

SYSTANZ
General Meeting
and
Plant Species
Radiation Workshop

Skotel, Whakapapa Village,
12th-13th February, 2004

Wednesday 11th

8pm-9pm registration at the Skotel for the 2 day meeting

Note that you can also pay your subscription to SYSTANZ at registration!! Dianne will be able to accept cash or cheques for the latter. The registration costs for the actual meeting can be paid by EFTPOS/Mastercard/Visa or cash

The registration fee is requested from all participants and partners as the fee covers the cost of food.

2 day fee: \$80 NZ

The 2 day registration fee includes 2xbreakfasts, 2xmorning and afternoon teas, 2xlunches and the barbeque on Thursday evening.

Thursday 12th

Plant species radiation workshop

9.00-9.10am welcome

9.10-10.30am Contributions to themes identified for IBC symposium*

10.30-11am morning tea

11.00-12.30pm Contributions to themes identified for IBC symposium*

12.30 – 2pm lunch

2.00-3.30pm Identification of new themes; plant species radiation in the Pacific/ memo of understanding between AWCME and Univ. of the South Pacific; writing a plant species radiation book and web resources; Funding attempts made in 2003; proposals for 2004; the BioQUEST consortium and producing educational modules; proposals for symposia at MBE 2005 and the US Evolution meeting 2007

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1. New Zealand as a model system for investigating plant biodiversity: a comparison with volcanic island archipelagos.
2. New Zealand as a testing ground for evaluating the relative importance of vicariance and dispersal in the Southern Hemisphere
3. The impact of tectonic and climate change on the evolution of the New Zealand flora
4. Morphological and Ecological Diversity in the New Zealand flora
5. Plant breeding systems and their role in adaptive radiation
6. Radiation with and without polyploid series
7. Model (and non-model) plants in the study of species radiation

3.30-3.50pm afternoon tea

Following afternoon tea the general SYSTANZ meeting begins

Thursday 12th

3.50- 4.00pm

welcome

4.00- 4.20pm

Michael Knapp Fangorn Forest is not a Gondwanan relic

4.20- 4.40pm

Ellen Cieraad New Zealand Cenozoic fossil ferns, species radiation and long-distance dispersal

4.40- 5.00pm

Adrienne Markey *Coprosma talbrockiei*: an oddball sheds light on the Coprosminae

5.30-6.00pm

registration for those attending only the general SYSTANZ meeting

Note that you can also pay your subscription to SYSTANZ at registration!! Dianne will be able to accept cash or cheques for the latter. The registration costs for the actual meeting can be paid by EFTPOS/Mastercard/Visa or cash.

The registration fee is requested from all participants and partners as the fee covers the cost of food.

1 day fee: \$45 NZ

The 1 day registration fee includes 1xbreakfast, 1xmorning and afternoon tea, 1xlunch and the barbeque on Thursday evening.

6.00-7.30pm

barbecue

8pm- 8.20pm

Phil Novis New Zealand snow algae – relevance to the origins of green plant diversity

8.20- 8.40pm

Lara Shepherd Genetic Diversity of Ancient and Modern Kiwi

8.40- 9.00pm

Quentin Atkinson How old is the Indo-European language family? A biological solution to a linguistic problem

9.00-9.20pm

Sharyn Goldstien - Phylogeny and evolution of the Nacellidae limpets of New Zealand: a Tethyan influx or southern radiation?

Friday 13th

SYSTANZ presentations continue

9.00-9.10am welcome

9.10-9.30am Phil Garnock Jones Evolution, taxonomy, and biogeography of Southwest Pacific Gesneriaceae Trib. Coronanthereae

9.30-9.50am Ilse Breitwieser The relationships of *Haastia* (Asteraceae)

9.50-10.10am Steve Wagstaff Phylogeny and Classification of *Brachyglottis* (Senecioneae, Asteraceae): an example of a rapid species radiation in New Zealand

10.10-10.30am Rob Smissen Phylogenetic and phylogeographic investigations in New Zealand endemic Gnaphalieae (Asteraceae)

10.30-11.00am morning tea

11.00-11.20am Kylee Simpson Research and Collection Application/Permits

11.20-11.40am Rod Hitchmough Re-establishing a workable national tissue collection as a resource for systematics and population genetics research on New Zealand indigenous biota

11.40-12.00am Peter Lockhart Progress and directions for SYSTANZ?

12.00-12.30pm Session Discussion

12.30-2.00pm lunch and AGM

2.00-2.20pm Richard Gardner *Meterosideros*: interspecific hybridization and ice age refugia

2.20-2.40pm Kuo-fang Chung Global Alpine Biogeography: Insights from Phylogenetics and Phylogeography of Trans-Pacific Genus *Oreomyrrhis* (Apiaceae)

2.40-3.00pm Leon Perrie Genetic variation is not concordant with the discrete morphology of Hooker's and Colenso's spleenwort ferns

3.00-3.20pm Tristan Armstrong The genetics of speciation in Australian alpine *Ranunculus*

3.30-4.00pm afternoon tea

4.00- 4.20pm Adrian Patterson Too many hosts, too few parasites: the effect of multiple hosts in co-evolutionary analyses

4.20- 4.40pm Martyn Kennedy Cophylogeny of the Pelecaniformes and their parasitic lice

4.40- 5.00pm Steve Trewick and Mary Morgan Richards Estimating the Age of New Zealand's Fauna

Michael Knapp¹, Karen Stöckler¹, David Havell^{1,2}, Frédéric Delsuc¹, Federico Sebastiani³ and Peter J. Lockhart¹

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Fangorn Forest is not a Gondwanan Relic

With acceptance of Alfred Wegeners' theory of the "Kontinentaldrift" in the 1960's, the distributions of Southern Hemisphere *Nothofagus* (beech) species has become iconic for ancient Gondwanan relationships that reach back into the Cretaceous. This paradigm has New Zealand *Nothofagus*, like the ratites and tuatara, as passive sailors upon a "Moa's Ark" that rafted away from other Gondwanan landmasses 80 million years (Myr) ago. Mysterious and ancient, the New Zealand beech forests are associated with imagery of "Walking with Dinosaurs" and "Lord of the Rings". An alternative explanation for their origins seems almost inconceivable given that *Nothofagus* seeds are generally thought to be poorly suited for dispersal across large distances or oceans. However, palynological evidence poses a dilemma. The fossil record raises the possibility that *Nothofagus* species reached the New Zealand archipelago by Tertiary trans-oceanic distance dispersal, and not by continental drift during the Cretaceous. Our aim has been to test the Moa's Ark hypothesis with phylogenetic, and in particular, molecular clock analyses of chloroplast DNA sequences. In this talk we present some of our results.

Ellen Cieraad and Daphne E. Lee

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New Zealand Cenozoic fossil ferns, species radiation and long-distance dispersal

The excellent Cenozoic fossil record of New Zealand fern spores and macrofossils provides an informative basis for understanding fern biogeography, speciation, radiations, extinctions and ecosystem stability. A new database of all published fern fossil records for the past 70 million years shows which fern families and lineages have been present in the New Zealand region since the breakup of Gondwana and which have arrived in the Late Cenozoic. It also allows for estimates to be made of times of species radiation. The database gives an indication of the duration of fern species, based on spore morphology, and the time of origin of extant species. Ferns have been a major component of forest ecosystems in the New Zealand region for at least the past 40 million years. There is no biotic imprint reflecting the reduced land area during the Late Oligocene – Early Miocene marine transgression. Additionally, the database makes it possible to assess the relative importance of long-distance dispersal in the New Zealand fern flora at various time intervals.

Adrienne S. Markey, Janice M. Lord and David A. Orlovich

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***Coprosma talbrockiei*: an oddball sheds light on the Coprosminae**

Although the Rubiaceae is a characteristically pantropical family, it is represented in southern temperate regions primarily by the austral tribe, Anthospermeae. One subtribe, Coprosminae is a small, closely-related group distributed in and around the Melasian-Australasian-South Pacific region. There is considerable overlap in the geographical ranges of three genera (*Nertera*, *Coprosma* and *Leptostigma*), whilst two genera persist as isolated, monotypic outliers in Australia, (*Durrintonia*) and New Caledonia (*Normandia*). Anderson *et al.* (2001) produced the first systematic investigation into subtribal relationships using sequences from both the ITS region of nrDNA and rps-16-intron from cpDNA. This clearly demonstrated that not only were *Leptostigma*, *Nertera* and *Coprosma* three, distinct, monophyletic genera, but that both *Durrintonia* and *Leptostigma* had diverged relatively early (early Tertiary?) from the progenitors of both *Coprosma* and *Nertera*, whilst the divergence of *Coprosma* from *Nertera* was more recent (late Tertiary?).

However, *Coprosma talbrockiei* was omitted from these analyses. This hermaphroditic, diminutive herb has always been regarded as aberrant for the genus, and was used as one justification for reducing both *Nertera* and *Leptostigma* to sections within *Coprosma* (Heads 1996). Furthermore, the sequence for *Normandia* used in the analyses of Anderson *et al.* (2001) appears to be incorrect. In this study, phylogenetic relationships within the *Coprosminae* have been reconstructed from both nrDNA sequences and the rps 16-intron of cpDNA. Results have clearly placed *C. talbrockiei* outside of *Coprosma* and *Nertera*, and allied it with *Durrintonia*. *C. talbrockiei*, *Durrintonia* and *Normandia* appear to be deeply divergent from the *Coprosma-Nertera* clade. Both phylogeographic patterns within the Coprosminae and the taxonomic status of *C. talbrockiei* are discussed.

Anderson, C.L., J.H.E. Rova and L. Andersson (2001). Molecular phylogeny of the tribe Anthospermeae (Rubiaceae): systematic and biogeographic implications. *Australian Systematic Botany* 14: 231-244.

Heads, M.J. (1996). Biogeography, taxonomy and evolution in the Pacific genus, *Coprosma* (Rubiaceae). *Candollea* 51, 382-405.

Phil Novis

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New Zealand snow algae – relevance to the origins of green plant diversity

Chlainomonas kolii is a rare and extremely unusual unicellular alga that occurs in summer snowfields. So far it has been found in two collection sites in New Zealand, and six sites in the Pacific Northwest of the United States.

Most obligate snow algae belong to the biflagellate genera *Chlamydomonas* and *Chloromonas*, which reproduce by means of zoosporangia and produce hypnozygotes (sexually produced resting cysts). By contrast, a sexual cycle is unknown in the quadriflagellate *Chlainomonas*, and vegetative division occurs by a budding-like process. *C. kolii* cells are surrounded by a unique outermost wall of lattice-like material.

These features suggest that *Chlainomonas* may be an early-divergent member of the UTC clade (sister group to the land plant lineage). Early evolutionary events leading to modern UTC diversity are still controversial. Firstly, the conservation of flagellar apparatus structure as displayed by other algal groups appears to be violated by the most popularly accepted phylogenetic tree. Secondly, support for the order of divergence of the three major groups is not always high in phylogenetic trees constructed using 18S rDNA and *rbcL* data. However, the common ancestor of all UTC organisms is universally believed to be a

quadriflagellate unicell. Therefore, study of *Chlainomonas kolii* will make an important contribution to knowledge of UTC evolution.

Lara Shepherd and David Lambert

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Genetic Diversity of Ancient and Modern Kiwi

Fossil evidence suggests that kiwi were once distributed across the whole of New Zealand. However, the populations of the four currently recognised kiwi species have been greatly reduced through habitat loss and introduced predators, such that kiwi are now considered endangered and their conservation is actively managed. A primary goal of conservation programmes for endangered species is an understanding of genetic diversity so that this diversity can be best maintained and problems like inbreeding can be avoided.

Our current research involves identifying DNA markers from modern kiwi samples to provide an understanding of the types and levels of genetic variation currently present. To compare present day diversity with that that existed pre-decline, we will assay genetic variation using ancient DNA methodology from museum skins and subfossil kiwi bones. Furthermore, only little spotted kiwi can currently be identified from bone morphology (Worthy, 1997). DNA identification may allow the determination of the former ranges of both great spotted kiwi and brown kiwi that may also be of importance for the re-introduction of kiwi to areas where they are locally extinct.

The results obtained from this study will give us a better understanding of present and past patterns of genetic variation in kiwi and thus allow conservation management to make more informed decisions regarding the kiwi recovery programme.

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How old is the Indo-European language family? A biological solution to a linguistic problem

Languages, like genes, provide vital clues about human history (Gray & Jordan, 2000). The origin of the Indo-European language family is 'the most intensively studied, yet still most recalcitrant, problem of historical linguistics' (Diamond & Bellwood, 2003). Due to slow rates of genetic change, admixture, and the relatively recent timescales involved, genetic analyses have not conclusively resolved debates about time-depth in Indo-European. Languages, however, change much faster than genes and so contain more historical information at shallower time-depths. Despite this, traditional means of linguistic analysis have also been unable to provide convincing evidence of Indo-European origins. This is primarily due to problems associated with variable rates of language evolution and an inability to quantify the degree of statistical uncertainty in estimated ages. Here, we explore the application of new phylogenetic date estimation techniques to linguistic data. These methods are able to estimate divergence times and the uncertainty associated with each estimate, even under conditions of rate heterogeneity. We combine maximum-likelihood models of language evolution, Bayesian inference of phylogeny and rate smoothing algorithms to test between two theories of Indo-European origin - the 'Kurgan expansion' and 'Anatolian farming' hypotheses. The Kurgan hypothesis centres on possible archaeological evidence for an expansion into Europe and the near-East by Kurgan horsemen beginning in the sixth millennium BP (Gimbutas, 1973). The Anatolian hypothesis claims that Indo-European languages expanded with the spread of

agriculture from Anatolia around 8,000 to 9,500BP (Renfrew, 1987). In striking agreement with the Anatolian hypothesis, our analysis of a matrix of 87 languages with 2,449 lexical items produced an estimated age range for the initial Indo-European divergence of between 7,800BP and 9,800BP (Gray & Atkinson, 2003). The results were robust to changes in coding procedures, calibration points, rooting of the trees and priors in the Bayesian analysis.

Diamond, J. & Bellwood, P. Farmers and Their Languages: The First Expansions. *Science* 300, 597 (2003).

Gimbutas, M. The beginning of the Bronze Age in Europe and the Indo-Europeans 3500-2500 B.C. *Journal of Indo-European Studies* 1, 163-214 (1973).

Gray, R. D. & Atkinson, Q. D. Language-tree divergence times support the Anatolian theory of Indo-European origin. *Nature* 426, 435-439 (2003).

Gray, R.D. & Jordan, F.M. Language trees support the express-train sequence of Austronesian expansion. *Nature* 405, 1052-1055 (2000).

Renfrew, C. *Archaeology and Language: the Puzzle of Indo-European origins*. London: Jonathan Cape (1987).

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Phylogeny and evolution of the Nacellidae limpets of New Zealand: a Tethyan influx or southern radiation?

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The biogeography of the limpet genus *Cellana* is based on shell morphology and a poorly represented fossil record. The genus is primarily distributed within the Indo-West Pacific (IWP), but reaching out to the Juan Fernandez Island and South as far as Campbell Island in the Sub-Antarctic region. The sister taxa, *Nacella*, are restricted to the southern waters, concentrated around the Magellanic area. It has been suggested that *Cellana* are of warm-water derivation, such as the Tethys Sea, with southern relicts from these warmer geological times reaching to the Sub-Antarctic. Phylogenetic analysis of partial sequence of the 12S mitochondrial gene, from 34 limpet species: 23 *Cellana*, 1 *Nacella* and 10 Patellids, allowed us to test this hypothesis of Northern origin against an alternative southern radiation. Marine regions represented by the *Cellana* samples included the IWP, Australia and New Zealand. The main feature of the analysis was the monophyletic clade of New Zealand species, excluding *C.ornata* which is basal to all other species. We show strong support for southern radiation of the New Zealand clade and suggest Gondwana links and southern radiation for the entire family.

Vincent Woo ¹, Phil Garnock-Jones ¹, Peter Lockhart ².

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Evolution, taxonomy, and biogeography of Southwest Pacific Gesneriaceae Trib. Coronanthereae.

The tropical family Gesneriaceae is related to Scrophulariaceae and Plantaginaceae and is usually divided into two subfamilies, Gesnerioideae and Cyrtandroideae. Coronanthereae is an anomalous South Pacific tribe with 20 species in 9 genera. Molecular characters (ITS, *trnL-F*, and *trnE-T* sequences) tell consistent stories, but ITS is more informative than the chloroplast sequences. Preliminary analyses suggest the tribe is monophyletic and sister to other Gesnerioideae, supporting classifications that place it as a tribe within that subfamily. The primary division of the tribe is into two sister clades, one largely South American, but including the Australian *Fieldia*, the other comprising the Australian *Lenbrassia* and four Pacific genera. Thus the recent taxonomic combining of *Fieldia* and *Lenbrassia* is not supported. The New Caledonian genera, *Coronanthera* and *Depanthus*, are not each other's nearest relatives despite their very similar flowers. *Coronanthera* is monophyletic, and comprises a rough-leaved clade nested in a smooth-leaved grade. It is sister to rough-leaved *Rhabdothamnus* of New Zealand. *Depanthus* is sister to *Negria* of Lord Howe Island; both are trees with large leaves. *Lenbrassia* of Queensland is sister to *Depanthus* + *Negria*. The young fossil record of the family suggests this distribution could be of mid to late tertiary age, and might have involved two dispersals from South America to Australasia, perhaps across Antarctica, and Pacific island-hopping. The tribe seems to have undergone four independent losses of brightly coloured flowers associated with bird pollination, which was probably the condition in its common ancestor, whereas vegetative characters might be more conservative indicators of relationships.

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The relationships of *Haastia* (Asteraceae)

The tribal and generic affinities of *Haastia*, an endemic New Zealand genus of three species, are discussed. *Haastia* has been placed with both the Gnaphalieae and Astereae, and more recently listed as unassigned to a tribe within the Asteroideae. Secretory canals in the leaves or leaf sheaths exclude *Haastia* from the Gnaphalieae, and senecioid pollen excludes it from the Gnaphalieae and the Astereae. In recent phylogenetic analyses of New Zealand Asteraceae *Haastia* is nested in the genus *Brachyglottis* (Senecioneae). Results from preliminary ITS and *trnK/matK* sequence analyses of New Zealand Senecioneae are presented and key characters of *Haastia* are compared with other genera in Senecioneae.

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Phylogeny and Classification of *Brachyglottis* (Senecioneae, Asteraceae): an example of a rapid species radiation in New Zealand

Phylogenetic analyses of ITS and 5' *trnK* / *matK* spacer sequences were undertaken of 39 species representing the range of morphological variation in the genus *Brachyglottis* and putative outgroups. Independent analyses of the sequence data were largely congruent and when combined provided stronger support for relationships. The results suggest that *Brachyglottis* as currently circumscribed is paraphyletic. However, a more inclusive monophyletic group was supported that consists of the genera *Bedfordia*, *Brachyglottis*, *Dolichoglottis*, *Haastia*, and *Traversia*. Short branch lengths suggest there has been a spectacular adaptive radiation of the *Brachyglottis* alliance in recent times. The species are morphologically diverse and occupy a wide range of ecological niches in New Zealand, and yet exhibit very little sequence variation.

Rob Smissen

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Phylogenetic and phylogeographic investigations in New Zealand endemic Gnaphalieae (Asteraceae)

Sequencing of the chloroplast *trnL* intron, *trnL-trnF* intergenic spacer and *psbA-trnH* intergenic spacer in *Raoulia* and allied genera has revealed considerable cpDNA polymorphism. Much of this polymorphism is within species, and even within individual populations. One species, *Raoulia eximia*, appears to have a considerable geographic component to genetic variation based on multi-locus fingerprinting and chloroplast DNA polymorphism, and may be continuing to interbreed with other species. However a second species, *Helichrysum lanceolatum*, has little geographic component to multi-locus genetic variation and appears to be more completely reproductively isolated.

Kylee Simpson

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Research and Collection Application/Permits

I will be giving a presentation on the new process for applying for collection and research permits from land managed by the Department of Conservation. This new system aims to protect resources on Departmental managed land, provide a consistent approach throughout the country and to minimise administrative costs to the applicants and the Department.

The new system has two processes, a “high impact” and “low impact”. The criteria for deciding which process applies to an application are determined by the effects of the collection methods. The purpose for providing the two processes is to ensure that applications with potentially significant effects are given proper consideration and those that will have little or no effect are not subjected to an unnecessary process.

I will outline how to go about applying for a permit, including how to complete an assessment of effects. I will also outline the standard conditions that will be in any permit granted. I will give out information sheets and facilitate any questions that there may be.

Rod Hitchmough

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Re-establishing a workable national tissue collection as a resource for systematics and population genetics research on New Zealand indigenous biota

DOC needs to address the curation of samples collected for genetics research by DOC staff or under DOC permits. For example, samples have been passed to third parties, sometimes overseas, without DOC’s knowledge. DOC has an obligation to address Iwi concerns about such samples. During the 1980s the National Frozen Tissue Collection was set up as a repository for frozen specimens. It was initially housed at Te Papa, but problems with -80 degree freezers meant that the collection was transferred to Victoria University to allow easier transfer of contents between freezers in the case of breakdown. Since then the university has carried the entire cost of curation, including replacement of freezers, but its ability to service outside users is extremely limited. The Department would like to see the collection revitalised, so that we can make it a condition of collecting permits for researchers that all material collected be accessioned to the collection, and subsampled for specific research projects. Te Papa has no genetics research capability itself, and is therefore free of vested interest in the use of the material. We would like to receive feedback on this proposal and will distribute a submission form.

Peter Lockhart¹ and Dietrich Radel²

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Progress and Directions for SYSTANZ?

This year we have been reconstructing the SYSTANZ web site. In this short talk we will present the latest version and discuss some future plans

^{1,2}Kuo-fang Chung, ¹Barbara A. Schaal, ³Ching-I Peng and ²Peter H. Raven

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Global Alpine Biogeography: Insights from Phylogenetics and Phylogeography of Trans-Pacific Genus *Oreomyrrhis* (Apiaceae)

The alpine biome is the only terrestrial ecosystem that is distributed globally. Understanding the evolution of plant species in this widespread ecosystem will provide insight into the origins of global biodiversity. Recent studies in Europe suggest that Pleistocene glaciations, landscape heterogeneity and dispersal dynamics have been the major factors shaping geographic distribution and genetic variation in alpine plants. However, few studies have attempted to test these ideas outside of Europe, on a global scale. The trans-Pacific disjunct genus *Oreomyrrhis*, found in isolated alpine systems of different South Pacific latitudes, presents an ideal study system to investigate global alpine biogeography. A phylogeny of *Oreomyrrhis* based on nuclear ITS data places *Oreomyrrhis* into Subtribe Scandicinae of tribe Scandiceae, Apiaceae. Within Scandicinae, *Oreomyrrhis* is nested within *Chaerophyllum* and, along with North American *C. procumbens* and *C. tainturieri*, forms a monophyletic clade. The low sequence divergence and poorly resolved phylogenetic relationships suggest a recent origin of *Oreomyrrhis* and support long-distance dispersal as a biogeographic hypothesis. These data are inconsistent with a vicariant scenario that invokes landbridges or Gondwanaland breakup. Preliminary phylogeographic studies of Taiwanese *Oreomyrrhis* using the chloroplast atpB-rbcL intergenic spacer region reveals high genetic variation and low geographic structure for the haplotypes sampled. These findings support the predictions of the displacement refugia model which postulates that repeat population range expansions and contractions in response to glacial cycles have produced low phylogeographic structure and subdivision among current alpine populations.

Leon Perrie and Patrick Brownsey

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Genetic variation is not concordant with the discrete morphology of Hooker's and Colenso's spleenwort ferns

William Colenso described *Asplenium hookerianum* and *A. colensoi* in the same 1845 publication. Morphologically, they are discrete and readily recognisable, with the frond segments of *A. hookerianum* being broad, while those of *A. (hookerianum* var.) *colensoi* are narrow. They often occur together, and while populations with only broad frond segments are also common, populations of 'pure' *colensoi* are unknown. Genetic variation as detected by (1) AFLP DNA-fingerprinting and (2) DNA sequencing of chloroplast loci is not concordant with this discrete morphological polymorphism. This suggests that, despite being morphologically diagnosable, *hookerianum* and *colensoi* are best treated at the varietal level.

Richard C. Gardner, Peter J. de Lange, D. Jeanette Keeling, Tharushini Bowala, Heather A. Brown, Megan Too, Robin Gardner-Gee, Shane D. Wright
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***Metrosideros*: Interspecific hybridization and ice age refugia**

Nucleotide sequences of the ITS region of nrDNA from 45 individual trees has confirmed that inter-specific hybridisation occurs naturally between all three main species of *Metrosideros* in New Zealand: *M. umbellata* (Southern rata), *M. robusta* (Northern rata) and *M. excelsa* (pohutukawa). Morphological hybrids typically showed sequence mixtures, while a few phenotypically normal individuals of each species showed evidence of sequence mixtures or mosaic sequences. These results suggest a history of ongoing hybridisation and introgression between the three species.

Chloroplast DNA sequence for the trnL region was also obtained for over 200 individual trees sampled across the entire geographic range of each species. Twelve different haplotypes were shared across the species, but the haplotypes showed a strong phylogeographic pattern. A single chloroplast haplotype was found in most areas of each island (independent of host species), but there was considerable haplotype diversity in the northern and coastal regions of both islands. We suggest that these regions of haplotype diversity (Nelson, the Far North and Coromandel) represent ice age refugia. The proposed refugia correspond to current localities of the highest average winter temperatures. The sharing of chloroplast haplotypes between species of *Metrosideros* confirms a history of repeated hybridisation and introgression for these plants, possibly initiated by periods of refugial confinement.

Tristan Armstrong

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The genetics of speciation in Australian alpine *Ranunculus*

Adaptive speciation is typically associated with the rapid evolution of diverse and contrasting morphologies among sister lineages. Little is understood about the nature of genetic changes contributing to this fundamental evolutionary process. Although studies of morphogenesis in model systems suggest increasingly that few genes may be responsible for dramatic alterations in plant architecture, natural case studies are almost absent. Here, a biometrical quantitative genetic approach is used to investigate leaf shape inheritance in two morphologically divergent species of Australian alpine *Ranunculus*. The contrasting morphologies exhibited by each taxon imply direct adaptation to specific environmental stresses associated with distinct alpine microhabitats. Despite high levels of interspecific reproductive compatibility and frequent local hybridization, distinctive parental morphologies are consistently maintained in natural populations.

Leaf shape inheritance was examined quantitatively using artificially generated parental lines and F₁, F₂ and backcross hybrid progeny arrays. Simple quantitative models were fitted to the generation means and variances of six leaf shape traits. Models indicated that leaf morphology is controlled by a number of independently segregating genes with simple additive and dominance effects. No linkage or pleiotropy was detected. Continuous variation in trait expression in segregating generations and the absence of bounded character states suggested that many genes are involved in the control of each trait. This finding conflicts with recent research in *Arabidopsis* and model crop species where leaf architecture is often controlled by only one or two genes with major effect. The data support a model under which parental phenotypes are determined by natural selection on traits under polygenic control involving independent genes. This finding provides a contrast with many other studies of hybridization where parental phenotypes are controlled by strongly linked genes.

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Too many hosts, too few parasites: the effect of multiple hosts in co-evolutionary analyses

One of the main assumptions of cospeciation studies over the last decade is that associate species, e.g. parasites, are relatively host specific. However, parasite species are usually found on multiple host species. Even louse species, considered model cospeciation organisms, are found on an average of two bird species. The effect that multiple hosts have on cophylogenetic analyses has not been examined. In this study, penguins and their *Austrogoniodes* louse species were used to understand coevolution in this group. Widespread louse species were found to be critically important in determining whether this group was cospeciating with their hosts. As a result of this analysis a new type of coevolutionary event, cophylogenetic inertia, was created.

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***Pectinopygus*: heirlooms or souvenirs? Cophylogeny of the Pelecaniformes and their parasitic lice**

What is the cophylogenetic history of these groups? Does it represent a nice, simple, elegant story of codivergence, where *Pectinopygus* tracks the evolutionary history of their pelecaniform hosts? Or do these lice present a complex story of host switching, perhaps even further confused by duplication events and the loss of lineages? Or do these lice, like many other cophylogenetic systems, present a story that is the combination of all these processes?

Inferences about the relative importance of these processes for this host/associate system were made using molecular trees for the hosts and parasites and TreeMap2. The results suggest that this mostly appears to represent a story of codivergence, where *Pectinopygus* tracks the evolutionary history of their hosts. Some host-switching has occurred (e.g., the red-footed booby louse), whereas other host switches and losses have been postulated in areas where the louse phylogeny is poorly supported.

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How old is New Zealand's extant biodiversity? Estimates from invertebrate DNA

Studies of New Zealand's endemic fauna using DNA sequences have allowed us to test hypothesis about the processes that have lead to the current distribution and abundance of extant species and given us estimates of the approximate age of that diversity. Species radiations can be linked with geological events and era. Recent mountain building and Pliocene Islands have apparently had a major role in the origin of new insect species. Most invertebrate studies have found that many species in New Zealand are older than the Pleistocene but younger than the Miocene. In contrast, the New Zealand weta have multiple lineages that data back to the Oligocene and provide evidence of speciation during the Miocene, Pliocene and Pleistocene.

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