

Allan Wilson Centre for Molecular Ecology and Evolution

Annual Report 2003/2004



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¹ Unless otherwise indicated, Massey University appointments are based on the Palmerston North campus

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CHAIRMAN'S REPORT

The Allan Wilson Centre was established as part of the New Zealand Government's Research Excellence initiative and incorporates scientists and support staff located in five institutions throughout the country with its "Head Office" at Massey University's Palmerston North campus. The Centre has been named for Professor Allan Wilson a New Zealander at the University of California, Berkley, whose outstanding work on the power of molecular information to interpret and re-interpret many issues in ecology, and in biology more generally, received wide acclaim. The Centre began its initial operation in July 2002 with its formal opening by the Hon Pete Hodgson, Minister of Research, Science and Technology, occurring on 12 September 2002 in the presence of Mrs Leona Wilson and other members of Allan Wilson's family.



The Centre has the over-arching aim of fully understanding the past and the future of New Zealand's biota. How did living organisms get here? How fast did their evolution proceed? What are the processes underlying the evolution of our biota? To paraphrase the Centre's Vision Statement it will "by undertaking research on New Zealand biota contribute to the understanding of evolutionary processes".

As part of the administration of the Centre a Governance Board of five experienced scientists has been established to assist the Directors and to monitor their work and, as well, to oversee the strategic directions of the Centre and to approve and audit budgets. The Board first met in August 2003 and then again in May 2004. As the current Chairman I am pleased to have the opportunity to express my grateful appreciation of the contribution my distinguished colleagues have already made to the oversight of the Centre and for their expertise and active interest in its work.

At its May meeting the Governance Board received reports from a number of subsidiary groups which have vital functions in the overall management of the Centre. They are; the Scientific Advisory Panel with all ten members being eminent overseas specialist in aspects of molecular evolution; the Research Management Group consisting of the Centre's two Directors plus the leaders of its four main research projects; the Centre Management Group of the two Directors, the Centre's Business Manager plus the leaders of its four main research projects; the Centre Management Group of the two Directors, the Centre's Business Manager and a senior University representative; and the Massey University Advisory Board of four senior University staff with an interest in the administrative and scientific endeavours of the University.

It also received Reports from the Leaders of the four over-arching research projects being undertaken by the Centre. These projects are:

1. Rates and Modes of Evolution
2. Biodiversity
3. Human Settlement of Aotearoa/New Zealand
4. New Ecological and Evolutionary Models

It has been a busy time for all concerned with the Centre, not least for the Board as it moves to put in place a helpful but effective system of advice and scrutiny to guide the Centre and its staff and to give assurance that funds are being appropriately disbursed and used.

In conclusion I congratulate the staff of the Centre on the progress and accomplishments achieved during the last year and commend this Annual Report to readers interested in these advances and in the science contained in them.

TNM Waters

Chairman

Allan Wilson Centre for Molecular Ecology and Evolution

DIRECTOR'S REPORT - MIKE HENDY

As we complete the second year of the Allan Wilson Centre we are beginning to see the added value of the Centre's establishment. The process of selecting the seven Government funded Centres of Research Excellence (CoREs) ensured that its members were already very active researchers of international repute. Thus the continued high productivity of quality science outputs is not unexpected, what we need to identify are those additional beneficial outcomes that have resulted from the Government's initiative. We will soon be reviewed by our funders, and it is incumbent on us to ensure that tangible additional benefits are highlighted.



So what have we achieved, that would have not happened if the CoRE had not been established?

The first obvious outcomes are the benefits resulting from the capital investment in equipment such as the AWC lab at Albany, the sequencing service, the HELIX high performance computer cluster. We are already seeing research papers produced as a consequence of access to these valuable tools. We have been able to significantly increase the generation and analysis of data. We hope that with the long foreshadowed Advanced Research Network of Aotearoa (AReNA), we will be able to realise our Biomirror goal of daily updating a local copy of the world's major biological databases. It is important to note that as we share these items with other users, the additional benefits are spread to the wider scientific community.

A second benefit has resulted from the increased interaction between researchers, both within the Centre, and internationally. The national meetings have resulted in a significant interaction across universities and across disciplines. We have been exposed to each other's research endeavours, and inspired by the energy and insight of our colleagues. Our investigators and our newer researchers have been enabled to present to more international

meetings, have had the opportunity to visit other labs and establish effective international collaborations.

The legacy of Allan Wilson is well known internationally, we are grateful to be able be associated with this New Zealand pioneer of interpreting molecular data. This has been a catalyst in raising our profile, an exposure we have a responsibility to use productively. In 2005 we will be hosting the SMBE meeting in Auckland, a major opportunity to showcase the current New Zealand pioneers in molecular ecology and evolution, and to expose our researchers to an international conference of exceptional reputation. Allan's legacy is also inspirational to our many new researchers. It humbling to note the significant number of students and post-docs who have been enabled to commence their research careers in these fields.

We must also acknowledge the benefit of our Scientific Advisory Panel, whose members have undertaken to ensure our research activities can be bench marked against the world's best. They are also able to offer guidance from an external viewpoint. Our most recent report from Professor Andreas Dress, Leipzig, challenges us to looking ahead, not just to 2008, when we can expect our current CoRE funding to end, but to 2015, when we must expect our newer researchers to be the new generation of senior researchers. He challenges us to see the Allan Wilson Centre to have a long-term future so that this new generation will continue to benefit from its establishment. We must plan for dynamic change, for longevity, and consider both the long-term scientific interests of New Zealand, of the researchers who will empower this country's future.

Mike Hendy

Executive Director

DIRECTOR'S REPORT – DAVID PENNY



Research advances in many ways. One important way is conceptual advances and to start this year's report I would like to celebrate some examples that blossomed during the year. One of the most interesting has involved one of our investigators with an international group and it has come from analysis of large data sets. It involves 'predictive adaptive responses' (PARs) - during fetal growth the young embryo is (for viviparous animals) sensing the nutritional status of its mother and is adjusting its growth and physiology in anticipation of conditions after the fetus is born. For humans, the information about such effects comes from some major long-term longitudinal studies, but equivalent data is found for invertebrates. The concept has led to an both article in *Nature* and a review in press at *Trends in Ecology and Evolution*. Such results are sending both theoreticians and experimentalists back to the proverbial drawing board to understand the dynamic interplay between genotype, phenotype and the environment. The model of one gene, one enzyme, one genotypic effect, is far too simple for the complexity of biology.

Perhaps to have one for the theoreticians, research at Canterbury University has found extremely powerful results to the effect that autocatalytic cycles of chemical reactions are quite likely to arise in a pre-biotic environment. Given a complex mixture of chemical compounds and minerals, it is not unreasonable that an autocatalytic cycle could occur. This finding has the potential to encourage origin of life experimentalists to design equipment where large numbers of sets of conditions can be tested simultaneously. With *in vitro* evolution studies, or combinatorial chemistry, extremely large combinations of variants can be evaluated simultaneously. Now we need the equivalent for studies of the earliest stages of the origin of life.

Continuing with the theme of conceptual advances but for computing, my third example is the development of the "Minmax Squeeze" computer program. This can guarantee a phylogenetic tree is minimal for large numbers of closely related sequences, such as may be found from within a population or a single species. This approach should lead to a breakthrough from relying solely on heuristic searches in analyzing DNA sequences, to a realisation that exact solutions (or a range of them) are now possible for maximum

parsimony, and where it is a maximum likelihood estimator. In the past, ideas were transferred inappropriately from classical phylogeny to population data, and the Squeeze program gives the possibility new approaches to analyzing population data.

Yes, conceptual advances are important, but they are just one of many ways that research progresses. Researchers are always central. We are pleased at the number and range of papers being published, it is a major achievement by active researchers. It is pleasing that we are now close to a full complement of staff, and the new members are of course younger. It is these younger researchers that are the focus for longer term, our task is to help them to new levels that we could not have got to by ourselves. This is a major responsibility for both the established and the younger researchers.

Most of my focus has been on the researchers, but we all know that much of our work requires better technology allowing both faster, cheaper and more accurate data collection, and more powerful computers for analysis. Our DNA Sequencers give ourselves (and many other researchers in New Zealand) access to better and longer sequencing runs at lower cost. Helix, our super-computing cluster is developing very well, but has the potential to benefit more of our own researchers. We have had several analyses that could not have been done without the cluster, and we foresee a big increase in usage this year. We were already experienced with DNA sequencing but have needed to build up our experience with supercomputing previously inaccessible to our researchers.

None of us can keep up on all fronts, but we expect that members on the Allan Wilson Center will be learning new and better ideas and techniques, and sharing that knowledge. Much of this continued learning is informal, but we also provide formal short-term courses. At the Allan Wilson Center we have an opportunity that is almost unique in the world because we have a wide variety of skills from innovative biologists, to excellent mathematicians. The biggest disaster would be to rest on our laurels and not keep developing, learning and sharing new knowledge. Next year we expect further conceptual and other advances, that is what we are contracted to do.

David Penny

Director, Research

RESEARCH PROGRAMME OVERVIEW

The research goal of the AWC is to combine fundamental biological questions, molecular (DNA sequence) data, and mathematics, in order to understand important processes that helped shape present day plants and animals, especially those of New Zealand. On a world scale, our combination of biologists and mathematicians is probably unique, and therefore we aim for research that is at the very best world standard. For convenience, we divide our research into four projects.

Under Rates and Modes of Evolution we test whether measuring rates of DNA sequence change at different times gives the expected acceleration of evolution at shorter times. A related sub-project seeks to understand how changes in the secondary and tertiary structure of proteins affects rates of evolution. Furthermore, we are testing the extent to which the measurable processes of microevolution (as measured in this Project) are sufficient for long term evolution.

Our second Project on Biodiversity is very broad and particularly focuses on New Zealand biota. We have an excellent opportunity to identify dispersal methods that have helped establish the main groups. We have unique animals from which we can learn about probable past events. The (geologically) recent uplift that gave the Southern Alps is a unique opportunity to study recent speciation as new niches become available, and in one case is challenging long held paradigms about the nature of species themselves.

Our Project 3 is on the peopling of the Pacific, and their plants and animals. Given the relative recency of occupation, and the strong archaeological evidence, the Pacific Islands are arguably the best place in the world to understand the processes involved whether it be of the peoples, their animals (pigs, chickens, dogs, rats), the food plants they brought with them, or used subsequently.

Finally, Project 4 on new ecological and evolutionary models uses the power of mathematics, together with a strong interaction with biologists, to develop and implement testable models for ecology and evolution. These range from short-term effects such as

viral evolution, to very distant events such as optimal conditions for the origin of life. Another sub-project develops better ways for detecting hybridization from sequence data, a topic much neglected by other groups as being far too hard. Project 4 gives us a major competitive advantage with respect to other groups in the world, but needs the strong input from biologists in order to be effective.

In summary, the AWC strives to be at the forefront of Molecular Ecology and Evolution, and we believe we have the ability to maintain ourselves there.

RESEARCH HIGHLIGHTS

Project One

Rates and Modes of Evolution

Researchers David Lambert, Craig Millar, Peter Lockhart, David Penny, Jennie Hay, Leon Huynen, Peter Ritchie, Jennifer Anderson, Lara Shepherd, Oliver Berry, Hayley Lawrence, Mary Morgan-Richards, Steve Trewick, Mark Stevens, Gillian Gibb, Renae Pratt, Julia Goldberg, Kerryn Slack, Barbara Binney

Objective 1: To determine rates of evolution in kiwi and tuatara

Tuatara: Over the last year we have designed PCR primers that amplify the entire HVRI region of the tuatara mitochondrial genome. This was done to be able to make a direct comparison with the Adelie penguin evolutionary rate estimation. We have completely sequenced the HVRI of two tuatara bones and have amplified shorter fragments from many other bones. In addition, we have also sequenced HVRII as this has many variable sites in living populations and will be useful for comparing genetic and geographic variation of extinct and extant populations. The sequence from the bones has variation not seen in any living populations.

We have been able to secure ~40 bones from mostly North Island sites, from both sand dune and caves, and have requested bones from a number of South Island localities.

We have complete control region sequence for 40 living tuatara ranging across all 26 populations in all 12 island groups. As new individuals are added, more variation within populations is found, but also individuals within populations and island groups cluster more closely, revealing genetic structure among populations and island groups.

A research highlight was the DNA identification of a mounted tuatara specimen, reputedly from the extinct East Island. Our analysis however showed that it had the same mitochondrial sequence as Brothers tuatara, thus demonstrating the use of these methods in identifying the provenance of tuatara. Genuine East Island samples are being obtained from Otago Museum to identify the closest living population for repopulation – this is part of a DoC restoration of East Island.

Kiwi: We have sequenced 654 bp of cytochrome b from a further 4 ancient brown kiwi samples. Furthermore, we have sequenced 200 bp of the HVRI of the mitochondrial control region in 35 ancient bone and skin samples of brown kiwi. Brown kiwi demonstrates a high level of genetic structuring with many of the ancient brown kiwi samples exhibiting unique control region sequences. We have also extracted and sequenced 190 bp of the HVRI of the mitochondrial control region and 250 bp of cytochrome b sequence in 28 ancient samples of little spotted kiwi. In contrast to brown kiwi, little spotted kiwi demonstrate considerably less genetic variation and structuring.

Objective 2: To estimate rates of mutation in birds

During the Antarctic field season 2003/04 we collected 150 sets of blood samples from known families of Adélie penguins. This was somewhat less than expected due to poor weather conditions. As a result we will conduct a final field season in 2004/05 to collect from a further 200 families. This will provide us with the required sample size for an accurate estimate of HVRI mutation rates in penguins.

All material collected to date has now been sequenced for the HVRI region and our current estimate of the rate of mutation is 0.68s/s/Myrs. This estimate lies within the range of evolutionary rates we have calculated using ancient DNA from Adélie penguin colonies in the Antarctic. Consequently this objective is progressing very well and we expect a series of high profile publications to result.

Objective 5. Rates and modes of early bird and mammalian evolution

Eight mammalian mitochondrial genomes were completed, and we are working on the NZ short-tailed bat mitochondrial genome. An additional 12 mitochondrial genomes of birds were completed. A collaborative arrangement with three avian paleontologists has led to a manuscript describing the oldest penguin fossils (which are from North Canterbury), together with three mitochondrial genomes from seabirds. The fossils give a calibration point for estimating long term evolutionary rates. Another 12 mitochondrial genomes of birds are being sequenced. The chloroplast sequences (to test similar ideas about the earlier ‘Cambrian explosion’) is well underway by sequencing ‘lower’ green plants (ferns, mosses and liverworts), and freshwater green alga. A significant achievement was the general overview of our approach which appeared in Trends in Ecology and Evolution.



Prodigious Birds; Moas and Moa Hunting in Prehistoric New Zealand (Cambridge Press, UK, 1989).
Acknowledgements to Athol Anderson

Project Two

Biodiversity

Researchers Charles Daugherty, David Lambert, Peter Lockhart, Hamish Spencer, Craig Millar, Kirsten Donald, Nicky Nelson, Kim McBreen, Martyn Kennedy, Sue Keall, Trish McLenachan, Olga Kardialsky, Ravikumar Gaddam, Kelly Hare, Joanne Hoare, Michael Knapp, Carlos Lehnebach, Hilary Miller, Mort Piripi, Anna Santure, Cielle Stephens, Kevin Woo, Tanya King, Kristina Ramstead, Richard Carter

Objective 1: To test for adaptation: morphological innovation in alpine plants

This objective researches the nature of plant species radiation in New Zealand [http://awcmee.massey.ac.nz/~NZ Plant Species Radiation Group](http://awcmee.massey.ac.nz/~NZ_Plant_Species_Radiation_Group) involving:

- a) comparative studies of groups that have radiated extensively in the alpine New Zealand zone,
- b) assessment of the potential of *Pachycladon* (a close relative of *Arabidopsis*) as a model system for functional and evolutionary genomics and
- c) the development of analytical methodology for describing species radiation.

Completed sequence data sets are being analysed using a SuperTree network method (Z closure). Data sets are also near completion that will allow comparative analyses of nuclear and chloroplast gene loci for *Ranunculus* and *Nothofagus* species in respect of their distribution south and north of the “beech gap”. Studies of *Ranunculus* morphology has led to the identification of 100 characters that are of interest for studying morphological convergence in alpine habitats.

A study of New Zealand *Ranunculus* species discussing morphological diversity and the importance of hybridization as an explanation for observed diversity, has been completed. Molecular clock studies on the *Nothofagus* provides strong evidence for multiple transoceanic dispersals of *Nothofagus*.

Objective 2: To investigate the relationship between genetic variation and extinction

We now have a collection of 132 blood samples from 121 individual Taiko (*Pterodroma magentae*), as well as a range of feathers and other tissue samples. This is remarkable given that the existing population is estimated only to be about 100-120 birds. A field trip to the Chatham Islands to collect new Taiko material resulted in ~80 sub-fossil bones being collected from a number of sites.

We have sexed all the samples collected to date. In addition, we have amplified the cytochrome b region of the Taiko mitochondrial genome for 20 birds. We are also working on the HVRI region of this species. Owing to variation in the PCR primers binding sites this region has proved more difficult than originally anticipated but we are confident that this technical difficulty will be resolved.

We have now completed the construction of the genomic library of Taiko and isolated 9 microsatellite DNA loci. Two of these have now been shown to be polymorphic across a sample of 12 birds. The remaining loci are currently under development.

Objective 3: Quarternary Plant Extinction & Stepping Stone Hypotheses

Preliminary work for this objective started in Year Two in preparation for full commencement of the objective in Year Three.

Objective 4: MHC and mate choice in tuatara

Major Histocompatibility Complex (MHC) genes play an important role in disease resistance in vertebrates, and are thought to help determine mate choice in some species. Variation at MHC genes is central to their role in immune function and appears to be maintained by natural selection. This study aims to identify the levels and patterns of variation at these loci and to investigate their role in the evolution of a New Zealand icon species, tuatara. We have isolated MHC genes from tuatara and have carried out preliminary investigations of variation at these genes in 2 populations of tuatara and are

investigating how MHC genes are organised within the tuatara genome with the long-term aim of understanding how MHC genes evolve in reptiles.

Sensory perception of tuatara: A study incorporating both ecological and psychological perspectives to test learning and visual perception using a novel operant technique and flicker-fusion rates to measure visual discrimination in tuatara has been completed. Tuatara (*Sphenodon punctatus*) were trained, using an operant conditioning procedure with food reinforcement to respond to discriminative stimuli of various flicker-fusion rates, and ignore a non-discriminative stimulus. Tuatara demonstrated a learning capacity for acquisition of an operant task as well as cognitive development for learning and memory strategies. Visual discrimination is important to tuatara and may facilitate behavioural responses to many context-dependent ecological processes (i.e. predator/prey/kin recognition, mate selection, environmental discrimination, optimal foraging strategies, and communication). By understanding the importance of visual stimuli, the study provides a better perspective of the tuatara natural sensory world. Additionally, a reliable method was established that could be used for more comprehensive psychophysical experiments to further access visual perception and learning in all reptiles, with the potential to examine other sensory mechanisms such as audition, chemoreception, and tactility.

Behaviour of juvenile tuatara: Activity patterns of juvenile tuatara have been videoed in 3 age groups in captivity. Video footage is currently being analysed.

Restoration of Rangitoto Island: Tuatara were translocated to a new island location as part an ecological restoration programme in collaboration with the Department of Conservation and the local Maori tribe, Ngati Koata. It provided a chance to test translocation techniques and their effect on subsequent success of populations. The Whakatere-papanui Island population was set up to enable assessment of whether knowing your neighbour affects dispersal post-translocation, with an aim to reduce dispersal from release sites. The tuatara were translocated from an area of Stephens Island where their predatory habits threatened expansion of the only population of the endangered Hamilton's frog. Forty four

Marlborough green geckos and 44 Cook Strait giant wetas were also translocated to Whakatere-papanui Island, as part of a long-term plan to ecologically restore the island.

Replanting on Stephens Island and its effect on skink populations: Plant succession and the active planting of bush by the Department of Conservation has changed the plant structure of the island and this in turn may have changed the distribution and/or abundance of the skinks on Stephens Island. Results indicate that revegetation is currently beneficial for all skink species. However revegetation is still in its early stages, and low captures from the forest indicates that over time revegetation may have a negative effect for the skinks of Stephens Island.

Objective 5: Nocturnality in New Zealand lizards

As reptiles are ectothermic they are highly influenced by environmental temperature. Most reptiles are diurnal. However, some lizards are nocturnal and forage at cool night-time temperatures, even though research shows that they prefer body temperature ranges only attainable during day hours. This study aims to unravel this paradox and understand why and how ectotherms function so well in apparently sub-optimal conditions. We compare both nocturnal and diurnal species of lizard to answer this question. Our research encompasses three major physiological measures: rate of oxygen consumption, locomotor efficiency and muscle enzyme function.

To date we have collected oxygen consumption measurements of four nocturnal, three diurnal and one crepuscular species of lizard. Locomotor efficiency experiments have also been undertaken in three species of lizard. One more species will have its locomotor efficiency measured this November on Mana Island. Data is currently being analysed for phylogenetic comparisons. Enzyme assays are currently being undertaken.

Objective 6: Co-evolution of trematodes and topshells

We have completed a large amount of the necessary field work in both Australia and New Zealand. The sequencing of mitochondrial DNA from both trematodes and their first-intermediate host snails has also largely been completed. These results have revealed a

number of interesting aspects of this host-parasite relationship. For instance, we have documented the first known example of more than one cryptic trematode species simultaneously infecting a single snail population. We also show that these two trematode species infect just one snail species, even though there is ample opportunity each generation to infect other closely related snails. A third cryptic trematode species, sister to one of this pair, infects at least 3 snail species, however, and two Australian snail species share a fourth cryptic trematode. One New Zealand and three Australian snail species were not found to be infected.

We have completed our estimate of the snails' phylogeny and show how dispersal of adults via rafting on bull kelp has repeatedly played an important role in the evolutionary history of this group.

Objective 7: Effects of global warming on tuatara populations

After two seasons, our study of natural nesting in tuatara has resulted in the following: 900 permanently marked female tuatara at nesting areas, data loggers in 90 nests recording hourly temperatures for 12 months, and temperature data loggers inserted at 14 locations and two depths associated with nesting areas. Hatchlings produced from nests monitored in the first season are predicted to have produced an even sex ratio, contrasting with data from the 1998/99 season which produced a male-biased sex ratio. Nest depths were not significantly different between years, but mean temperatures in nests in 1998/99 were significantly warmer than in 2002/03. Hatchling sex ratio varies with nesting rookery, but no rookeries have produced a female-biased sex ratio.

Additional work in Project 2:

(a) Integrating Traditional Maori and Scientific Ecological Knowledge of the Tuatara:

We are integrating Maori traditional ecological knowledge (TEK) and scientific ecological knowledge of tuatara. The objectives of this project are to (1) gain insight into past and present tuatara ecology, (2) document valuable Maori TEK, (3) foster a deeper understanding between project collaborators and (4) provide a case study for comparison with other TEK studies. During 2004, TEK was recorded through semi-directed interviews

of sixteen kaumatua (elders) of Te Atiawa and Ngati Koata iwi. These iwi are the kaitiaki, or guardians, of North Brother and Stephens Islands, some of the few remaining islands that tuatara still inhabit today. Digital audio and video interview records were collected to produce a TEK archive for each collaborating iwi. A flexible informed consent process was developed to allow balance between intellectual property rights and confidentiality. Kaumatua reviewed their interview transcripts for accuracy and kaumatua and iwi trusts jointly determined which information to disseminate publicly. Final interview transcripts are archived with and available from Te Atiawa and Ngati Koata Trusts (see references below). These transcripts will be analysed for ecological and cultural content and provide the basis for a peer-reviewed, public report expected in May 2005. There is concern that both tuatara and TEK may be lost over time. This study is therefore relevant to the conservation of both tuatara and the oral history of the Maori people of New Zealand.

(b) *Predator-prey interactions between New Zealand lizards and their native and introduced predators:* Predator-prey interactions are often viewed as an ‘arms race’ where predators evolve mechanisms to capture prey, and prey simultaneously evolve mechanisms to avoid capture. New Zealand lizards coevolved with both predatory birds and with tuatara, and exhibit a suite of antipredator defences directed at these visual predators. However, when mammals were introduced to New Zealand many reptile populations went extinct and others continue to decline. This research addresses the question of why New Zealand lizards are so susceptible to predation by mammals. Experiments into the behavioural responses of lizards to scent of their native and introduced predators have been undertaken for 2 lizard species in 3 locations (2 in the absence of mammals, and 1 in the presence of mammals) and data are currently being statistically analysed.

Project Three

Human settlement of Aotearoa/New Zealand

Researchers Lisa Matisoo-Smith, David Penny, Judith Robins, Simon Hills, Abby Harrison, Lorraine Berry, Melanie Pierson, Andrew Clarke

Objective 1: The settlement of the Pacific

A total of 20 complete mitochondrial genomes have been sequenced and are ready for analysis. A new computer program (MinMax Squeeze) has been developed that is particularly effective on this class of sequence data. Samples collected for Y-chromosome analysis include ethical approval for analysis of relevant nuclear genes. Several hundred blood samples have been collected from Papua/New Guinea, Fiji and Kiribati.

Objective 2: Use of commensal animals and plants to trace human settlement patterns

We have now sequenced 13,000 bp of a 16,000 bp genome for the New Zealand kiore. We anticipate finishing this first genome by the end of 2004, at which point the second (Southeast Asian) genome will proceed rapidly.

We have obtained fresh tissue samples for *R. exulans* from Thailand, Island Southeast Asia and PNG, *R. praetor* tissues from PNG and *R. tanezumi* tissues from PNG and Fais. We have recently acquired additional kiore samples from Easter Island and Vanuatu, and have been granted access to samples collected from the Bismarck Archipelago and coastal PNG.

Germplasm Acquisition: Seeds from 27 cultivars of bottle gourd have been obtained representing South American and Asian germplasm and will be crucial in testing our hypothesis of a South American origin for the Polynesian bottle gourd. Over 300 cultivars of sweet potato have been sampled for DNA analysis, representing cultivars from South America, Polynesia and island South East Asia and will be used to infer the origin and dispersal of the sweet potato in Oceania.

Marker Systems Development: Approximately 40 potential markers have now been isolated for sweet potato. Two AFLP-derived sequencing markers have been developed for sweet potato and are ready to use on the sweet potato samples collected from Japan. A new technique has been developed for isolating polymorphic regions from bottle gourd and converting these regions into DNA sequencing markers. Collaborations will accelerate DNA marker development in the bottle gourd and will allow us access to Polynesian bottle gourd samples held by the Smithsonian Institution. Data collection is ongoing, once enough data are obtained for sweet potato variation, phylogenies will be constructed.

Objective 3: Pacific biodiversity and human impacts

Linkages with Pacific institutions are continuing to be developed.

Additional work in Project 3:

Easter Island Palm is now extinct, but we have sourced seeds. Appropriate markers from existing palms from around the South Pacific are being sequenced and this information is being used to sequence markers from the Easter Island palm. This will allow a firm identification of the palm.

We have sequenced the nuclear intergenic spacer (IGS) from taro, which was found to contain a large repeat region. This project is now proceeding in two directions: the first, to develop the taro IGS as a useful marker for reconstructing patterns of human mobility in the Pacific, and the second, to use the taro IGS sequence data to develop a model for the evolution of repeat sequences.



Cover of the 15 June 2004 issue of PNAS submitted by Lisa Matisoo-Smith. Acknowledgements: Tim Mackrell

Project Four

New ecological and evolutionary models

Researchers Mike Steel, Mike Hendy, Allen Rodrigo, David Penny, Barbara Holland, Tim White, Lesley Collins, Bhalchandra Thatte, Stephane Guidon, Michael Woodhams, Stefan Grunewald, Dietrich Radel, Philip Daniel, Greg Ewing, Matt Goode, James Matheson, Philip Daniel, Michaela Baroni, Sylvia Chen, Klaus Schliep, Jessica Hayward,

Objective 1: New phylogenetic approaches to rapidly evolving populations

The successful incorporation of migration into population genetic demographic models has paved the way for the incorporation of changing parameters (i.e., population size, mutation rate), the development of a parallel MCMC platform for the analysis, and will allow for changing numbers of demes over time. Further extensions are planned following integrated models of virus/parasite and host genealogies.

A simple frequency-dependent selection akin to the game-theoretic model of the “prisoner's dilemma” is being investigated following the showing that non-intuitive behaviour (a decrease in mean fitness over time) can potentially occur in large parts of parameter space. We are also the first to report on maternal selection perpetual cycling of allele frequencies in this multi-generational form of selection. Again, this is not an intuitively expected outcome of selection. Work on genomic imprinting has shown that no single evolutionary hypothesis is currently capable of explaining all the aspects of imprinting.

New relationships between the maximum likelihood and maximum parsimony tree reconstruction methods have been published; the significance of these results - particularly for constructing phylogenies on populations of the same species will be developed further. These new results apply when the sequences are relatively similar to each other, such as from individuals within a species.

Objective 2: Mathematical modelling of species radiations, extinction and reticulation

Algorithms to allow nested taxa and multi-layer supertrees, as well as dated supertrees, were developed, published and programmed, with applications to biological data. Techniques for analysing hybrid phylogenies were developed with results being applied to the published alpine buttercup data from Project 2.

Objective 3: Phylogenetic bioinformatics

New phylogenetic methods have been developed based on gene content. Techniques for analysing gene order data were developed - fundamental statistical limits for inferring ancestral sequences from sequences were derived

Lineage specific selection under covarion models and “standard” models is being investigated. A MinMax Squeeze computer program that can prove a tree to be minimal has been implemented; the program was tested with 53 complete mitochondrial genomes of humans, and found a minimal tree requiring two mutations less than in the original publication. The new method will be tested further and is expected to have wide applicability in the study of intra-specific sequence data.

Objective 4: Developing simulation to study the origin of life and earliest divergences

An algorithm has been developed to determine if an arbitrary biochemical system can support a self-sustaining, autocatalytic subsystem, then be applied to analyse Stuart Kauffman’s simple model for the emergence of autocatalysis in the origin of life. Subsequent work has led to a much more extensive mathematical analysis of the properties of autocatalytic biochemical systems. A wide-ranging review on the origin of life has been completed with theoretical and experimental results integrated, and new approaches suggested for some questions.

Non-coding RNA genes and inferring ancestral character states of the spliceosome for deeply diverging eukaryotes have been identified. A programme has been developed to identify some other non-coding RNA which is being tested experimentally with some of the predictions from bioinformatics.

CAPITAL EQUIPMENT - HELIX

In October 2002, the Allan Wilson Centre's parallel processor, a Beowulf cluster "HELIX" was commissioned. HELIX comprises 66 off-the-shelf IBM PC-compatible computers connected to each other on a high speed network, which together function as a single unit. Additionally, whereas a typical desktop computer contains one CPU, each computer (or "node") that is part of HELIX has two CPUs, giving HELIX an overall processing power equivalent to 132 modern PC computers. At the time of commissioning HELIX was benchmarked at number 304 in the ranking of the world's 500 most powerful computers.

HELIX has become an important bioinformatics tool for researchers in the Allan Wilson Centre, undertaking computationally intensive tasks including RNA and protein folding prediction, "in-silico" reactor simulations, extensive boot-strap phylogenetic analyses and multi-parameter simulations to test the accuracy of phylogenetic heuristic software. Having HELIX has greatly extended the analytic capacity of researchers in the Centre, and lead to several significant research publications.

HELIX was constructed and maintained by scientists of the Institute of Information and Mathematical Sciences, at Massey University's Albany campus. It is a facility that is available to other researchers with high performance computational needs. Demand for time on this facility has lead to a recent increase in its capacity, funded by Massey University, with an additional 20 dual processors using 64-bit chips and greatly increased memory, in a new initiative now referred to as "Double HELIX". An on-going programme of upgrading is planned. The Allan Wilson Centre also will be hosting a Biomirrors server linked to HELIX, in partnership with the Biomirrors initiative of the Bioinformatics Institute at the University of Auckland.

PRESENTATIONS

Total: 64

Baroni, M. Using directed graphs to represent reticulate evolution. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.

Burnham, K. Dendritic cells, little green microbes and the watchtowers of immunity. Annual meeting of Immunet, University of Otago, Dunedin. 3 September 2003.

Burnham, K., Keall, S.N., Nelson, N.J. and Daugherty, C.H. Effects of season, sex and ticks on peripheral blood cells of captive and wild tuatara. Joint Annual Meeting of Ichthyologists and Herpetologists, Norman, Oklahoma, USA, 30 May 2004.

Burnham, K., Keall, S.N., Nelson, N.J. and Daugherty, C.H. T cell function in tuatara (*Sphenodon punctatus*). Joint Annual Meeting of Ichthyologists and Herpetologists, Norman, Oklahoma, USA, 30 May 2004.

Clarke, A., 2004. Using DNA sequence data to trace the origins and dispersal of sweet potato and bottle gourd in Polynesia: Implications for human mobility. Paper presented at the Australasian Society for Human Biology Conference, Auckland, New Zealand, 7-10 December 2003.

Clarke, A. C., McLenachan, P. A., Penny, D., 2004. Reconstructing prehistoric human contact between Polynesia and South America: Molecular analysis of the sweet potato and bottle gourd. Poster presented at the Evolution Conference 2004, Fort Collins, Colorado, United States of America, 26-30 June 2004.

Daniel, D. New supertree methods. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.

Ewing, G. The structured coalescent with serially-sampled sequences. International Conference on Bioinformatics, Auckland, New Zealand. 5-8 September 2004.

Ewing, G. Using temporarily spaced sequences to simultaneously estimate migration rates, mutation rate and population sizes in two subpopulations. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.

Goode, M. Modeling change in codon substitution using serially sampled sequence data. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.

Grunewald, S. A method to construct phylogenetic networks from quartet data. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.

Guidon, S. Modelling the site-specific variation of selection patterns along lineages. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.

Hare, K.M., Pledger, S., Thompson, M.B., Miller, J.H. and Daugherty, C.H. Conditioning reduces resting metabolic rates of lizards. Joint Annual Meeting of Ichthyologists and Herpetologists, Norman, Oklahoma, USA, 30 May 2004.

Hare, K.M., Thompson, M.B., Miller, J.H. and Daugherty, C.H. Conditioning reduces resting metabolic rates of lizards. Animal Behaviour Meeting, Oaxaca, Mexico, 16 June 2004.

Hay, J. Fossil molecular outgroup for a phylogenetically isolated taxon, *Sphenodon*. Genomes and Evolution, Penn State University, Pennsylvania, USA, 17-20 June 2003.

- Hendy, M. Interpreting interleaved mini-satellite repeats, Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.
- Hendy, M. Combinatorics of tandem duplication trees. Humboldt University of Berlin, Germany, 23 September 2003.
- Hendy, M. Combinatorics of tandem duplication trees. University of Greifswald, Germany, 23 September 2003.
- Hendy, M. Upper bounds on maximum likelihood for phylogenetic trees. European Conference on Computational Biology, Paris, 28 September 2003.
- Hoare, J.M. Why have lizards disappeared from the New Zealand mainland? Australian Society of Herpetologists, Inc., Conference 2003, Darwin, Australia, 5 December, 2003.
- Hoare, J.M., Keall, S.N., Nelson, N.J., Mitchell, N., Daugherty, C.H. and Pledger, S. Downward spiral for the Brothers Island tuatara. Australian Society of Herpetologists, Inc., Conference 2003, Darwin, Australia, 5 December, 2003.
- Holland, B. Consensus networks or phylogenetic ink blots? Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.
- Huynen, L., Millar, C.D. and D.M. Lambert. Nuclear DNA Detects Species Limits in Ancient Moa. Evolution 2003, State University of California, Chico, California, June 2003.
- Keall, S.N. and Daugherty, C.H. and Pledger, S. Population ecology of Duvaucel's gecko on North Brother Island. Australian Society of Herpetologists, Inc., Conference 2003, Darwin, Australia, 5 December 2003.
- Kennedy, M. Cophylogeny of the Pelecaniformes and their parasitic lice. SYSTANZ General Meeting and Plant Species Radiation Workshop. Whakapapa Village, New Zealand, 12-13 February 2004.
- Knapp, M. Fangorn forest is not a Gondwanan relic. SYSTANZ General Meeting and Plant Species Radiation Workshop. Whakapapa Village, New Zealand, 12-13 February 2004.
- Lambert, D. M. Invited presentation DNA *Barcoding Ancient Life*. Meeting of the Society for Molecular Biology and Evolution. Pennsylvania State University, June, 2004. Invited Chair of session on 'Molecules and Biodiversity', 17-20 June 2004.
- Lambert, D.M. *DNA Barcoding ancient life*. Invited presentation to 7th International Conference on Ancient DNA and Related Biomolecules. University of Queensland, May, 2004.
- Lambert, D.M. Biological Information and Knowledge: Ancient DNA and Ecology 2003. Plenary Talk, New Zealand Bioinformatics Conference, Te Papa, Wellington, 2003.
- Lawrence, H. Department of Conservation, Taiko Recovery Group Annual Meeting: Genetic Analysis of Taiko 29th April 2004.
- Lawrence, H. Molecular Ecology Conference: *Molecular Ecology of the Chatham Island Taiko*, 6th December 2003.
- Lockhart, P. Progress and directions for SYSTANZ? SYSTANZ General Meeting and Plant Species Radiation Workshop. Whakapapa Village, New Zealand, 12-13 February 2004.
- Longson, C., Hare, K.M., and Daugherty, C.H. Fluctuating asymmetry is not a sensitive indicator of environmental stress in the egg-laying skink, *Oligosoma suteri*. 10th Biennial Conference of the Society for Research on Amphibians and Reptiles in New Zealand, Whakatane, New Zealand, 2 February, 2003.

- Matheson, J. Analysis of historical NZ respiratory syncytial virus (RSV) data. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.
- Matisoo-Smith, E. and J. Robins, 2003. Historic pig introductions to New Zealand. Paper presented at the Pig Workshop, Durham, UK, September 2003.
- Matisoo-Smith, E., 2004. Kororareka Kiore and Russell Rats. Invited paper at 'The French Place in the Bay of Islands' Historic Places Trust Symposium, Russell, April 2004.
- McBreen, K. Obtaining a species phylogeny for close relatives of *Arabidopsis* in New Zealand. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.
- Miller, H. Molecular Phylogenetics of New Zealand's Petroica species. NZ Molecular Ecology Annual Meeting, Caitlins, Otago, 5 December 2003.
- Miller, H. The major histocompatibility complex (MHC) of an ancient reptile lineage, *Sphenodon* (tuatara). Genomes and Evolution, Penn State University, Pennsylvania, USA, 17-20 June 2003.
- Miller, H., Belov, K. and Daugherty, C.H. The Major Histocompatibility Complex (MHC) of an ancient reptile lineage, *Sphenodon* (Tuatara). Genomes and Evolution 2004, June 17th-20th, State College, Pennsylvania, USA, 17 June 2004.
- Mitchell, N., Allendorf, F., Nelson, N., Keall, S. and Daugherty, C. Demographic effects of temperature-dependent sex determination: can tuatara survive global warming? Australian Society of Herpetologists, Inc., Conference 2003, Darwin, Australia, 5 December 2003.
- Nelson, N.J. Conservation of Tuatara. San Diego Zoo Forum for Millenium Post-Docs, San Diego Zoo, San Diego. 24 September, 2003.
- Nelson, N.J., Mitchell, N.J., Pledger, S., Keall, S.N and Daugherty, C.H. Temperature-dependent sex determination in tuatara (*Sphenodon*). Joint Annual Meeting of Ichthyologists and Herpetologists, Norman, Oklahoma, USA, 30 May, 2004.
- Penny, D. RNA processing in the eukaryotic ancestor. Genomes and Evolution, Penn State University, Pennsylvania, USA, 17-20 June 2003.
- Penny, D. Where next in phylogeny? Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.
- Penny, D. Lessons from human and chimpanzee genomes. Paper presented at the Australasian Society for Human Biology Conference, Auckland, New Zealand, 7-10 December 2003.
- Penny, D. and Collins, L. RNA processing in the eukaryotic ancestor. Society Molecular Biology and Evolution, College Parl, PA. June 2004.
- Penny, D. and Phillips, M. Evolution of mammals and birds; are microevolutionary processes sufficient for macroevolution? Evolution 2004, Fort Collins, Colorado, June 2004.
- Pierson, M., 2003. Mites as markers of prehistoric mobility. paper presented at the Molecular Ecology Meeting, NZ. December 2003.
- Pierson, M., 2003. Mites as markers of prehistoric mobility. Paper presented at the Australasian Society for Human Biology Conference, Auckland, New Zealand, 7-10 December 2003.

- Ramstad, K., Allendorf, F., Daugherty, C.H., Nelson, N.J., Ngati Koata and Te Atiawa. Integrating traditional and scientific ecological knowledge: case studies from Alaska and New Zealand. National Institute of Water and Atmospheric Research, Christchurch, 24 June 2004.
- Ramstad, K, Nelson, N.J., Daugherty, C.H., and Allendorf, F. Does traditional ecological knowledge persist as species decline? Maori and tuatara of Aotearoa, New Zealand, 89th Annual meeting of The Ecological Society of America, Portland, Oregon, USA, 2 August, 2003.
- Romijn, R., Keall, S.N., Nelson, N.J., and Daugherty C.H. Using an endangered species, the tuatara, to promote conservation education. Science Communicators Conference, Heritage Hotel, Auckland, 23 June 2004.
- Shepherd, L. Genetic diversity of ancient and modern kiwi. SYSTANZ General Meeting and Plant Species Radiation Workshop. Whakapapa Village, New Zealand, 12-13 February 2004.
- Spencer, H. Frequency-dependent Selection with Dominance: The Behaviour of the Mean Fitness. Evolution 2004: Joint Meeting of the Society for the Study of Evolution, the Society of Systematic Biologists and the American Society of Naturalists, Colorado State University, Fort Collins, June 2004.
- Spencer, H. The Evolutionary Consequences of Phenotypic Plasticity: Adding a Spatial Dimension. SIRC 2003: 15th Annual Colloquium of the Spatial Information Research Centre, University of Otago, Dunedin, December 2003.
- Steel, M. Some open problems in phylogenetic combinatorics. Phylogenetics Combinatorics and Applications 2004, University of Uppsala, Sweden, July 5-9, 2004.
- Steel, M. The probability of self-sustaining autocatalysis in abstract origin of life models. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.
- Thatte, B. MANTRA – a multiple alignment and tree reconstruction algorithm. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.
- Thierier, T. A characteristic function approach to perfect and imperfect phylogenies. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.
- Trewick, S. and Morgan-Richards, M. Estimating the age of New Zealand's fauna. SYSTANZ General Meeting and Plant Species Radiation Workshop. Whakapapa Village, New Zealand, 12-13 February 2004.
- Welch, D. Reconstructing host genealogy and parasite history – an integrated model. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.
- White, T. Compressing DNA sequence databases with COIL. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.
- Woodhams, M. The modified closest Tree. Annual Phylogenetics Workshop. DOOM04. Whakapapa Village, New Zealand, 16-20 February 2004.

PUBLICATIONS

Total: 75

Allen, R., Cree, A., Darby, J., Davis, L., Patrick, B. and Spencer, H. (2003) Chapter 8: Forests and Shrublands. *Pages 153-190 In The Natural History of Southern New Zealand*, J. Darby, R.E. Fordyce, A. Mark, K. Probert and C. Townsend (eds). Otago University Press, Dunedin.

Anderson, J.P., Learn, G.H., Rodrigo, A.G., He, X., Wang, Y., Weinstock, H., Kalish, M.L., Robbins, K.E., Hood, L. and Mullins, J.I. (2003) Predicting Demographic Group Structures Based on DNA Sequence Data. *Molecular Biology and Evolution* 20: 1168-1180

Asmussen, M.A., R.A. Cartwright and Spencer, H.G. (2004) Frequency-dependent selection with dominance: A window onto the behavior of the mean fitness. *Genetics* 167: 499-512.

Barker, M., Brett, T., Darby, J., Dugan J., Hubbard, D., Johnson, P., Mladenov, P., Patrick, B., Peake, B., Probert, K., Smith, A., Spencer, H. and Walker, S. (2003) *Chapter 11: The coast. Pages 267-311 in The Natural History of Southern New Zealand*, J. Darby, R.E. Fordyce, A. Mark, K. Probert and C. Townsend (eds). Otago University Press, Dunedin.

Bateson, P. D., Barker, T., Clutton-Brock, D. Deb., Foley, R.A., Gluckman, P., Godfrey, K., Kirkwood, T., Mirazón Lahr, M., Macnamara, J., Metcalfe, N.B., Monaghan, P., Spencer, H.G. and S.E. Sultan, S.E. (2004) Developmental plasticity and human health. *Nature* 430: 419-421.

Bell, B.D., Daugherty, C.H., Hay, J.M. and Hitchmough, R.A. (2004). Species identification of allopatric populations with conflicting datasets: a Cook Strait islands case study and round-table discussion. *New Zealand Journal of Zoology* 31: 101. (Published abstract for 2003 conference of

the Society for Research on Amphibians and Reptiles in New Zealand)

Brett, T., Carter, L., Carter, R.M., Darby, J., Davis, L., Dawson, S., Jillett, J., Probert, K. and Spencer, H. (2003) Chapter 12: The open sea. *Pages 313-338 in The Natural History of Southern New Zealand*, J. Darby, R.E. Fordyce, A. Mark, K. Probert and C. Townsend (eds). Otago University Press, Dunedin

Castro, L., Mason, K.M., Armstrong, D.P. and Lambert, D.M. (2004). Effects of extra-pair paternity on effective population size in a reintroduced population of the endangered hihi, and potential for behavioural management. *Conservation Genetics* 5: 381-393.

Collins, L.J. and Penny, D. (2004) Lost in the RNA World – the genomics of ncRNA. *New Zealand Bio Science* 13: 38-40.

Collins, L.J., Macke T. and Penny D. (2004). Searching for ncRNAs in eukaryotic genomes: Maximizing biological input with RNAmotif. *Journal of Integrative Bioinformatics* 0001: Online Journal: http://journal.imbio.de/index.php?paper_id=6

Collins, L.J., Poole, A.M. and Penny, D. (2003). Using Ancestral Sequences to Uncover Potential Gene Homologues. *Applied Bioinformatics* 2, S85-S95.

Daugherty, C.H. and Allendorf, F. (2002) The numbers that really matter. *Conservation Biology* 16: 1-2

Daugherty, C.H. (2003) Understanding the past – discovering a future: how learning more about tuatara and its chequered past is helping to shape the future of New Zealand. *New Zealand Science Review* 60(4): 141-142.

Delsuc, F., Phillips, M.J. and Penny, D. (2003) Comment on "Hexapod Origins: Monophyletic or Paraphyletic?" *Science* 12 301: 1482-1483.

- Donald, K.M., Kennedy, M., Poulin, R. and Spencer, H.G. (2004) Host specificity and molecular phylogeny of larval Digenea isolated from New Zealand and Australian topshells (Gastropoda: Trochidae). *Int J Parasitol.* 34(5):557-68.
- Drake, D.R., Mulder, C.P.H., Towns, D.R. and Daugherty, C.H. (2002) The biology of insularity: an introduction. *Journal of Biogeography* 29: 563 - 572.
- Drummond, A.J., Nicholls, G.K., Rodrigo, A.G. and Solomon. Genealogies from time-stamped sequence data. In *Tools for Constructing Chronologies* (Eds. C. Buck and A. Millard) Springer Lecture Notes in Statistics, vol 171:pp. 151-174.
- Esser, C., Ahmadinejad, N., Wiegand, C., Rotte, C., Sebastaini, F., Gelius-Dietrich, G., Henze, K., Kretschmann, E., Richly, E., Leister, D., Bryant, D., Steel, M.A., Lockhart, P.J., Penny, D. and Martin, W. (2004) Loss of phylogenetic signal makes the source of mitochondria difficult, even with 62 complete procaryote genomes. *Molecular Biology and Evolution* 21: 1643-1660.
- Goode, M., and Rodrigo, A.G. (2004) Using PEBBLE for the evolutionary analysis of serially sampled molecular sequences. In *Current Protocols in Bioinformatics* (ed. A. Baxevanis). J. Wiley.
- Guindon, S., Rodrigo, A., Dyer, K.A. and Huelsenbeck, J.P. (2004). Modeling the site-specific variation of selection patterns along lineages. *PNAS* 2004 101: 12957-12962
- Hare, K., Longson, C., Pledger, S. and Daugherty, C. (2004). Size, growth and survival are reduced at cool incubation temperatures in the temperate lizard *Oligosoma suteri* (Lacertidae: Scincidae). *Copeia* 2004 (2), pp. 383-390
- Harrison, G.L., McLenachan, P.A., Phillips, M.J., Slack, K.E., Cooper, A. and Penny, D. (2004) Four new avian mitochondrial genomes help get to basic evolutionary questions in the Late Cretaceous. *Mol. Biol. Evol.* 21(6):974-983.
- Hay, J.M., Daugherty, C.H., Cree, A. and Maxson, L.R. (2003) Low genetic divergence obscures phylogeny amongst populations of *Sphenodon*, remnant of an ancient reptile lineage. *Mol. Phylog. Evol.* (1). 29: 1-19.
- Herbert, J. and Daugherty, C.H. (2002) Genetic variation, systematics, and management of kiwi (*Apteryx*). Pp. 11-34 in *Some early 1990s studies in kiwi (Apteryx) genetics and management. Science and Research Internal Report 191*.
- Hordijk, W. and Steel, M.A. (2004) Detecting autocatalytic, self-sustaining sets in chemical reaction systems. *J.Theoret. Biol.* 227: 451-461.
- Huynen, L., Lambert, D.M.; McLennan, J.A.; Rickard, C.; Robertson, H.A. (2003) A DNA test for sex assignment in kiwi (*Apteryx* spp.). *Notornis* 50(4): 231-233.
- Hurles, M. E., E. Matisoo-Smith, R. D. Gray and D. Penny. (2003) Untangling Pacific settlement: the edge of the knowable. *Trends in Ecology and Evolution* 18: 531-538
- Jolly, J.N., and Daugherty, C.H. (2002) Comparison of little spotted kiwi (*Apteryx owenii*) from Kapiti and D'Urville Islands. Pp. 57 – 65 *Some early 1990s studies in kiwi (Apteryx) genetics and management. Science and Research Internal Report 191*.
- Kennedy, M. and Spencer, H.G. (2004) Phylogeny of the Frigatebirds (Fregatidae) and Tropicbirds (Phaethonidae), two divergent groups of the traditional order Pelecaniformes, inferred from mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution* 31(1):31-8

- King, T.M., Kennedy, M. and Wallis, G.P. (2003) Phylogeographic genetic analysis of the alpine weta, *Hemideina maori*: The evolution of a colour polymorphism and the origins of a hybrid zone. *Journal of The Royal Society of New Zealand*, 33, 715-729.
- Lambert, D.M., Millar, C.D. and L. Huynen (2004). Ancient DNA of the Extinct Moa of New Zealand. *Australasian Science* September 14-16.
- Lettink, M., Jamieson, I.G., Millar, C.D., Lambert, D.M. (2002) Mating system and genetic variation in endangered New Zealand takahe. *Conservation Genetics* 3: 427-434.
- Mark, A., Lee, W., Patrick, B., Cree, A., Darby, J. and Spencer, H. (2003). Chapter 9: Tussock grasslands and associated mountain lands. Pages 191-235 in *The Natural History of Southern New Zealand*, J. Darby, R.E. Fordyce, A. Mark, K. Probert and C. Townsend (Eds.). Otago University Press, Dunedin.
- Markwell, T.J., and Daugherty, C.H. (2003) Variability in ^{15}N , ^{13}C and Kjeldahl nitrogen of soils from islands with and without seabirds in the Marlborough Sounds, New Zealand. *New Zealand Journal of Ecology* 27: 25-30.
- Markwell, T.J., and Daugherty, C.H. (2002) Invertebrate and lizard abundance is greater on seabird-inhabited islands than on seabird-free islands in the Marlborough Sounds, New Zealand. *Ecoscience* 9: 293-299.
- Matisoo-Smith, E. and J. Robins, 2004. Origins and dispersals of Pacific peoples: Evidence from mtDNA phylogenies of the Pacific rat. *Proceedings of the National Academy of Sciences, USA* 101(24):9167-9172.
- McBreen, K., Lockhart, P.J., McLenachan, P., Scheele, S., Robertson, A.W. (2003) The use of molecular techniques to resolve relationships among traditional weaving cultivars of Phormium. *NZ J Bot.* 41:301-310
- Miller H.C, and Lambert D.M (2003) An evaluation of methods of blood preservation for RT-PCR from endangered species. *Conservation Genetics* 4: 651-654
- Miller, H.C and Lambert, D.M (2004) Gene duplication and gene conversion in class II MHC genes of New Zealand robins (Petroicidae). *Immunogenetics* 56: 178-191.
- Miller, H.C. and Lambert, D.M. (2003). An evaluation of methods of blood preservation for RT-PCR from endangered species. *Conservation Genetics* 4: 651-654.
- Miller, H.C. and Lambert, D.M. (2004). Gene duplication and gene conversion in class II MHC genes of New Zealand robins (Petroicidae). *Immunogenetics* 56: 178-191.
- Morgan-Richards, M. and Wallis, G.P. (2003) Degree of cytogenetic differentiation fails to predict hybrid zone width in the weta *Hemideina thoracica* (Orthoptera: Anostostomatidae) *Evolution* 57: 849-861
- Morgan-Richards, M., Trewick, S. A., Chapman, H. M. (2004). Evidence of hybridisation among *Hieracium* species in New Zealand from flow cytometry. *Heredity*. (Published on line 12 May 2004).
- Nelson, N.J., Thompson, M.B., Pledger, S., Keall, S.N., and Daugherty, C.H. (2004) Egg mass determines hatchling size, and incubation temperature influences post-hatching growth, of tuatara, *Sphenodon punctatus*. *Journal of Zoology, London* 263: 77-87.
- Norris, T.B., Rickards, G.K. and Daugherty, C.H. (2004) Chromosomes of tuatara, *Sphenodon*, a chromosome heteromorphism and an archaic reptilian karyotype. *Cytogenetic and Genome Research* 105: 93-99.

- Page, R.D.M., Cruickshank, R.H., Dickens, M., Furness, R.W., Kennedy, M., Palma, R.L. and Smith, V.S.(2004.) Phylogeny of "Philoceanus-complex" seabird lice (Phthiraptera: Ischnocera) inferred from mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution*, 30, 633-652.
- Penny, D. (2002) Consequences of the continuity between the human and biological worlds. In "Learning, animals and the environment: changing the face of the future". (M.Fisher, J. Marbrook and G. Sutherland eds) *Pp 19-28 Royal Society of New Zealand, Wellington*.
- Penny, D. (2004) Darwin: I wish I were a Botanist. Book review of "The Correspondence of Charles Darwin, Volume 13 1865", Cambridge University Press. *Trends in Ecology and Evolution 19*: 67-68.
- Penny, D. (2004) Evolutionary trees for all. *Trends in Ecology and Evolution 19*(6): 273
- Penny, D. (2004) Life, the Universe, and Everything. Book review of "Life's Solutions: Inevitable humans in a lonely world." *Simon Conway Morris, Cambridge University Press. EMBO Reports 5*: 134-135.
- Penny, D. (2004) Our relative genetics. *Nature 427*, 208-209.
- Penny, D. and Phillips, M.J. (2004). The rise of birds and mammals: Are microevolutionary processes sufficient for macroevolution. *Trends in Ecology and Evolution 19*: 516-522
- Phillips, M.J., Delsuc, F. and Penny, D. (2004) Genome-Scale Phylogeny and the Detection of Systematic Biases. *Molecular Biology and Evolution. 21*(7): 1455-1458.
- Rest, J.S., Ast, J.C., Austin, C.C., Waddell, P.J., Tibbetts, E.A., Hay, J.M., and Mindell, D.P. (2003) Molecular systematics of primary reptilian lineages and the tuatara mitochondrial genome. *Mol. Phylog. Evol.* 29: 289-297.
- Ritchie, P.A., Millar, C.D., Gibb, G. Baroni, C. and Lambert, D.M. 2004. Ancient DNA Enables Timing of the Pleistocene Origin and Holocene Expansion of Two Adélie Penguin Lineages in Antarctica. *Molecular Biology and Evolution 21*(2): 240-248.
- Rodrigo, A.G., Goode, M., Forsberg, R., Ross, H.A. and Drummond, A. (2003) Inferring evolutionary rates using serially sampled sequences from several populations. *Mol. Biol. Evol.*, 20:2010–2018
- Savolainen, P., Leitner, T., Wilton, A.N., Matisoo-Smith, E., and Lundeberg, J. 2004 Detailed picture of the Origin of the Australian Dingo, obtained from the study of Mitochondrial DNA. *Proceedings of the National Academy of Sciences, USA.* 101(33):12387-12390.
- Sober, E. and Steel, M. (2002) Testing the hypothesis of common ancestry. *J. Theor. Biol. 218*: 395-408
- Spencer, H. and Darby, J. (2003) Birds of Freshwater Habitats in Southern New Zealand. Pages 264-265 in Chapter 10: *Inland Water and Wetlands, The Natural History of Southern New Zealand*, J. Darby, R.E. Fordyce, A. Mark, K. Probert and C. Townsend (eds). Otago University Press, Dunedin
- Spencer, H.G. (2002) Intragenomic conflict. In *Encyclopedia of Life Sciences*, G. Fullerlove (ed.). <http://www.els.net>. Nature Publishing Group, London.
- Spencer, H.G. (2002) Mutation-selection balance. Volume 12, pages 529-533 in *Encyclopedia of Life Sciences*, G. Fullerlove (ed.). [Http://www.els.net](http://www.els.net). Nature Publishing Group, London.

- Spencer, H.G. (2002) The correlation between relatives on the supposition of genomic imprinting. *Genetics* 161: 411-417.
- Spencer, H.G. 2003. Further properties of Gavrillet's one-locus two-allele model of maternal selection. *Genetics* 164: 1689-1692.
- Spencer, H.G. (2004) Population genetics. In *Biometrics*, S.R. Wilson and C. Burden (eds), in *Encyclopedia of Life Support Systems*, Developed under the Auspices of UNESCO, EOLSS Publishers, Oxford. <http://www.eolss.net>
- Spencer, H.G., and D.B. Paul. (2002) Eugenics. Pages 317-322 in *Encyclopedia of Evolution*, M. Pagel (ed.). Oxford University Press, New York.
- Spencer, H.G., Feldman, M.W., Clark, A.G. and A.E Weisstein, A.E. (2004) The effect of genetic conflict on genomic imprinting and modification of expression at a sex-linked locus. *Genetics* 166: 565-579.
- Steel, M.A. and Penny, D. (2004) Two further links between MP and ML under the Poisson model. *Applied Mathematics Letters* 17: 785-790.
- Stevens, M.I., Hogg, I.D. (2003) Long-term isolation and recent range expansion revealed for the endemic springtail *Gomphiocephalus hodgsoni* from southern Victoria Land, Antarctica. *Molecular Ecology* 12: 2357-2369.
- Stevens, M.I., Hogg, I.D. (2004) Population genetic structure of New Zealand's endemic corophiid amphipods: evidence for allopatric speciation. *Biological Journal of the Linnean Society* 81: 119-133.
- Sultan, S.E., and Spencer, H.G. (2002) Metapopulation structure favors plasticity over local adaptation. *American Naturalist* 160: 271-283.
- Suter, H.C., Kennedy, M. and Young, G. (2004) Neoteny or not? The distribution of the hypophysial duct within the Galaxioidea. *Journal of Fish Biology*, 64, 1217-1225.
- Trewick, S.A., Morgan-Richards, M. & Chapman, H.M. (2004) Chloroplast DNA diversity of *Hieracium pilosella* (Asteraceae) introduced to New Zealand: reticulation, hybridization, and invasion. *American Journal of Botany*, 91: 73-85
- Tutt, K. Daugherty, C.H. and Gibbs, G.W. (2002) Differential life-history characteristics of male and female *Peripatoides novaezealandiae* (Onychophora: Peripatopsidae). *Journal of Zoology, London* 258: 257-267
- Votier, S.C., Bearhop, S., Newell, R.G., Orr, K., Furness, R.W. and Kennedy, M. (2004). The first record of Brown Skua *Catharacta antarctica* in Europe. *Ibis*, 146, 95-102.
- Weisstein, A.E., and Spencer, H.G. (2003) The evolution of genomic imprinting via variance minimization: An evolutionary genetic model. *Genetics* 165: 205-222.

ADDITIONAL FUNDING SECURED IN YEAR TWO

Total additional funds secured in 2003/4: \$1,283,960

Hare, K. Faculties of Science and Architecture & Design Small Grants, New Zealand. \$1500.

Hare, K. New Zealand Vice Chancellors' Committee - Claude McCarthy Fellowship. NZ\$1000 for conference travel

Hare, K. Society for Research on Amphibians and Reptiles in NZ, Research Award 2004. \$1,500.

Hare, K. VUW Faculties of Science and Architecture & Design Small Grants. NZ\$1800 for conference travel.

Hoare, J. Nicola Grimmond Student Award. \$60.

Hoare, J. Society for Research on Amphibians and Reptiles in NZ, Research Award 2004. \$1,500.

Hoare, J. Tertiary Grant from Masterton Trust Lands Trust. \$600 one-off payment

Keall, S., Nelson, N. and Daugherty, C. Tuatara - A Taonga for all New Zealanders. \$85,000 from RSNZ Science and Technology Promotion Fund for Tuatara Roadshow in partnership with Te Atiawa iwi and San Diego Zoo

Lambert, D.M. and Milar, C.D. How variable are evolutionary rates across vertebrates? An ancient DNA approach. Marsden Award \$750,000 over three years.

Millar, C.D. Can past ecology enlighten future conservation?. University of Auckland Research Fund \$7,500.

Matisoo-Smith, L. 8,000€ per annum (5 years) from CNRS (French Research Funding) for Interdisciplinary Studies of the Societies of the Ancient Pacific.

Matisoo-Smith, L. \$120,000 from Nga Pae o te Maramatanga, The National Institute of Research Excellence for Maori Development and Advancement for A new paradigm for evolution: does the flow of energy determine the rate of evolutionary change?

Matisoo-Smith, L. US\$2500 from The Leakey Foundation for Ancient DNA analyses at Klasies River Mouth.

Matisoo-Smith, L. \$16,000 from The University of Auckland Research Fund for The dating of Me Aure Cave.

Nelson, N. Why are stable social groups rare in reptiles? \$20,000 from Victoria University Research Fund

Nelson, N., Daugherty, C. and Keall, S. Strategic Investment Fund, SBS, Victoria University. \$20,000 grant to develop laboratory work space on Stephens Island

Nelson, N. University Research Fund, Victoria University of Wellington - \$8,500 for Summer Students on Traditional Ecological Knowledge Project.

Nelson, N. School of Biological Sciences, Victoria University. \$10,000 for Summer Students on Traditional Ecological Knowledge Project

Romijn, R. The Royal Society of New Zealand Teacher Fellowship Scheme. \$2500 to attend Zoological Society of San Diego Conservation Education Workshop, October 2004.

Stevens, M. New Zealand Science and Technology Postdoctoral fellowship. \$217,500 over three years.

OVERSEAS VISITORS

The following scientists visited the Centre during Year Two:

Dr. Kellar Autumn
Lewis and Clark College, Oregon
USA

Dr. Geoff Birchard
George Mason University
USA

Prof. Daniel Blackburn
Trinity College, Hartford, Connecticut
USA

Dr. Dona Boggs
Eastern Washington University
USA

Dr. Kim Burnham
Oklahoma State University
USA

Dr Dietmar Cieslik
University of Griefswald
Germany

Dr. Alan Dixon
Zoological Society of San Diego
USA

Dr. Andreas Dress
University of Bielefeld
Germany

Tandora Grant
Zoological Society of San Diego
USA

Prof Masami Hasegawa
Institute of Statistical Mathematics, Tokyo
Japan

Prof Charles Kurland
Lund University
Sweden

Tom LoFaro
Gustavus Adolphus College
USA

Dr Peter Matthews
National Museum of Ethnology, Osaka,
Japan

Prof Brook Milligan
New Mexico State University
USA

Ragini Mudaliar
University of South Pacific
Fiji

Lee Pagni
Zoological Society of San Diego
USA

Art Risser
Zoological Society of San Diego
USA

Dr Carol Scaramizzi
University of Sydney
Australia

Alexandra Schulmeister
Germany

Professor Peter Waddell
University of North Carolina
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Lusheng Zhang
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