ann Horsburgh; PhD students: 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), 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
Ritchie	<p>The Population Genetic Structure of New Zealand Blue Cod (<i>Parapercis colias</i>) Stocks Team members: Clare Gebbie 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 population genetic structure of the New Zealand-wide stock.</p>	<ul style="list-style-type: none"> Ministry of Primary Industries Fishing Industry Recreational fishing groups
Ross	<p>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.)</p>	
Spencer	<p>Prof. Jon Waters, postdoc Dr Raisa Nikula and I are studying long-distance dispersal in the invertebrate community of bull-kelp holdfasts. Long-distance dispersal has been neglected in studies of population founding and connectivity.</p>	<ul style="list-style-type: none"> DoC, because it will increase our knowledge of NZ's subantarctic marine fauna Te Papa, Amateur shell collectors & naturalists, because it will improve our molluscan taxonomy Evolutionary biologists, because it will shed light on fundamental long-standing questions about the population founding and connectivity
Waters	<p>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>Phocarctos hookeri</i>. By studying ancient DNA of such species, we hope to better understand the biological consequences of human settlement in coastal New Zealand.</p>	<ul style="list-style-type: none"> NZ archaeologists Museum researchers Dept of Conservation Ngai Tahu

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

Investigator	Project	Stakeholders
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
Matisoo-Smith	<p>Identifying disease in ancient Pacific populations</p> <p>Team members: PhD student Anna Gosling. We are working with colleagues from the University of Otago (A/P Tony Merriman) 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</p> <p>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.).</p> <p>We are investigating the microbial diversity of NZ wildlife, including transmission, molecular epidemiology and potential 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.</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
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), Shelley Jeffries (RSNZ teacher fellow).</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
Poole Tylanakis	<p>Digging up the dirt on global environmental change: a comparative metatranscriptomic analysis of ecosystem functioning.</p> <p>Team members: Anthony Poole, Jason Tylanakis, Dr Stinus Lindgreen (EU Marie Curie Fellow), Dr Karen Adair (Lincoln)</p> <p>Human-generated carbon emissions drive temperature increases, but further change may be hastened by feedback loops. Specifically, nitrogen-based fertilisers may increase soil micro-organism respiration under elevated temperatures, releasing more carbon as CO₂. We predict that these drivers will alter invasive-plant and soil-microbial communities to include species (e.g., ammonia-oxidizing bacteria) with higher respiration rates, and thereby alter the metabolic processes carried out by the soil community as a whole. Using gene expression data generated with next generation sequencing, we will test the effects of warming and nitrogen deposition on microbial diversity, abundance and ecosystem functioning in a unique multi-year field experiment.</p>	
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</p>	<ul style="list-style-type: none"> • Cawthron Institute • Auckland Regional Council • Zespri International Ltd, Plant & Food Research, Dnature, Seeka, Green Growers Association

Investigator	Project	Stakeholders
	<p>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>	
Russell	<p>Testing ecological rules of community organisation Team members: James Russell, Alexei Drummond This project uses community datasets across taxonomic groupings collected on Little Barrier Island (Hauturu-O-Toi) within the current Model Ecosystem/Hidden Treasures Strategic Initiative and also historically (birds and insects) to develop analytical tools to model communities and test rules of ecological organisation.</p>	<ul style="list-style-type: none"> • DOC • Iwi (Ngati Manuhiri) • Statistical Ecologists • Hauturu Supporters
Spencer	<p>An overseas collaborator and I are writing about the evolutionary concept of genetic conflict and how it pertains to human health, sometimes even leading to an apparently paradoxical co-operation between those in conflict (e.g., mothers and offspring, whose evolutionary interests need not coincide). I am also working on a project with AWC Affiliate, Assoc. Prof. John Stenhouse, looking at the eugenics movement in New Zealand, a better understanding of which has implications today in debates about the rights of the disabled.</p>	<ul style="list-style-type: none"> • Medical research community, because there is current widespread misunderstanding of what genetic conflict entails • NZ & international historians, who have called for more international studies of eugenics movements in different countries • Ethicists, who argue that understanding eugenics sheds light on contemporary ethical debates • Groups caring for disabled people in NZ, who face ethical issues every day in their work.
Waters	<p>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.</p>	<ul style="list-style-type: none"> • NZ archaeologists • Museum researchers • Dept of Conservation • Ngai Tahu