2010 Australian Systematic Botany Society Conference

Lincoln University, Canterbury, New Zealand

29 November – 3 December 2010

"Systematic botany across the ditch: links between Australia and New Zealand"

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Welcome to ASBS 2010

The organising committee, on behalf of Landcare Research's Allan Herbarium and the New Zealand Plant Radiation Network, welcome you to Lincoln for the 2010 conference of the Australian Systematic Botany Society.

Lincoln is located on the Canterbury Plains to the west of Banks Peninsula, 22 kilometres south of Christchurch. The Canterbury Plains are a lowland area of east-central South Island, New Zealand. The plains cover an area of 240 by 70 km, bordering on the Pacific Ocean. The Rangitata, Rakaia, and Waimakariri are the principal rivers, flowing east from the Southern Alps to cross the plains, which have relatively hot summers and generally low humidity and a mean annual rainfall of less than 750 mm. The major earthquake on September 4, 2010 revealed a previously unknown geological fault beneath the Canterbury Plains and created a surface rift that offset features by as much as four meters in places.

Most activities for this year's ASBS Symposium will take place at the Stewart Lecture theatre of Lincoln University, in walking distance from Landcare Research. Landcare Research, a Government-owned Crown Research Institute, is New Zealand's foremost environmental research organisation. It is custodian of several biological research collections and databases that have been designated by the Government as being of "significant national importance". One of these is the Allan Herbarium, New Zealand's largest herbarium. The herbarium now holds about 600,000 specimens with the oldest samples collected during Captain Cook's first voyage to New Zealand, 1769 – 1770. It contains species from around the world, but specialises in plants from the New Zealand region and the South Pacific.

The United Nations declared 2010 to be the International Year of Biodiversity. It is a celebration of life on earth and of the value of biodiversity for our lives. New Zealand's biodiversity is of great importance to the world and especially New Zealanders. Our forests, rivers, lakes and coasts provide a backdrop to our way of life; and species such as kiwi, kauri and weta have come to symbolise the special relationship New Zealanders have with the environment.

The theme of the conference "Systematic botany across the ditch: links between Australia and New Zealand" will highlight the close botanical connections of Australia and New Zealand and will hopefully inspire even closer collaborations.

We have three interesting keynote speakers. Dr Matt McGlone, Landcare Research, and Dr Peter H. Weston, National Herbarium of New South Wales and current president of ASBS, will present some of their views on biogeography. Professor Phil Garnock-Jones, who is retiring from his position at Victoria University of Wellington, will reflect on national and international developments of plant taxonomy during his career.

The conference is dedicated to Dr Eric Godley (1919-2010). Dr Eric J. Godley OBE, Hon. DSc (Cantuar.), FRSNZ, AHRIH has made a sustained and distinguished contribution to New Zealand botany. After completing degrees in Auckland and Cambridge he spent most of his career as the Director of Botany Division of the Department of Scientific and Industrial Research. Under his leadership, the Division greatly expanded its research and extension programmes, established a network of regional stations, and became New Zealand's principal centre for research on native and naturalised plants. Eric Godley had wide research interests. In particular, he published extensively on the reproductive biology of the native flora, the biogeography of southern temperate floras, and botanical history.

We would like to thank the sponsors of this year's symposium, Landcare Research and the ASBS. We also thank CSIRO Publishing and Australian Systematic Botany for their sponsorship of the best student oral presentation (Pauline Ladiges Prize) and the award for the best poster.

Thanks go to all who have helped in the preparation of ASBS 2010. I would like to thank all Allan Herbarium staff, especially Peter Heenan for leading the organising committee. I would also like to thank Jan Latham of the Professional Development Group, Lincoln University.

The organising committee this year is Ilse Breitwieser, Murray Dawson, David Glenny, Peter Heenan, Phil Novis and Rob Smissen, all from the Allan Herbarium.

On behalf of the organising committee, I would like to thank you for coming to Lincoln. We hope you will enjoy the ASBS 2010 Symposium.

Dr Ilse Breitwieser
Director, Allan Herbarium
Chair, ASBS Symposium 2010

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Associated meetings

ASBS council meeting – Landcare Research, Waikirikiri video conference room

13.00 – 17.00 Monday 29 November

ASBS Annual General Meeting – Lincoln University, Stewart Lecture Theatre

16.00 – 17.00 Tuesday 30 November

ASBS editors meeting – Lincoln University, Forbes Building, first floor, room A

17.00 – 18.00 Thursday 2 December

NZPRN meeting – Lincoln University, Stewart Lecture Theatre

17.00 – 18.00 Thursday 2 December

Contacts

Conference website:
http://www.landcareresearch.co.nz/news/conferences/asbs2010

email: asbs2010@landcareresearch.co.nz

Lincoln University (venue). Ellesmere Junction Road/Springs Road, Lincoln, Canterbury, New Zealand.

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Conference program

Monday 29 November 2010

13.00 – 17.00	ASBS council meeting – Waikirikiri video conference room, Landcare Research
17.00 – 19.00	Registration mixer – Stewart lecture theatre foyer, Lincoln University

Tuesday 30 November 2010

08.30 – 09.00	Registration – Stewart lecture theatre foyer, Lincoln University
09.00 – 09.20	Conference Welcome (Ilse Breitwieser)
09.20 – 10.20	**Session 1 (chair: Ilse Breitwieser)**
09.20 – 10.00	Taking refuge: haplotypes and plant biogeography
	Keynote speaker: Matt McGlone, Landcare Research, Lincoln, New Zealand
10.00 – 10.20	The disjunct distribution of fierce lancewood (*Pseudopanax ferox*)
	Leon Perrie & Lara Shepherd
10.20 – 10.40	Morning tea
10.40 – 12.20	**Session 2 (chair: Patrick Brownsey)**
10.40 – 11.00	Rapid diversification in *Puya* (Bromeliaceae) and Cenozoic climate change: a case study in the Chilean *Puya* clade
	Katharina Schulte, Daniele Silvestro, Klaus Winter, J. Andrew C. Smith & Georg Zizka
11.00 – 11.20	Speciation and phylogeography of *Telopea* and *Lomatia* (Proteaceae)
	Melita L. Baum, Michael D. Crisp, Maurizio Rossetto & Peter H. Weston
11.20 – 11.40	Patterns of phylogenetic diversity in wirerush, *Empodisma minus* (Restionaceae).
	Steven J. Wagstaff & Bev Clarkson
11.40 – 12.00	Hybrid stories from the central North Island of New Zealand
	Bruce D. Clarkson
12.00 – 12.20	Relationships, hybridisation and phylogeography of *Sophora*, with a focus on the origins of putative translocated *S. chathamica*
	Lara Shepherd, Peter de Lange, Peter Heenan, Leon Perrie & Peter Lockhart
12.20 – 13.20	Lunch

13.20 – 15.00	**Session 3 (chair: Bruce Clarkson)**
13.20 – 13.40	A progress report on the relationships and taxonomy of the *Lepidium oleraceum* complex
	Peter Heenan, Peter de Lange, Gary Houliston, Anthony Mitchell & Emilie Robin
13.40 – 14.00	Systematics of native New Zealand *Plantago*
	Heidi M. Meudt
14.00 – 14.20	Genome and chromosome analysis of New Zealand *Plantago* species
	Charles Wong & Brian Murray
14.20 – 14.40	Australians making themselves at home: the population genetics of some recent New Zealand invaders
	Gary Houliston, Peter Heenan, Ana Ramon-Laca & Reema Jain
14.40 – 15.00	Latina lingua tirones tirone
	Wayne A. Gebert
15.00 – 15.20	Afternoon tea
15.20 – 16.00	**Session 4 (chair: Phil Novis)**
15.20 – 15.40	New Zealand alpine flora in a changing climate: a model based assessment of *Pachycladon* (Brassicaceae)
	Christopher P. Bickford, Adrian Walcroft, Margaret M. Barbour & Peter B. Heenan
15.40 – 16.00	Sensible Seasons
	Tim Entwisle
16.00 – 17.00	ASBS Annual General Meeting

Wednesday 1 December 2010

09.00 – 10.20	**Session 5 (chair: Bill Barker)**
09.00 – 09.40	Cenozoic environmental change and the systematics of southern hemisphere plants
	Keynote speaker: Peter H. Weston, National Herbarium of New South Wales, Royal Botanic Gardens
09.40 – 10.00	Late Oligocene spores and pollen from Cosy Dell, Southland, New Zealand: a preliminary account
	Dallas Mildenhall, Elizabeth Kennedy, Mike Isaac & Daphne Lee
10.00 – 10.20	What do we really know about the history of Australian rainforests?
	Greg Jordan & Kale Sniderman
10.20 – 10.40	Morning tea

10.40 – 12.20	**Session 6 (chair: Karen Wilson)**
10.40 – 11.00	New Zealand's plants: how long have they been here?
	Daphne Lee, Jennifer Bannister, John Conran, Dallas Mildenhall & Greg Jordan
11.00 – 11.20	Fossil flowers from the Early Miocene Foulden Maar, New Zealand
	Jennifer Bannister, Daphne Lee, Ian Raine, Dallas Mildenhall & John Conran
11.20 – 11.40	Lauraceae at Foulden Maar: diversity and identity
	John G. Conran, Jennifer M. Bannister & Daphne E. Lee
11.40 – 12.00	Crossing the ditch? Historical biogeography of the trans-Tasman Styphelieae (Styphelioideae, Ericaceae)
	C. Puente-Lelievre, M.G. Harrington, E.A. Brown & D.M. Crayn
12.00 – 12.20	New interpretations of Myrtaceae evolution and biogeography using a dated molecular phylogeny
	Andrew H. Thornhill, Simon Y.W. Ho & Michael D. Crisp
12.20 – 13.20	Lunch
13.20 – 15.00	**Session 7 (chair: Brian Murray)**
13.20 – 13.40	New Zealand ferns and liverworts: do they share a common biogeographic history?
	David Glenny & Patrick Brownsey
13.40 – 14.00	Biogeography and systematics of the genus *Macrozamia* (Zamiaceae)
	James A. Ingham, Lyn Cook, Paul Forster & Mike Crisp
14.00 – 14.20	Preliminary molecular phylogeny and biogeography of *Coprosma* (Rubiaceae)
	Jason T. Cantley & Sterling C. Keeley
14.20 – 14.40	The Australasian side of Loganiaceae: phylogenetics and biogeography of Loganieae
	K.L. Gibbons, B, M.J. Henwood & B.J. Conn
14.40 – 15.00	Cultural and economic importance of intra-specific variation in *Phormium*
	Sue Scheele & Katarina Tawiri
15.00 – 15.20	Afternoon tea
15.20 – 17.00	**Session 8 (chair: Tim Entwistle)**
15.20 – 15.40	Taxonomy of *Amblysperma/Trichocline* (Asteraceae: Mutsieae), Western Australia's South American link?
	Greg Keighery & Bronwen Keighery

15.40 – 16.00	Diversity and relationships of the NZ marine red algae: what do we know?
	Wendy Nelson
16.00 – 16.20	The taxonomy of *Klebsormidium*
	Phil Novis
16.20 – 16.40	Do green algal photobionts co-evolve with their ascomycete hosts? A case study using *Menegazzia* (Parmeliaceae, Lecanoromycetes)
	Ben Myles, Jon Waters & David Orlovich
16.40 – 17.00	*Megaceros* (Anthocerotophyta): More than meets the eye
	D. Christine Cargill, Ish Sharma & Joe Miller
17.00 – 17.30	**Poster session**
18.00	Buses depart Lincoln University for conference dinner
18.30 – 19.00	Pre-dinner drinks
19.00	Conference dinner

Thursday 2 December 2010

09.00 – 10.20	**Session 9 (chair: Mike Bayly)**
09.00 – 09.40	How to look, again, at hebe
	Keynote speaker: Phil Garnock-Jones, School of Biological Sciences, Victoria University of Wellington
09.40 – 10.00	Molecular phylogenetics of *Acacia*
	Joseph Miller & Daniel Murphy
10.00 – 10.20	The primrose and its relatives: an extreme case of species paraphyly
	Alexander N. Schmidt-Lebuhn, Barbara Keller, Jurriaan de Vos & Elena Conti
10.20 – 10.40	Morning tea
10.40 – 12.00	**Session 10 (chair: Heidi Meudt)**
10.40 – 11.00	The evolution of *Wahlenbergia* (Campanulaceae) in Australasia
	Jessie M. Prebble
11.00 – 11.20	Testing species limits in *Schoenus* L. (Schoeneae, Cyperaceae)
	P.M. Musili, A.K. Gibbs, K.L. Wilson & J.J. Bruhl

11.20 – 11.40	The fate of *Mukia* and *Cucumis* (Cucurbitaceae) in Australia: Unexpected relationships and diversity
	Ian R.H. Telford, Patrizia M. Sebastian, Hanno Schaefer, Jeremy J. Bruhl & Susanne S. Renner
11.40 – 12.00	The Virtual Compositae: novel solutions to global problems in the largest flowering plant family on earth
	V. A. Funk
12.00 – 12.30	New Zealand e-flora launch
12.30 – 13.20	Lunch
13.20 – 15.00	**Session 11 (chair: Jeremy Bruhl)**
13.20 – 13.40	Composition, biology, and phytogeography and conservation of Western Australian Asteraceae
	Bronwen Keighery & Greg Keighery
13.40 – 14.00	Evolution of gender dimorphism in Australasian Malveae (Malvoideae, Malvaceae): boys and girls jumping the ditch?
	Jennifer A. Tate, Cynthia Skema, Todd McLay, Steve Wagstaff, Greg Jordan & William R. Barker
14.00 – 14.20	Genetic assessment of relationships between genera of the Subtribe Agrostidinae
	Austin J. Brown, Hugh B. Cross, Duncan Jardine, Daniel J. Murphy, David J. Cantrill & Andrew J. Lowe
14.20 – 14.40	Evidence for a single origin of stellate hairs in Australian members of *Olearia* (Asterotriche)
	A. Messina, N.G. Walsh., P.T. Green, S. Hoebee & T. Whiffin
14.40 – 15.10	Afternoon tea
15.10 – 15.20	Award of prizes
15.20 – 17.00	**Session 12 (chair: Ilse Breitwieser)**
15.20 – 15.40	Flora from the inside out: Camel diet and impact on vegetation of outback South Australia
	Hugh Cross, Vicki Thomson, Duncan Jardine & Kyle Armstrong
15.40 – 16.00	Re-delimiting species in *Uncinia*: a morphometric study of *Uncinia angustifolia*, *U. rupestris* and *U. zotovii*.
	Carlos A. Lehnebach
16.00 – 16.20	Impact of *Cytisus scoparius* (broom) on native vegetation at the Barrington Tops, New South Wales, including a comparison of a species list published in 1939 and species recorded since 2000 for this area - the case for voucher herbarium specimens
	John Hosking

16.20 – 16.40	*Kunzea ericoides* - a shared weed between countries or a remarkable example of a rapid species radiation?
	P.J. de Lange
16.40 – 17.00	Interspecific hybridisation and reproductive isolation among New Zealand plants
	Rob Smissen
17.00 – 18.00	**Concurrent meetings**
	ASBS editors meeting
	NZPRN meeting

Friday 3 December 2010

07.00 – 19.00	Field trip
07.30	Field trip bus departs Lincoln University
19.00	Field trip returns

Conference program overview

Mon. time	Monday item	Tue. time	Tuesday item	Wed. time	Wednesday item	Thu. time	Thursday item	Fri. time	Friday item
13.00-17.00	ASBS council meeting	08.30-0900	Registration	09.00-09.40	Keynote address - Peter Weston	09.00-09.40	Keynote address - Phil Garnock-Jones	07.00-19.00	Field trip
17.00-19.00	Registration function	09.00-09.20	Welcome - Ilse Breitwieser	09.40-10.00	Mildenhall *et al.*- Cosy dell	09.40-10.00	Miller & Murphy - *Accacia* phylogenetics		
		09.20-10.00	Keynote address - Matt McGlone	10.00-10.20	Jordan & Sniderman - rainforests	10.00-10.20	Schmidt-Lebuhn *et al.* - primrose		
		10.00-10.20	Perrie & Shepherd - *Pseudopanax*	10.20-10.40	Morning tea	10.20-10.40	Morning tea		
		10.20-10.40	Morning tea	10.40-11.00	Lee *et al.* - NZ plants: how long?	10.40-11.00	Prebble - *Wahlenbergia*		
		10.40-11.00	Schulte *et al.* - *Puya*	11.00-11.20	Bannister *et al.* - fossil flowers	11.00-11.20	Musili *et al.*- *Schoenus* species limits		
		11.00-11.20	Baum et al. - *Teopea & Lomatia*	11.20-11.40	Conran *et al.*- Foulden Maar	11.20-11.40	Telford *et al.*- *Mukia* & *Cucumis*		
		11.20-11.40	Wagstaff & Clarkson - *Empodisma*	11.40-12.00	Puente-Lelievre *et al.* - Styphelieae	11.40-12.00	Funk - The virtual Compositae		
		11.40-12.00	Clarkson - hybrid stories from NZ	12.00-12.20	Thornhill *et al.* - Myrtaceae	12.00-12.30	NZ eflora launch		
		12.00-12.20	Shepherd *et al.* *Sophora*	12.20-13.20	Lunch	12.30-13.20	Lunch		
		12.20-13.20	Lunch	13.20-13.40	Glenny & Brownsey - ferns and liverworts	13.20-13.40	Keighery & Keighery - WA Asteraceae		
		13.20-13.40	Heenan *et al.*- *Lepidium*	13.40-14.00	Ingham *et al.*- *Macrozamia*	13.40-14.00	Tate *et al.* - gender dimorphism		
		13.40-14.00	Meudt - *Plantago*	14.00-14.20	Cantley & Keeley - *Coprosma*	14.00-14.20	Brown *et al.*- Agrostidinae		

14.00-14.20	Wong & Murray - *Plantago*	14.20-14.40	Gibbons *et al.* - Loganieae	14.20-14.40	Messina *et al.* - *Olearia* stellate hairs
14.20-14.40	Houliston *et al.* - Australian invaders	14.40-15.00	Scheele & Tawiri - *Phormium*	14.40-15.10	Afternoon tea
14.40-15.00	Gebert - *Latina lingua*	15.00-15.20	Afternoon tea	15.10-15.20	Award of prizes
15.00-15.20	Afternoon tea	15.20-15.40	Keighery & Keighery - Mutsieae	15.20-15.40	Cross *et al.* - camel diet
15.20-15.40	Bickford *et al.* - *Pachycladon*	15.40-16.00	Nelson - NZ Marine red algae	15.40-16.00	Lehneback - *Uncinia*
15.40-16.00	Entwistle - sensible seasons	16.00-16.20	Novis - *Klebsormidium*	16.00-16.20	Hosking - *Cytisus scoparius* impact
16.00-17.00	ASBS AGM	16.20-16.40	Myles *et al.* - coevolution	16.20-16.40	de Lange - *Kunzea ericoides*
		16.40-17.00	Cargill *et al.* - *Megaceros*	16.40-17.00	Smissen - hybrids
		17.00-17.30	Poster session	17.00-18.00	ASBS editors and NZPRN meetings
		18.00	Buses depart for dinner		
		18.30	Pre-dinner drinks		
		19.00	Conference dinner		

Abstracts of talks

Fossil flowers from the Early Miocene Foulden Maar, New Zealand

Jennifer Bannister[A], Daphne Lee[B], Ian Raine[C], Dallas Mildenhall[C] & John Conran[D]
[a]Department of Botany, University of Otago, PO Box 56, Dunedin, New Zealand; [B]Department of Geology, University of Otago, PO Box 56, Dunedin, New Zealand; [C]GNS Science, PO Box 30-368, Lower Hutt, New Zealand; [D]Australian Centre for Evolutionary Biology and Biodiversity, School of Earth and Environmental Sciences, Benham Bldg DX 650 312, The University of Adelaide, SA 5005, Australia

Flowers are uncommon as fossils, and flowers with *in situ* pollen are extremely rare. In the laminated diatomite deposit at Foulden Maar, southern South Island, New Zealand, female flowers, male flowers and inflorescences, buds, and clusters of anthers are present, generally on the light-coloured spring-summer layers. Families recognised to date include Euphorbiaceae, Onagraceae, Picrodendraceae, and probable Rutaceae. Flowers range in size from 2 to 20 mm in diameter, and most appear to have been insect-pollinated. The flowers all fell from or were blown in from forest trees and shrubs growing around the perimeter of the 1500 m diameter volcanic lake. Some of the flowers are from genera no longer present in New Zealand. Others, including *Fuchsia* are still important components of the modern New Zealand flora, but the flowers and pollen at Foulden are from an extinct species, as might be expected after >20 million years.

Speciation and phylogeography of *Telopea* and *Lomatia* (Proteaceae)

Melita L. Baum[A,B], Michael D. Crisp[A], Maurizio Rossetto[B] & Peter H Weston[B]
[A]Evolution, Ecology & Genetics, School of Biology, Australian National University, Acton ACT 0200; [B] National Herbarium of NSW, Botanic Gardens Trust, Mrs Macquaries Rd, Sydney, NSW 2000

Lomatia and *Telopea* (Proteaceae) are sister genera that have an almost identical distribution in eastern Australia, but a different geographical pattern. *Lomatia* consists of 9 Australian species with broadly sympatric distributions and high occurrence of hybridisation. In contrast, *Telopea* has 5 species with a mostly allopatric distribution and few known cases of hybridisation. The overlap in distribution suggests that if historical events, such as climate change, have led to allopatric speciation, congruent geographic patterns should have resulted in both genera.

A comparative phylogeography of *Telopea* and Australian *Lomatia* can test whether major geographic and environmental disjunctions correspond with genetic disjunctions.

By using variable chloroplast and nuclear DNA regions we will investigate differences and similarities of genetic structure across and within genera, to reveal the major contributors to distribution and gene flow.

Discovering what genetic and environmental processes are dominant within *Lomatia* and *Telopea* will assist in determining what historical events have been important for the speciation of eastern Australian flora.

New Zealand alpine flora in a changing climate: a model based assessment of *Pachycladon* (Brassicaceae)

Christopher P. Bickford[A], Adrian Walcroft[B], Margaret M. Barbour[C] & Peter B. Heenan[A]
[A] Landcare Research, Biosystematics, PO Box 40, Lincoln 7640, New Zealand; [B] Landcare Research, Global Change Processes, Palmerston North, New Zealand; [C] University of Sydney, Faculty of Agriculture, Food and Natural Resources, Narellen, Australia

Current climate change projections pose unique threats to alpine plants, but the effects of increased temperature on the alpine plant community are poorly understood. *Pachycladon* is a genus of largely alpine plants that has experienced rapid evolutionary radiation in New Zealand since the Pliocene and whose present distribution is hypothesized to relate to Pleistocene climate change. Using four species within *Pachycladon* we assessed the effects of elevated temperature on plant carbon balance using a synthesis of empirical data and simulation modelling. Intrinsic differences in physiological traits associated with photosynthetic carbon uptake and respiratory carbon losses, combined with differences in growth habitat microclimate, resulted in stronger impacts on plant carbon balance as altitude increased. In *Pachycladon cheesemanii*, the lowest altitude species within the group, model results from the 2009 growing season demonstrate a 5.3% increase in gross carbon uptake and 141% increase in respiratory carbon losses as mean temperature was elevated 2°C above measured ambient field temperature. In contrast, model results from the 2009 growing season for the highest altitude species, *Pachycladon enysii*, demonstrate a 5.9% increase in gross carbon uptake, but a 267% increase in respiratory carbon losses when mean temperature was elevated 2°C above measured ambient field temperature. These model results support the hypothesis that warmer air temperatures due to global warming will negatively impact plant carbon balance in these alpine plants, and portend poor prospects for *Pachycladon* survivorship under a warmer climate regime.

Genetic assessment of relationships between genera of the Subtribe Agrostidinae

Austin J. Brown[A,B], Hugh B. Cross[B,C], Duncan Jardine[B], Daniel J. Murphy[A], David J. Cantrill[A] & Andrew J. Lowe[B,C]
[A]National Herbarium of Victoria, Royal Botanic Gardens Melbourne, Private Bag 2000, South Yarra, Vic 3141; [B]School of Earth and Environmental Sciences, The University of Adelaide, SA 5050, [C]State Herbarium of South Australia, Dept Environment and Natural Resources, PO Box 3732, Kent Town, SA 5000

Lachnagrostis Trin. (Poaceae) is a genus of Australasian grasses in the subfamily Pooideae. Known as Blown-grasses in Australia and as Wind-grasses in New Zealand, the genus has only been segregated from *Agrostis* L. since 1995 and is still not recognised by a number of major northern hemisphere authorities. In previous treatments, *Lachnagrostis* and *Agrostis* taxa have also been included in *Deyeuxia* Clarion ex P.Beauv., the separation of *Deyeuxia* from *Calamagrostis* Adans. continues to prove difficult and members of *Polypogon* Desf. have been and continue to be, variously assigned to *Agrostis*, *Alopecurus* L. or to newly raised genera. In order to better circumscribe *Lachnagrostis*, a phylogeny of subtribe Agrostidinae Fr. based on sequences of the nDNA ITS and cpDNA *mat*K and *rbc*L regions was constructed. Preliminary work supports the separation of Agrostidinae from other Tribes of Aveneae. However, relationships among genera of Agrostidinae are not always clearly defined or consistent between DNA regions. The Australasian endemic genera, *Echinopogon* P.Beauv. and *Pentapogon* R.Br. appear to be confirmed members of the subtribe. Preliminary results suggests that *Deyeuxia* taxa from the southern hemisphere are more closely related to the Australasian endemic *Dichelachne* Endl. rather than to the northern hemisphere *Calamagrostis*. *Agrostis* forms separate clades in the rbcL analysis, with the Australasian representatives in a clade with *Agrostis stolonifera* L. and *A. gigantea* Roth, rather than with *A. capillaris* L. *Lachnagrostis* is monophyletic for *rbc*L and supports its retention as a separate genus to *Agrostis*, but for ITS, the New Zealand and Australian taxa largely form separate clades. *Lachnagrostis punicea* (A.J.Br. & N.G.Walsh) S.W.L.Jacobs is separated from the other Australian *Lachnagrostis* and, appears more closely aligned to the South African *Lachnagrostis/Agrostis*. Overall, a number of genera in Agrostidinae appear non-monophyletic and further revision of the entire subtribe is warranted.

Preliminary molecular phylogeny and biogeography of *Coprosma* (Rubiaceae)

Jason T. Cantley[A] & Sterling C. Keeley[A]
[A]University of Hawaii, Department of Botany, 3190 Maile Way,
Room #101, Honolulu, Hawaii, 96822-2279, USA

The genus *Coprosma* (Rubiaceae) consists of over 120 species widely distributed throughout the Pacific. The center of diversity is New Zealand with secondary centers in New Guinea and Hawaii. A molecular phylogeny using the nuclear ITS and ETS regions and the rps16 cpDNA region is presented for 71 *Coprosma* taxa from representative locations across the Pacific. Preliminary results suggest an origin in New Zealand and subsequent dispersal(s) to Australia, New Guinea and the wider Pacific. Possible dispersal pathways through the Pacific towards Hawaii are also discussed. This is the first molecular study to document the phylogenetic and biogeographic connections of *Coprosma* species in the Pacific. The phylogeny also provides information on the distribution of reproductive and morphological characters (e.g., fleshy red-orange fruits, shrubby habit) that have been important in successful dispersal and establishment across large distances between land masses in the Pacific Ocean.

Megaceros (Anthocerotophyta): More than meets the eye

D. Christine Cargill[A], Ish Sharma[A] & Joe Miller[A]
[A]Centre for Plant Biodiversity Research, CSIRO, Canberra, ACT

Recent molecular studies have separated the hornwort genus *Megaceros* s.l. into two distinct genera. Not only found to be separated genetically, but also geographically. However, species boundaries based on morphology within each group are still unclear. Australasian species initially appeared to correlate with spore patterns, and fell into two distinct groups, one confined to the Wet Tropics of Queensland and the other a widespread species occurring throughout eastern Australia, and also New Caledonia and Lord Howe Island. Based on the spore characters, it was hypothesised that this widespread species extended to New Zealand. Instead, molecular data has revealed two cryptic species within the widespread Australian/New Caledonian/Lord Howe Island populations and a highly divergent tropical species.

Recent collections of *Megaceros* from the South Island of New Zealand have unexpectedly revealed a morphologically diverse group, including the first reports of gemmae for the genus. Molecular data has shown, at least for South Island populations of *Megaceros*, that they are not conspecific with Australia/New Caledonia/Lord Howe Island populations.

Hybrid stories from the central North Island of New Zealand

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Over the last 30 years or more I have been surveying indigenous vegetation in the central North Island. This has provided opportunities to measure the frequency and abundance of hybrids and consider the ecological and evolutionary significance of hybridism. Examples encountered cover a wide range of types including:

- Emphemeral and persistent introgressive hybridism (long and short distance pollen dispersal) e.g., *Podocarpus*, *Lepidothamnus* and *Coprosma*;
- Relictual population hybridisation (swamping) e.g., *Phyllocladus* and *Melicytus*;
- Natural disturbance hybridism (open sites) e.g., *Metrosideros*, *Gaultheria*, *Raoulia*, *Celmisia* and *Olearia*;
- Human induced disturbance hybridism (including spontaneous garden hybrids) e.g. *Hebe* and *Coprosma*;
- Possible cyclic hybridisation; evidence for climate induced constitution and reconstitution of hybrids e.g., *Hoheria* and *Podocarpus*;
- Stable hybrids e.g., *Pittosporum*.

Speciation by homoploidy is rare. On the other hand, recent polyploidy drives speciation. Hybridism is common in certain genera concentrated in New Zealand e.g., *Hebe*, *Coprosma* and *Melicytus* but other genera and families with high levels of hybridism elsewhere have high levels in New Zealand also e.g., Asteraceae. Stable hybrids and cyclic hybridisation seem possible but remain unproven

Lauraceae at Foulden Maar: diversity and identity

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The macrofossil assemblage of the Early Miocene Foulden Maar deposit in Otago is dominated by abundant well-preserved Lauraceae leaves as well as some fruits. Numerical examination of cuticular patterns in these leaves indicates that there are three or four genera present, including (in order of sample abundance) *Litsea*, *Cryptocarya*, *Endiandra* and possibly *Beilschmiedia*. Based on a combination of the cuticular features as well as additional gross leaf morphology, there seems to be a single *Litsea*, at least two species of *Cryptocarya* and several species within the *Endiandra–Beilschmiedia* group. There are also well-preserved fossil fruits which are good matches for Lauraceae with possible affinities to *Cryptocarya, Endiandra* or *Beilschmiedia.* The numerical dominance of Lauraceae leaves in the lake bed sediments indicates that the forest around the margins appears to have been Lauraceae-dominated, and in combination with the other families present as either macro- or microfossils suggests that the assemblage was a warm-temperate forest, similar to parts of modern south-east Queensland and New South Wales, but with a mixture of modern New Zealand, Australian and New Caledonian elements.

Flora from the Inside Out: Camel Diet and Impact on Vegetation of Outback South Australia

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Camels were introduced to Australia in the 19th century and their feral descendents now roam across the outback. Little is known about their effect on native vegetation and whether they are a vector in the spread of weedy species, however, their rising numbers are recognised as having a negative impact on the fragile ecosystems and biodiversity of arid Australia. In this study, we investigated the impact of these feral animals on Australian outback vegetation through plant genetic analysis of camel stomach contents. Samples were collected from 150 camels culled from wild populations in the Lake Gairdner region of outback South Australia. DNA was extracted from selected stomach samples, and chloroplast and nuclear ribosomal markers were amplified, cloned, and sequenced to obtain information on dietary patterns of the camels. These molecular markers were designed to amplify a broad range of plants and are standard loci for plant DNA barcoding projects. The plant sequences detected in the stomach contents were then compared to both online databases and reference sequences produced from collections housed in the State Herbarium of South Australia. Preliminary results indicate that the camels ate a wide range of plants, generally species that are representative of the region's flora, including plants identified in previous studies as highly palatable to camels. Plant taxa included acacias (Fabaceae), chenopods (Chenopodiaceae), and species of the Sapindaceae family, but interestingly, no grass species (Poaceae) were detected. Species of sandalwood (*Santalum* spp.; Santalaceae) were also identified from DNA sequences, which is of concern as extensive targeted browsing by growing camel populations is a possible cause of the decline in this genus in South Australia. The overall impact of camel feeding habits in comparison to the diet of native fauna will also be discussed.

Kunzea ericoides - a shared weed between countries or a remarkable example of a rapid species radiation?

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Kunzea ericoides is an Australasian species aggregate. Belonging to the newly erected subgenus *Niviferae* sect. *Niviferae*, members of the *Kunzea ericoides* complex have long suffered from taxonomic neglect, neglect that has resulted in them being collectively (as *K. ericoides*) touted as one of the world's top worst 100 weeds! In a series of papers examining the cytology, ability to hybridise and DNA sequence data I have argued that *Kunzea ericoides* s. s. is a New Zealand endemic and that the species aggregate is divisable. Australia has seven endemic segregates, three of which have valid names (*K. leptospermoides*, *K. peduncularis*, *K. phylicoides*) and New Zealand ten endemics, four of which have valid names (*K. ericoides* var. *ericoides*, var. *linearis*, var. *microflora*, *K. sinclairii*). In this paper I briefly explore the basis for the upcoming formal segregation of these entities.

Sensible Seasons

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To detect and measure changes due to global warming, it helps to be 'in tune' with our environment. One excellent way is to use seasons that relate to significant changes in the biological world, and particularly in our gardens and native vegetation. Most people around the world use the European-devised system of four seasons – summer, autumn, winter and spring – even though these seasons often have little relevance to the biological changes in their region. Indigenous communities in Australia have long had systems of six or more seasons. I've recommended a five-season system for the coastal Sydney region, including an early spring ('sprinter' – beginning with the mass flowering of wattles in southern Australia) in August and September, a pre-summer season ('sprummer') in November and December, a longer summer (December to March), and a short autumn (April and May) and winter (June and July). While every year is different, this system better reflects the environmental changes around Sydney. We need better phenological data and a willingness to untie ourselves from four seasons based on the distance of the sun from the earth and/or environmental changes in a distant land. Botanic gardens can lead this debate, but clearly poets or Indigenous people should provide the new names…

The Virtual Compositae:

Novel Solutions to Global Problems in the Largest Flowering Plant Family on Earth

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Examining evolution in large clades poses special challenges. There are new ways to identify problems, create solutions, and pool data to answer questions. Under the umbrella of TICA (The International Compositae Alliance) three projects are underway: the Global Compositae Checklist (GCC; establish agreed upon names), the Virtual Key for the Compositae (VKComp; global key to species), and Life Desks (C-EOL; which feeds into the Encyclopedia of Life). Soon, we hope, trees will be added through collaboration with WebTol. All this will provide rapid availability of the latest information and greatly speed up science while making this large family accessible to conservation biologists and the general public. **The Global Compositae Checklist** underpins all of our efforts. The Checklist is under the direction of Christina Flann. A preliminary checklist is available to experts so they can check their groups; we estimate that this list is about 80% complete. First regional lists, where available, were combined (e.g. Checklists from Australia and New Zealand). At the same time some experts had complete lists of some super generic taxa. These two types of data were prepared one set at a time and loaded into the new software developed by Landcare Systems which provides the users with all of the variations of names that have been supplied and allows them to select the preferred name. Lists that were available as spreadsheets had first priority, followed by those in text documents. Hard copy literature is done last or when it represents a critical area. **The Virtual Key to the Compositae** began in 2009 and is an international effort to build an electronic key to identify any member of the Compositae. Under the direction of Mauricio Bonifacino, this effort is beginning with Phase I: North America. There are three main issues revolving around the process of building the key: a) the construction of a list of characters and states, c) the standardization of terminology, and c) the scoring of the matrix upon which the key is based. Keys to some North American species are available on line. **Lifedesks and the Encyclopedia of Life** are the result of a consortium of institutions that are working to make reliable information on organisms that inhabit Earth available to everyone. A new addition to this effort is “Lifdesks” that allows “curators” to build WebPages in a simple fashion before they are released to the public. TICA is working to promote the use of Lifedesks as a way or organizing and sharing information on taxa as it becomes available. **Organizing the Community** is done by TICA(started 2001; www.compositae.org). The first International meeting was in 2003 and other meetings have followed; the most recent meeting resulted in a book that summarized the status of research in the family. A 2010 workshop, funded by the Synthesis Center of EOL decided that TICA should create “tribal coordinators” and “regional coordinators” for the family. These coordinators are responsible for identifying team members and communicating with them on a regular basis. **Answering Scientific Questions is the ultimate goal** and we can use the products of these digital efforts to study questions about systematics, biogeography, and evolution. Imagine the power of knowing the correct name for each of the 25,000+ species in the family, their distribution, and their position on the phylogeny. Go further and imagine that this complex and fascinating family is made accessible to everyone by means of a virtual key and an EOL page, all available online, continuously updated and receiving feeds from experts and users alike. We could learn the origin of floras, which clades are the result of adaptive radiations, reconstruct ancestral groups, determine the accuracy of various hypotheses about the origin of the family, and much more. These coming years are destined to be wonderful times for the practicing Compositae systematist, but only if we work together.

How to look, again, at hebe

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The hebe complex (*Veronica* sect. *Hebe*, Plantaginaceae) is one of the great species radiations in the New Zealand flora and recent progress in understanding its patterns and processes parallels our understanding of the flora as a whole. Lucy Moore wrote an important paper in 1967 that analysed the variation in morphological characters. Although methodologically pre-cladistic, she presented branching diagrams that indicated relationships, based on her 1961 Flora treatment with Margot Ashwin. Since Lucy's and Margot's time, numerous botanists have added ideas and data to the hebe story. New species have been discovered and described and old ones resurrected from synonymy. Different classifications have been proposed and their circumscriptions tested. We have a much firmer idea where hebes came from and when, if not how. However, we still lack a well-resolved phylogeny because standard molecular markers haven't yet been informative about the crown hebe clade. The future is likely to include improved molecular analyses, deeper appreciation of morphological and chemical evolution, understanding of the roles of hybridism and polyploidy, and our progress will be based on seeing hebes in context as divergent veronicas. I would encourage an international perspective, increased collaboration and competition, and explicit framing and testing of questions. Lucy Moore's conclusion that "there is still much to be learned from looking hard at hebe" and her verbal advice that "it pays to be suspicious" are as relevant today as they were in 1967.

Latina lingua tirones tirone

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Have you every tried to read latin only to be baffled by a jumble of words that don't seem to match? Have you tried looking up a latin word in a dictionary but couldn't find a match? In this talk I will take you through parts of the Latin language and highlight ways to make sense of this classical language. I will focus on areas that are commonly used in Botanical Latin such as nouns, adjectives, comparatives and superlatives and I will touch on numerals and verbs.

The Australasian side of Loganiaceae: phylogenetics and biogeography of Loganieae

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Loganiaceae is a predominantly tropical to subtropical family with occasional extensions into higher latitudes. Areas of highest generic diversity include the Americas, Africa and Australasia. The morphological heterogeneity of the family has long been noted and recent molecular and morphological cladistic analyses have confirmed the polyphyletic nature of Loganiaceae as traditionally circumscribed. A monophyletic core Loganiaceae has been resolved, and is best represented in Australia and New Zealand by *Logania* R. Br., *Mitrasacme* Labill. and *Geniostoma* J.R.Forst. & G.Forst. Tribal circumscriptions have varied widely. As a result of recent molecular phylogenetic analyses, the circumscription of Loganieae has been broadened to include all Australian and New Zealand genera except the pantropical *Strychnos* L. (Strychneae). Generic limits and relationships, however, remain largely untested. Loganieae, therefore, provide an excellent model with which to explore the biogeographical history of the Australasian region.

Nuclear ribosomal and chloroplast nucleotide sequence data were used to conduct maximum parsimony and Bayesian phylogenetic analyses of Loganieae to test generic limits and to resolve intergeneric relationships. The Hawaiian endemic genus *Labordia* Guidich. was found to nest within the more geographically widespread *Geniostoma*, as previously proposed on morphological data. *Logania* Section *Logania* and *Logania* Section *Stomandra* (R.Br.) DC. each appear to be monophyletic; however, *Logania* was found to be paraphyletic. The evolution of selected morphological characters within Loganieae will be discussed and the historical biogeographical implications of relationships within the tribe will be explored.

New Zealand ferns and liverworts: do they share a common biogeographic history?

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The two groups of plants have same level of endemism at species level, 50%. The null hypothesis taken here is that the level of endemism is correlated to, and a result of, dispersability averaged over a group of organisms. Are there differences between the ferns and liverworts that suggest that they have a different history, or is the degree of endemism purely a reflection of dispersability? The question is interesting to ask because pteridologists have in recent decades have been dispersalists (although vicariance views were earlier held by some authors (e.g. Copeland 1939, Lovis 1959) while in hepaticology, the vicariance views of Rudolf Schuster (e.g. Schuster 1979) have dominated liverwort biogeography up to the present day, and Schuster demonstrated his views using mainly examples from the New Zealand liverwort flora.

A progress report on the relationships and taxonomy of the *Lepidium oleraceum* complex

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Cook's Scurvy Grass (*Lepidium oleraceum*) is a widespread (Kermadec to Subantarctic islands), coastal, and threatened species endemic to New Zealand. It is a difficult species to study as it is mostly known from small and scattered populations on offshore islands or rock stacks and islets close to the main New Zealand islands; there are few populations on the North and South islands. nrDNA ETS sequence data suggest that *L. oleraceum* comprises several lineages whose relationships are closely linked with the New Zealand *L. banksii* and *L. obtusatum* and also *L. nesophilum* (Lord Howe Island) and *L. foliosum* (Australia). The lineages of *L. oleraceum* include plants from: a) Kermadec Islands to Marlborough Sounds - *L. oleraceum* s.s.; b) Chatham Islands & Antipodes; c) Snares Island; d) southern South Island & Stewart Island. Morphological studies have been undertaken of plants grown in common garden environments (Auckland & Lincoln), with the plants being collected in the wild from several populations of each lineage. The morphological variation between and within the lineages is considerable, with variation in growth habit, leaf shape, size and teeth, stamen number, silicle shape and size, and hairs. As a result of the DNA and morphological studies a number of new species will be segreagated from *L. oleraceum*.

Impact of *Cytisus scoparius* (broom) on native vegetation at the Barrington Tops, New South Wales, including a comparison of a species list published in 1939 and species recorded since 2000 for this area - the case for voucher herbarium specimens

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At the Barrington Tops *Cytisus scoparius* has a significant impact on vegetation growing in frost hollows and open forest without a native shrub and vine understorey. In open forest areas with a native shrub and vine understorey impact appears to be minor. In 1939 Fraser and Vickery published a list of species occurring in these areas. Vouchers of many of the species they recorded were collected and lodged at the National Herbarium of New South Wales (NSW). Other specimens are likely to be present in the John Ray Herbarium at Sydney University (SYD) but these have not been accessed to date. Without these vouchers many of the names used by Fraser and Vickery could not be linked to species currently found in various areas on the Barrington Tops. Fraser and Vickery did not record *C. scoparius* at the Barrington Tops. In the area currently impacted by *C. scoparius* they recorded 143 species, 64 of which are still under the same name and 26 of which were not vouchered. Nine names that they used cannot be associated with current names in the absence of vouchers. Since 2000 285 species have been recorded from *C. scoparius* infested areas at the Barrington Tops, 101% more than were recorded by Fraser and Vickery. Most of the increase is due to native species not recorded by Fraser and Vickery for this area. Recent records also indicate that probably all of the species present in 1939 still occur in the area. Many of the species at the Barrington Tops have been named in recent years and many more still require names. Current and future vegetation studies at the Barrington Tops need to be backed up by herbarium vouchers.

Australians making themselves at home; the population genetics of some recent New Zealand invaders

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Reconstruction of the introduction history of a plant emerging from the so-called 'lag-phase' and becoming a serious threat outside their native biogeographical ranges is an important step towards understanding and designing strategies that prevent or manage invasions. New Zealand has a high number of weed species (700 new emerging weeds have been recorded in the past 20 years), and an even higher number of naturalised plants (ca. 3500). Despite this, we have a poor understanding of the ecological and evolutionary processes between naturalisation and weediness. Using two Australian species that are emerging weeds in New Zealand (Alpine wattle, *Acacia pravissima*; Coastal Banksia, *Banksia integrifolia*), we will compare the population genetics in the native range with both the cultivated and naturalised populations in New Zealand. By comparing the amount of genetic variation in naturalised and native species, we may gain insights into what factors determine the success of new invaders.

Biogeography and Systematics of the genus *Macrozamia* (Zamiaceae)

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Macrozamia is a genus of cycad endemic to Australia. It occurs in three broadly-disjunct regions from south-west Western Australia, central Australia and eastern Australia. Forty-one species have been described using geographic location and differences in morphology. Analyses of allozymes generally support current morpho-geographic species, but find low genetic diversity overall. This suggests a recent divergence or a divergence from a genetically depauperate ancestor. Allozyme studies focused on a single morpho-species group or morpho-species complex. Therefore, relationships within the genus are still unclear. We used sequence data to assess genetic relatedness across all species within the genus by using two intergenic chloroplast loci, atpH-atpI and trnL-trnF (~1300bp), for a total of 169 individuals from 40 of the 41 described species of *Macrozamia*. We found widespread sharing of chloroplast DNA haplotypes among described morpho-geographic species from eastern and central Australia, whereas western Australian species were differentiated from the rest by several base-substitutions. Despite widespread sharing of internal haplotypes, some geographic structuring was observed in the eastern populations. Three haplotype clusters were restricted to coastal central Queensland and another was restricted to northern NSW. Although hybridisation between populations within these clusters cannot be ruled out, two haplotype clusters that are six base-substitutions different from each other were obtained from co-occurring populations in Queensland. This indicates that hybridisation between populations from different haplotype clusters is highly unlikely. Overall, these results suggest that species within the genus have recently diverged. The incomplete lineage sorting observed is most likely due to retainment of ancestral polymorphisms rather than to hybridisation. Nuclear loci and possibly other, more-variable genetic markers such as microsatellites will be investigated in order to further test this hypothesis.

What do we really know about the history of Australian rainforests?

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In spite of decades of discussion, there has never been an overview of the history of the Australian rainforest that simultaneously analyses the fossil record and living rainforest flora *in toto*. Previous treatments have been anecdotal or have used small (and, arguably, biased) subsets of the taxa. This talks describes an analysis of the whole of the woody component of the Australian rainforest flora. We address the questions:

(1) For what proportion of the rainforest flora do we have fossil evidence?
(2) How old are these fossils?
(3) What proportions of the rainforest flora are related to Asian taxa?

We segregated the woody flora into over 1000 clades defined by disjunctions between Australia and any other landmass (excluding New Guinea). We defined five mutually exclusive categories representing the diverse array of Australian rainforests (microthermal; mesothermal; lowland tropical; dry types; littoral and mangrove). Where possible we used published phylogenies to identify disjunctions, otherwise we depended on assumptions of monophyly of species, genera, families etc. We related fossil records (both micro- and macrofossils) to these disjunctions.

Consistent with established narrative, the microthermal rainforest has few disjunctions, mostly with other southern landmasses and associated with Late Cretaceous and Palaeogene fossil records. In contrast, few (<10%) the disjunct clades in the other rainforest types are associated with fossils, and these fossils tend to be very young (Late Quaternary). Almost 50% of the disjunctions in these northern forests are within species, indicating recent interchange between Australia and Asia. Comparison of recent and Early Miocene pollen assemblages suggests that much of this interchange has been immigration from Asia. Mesothermal rainforests have the strongest fossil record and the smallest proportion of within-species disjunction of the four northern forest types.

Composition, Biology, and Phytogeography and Conservation of Western Australian Asteraceae

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Australia has approximately 1,000 taxa of Asteraceae distributed in 205 genera. The state of Western Australia, occupies the western third of the continent and contains habitats ranging from tropical to arid to temperate Mediterranean. The State has a flora exceeding 12,000 species, of which about 8,000 taxa are concentrated in the Mediterranean region which is a mega-diverse region for flowering plants. Western Australia contains 513 native taxa of Asteraceae distributed in 117 genera. The largest genera are *Olearia* (48 taxa), *Rhodanthe* (39), *Senecio* (35) and *Brachyscome* (21). Seventy one genera have only 1-2 species recorded for Western Australia.

A feature of this family is the 116 weed species, from 76 genera. The Asteraceae contribute the second largest number of weeds after the Poaceae (196) to the total Western Australian weed flora of 1234 weeds. Major weeds are *Arctotheca calendula*, *Cirsium vulgare*, *Carduus pycnocephalus*, *Centaurea melitensis*, *Senecio glastifolius* and *Xanthium* species.

Currently 18 genera and approximately 275 taxa (54%) are endemic to the state, a lower figure compared to other large families such as the Fabaceae (71% of species endemic), Myrtaceae (68%) and Proteaceae (74%). Current revisions suggest that at least another 50-60 taxa await description/recognition, most of which will be endemic. Centres of species richness are the dry Mediterranean shrub lands, woodlands and saline lake systems of southern Western Australia. The arid Pilbara Ranges and West Kimberley uplands are secondary centres. Centres of endemism are the Mediterranean and the Semi-arid areas of southern Western Australia. Secondary centres are the wet tropical North-west Kimberley and Pilbara uplands.

Most taxa (341) are annuals and members of the genera *Cephalipterum*, *Lawrencella*, *Rhodanthe* and *Schoenia* mass flower after rain in the semi-arid, making a substantial but ephemeral biomass contribution. The family contains a wide variety of breeding systems, with frequent polyploidy and inbreeding. Pollination is by insects, chiefly solitary bees. Fruits are normally dry and wind dispersed.

Four taxa are presumed extinct are 65 are listed as conservation priorities, but only one is legally protected. This is much lower than other groups, eg: Orchidaceae.

Taxonomy of *Amblysperma/Trichocline* (Asteraceae: Mutsieae), Western Australia's South American link?

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Although frequently combined into the South American genus *Trichocline* on morphological grounds as a monotypic section, the Western Australian genus *Amblysperma* could be closer to the African *Gerbera*. There are several other obvious links to Southern Africa in the Asteraceae of Western Australia in *Cymbonotus* and *Sonchus*, suggesting a western not eastern link. Further *Amblysperma* shows considerable ecological and morphological variation in Western Australia, suggesting a long residence.

All species are tuberous perennial herbs with a basal rosette of leaves dyeing back to a rootstock and often flowering when leafless in summer. All members studied have showy inflorescences pollinated by solitary bees and are out-breeding.

The genus currently consists of at least three, possibly 4 species. These are *Amblysperma spathulata*, a common and widespread species of the Jarrah Forest, *A. scapigera* a common component of the Wandoo woodlands of Western Australia, *A. minor* a component of claypans and winter wet sites and *A.* sp. nov. restricted to the lateritic uplands of the Mount Leseur area north of Perth.

New Zealand's plants: how long have they been here?

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There is ongoing debate over the antiquity and origins of the present-day New Zealand vegetation. The issue centres on whether the ferns, conifers, monocots and dicots of the modern flora are firmly rooted in the geological past in the region, or whether they are relatively recent arrivals. Molecular phylogenies have yielded a range of conflicting dates for colonisation, but until now there has been sparse fossil evidence for the presence of some groups. Research on macrofossils, mostly leaves with well-preserved distinctive and diagnostic cuticle from lake deposits and lignites of Late Oligocene and Early Miocene age from Otago and Southland, suggest that many iconic New Zealand plants have been present for a minimum of 25-23 million years. For example, we have documented macrofossils and/or pollen records of this age for all the extant New Zealand conifer genera (with the exception of *Manoao* which lacks distinctive pollen): *Agathis* (Araucariaceae), *Libocedrus* (Cupressaceae), and *Dacrycarpus*, *Dacrydium*, *Halocarpus*, *Lepidothamnus*, *Phyllocladus*, *Podocarpus* and *Prumnopitys* (Podocarpaceae). Many modern New Zealand monocots now have macrofossil records extending back to the Late Oligocene-Early Miocene, including *Astelia*, *Cordyline*, *Dianella*, *Luzuriaga*, *Phormium*, *Rhopalostylis*, *Ripogonum* and *Typha* as well as two epiphytic orchids: *Dendrobium* and *Earina*. Forest trees with macrofossil records include species of *Alectryon*, *Elaeocarpus*, *Fuchsia*, *Hedycarya*, *Laurelia*, *Litsea*, *Myrsine, Pseudopanax, Nothofagus (fusca-type),* and *Weinmannia*. When combined with the pollen records from the same sites, the list increases, and long fossil records are now available for a large proportion of modern New Zealand forest genera including *Ascarina, Dysoxylon, Ixerba, Knightia, Metrosideros* and *Quintinia.*

For several New Zealand groups such as conifers, the generic and specific diversity in the Late Oligocene-Early Miocene was considerably greater than today and was probably even richer, given that the fossil record underestimates the true diversity. Some of the fossil types (*Dacrycarpus*, *Halocarpus* and *Lepidothamnus*) appear to be close to extant New Zealand species, lending support to the idea of continuous presence of the modern conifer groups in New Zealand since at least the Late Oligocene. Thus, evidence is accumulating that shows that instead of being the "flypaper of the Pacific" or a sink for plant taxa blown in recently from the continent to the west, New Zealand has had highly diverse forests for at least the past 25 million years. None of the species are identical with those living in New Zealand today. However, they are likely to be the ancestors of many of the extant forest genera, and they represent the "survivors" of a considerably more diverse vegetation that included taxa such as *Cryptocarya*, *Gymnostoma*, *Mallotus/Macaranga*, Proteaceae (*Banksia*, *Beauprea*, *Persoonia*), and *brassii*-type *Nothofagus*.

Re-delimiting species in *Uncinia*: a morphometric study of *Uncinia angustifolia*, *U. rupestris* and *U. zotovii*

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There are about 34 species of *Uncinia* in New Zealand, most of them are endemic and only three are found elsewhere. Species identification in *Uncinia* can be a difficult task, especially when the material is not fertile or flowering spikes are immature. The absence of discrete differences among some species, however, is what makes species identification even more difficult. Difficulty in delimiting species within this genus is such that researchers have considered many species to be ecological races only and have radically reduced the number of accepted species.

There are several species pairs or groups of species in New Zealand in which identification, using the keys and descriptions currently available, is extremely difficult. One of these groups is formed by *Uncinia angustifolia*, *U. rupestris* and *U. zotovii*. Boundaries between these three species overlap considerably and they have been regarded as a species complex. All three species have a complicated taxonomic history. *Uncinia angustifolia* has been considered a variety of *U. rupestris*, which, in turn, has been considered a variety of *U. caespitosa* or included in two other species. As for *U. zotovii*, this was originally part of *U. caespitosa* along with the grassland species *U. viridis*. This study re-examines historical and recently collected material, and re-evaluates species limits for these three species using multivariate statistic analyses of morphological characters.

Results confirm the circumscription of *U. caespitosa* s.s. and the segregation of *U. viridis* and *U. zotovii* from *U. caespitosa* s.l. but they also indicate current species descriptions are inaccurate and based on material of mixed identity. Results also suggest that *U. angustifolia*, *U. rupestris* and *U. zotovii* should be considered as three different species. Furthermore, *U. viridis* and *U. rupestris* are conspecific; the latter name has priority and should be maintained.

Taking refuge: haplotypes and plant biogeography

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All landscapes are palimpsests: they have been partially scraped clean and reused, not once, but innumerable times, by extremes of temperature and rainfall, by glaciers, rivers, and tectonic change. Contingent, messy ecological processes have distributed plants over space and time, creating rich, but confusing plant historical landscapes. Chloroplast haplotypes offer the opportunity to track plant species responses to change, and thus to develop satisfying narratives. However, haplotype analyses have been most often employed in the service of excessively simplistic concepts, chief of these being that of glacial refugia. In Australasia, aside from areas that were actually covered with glacial ice, the refugial concept has extremely limited applicability. Here I outline a new approach to the problem of making sense of haplotype distributions.

Evidence for a single origin of stellate hairs in Australian members of *Olearia* (Asterotriche)

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Olearia, the daisy bush genus is a large genus containing approximately 180 species, occurring in Australasia. Classification of *Olearia* based primarily on leaf hair types by Bentham, modified by Heads recognises six sections. Recent studies on *Olearia* and related daisy genera have not shown support for a single origin of *Olearia*, suggesting it may represent more than one genus. Similarly, the current infra-generic classification of *Olearia* has not been supported by a molecular study by Cross *et al.* (2002). Section *Asterotriche* (defined by the presence of stellate hairs) was not shown to be monophyletic, with representative taxa from Australia and New Zealand forming two different groups based on country of origin. However, it does appear that Australian members of this group form a monophyletic group. The current study aims to test the monophyly of Australian members of section *Asterotriche*, and to assist in the delimitation of morphologically variable taxa within the group. Building on work by Cross, ITS has been sequenced from 41 samples, representing all but one of the 18 currently recognised species in section *Asterotriche* from Australia. Three chloroplast regions (*rpl32- trnL*, *psbA- trnH* and *MatK*) have also been sequenced for some members of this group. Preliminary analysis of ITS sequence data shows support for a monophyletic stellate-haired Australian group, with little sequence variation seen between ingroup taxa. Subsets of chloroplast regions have shown even less variation, with little to no variation seen in members of section *Asterotriche*. While these molecular markers appear to be valuable in showing the close relationship between Australian members of section Asterotriche, other markers need to be explored to reveal relationships within the section.

Systematics of native New Zealand *Plantago*

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In this talk I will summarize the results of recent phylogenetic, cytological, and morphological studies regarding the systematics of ca. 12 species and subspecies of native New Zealand *Plantago.* Molecular phylogenetic analyses show that the New Zealand species are not monophyletic, and instead comprise three separate lineages whose ancestors dispersed independently from Australia to New Zealand between 0.5-2.2 Mya. New chromosome counts for several individuals of most species confirm previous counts, expand coverage of species' ranges, and also add one new number (2*n* = 72) to a group with a wide range of ploidy levels (2*n* = 12, 24, 48, 60, 72, 96). Separate studies, which sampled multiple individuals of each New Zealand species for internal transcribe spacer (ITS) nuclear ribosomal DNA and amplified fragment length polymorphism (AFLP), respectively, allowed testing of species boundaries and interpretation of polyploid origins. I will highlight the key results of these studies and discuss them in light of unpublished morphological analyses, with the aim of integrating all data into a new taxonomic revision of New Zealand *Plantago.*

Late Oligocene spores and pollen from Cosy Dell, Southland, New Zealand: a preliminary account

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The Chatton Formation of eastern Southland is a widespread, near-shore to off-shore shelf unit of Late Oligocene to Early Miocene age, deposited at or close to the time of the maximum marine inundation of New Zealand. The Chatton is overlain by the mainly fluvio-deltaic Gore Lignite Measures and at least locally the units probably inter-finger.

At Cosy Dell, 11 km west-southwest of Gore, an isolated exposure of the Chatton Formation contains abundant near-shore macrofossils including mollusca, brachiopods, corals, echinoids, bryozoans, encrusting algae, fragmented whale and penguin bones, and teredo-bored wood, within a calcareous sandy matrix which includes encrusted boulders and cobbles from an adjacent shoreline Microfossils including ostracods, dinoflagellates and foraminifera support a Late Oligocene age indicated by the diverse molluscan fauna (Duntroonian: 27.3-25.2 Ma) for the Chatton Formation at this locality. The fauna implies a subtropical environment proximal to a rocky shoreline and an estuary.

Any terrestrial pollen flora obtained from the locality are inferred to represent a paleoenvironment recovering either from total inundation, if total inundation did actually occur, or from widespread but not total inundation.

The preservation of the recovered palynomorphs ranges from poor to excellent, reflecting differences from mechanical breakdown as a result of varying distances travelled from source and the range of depositional processes. Rare recycled, darker coloured spores and pollen do not appear to have come from significantly older sediments. The pollen assemblage is dominated by *Dacrydiumites praecupressinoides* (rimu), *Podocarpidites* spp. (*Podocarpus/Prumnopitys*), *Haloragacidites harrisii* (*Casuarina*), *Nothofagidites* subgenus *Brassospora* (broad-leafed southern beech) and *Milfordia homeopunctata* (cf. Restionaceae). This assemblage suggests an age no older than Duntroonian. The pre-dominance of pollen from emergent forest trees and a variety of fern spores suggests sub-tropical lowland coastal forest growing under a high rainfall regime. Further support for sub-tropical conditions is provided by the presence of *Bluffopollis maculatus* (Strasburgeriaceae – restricted to montane forest of New Caledonia today), *Monogemmites gemmatus* (*Hymenocallis* – tropical to sub-tropical America) and *Kuylisporites waterbolkii* (*Hemitelia* – tropical to sub-tropical America).

Palynomorphs are sparse in the samples examined but the diversity is high. This study is a work in progress; so far there is nothing in the palynoflora which would indicate that the source vegetation was from an emergent landscape recovering from recent inundation. However, the timing of the maximum inundation is still not well constrained and the possibility that the Cosy Dell Chatton postdates maximum inundation by several million years cannot yet be dismissed i.e., plenty of time may have elapsed for the vegetation to recover and re-colonise.

Molecular phylogenetics of *Acacia*

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The genus *Acacia* is the largest plant genus in Australia and is a key component of many ecosystems, especially in arid regions. We present molecular phylogenetic results from plastid and nuclear DNA regions for over 200 species. These data resolve major lineages of *Acacia* that have not been previously reported. We will present the phylogenetic data and present a foundation for a new informal classification of *Acacia*.

Genome size variation and cell size in *Plantago* (Plantaginaceae)

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Flow cytometric analysis of propidium iodide stained nuclei of eight endemic and two introduced species of *Plantago* that span a wide range of ploidy levels (from 2*x* to 16*x*) show the expected increase in total genome size or C-value with ploidy. However, when the sizes of the component genomes of the species, the Cx-values, are calculated it is clear that there has been a massive downsizing of the component genomes associated with the increase in ploidy level. This downsizing has not occurred at a uniform rate with a significantly greater DNA loss in the transition from diploid to octoploid than from octoploid to higher ploidy levels. Our results provide an excellent illustration of why flow cytometry alone cannot always be used to identify polyploids. Pollen diameter, stomatal guard cell length and the number of chloroplasts in the guard cells have also been measured in the various species and these also illustrate the potential pitfalls of using these parameters for identifying ploidy levels.

Testing species limits in *Schoenus* L. (Schoeneae, Cyperaceae)

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Schoenus L. is a predominantly Australian genus of the Cyperaceae composed of c. 120 species. Species limits, definitions and relationships within this genus have been uncertain. Previous analyses of *Schoenus* using molecular data (*trn*L-F and ETS regions) have revealed three main clades. Preliminary results based on molecules and morphology for one of the main clades with c. 57 taxa will be discussed. Phenetic analyses of morphological characters and anatomy has been used to test species limits, and have revealed numerous species complexes. The *S. melanostachys* complex will be used as a case study to show how morphology, anatomy, geography and geology can define at least two distinct groups. Separation of these groups is strongly supported by principal components correlations (PCCs) and Kruskal-Wallis tests in ordinations and clustering respectively.

Do green algal photobionts co-evolve with their ascomycete hosts? A case study using *Menegazzia* (Parmeliaceae, Lecanoromycetes)

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Only recently has the ability to study the separate evolutionary histories of lichen photobionts and mycobionts become widely available. With universal primers for numerous genomic regions now obtainable for both groups, co-evolutionary questions that could only be speculated on in the past can now be thoroughly investigated. Such methods were employed here on the lichenized ascomycete genus *Menegazzia* and its green algal photobiont *Trebouxia*. To achieve this multiple collections were made of 15 *Menegazzia* species in New Zealand and Australia. The ascomycete phylogeny was then constructed using the nuclear regions ITS, 28S and EF1α, and the mitochondrial region 12S, while the algal phylogeny was constructed from the same vouchers using nuclear ITS, and chloroplast *psb*J-L. The evolutionary histories of both groups were compared for similarity, under the assumption that high levels of topological concordance would indicate co-evolution. The result is in agreement with several other recent studies which have looked at this relationship: genus-wide co-evolution is not supported. The algal diversity is found to be much lower than that of the fungal diversity, with the most common photobiont, *Trebouxia jamesii*, involved in symbiotic relationships with several different *Menegazzia* species. However, in contrast to other studies, we also find evidence for fungal-algal host specificity within some clades. These patterns are discussed in light of lichen dispersal strategy differences.

Diversity and relationships of the NZ marine red algae: what do we know?

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The red algae are a very diverse and ancient lineage, with the earliest fossils of putative red algae dating from ca 1.25 billon years ago, and evidence that five major lineages of florideophyte red algae were established by 600–550 Ma. The understanding of the systematics of the Rhodophyta has been undergoing a period of change and instability over the past two decades, and very significant discoveries, within both the bangiophyte and florideophyte lines, have substantially altered the numbers of orders recognised (an additional 19 orders circumscribed) and the understanding of how these orders relate to one another. The antiquity of the red algae, and the diversity of evolutionary histories represented amongst the orders and families, presents a very complex setting in which to develop hypotheses about biogeographic relationships. About 500 species of marine red algae have been reported to occur in New Zealand in comparison to the ca. 850 species recorded from southern Australia. Recent work suggests that the diversity in the New Zealand flora has been underestimated in a number of ways. The poor state of knowledge and the critical lack of monographic studies of most red-algal taxa in New Zealand have placed a significant constraint on biogeographic analyses of the flora. Recent research, including investigations of the Bangiales, Halymeniales, Gigartinales, Corallinales, Delesseriaceae, is challenging previously held views about the diversity and the relationships of the flora.

The taxonomy of *Klebsormidium*

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Klebsormidium is a simple filamentous green plant. However, its nomenclatural history is anything but simple. The name references the legacy of the genus *Hormidium*, used by Kützing in 1843, but first applied to the species we would now recognise as *Klebsormidium* by Klebs in 1896. *Hormidium* has priority as a genus of orchids, and it subsequently transpired that some species of *Ulothrix* and other genera were close relatives of *Hormidium* sensu Klebs, Thanks to ultrastructural and molecular investigation, species of *Ulothrix* have now been separated into at least 3 genera in 3 different divisions of green algae, including *U. flaccida*, which is now the basionym for the type species of *Klebsormidium*. Furthermore, it became recognised that *Klebsormidium* belonged to the land plant lineage rather than the Chlorophyta, with zoospores possessing parallel basal bodies that emerge laterally from the cell.

Recent studies of *Klebsormidium* promise further upheaval, in which the status of the genus as circumscribing filamentous forms is now under threat. The unicellular genus *Interfilum* has been found to share ultrastructural features with *Klebsormidium*, and molecular phylogenetics indicates that *Interfilum* is closely related to some strains of *K. flaccidum* – a filamentous species that can, interestingly, be prone to dissociation of cells. These species form a clade separated from another that contains the larger species of *Klebsormidium*: *K. crenulatum* and *K. mucosum*. The closest relative of *Klebsormidium* is the recently described *Entransia fimbriata*, which shares this larger size; consequently, the tentative phylogeny currently available makes some intuitive sense. Although analysis is still hampered by fragmented datasets and a problematic outgroup, the prospects for resolving relationships in Klebsormidiales in the future look bright.

The disjunct distribution of fierce lancewood (*Pseudopanax ferox*)

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The twelve species of *Pseudopanax* (Araliaceae) are all endemic to New Zealand. They exhibit a range of distributions, from highly restricted to almost continuous throughout the main islands. The fierce lancewood, *P. ferox*, is a small tree that occurs from the northern North Island to the southern South Island but, like many New Zealand plants, it has a highly disjunct distribution. We used nuclear microsatellites to investigate the population genetics of fierce lancewood. Four principal genetic subgroups were identified: northern and central North Island; southern North Island (= one hillside population); northern South Island; and eastern and southern South Island. A presence through the Last Glacial Maximum in even the south-eastern South Island is indicated. We develop a hypothesis for the origin of fierce lancewood's disjunct distribution, and extend this to other lowland species of drought-prone and/or fertile habitats that are similarly disjunct. We also comment on the conservation of disjunct species.

The Evolution of *Wahlenbergia* (Campanulaceae) in Australasia

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The first molecular phylogeny of *Wahlenbergia* was reconstructed from approximately 20% of the species in the genus, based on nuclear ribosomal ITS (nrITS) and chloroplast *trnL-F* DNA markers, and including samples from South Africa, Europe, Australia, and New Zealand. Molecular dating estimates indicated the genus diversified in South Africa about 25 mya, and then dispersed to Australasia about 5 mya. Two radiations are evident within New Zealand, corresponding to two introductions from Australia, dated about 1.0 and 0.5 mya. Additionally, a large phylogeny with increased within-species sampling focusing on addressing taxonomic questions among the 45 Australasian species of *Wahlenbergia* was also reconstructed based on nrITS and *trnL-F*, plus an additional chloroplast DNA marker, *trnK*. Relationships and species limits of the New Zealand species of *Wahlenbergia* were further analysed using amplified fragment length polymorphisms (AFLPs). I will focus on the relationships between the Australian and New Zealand *Wahlenbergia*, using the New Zealand *Wahlenbergia littoricola* subsp. *vernicosa* as an example.

Crossing the ditch? Historical biogeography of the trans-tasman Styphelieae (Styphelioideae, Ericaceae)

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The possible contributions of long-distance dispersal versus Gondwanan vicariance to the New Zealand flora have been long debated. The subfamily Styphelioideae Sweet of Ericaceae Juss. (formerly Epacridaceae) typify many of the controversies in the historical biogeography of Australasia. The epacrids are mostly restricted to Gondwanan fragments (Australia, New Zealand, New Caledonia, and South America) with outliers extending the range to SE Asia and Hawaii. Some aspects of their ecology would likely decrease the probability of transoceanic dispersal (e.g. woodiness and a strong tendency to occur in heaths and montane forests), whereas others should increase their capacity to disperse (e.g. small fleshy fruit and/or small seeds). In addition, recent evidence from fossils suggests relatively recent origins for extant New Zealand Styphelioideae.

We used clades inside the tribe Styphelieae Bartl. that include New Zealand and Australian congeners, such as *Leptecophylla* C.M.Weiller, *Acrothamnus* Quinn, *Leucopogon* R.Br. and *Pentachondra* R.Br., and estimated the phylogenetic relationships and tempo of evolution of these lineages. Molecular phylogenetic analyses based on plastid loci and Bayesian relaxed molecular clock methods provide new insights into the biogeographic history of the Styphelieae in New Zealand.

Cultural and economic importance of intra-specific variation in *Phormium*

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Phormium tenax, harakeke, was essential to both subsistence Maori and early European economies in New Zealand. Leaf and fibre characters are described, demonstrated, and compared to other important fibre plants used for similar purposes (cordage, containers, mats, nets and garments). Users took advantage of natural variation in the genus and selected and cultivated plants with particular characteristics. The results of recent DNA fingerprinting on traditional weaving cultivars and the connotations for trade and exchange of valued plants are discussed. Leaf and chemical properties relevant to potential new uses of *Phormium* are described. A perspective is offered on the native versus introduced debate re the distribution of *Phormium* on Norfolk and Chatham Islands, and the facts of a commonly told story of early flax processing on Norfolk Island are challenged and reinterpreted.

The primrose and its relatives: an extreme case of species paraphyly

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The type section of *Primula* (Primulaceae) is currently considered to include seven species. Two of them are widely distributed throughout temperate Eurasia, one (the primrose) is found in Europe and N Africa, and the remaining four are restricted to the Caucasus and its immediate surroundings. Together, they are phylogenetically isolated in their genus. Although its species are important ornamentals, traditional medicinal plants and model organisms for the study of heterostyly, the section has not yet been studied from a phylogenetic or evolutionary perspective. Using network and tree inference approaches on nuclear ITS and plastid data from all species and subspecies, we find that widespread *Primula elatior* is genetically extremely heterogeneous and paraphyletic to most if not all of the other taxa, and in its current circumscription may represent the disjointed remnant of an ancestral species from which the other recognized species diverged. It remains unclear how large a role introgression plays in shaping the current genetic structure of the species. Morphologically very divergent *Primula grandis*, previously treated as part of a separate section or even as the monotypic genus *Sredinskya*, is genetically very close to the other representatives of section *Primula* and presumably nested within it. A comparison of the genetic data for different geographic regions indicates that the Caucasus region is the centre not only of taxonomic, but also of genetic and phylogenetic diversity for the section. Additional studies using population genetic and phylogeographic approaches are needed to examine the prevalence of introgression between species and historical patterns of migration.

Rapid diversification in *Puya* (Bromeliaceae) and Cenozoic climate change: a case study in the Chilean *Puya* clade

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The terrestrial genus *Puya* (219 species) is a prime example for a neotropical plant group that diversified rapidly along the Andean cordillera, where it is a characteristic element of high elevation habitats. Under the current climate, *Puya* exhibits a very fragmented distribution, with approx. two thirds of the species occurring in allopatry, often possessing only a small distribution. During the Cenozoic, *Puya* repeatedly underwent dramatic range expansions and contractions, which promoted either contact or geographic isolation between closely related species. To study the effects of sympatry on species diversity during cycles of area expansion the Chilean *Puya* species constitute a suitable model case. Today, this geographically isolated group of closely related species exhibits an outstanding distributional pattern within the genus due to the high extent of areas where species co-occur in different species combinations.

Here we present the results of an AFLP analysis of the Chilean *Puya* clade in which we reconstructed complex phylogenetic relationships, explore species boundaries and isolation mechanisms, and discuss the role of Crassulacean acid metabolism - a novel physiological feature within the clade - in relation to different environmental conditions.

Relationships, hybridization and phylogeography of *Sophora*, with a focus on the origins of putative translocated *S. chathamica*

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We have sequenced the chloroplast trnQ-rps16 intergenic spacer from over 350 samples of New Zealand *Sophora* revealing 22 haplotypes. Chloroplast haplotypes were shared between the 7 *Sophora* species, suggesting an important role for hybridization and introgression in this genus. Phylogeographic structuring of chloroplast haplotypes was evident and a greater number of both total and endemic haplotypes occurred in the North versus South Island.

Sophora chathamica from Wellington and the Chatham Islands has been suggested to have potentially derived from Maori translocations. Chloroplast sequences and AFLP data demonstrated a high level of diversity in these populations suggesting that they may be natural. Chloroplast sequences obtained from seeds collected from Chatham and Kermadec Island beaches also revealed considerable variation, indicating the effectiveness of oceanic dispersal for this genus.

Interspecific hybridisation and reproductive isolation among New Zealand plants

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Reproductive isolating mechanisms, or hybridisation barriers, have been defined as the collection of mechanisms, behaviours and physiological processes that prevent the members of two different species from mating and producing offspring, or which ensure that any offspring that may be produced are not fertile. These barriers maintain the integrity of species over time, reducing or directly impeding gene flow between them.

And yet, many plant species hybridise frequently producing partially- to fully-fertile hybrids. Often these hybrids are vigorous and common. So why don't the hybrids take-over, and why do the species remain morphologically and genetically distinct? In this talk I will examine some examples of hybridising species from the New Zealand angiosperm flora (including *Convolvulus, Phormium* and the everlasting daisies) and discuss some reasons why their hybrids so often don't conquer, and what some of the possible outcomes of hybridisation are.

Evolution of gender dimorphism in Australasian Malveae (Malvoideae, Malvaceae): boys and girls jumping the ditch?

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While most plants are hermaphroditic, gender dimorphism, with male and female functions separated in different flowers, has evolved repeatedly in unrelated families and is particularly prevalent on oceanic islands. New Zealand has the highest reported incidence of gender dimorphism with 23% of the indigenous taxa showing some form of separate male and female function in flowers. Two prevailing hypotheses for the high frequency of this breeding system on islands have been proposed: 1) gender dimorphism evolves on islands from an initially hermaphroditic, self-compatible founder (to promote outcrossing) or 2) gender dimorphic groups are favored to establish on islands and are most closely related to gender dimorphic taxa from the source area. To distinguish between these hypotheses, a phylogenetic framework is required. The Australasian members of Malvaceae (tribe Malveae, subfamily Malvoideae) provide an ideal system to evaluate these alternative scenarios. The widely distributed Australian genus *Lawrencia* includes both hermaphroditic (5 spp.) and dioecious (7 spp.) species. Two more narrowly distributed dioecious genera, *Asterotrichion* (1 sp.) and *Gynatrix* (2 spp.), occur in Tasmania and mainland Australia, and two genera are endemic to New Zealand: *Hoheria* (6 hermaphroditic spp.) and *Plagianthus* (2 dioecious spp.). Previous phylogenetic hypotheses based on chloroplast and ITS sequence data lacked resolution at key nodes for interpreting the origin(s) of gender dimorphism in these genera. We are increasing sampling within *Lawrencia* and sequencing additional chloroplast markers and low-copy nuclear genes to refine phylogenetic resolution. The inferred phylogeny will be used to determine which of these two alternate hypotheses apply to this group.

The fate of *Mukia* and *Cucumis* (Cucurbitaceae) in Australia: Unexpected relationships and diversity

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Phylogenetic analyses using multigene datasets have radically changed the systematics of Cucurbitaceae in Australia from earlier classifications based on morphology. *Mukia* Arn. has been shown to be nested in *Cucumis* L. (tribe Benincaseae) except for four endemic Australian species unexpectedly placed on a clade sister to the Mediterranean *Ecballium*/*Bryonia* clade (tribe Bryonieae). A new genus, *Austrobryonia* H.Schaef., was erected to accommodate them: *A. micrantha* (F.Muell.) I.Telford, *A. argillicola* I.Telford, *A. centralis* I.Telford and *A. pilbarensis* I.Telford. *Cucumis sativus* L., cucumber, and *C. melo* L., melon, are part of a clade comprised of c. 25 poorly collected and understudied species-level entities from India, SE Asia, Malesia, Australia, Africa and islands of the Indian Ocean in addition to the c. 30 African species of *Cucumis*. Of the 25, seven are indigenous Australian species belonging to four clades of Asian ancestry. *Cucumis picrocarpus* F.Muell., sister to *C. melo* has been reinstated. The dismembered polyphyletic *C.* (formerly *Mukia*) *maderaspatanus* L. assemblage revealed cryptic species, some new, some requiring new combinations, of which three occur in Australia: *C. althaeoides* (Ser.) P.Sebastian & I.Telford, *C. argenteus* (Domin) P.Sebastian & I.Telford and *C. variabilis* P.Sebastian & I.Telford. Also, three new endemic tropical Australian species constitute a clade sister to the Asian–Malesian *C. javanicus* (Miq.) Ghebret. & Thulin. These new relationships and their biogeographic implications show how poorly known Australian Cucurbitaceae were prior to phylogenetic reconstruction using molecular data.

New interpretations of Myrtaceae evolution and biogeography using a dated molecular phylogeny

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The plant family Myrtaceae has major centres of diversity in Australia and South America, but is distributed around the Southern Hemisphere and also some parts of the Northern Hemisphere. The origin of the family has previously been suggested as Gondwanan and hypotheses as to how the family has diversified have suggested vicariance or dispersal events. In the current study, we test these hypotheses using a well resolved chronogram attained from a Bayesian phylogenetic analysis using a calibrated relaxed molecular clock. Our results suggest that many of the divergence events within Myrtaceae tribes have occurred since the Miocene, but vicariance cannot be discounted for some of the disjunct distributions that are seen in extant Myrtaceae.

Patterns of phylogenetic diversity in wirerush, *Empodisma minus* (Restionaceae)

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As presently circumscribed the genus *Empodisma* includes 2 species. *Empodisma gracillimum* is restricted to southwestern Australia, whereas *Empodima minus* is found in Tasmania, Eastern Australia and New Zealand. We sequenced three cpDNA genes for 13 individuals of *Empodisma minus* collected in New Zealand, Tasmania and eastern Australia. These sequences were aligned with *Empodisma gracillimum* and a diverse sample of outgroups from the Restionaceae. Our results suggest the genus *Empodisma* is monophyletic and supports an ancient split between *Empodisma gracillimum* and *E. minus* that may predate the expansion of the arid treeless Nullarbor Plain. We recovered two genetically distinct lineages within *Empodisma minus,* a wide-ranging cpDNA haplotype found in Eastern Australia, Tasmania and New Zealand south of 38-39° S latitude and a distinct cpDNA haplotype restricted to the populations on the North Island of New Zealand north of 38-39° S latitude. This split conforms to a broad phytogeographical boundary that has long been recognized by New Zealand ecologists known as the kauri line. The kauri line is the southern distributional limit of *Agathis australis* and several other northern plant species. The region north of the kauri line is the warmest in New Zealand, and the pre-European vegetation consisted primarily of warm-temperate forests and restiad wetlands. The disruptive effects of ice and severe climates during past episodes of glaciation or alternately the effect of active tectonic movements have been offered as competing hypotheses to account for the kauri line.

Cenozoic environmental change and the systematics of southern hemisphere plants

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Systematists traditionally justify their science on the grounds that it enables other scientific research by providing a logical framework for generalisations about organisms. However, systematists since Linnaeus have also taken a specific interest in reconciling their knowledge of organismal relationships and distributions with theories of environmental change. Joseph Hooker, for instance, armed only with species lists, distributional information and intuitively assessed ideas of interspecific relationships, was able to formulate a remarkably prescient theory explaining disjunct plant distributions in the southern hemisphere as the result of changes in climate and the distribution of land and sea. The development of explicit methods for reconstructing phylogeny in the second half of the twentieth century was the catalyst for significant advances in biogeographic methodology, which allowed systematists to test macroevolutionary hypotheses of vicariance, dispersal, biome shifts and diversification far more rigorously than before. The recent addition of relaxed molecular clock dating techniques to the systematist's tool kit has provided yet another potentially powerful method that allows us to augment knowledge of the relative ages of clades with estimates of their minimum absolute age. These advances have enabled ever more detailed reconciliation of phylogeny with knowledge from earth and climate sciences. The results of this work have been surprising in suggesting that most taxa are more vagile but also more ecologically conservative than many of us had expected. They have also reminded us of the likely inability of most plant groups to adapt successfully to abrupt climate change. Systematic research at and below the species level has also been recently invigorated by the addition of molecular data and new analytical tools from population genetics. The exquisitely detailed descriptions of geographic variation that these advances have enabled suggest how populations have evolved and moved in response to recent climatic change. These studies also give us an insight into likely microevolutionary responses of plant populations to future climate change.

Genome and chromosome analysis of New Zealand *Plantago* species

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The taxonomic status of New Zealand species of *Plantago* (Plantaginaceae) is not fully resolved but approximately eight taxa have been recognized. These encompass a wide range of ploidy levels from diploid to 16-ploid, with a recently discovered 12*x* entity. Little is known, beyond their chromosome number, about the chromosomal relationships of these polyploids. Measurements of monoploid genome size (C_x-value, the DNA amount of the constituent genomes of diploids and polyploids) using flow cytometry show that there has been a large reduction in genome size with increasing ploidy level. Using genomic *in situ* hybridization (GISH) with a variety of whole genomic probes has revealed a complex evolutionary pattern suggesting both allopolyploid and autopolyploid formation events. However, meiotic analyses reveal that species of all ploidy levels are bivalent-forming, suggesting instead that they are all allopolyploids. More work is currently being done using fluorescent *in situ* hybridization (FISH) with the 5S and 45S ribosomal genes as probes to further study the evolutionary relationships and homogeneity between the different species.

Abstracts of posters

VKC: Virtual Key to the Compositae

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The accurate identification of species in difficult or diverse groups has always been a central element in gaining a better understanding of those groups. The Compositae family is a prime example of a this type of group and has been always associated with a idea that they are hard to identify. As a result its members are often consigned to DYC folders in the herbarium. An international effort is currently underway to build an electronic key that will simplify the task of identifying any Compositae. A list of characters and states has been built and recently revisited and expanded. The project, thanks to the generous support of USDA is currently on phase I, Compositae in the United States. The scoring of a matrix is advancing rapidly for the over 2500 species present in the US, and a final product is expected by March 2011. The Virtual Key is built on a Lucid platform and keys to each tribe will be made available at the project web site (www.vkcomp.org) as they are completed.

Broader Impacts: The results of this project will allow anyone with a modest botanical knowledge to key out members of this large and important family.

Related Links:
www.VKComp.org

Morphological comparisons in *Lachnagrostis* across the ditch

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The Blown-grasses of Australia and the Wind-grasses of New Zealand comprise the genus *Lachnagrotis* Trin. (Poaceae). Two taxa; *L. filiformis* (G.Forst.) Trin. (Common Blown-grass, Fairy-grass, New Zealand Wind-grass) and *L. billardierei* (R.Br.) Trin. subsp. *billardierei* (Coast Blown-grass, Sand Wind-grass) are shared between the countries but most are endemic to one or the other and many have rather restricted, geographical or ecological distributions. While examining the New Zealand endemics of *Lachnagrostis* it became apparent that in a number of cases, species displayed morphological similarities to Australian taxa. Examples are: *L. lacunarum* (D.I.Morris) S.W.L.Jacobs (Tarn Blown-grass) from the Tasmanian Alps with *L. striata* (Colenso) Zotov (Purple Wind-grass) from lowland to subalpine New Zealand; *L. scabra* (P.Beauv.) Nees ex Steud. (Rough Blown-grass) from coastal Australia with *L. glabra* (Petrie) Edgar (Salt-marsh Wind-grass) from coastal New Zealand; and *L. robusta* (Vickery) S.W.L.Jacobs (Salt Blown-grass) from Australian salt marshes with *L. tenuis* (Cheeseman) Edgar (Slender Wind-grass) from coastal salt-marshes of New Zealand. This morphological similarity could be homologous and have arisen from adaptive radiation (and possibly multiple extinctions) following the introduction of one taxon from one country to the other or from allopatric speciation of a taxon, common to both countries. On the other hand, speciation may have derived from independent ecological adaptive speciation from separate lineages in each country (i.e. homoplasy). The current poster is a preliminary comparison of morphological measures which awaits DNA sequence data to test taxon relationships.

Redevelopment of the database of the N.C.W. Beadle Herbarium

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The N.C.W. Beadle Herbarium (NE) is an important regional herbarium with strong coverage of northeastern NSW, good coverage of Australia and a selection of gatherings worldwide. NE was one of the first herbaria to be databased, in the mid 1980s. After several changes in platforms, the NEDB has been in urgent need of redevelopment. With support from ANDS, ALA and UNE and in collaboration with INTERSECT, the N.C.W. Beadle Herbarium is being redeveloped for data integrity, and data delivery via UNE website as well as to AVH and ALA. Here, we report on progress on phase one of the redevelopment of the NEDB.

The evolutionary history of austral *Myosotis* (Boraginaceae)

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The genus *Myosotis* comprises around 100 species of herbs distributed primarily in temperate areas of both hemispheres, or the high mountains of the tropics. Molecular evidence points to an origin of the genus in Europe and subsequent dispersal to other regions of the world including to New Zealand. Species belonging to the austral clade currently include 41 from New Zealand, 2 from Australia, and 1 each from Papua New Guinea and South America. These represent a species radiation derived from a single long-distance dispersal event. Relationships within this clade are poorly understood. The main aim of my masters' research is to reconstruct a full phylogeny of all the austral taxa using molecular phylogenetic techniques. At a finer scale, I will investigate species boundaries between morphologically similar species. A preliminary reanalysis of the only partial phylogeny of the genus has revealed striking biogeographic patterns as well as insights into the evolution of flower colour in the genus. Northern members of the genus are known for their 'forget-me-not' blue flowers, but in the south white is by far the dominant hue. Only two species in the austral clade exhibit blue flowers; both are residents of New Zealand's sub-Antarctic Auckland and Campbell islands.

New interactive keys to New Zealand weeds

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New interactive keys are being developed for rapid and accurate identification and management of New Zealand weeds and pest plants. These powerful but simple to use plant identification tools are created using Lucid™ software.

The first key, completed July 2009, is for the identification of all 150 National Pest Plant Accord (NPPA) species banned from sale, propagation and distribution in New Zealand (www.tinyurl.com/nppakey). In addition to the NPPA species, a further 150 similar and related species are included. This key is comprehensively illustrated with >5000 images. The key links to an electronic version of the naturalised plants flora (Flora of New Zealand Vol. 4) and other New Zealand plant resources: MAF Biosecurity New Zealand (MAF-BNZ), Ngā Tipu o Aotearoa – New Zealand Plants (http://nzflora.landcareresearch.co.nz), and the Weedbusters (http://weedbusters.co.nz) websites.

The NPPA key is currently being extended to include all 328 species on the Department of Conservation Consolidated List of Environmental Weeds in New Zealand (www.doc.govt.nz/upload/documents/science-and-technical/drds292.pdf). This project is scheduled for completion in March 2011. The combined key covers many weed species and we hope to add further weeds in the future.

These new keys include some 50 characters and more than 200 character states and are freely available from the Landcare Research website. For consistency they share data with and are closely modelled on three keys to Australian weeds developed and distributed by the Centre for Biological Information Technology (CBIT) (Declared plants of Australia, Suburban and environmental weeds of SE Queensland – version 2, and Environmental weeds of Australia; all in CD/DVD format).

In the course of this work, the correct names following the most up-to-date botanical treatments were resolved for many weed taxa. These updated names have been incorporated into the interactive keys, the Landcare Research Plant Names database, the new edition of *An Illustrated Guide to Common Weeds of New Zealand*, and the MAF-BNZ NPPA list (www.biosecurity.govt.nz/pests/surv-mgmt/mgmt/prog/nppa). This provides an important consistency of usage of weed names in New Zealand.

ACKNOWLEDGMENTS

The New Zealand weed and pest plant keys outlined here were funded by the Terrestrial & Freshwater Biodiversity Information System (TFBIS) Programme. We also thank many contributors for images used in the keys.

Global Compositae Checklist – Progress and Prospects

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The days of manually compiling checklists are coming to an end as the options offered by Biodiversity Informatics change the systematic landscape. The Global Compositae Checklist (GCC) is a project that utilizes the possibilities of computer assisted checklist generation by integrating existing electronic datasets from around the world for this large plant family (approx 25,000 species). The purpose built program (C-INT) retains all original data and links names that are deemed the same to a “consensus” name which reflects a summary of all contributed data. To date the project has included more than 50 individual data sources covering the cosmopolitan distribution of the Compositae. The family is estimated as having 25,000 described species and the accumulated data contributed to this project has yielded 26,000 accepted species, 58,000 species synonyms as well as significant infraspecific data. In total more than 420,000 individual records have been matched to create around 150,000 consensus names, approximately 60% of which have preferred concepts. This data represents significant progress towards a global checklist and is now being presented to Compositae taxonomists from around the world via The International Compositae Alliance (TICA) for feedback and vetting.

Broader Impacts:
This project will provide up-to-date nomenclature for the largest and most successful flowering plant family. It will assist amateurs and professions in using the correct names for the family and will help with conservation efforts.

Related Links:
http://www.compositae.org

Genetic Diversity of the Quandong (*Santalum acuminatum*) in South Australia

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The native Australian fruit quandong, *Santalum acuminatum*, is widely dispersed across the southern arid regions of Australia. The quandong, along with two other endemic species of *Santalum* (*S. spicatum* and *S. murrayanum*) have been listed as threatened. Their populations are impacted by wild harvesting for their fruit, browsing by feral animals, and habitat fragmentation. We use a phylogeographic approach to study remnant populations in South Australia, reconstruct the historical processes underlying their geographic distributions, reveal their current genetic structure, and determine which of the external stresses have had the greatest impact. We collected leaf samples from extant populations of *Santalum* species across South Australia and from the state herbarium. These samples have been genotyped using chloroplast and nuclear microsatellite markers, and DNA sequences were obtained from the nrDNA marker ITS. Preliminary results indicate a high degree of genetic variation both between and within populations of South Australia. This was found in DNA sequences of both ITS and chloroplast regions. Both DNA sequence and microsatellite data suggest that populations from western South Australia, in the Nullarbor region, were genetically distinct from all other populations sampled. This corresponds with morphological variation observed in these populations. More detailed genetic and morphological study of quandong will help to uncover the historical processed underlying the current distribution of the species, and determine what biotic and abiotic factors have had the largest impacts on their genetic diversity.

Fruit diversity within *Schoenus* section *Helothrix*

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Schoenus section *Helothrix* (Nees) Kük. comprises c. 30 taxa that are predominately tufted annual or short lived perennial sedges. Scanning electron microscopy was used to illustrate fruit characters such as size, shape and surface ornamentation. Characters associated with the perianth segments, i.e. number, length and indumentum, were also investigated. These results will contribute to the morphological analysis of *Schoenus*. Fruit from three taxa (*Schoenus apogon*, *S. fluitans* and *S. maschalinus*) that occur in both Australia and New Zealand will be highlighted.

Conservation genetics of the endemic root holoparasite, *Dactylanthus taylorii*

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Identification of intraspecific genetic variation is important for management and conservation of endangered taxa. *Dactylanthus taylorii* (Balanophoraceae) is an endemic New Zealand root holoparasite that is endangered due to threats from introduced pests, particularly brush-tailed possums, and habitat degradation. *D. taylorii* is listed as Nationally Vulnerable and management is coordinated through a National Recovery Group, who actively monitor and protect populations throughout its North Island range. For this study, we are using microsatellite loci to evaluate genetic diversity within and between populations of *D. taylorii* from throughout its range to determine population structure and to aid in conservation management decisions. To isolate microsatellite loci, genomic DNA of *D. taylorii* was sequenced using 454 GS FLX. From the 61,709 random sequences that were generated, 4044 repeats were identified and 753 primer pairs were designed using MSATCOMMANDER and Primer3. Based on criteria related to sequence quality and repeat structure, 48 loci have been screened to identify consistently amplifiable and variable markers that will be suitable to evaluate the genetic structure of all known populations. Using these markers we will determine the levels of genetic variation within and between populations, as well as the degree of gene flow between populations and the level of inbreeding. This information will directly benefit future conservation efforts as the Department of Conservation and the National Recovery Group determine populations of national significance to conserve and potential seed sources for translocation to increase genetic diversity in existing populations and to establish new populations.

When males stop being females & vice versa: A case study of dioecious floral development in ribbonwood (*Plagianthus*, Malvaceae)

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Despite the remarkably high occurrence of dioecy in the New Zealand flora, very little is understood about the evolution, gender expression and floral development in these native species whose populations consist of distinct male plants and female plants. The dioecious genus *Plagianthus* (Malvaceae) is endemic to New Zealand and contains two species: the lowland tree *P. regius* and the estuarine shrub *P. divaricatus*. Both species are strictly dioecious, yet each possess whorls of the opposite gender in their functionally unisexual flowers (i.e., female flowers develop an androecium and male flowers a gynoecium). To characterize the floral development and determine when the non-functional reproductive parts are arrested, histological and scanning electron microscopy work was conducted on specimens of *P. regius* and *P. divaricatus* collected from floral inception through to anthesis. Stages of floral development in the two sexes are contrasted in images. Knowledge of floral developmental stages in *Plagianthus* will provide the framework for designing an investigation into the genetic differences underlying gender expression via a comparison of 454 sequence data of floral cDNA libraries of males versus females.

Gingidia montana (Apiaceae) in Australia, an unnamed endemic or waif from New Zealand

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Eight species are currently assigned to *Gingidia*; five endemic to New Zealand, two endemic to southern NSW. The remaining species, *Gingidia montana*, with its type from New Zealand, is known in Australia from two small extant populations on cliff tops of New England National Park in northern NSW. There was concern by Park staff that this may be a recently introduced weed from New Zealand, but we present evidence that the Australian populations are a new, rare, endemic species. A previous, preliminary phylogenetic study pointed to the non-monophyly of *Gingidia*. That study did not include Australian material of '*G. montana*'. We set out our plan for trans-Tasman collaboration to resolve species limits and the phylogeny of the group.

An example of species radiation and convergence on a piece of Pacific Gondwana: New Zealand gnaphalioid Asteraceae

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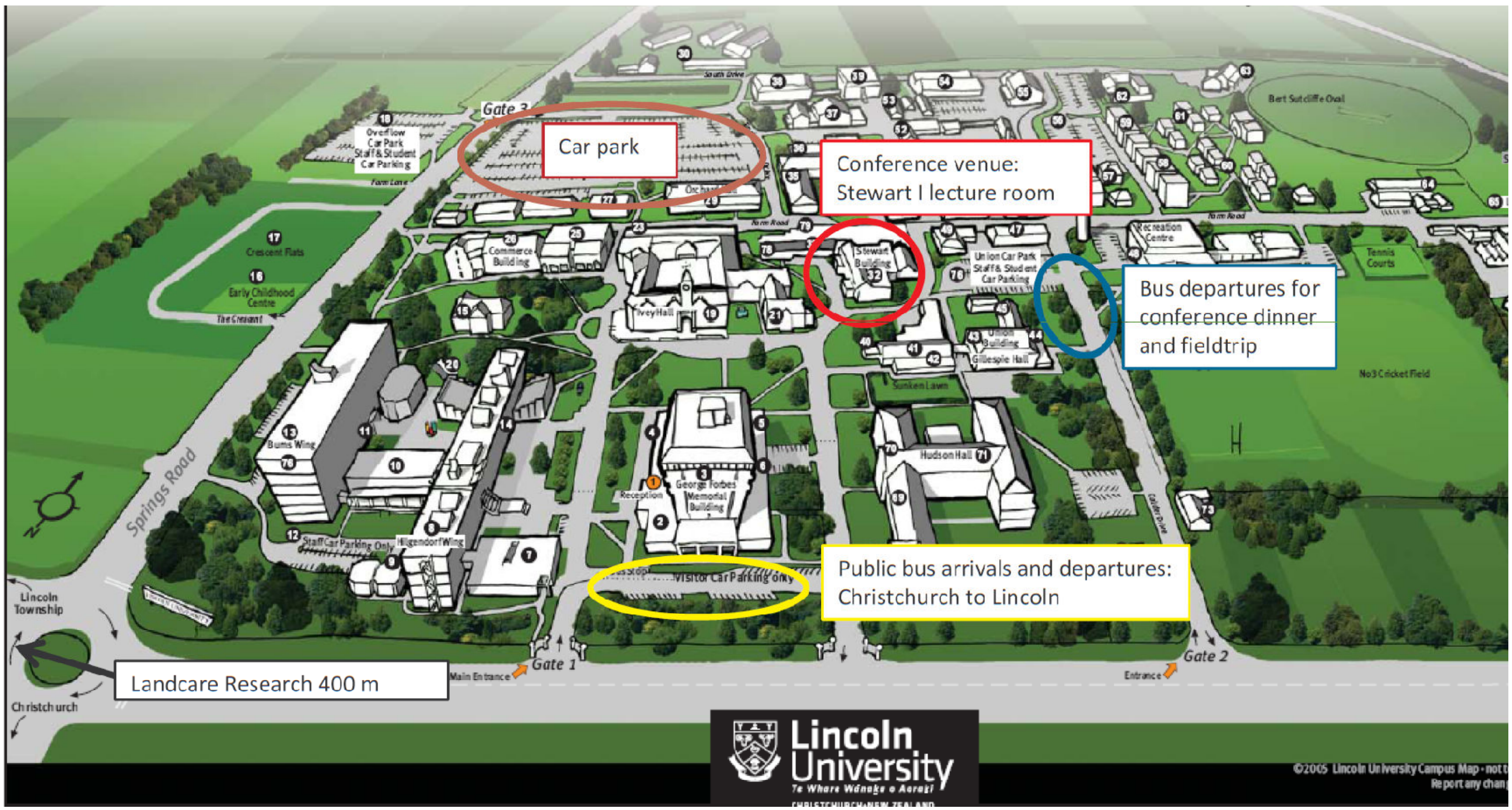
Most of the 70–80 species of gnaphalioid Asteraceae in New Zealand constitute a single lineage that is entirely endemic except for two species in New Guinea. Members of this lineage show poor phylogenetic signals from ITS sequence data but a remarkable morphological and ecological diversity. This is consistent with results from an increasing number of New Zealand’s plant groups. These have led researchers to infer rapid and recent species radiation associated with geological and climatic instability in New Zealand in the late Tertiary and early Quaternary. Curiously striking morphological similarities exist between this endemic gnaphalioid lineage and other Asteraceae lineages both in New Zealand and elsewhere. Such morphological convergences can cause taxonomic confusion if they are misinterpreted as synapomorphies. Currently we are using multilocus fingerprinting and low copy number nuclear gene sequencing to gain insight into the complex inter-relationships of New Zealand’s Gnaphalieae.


Car park
Conference venue:
Stewart I lecture room
Bus departures for
conference dinner
and fieldtrip
Public bus arrivals and departures:
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Landcare Research 400 m
Gate 1
Gate 2
Gate 3
Main Entrance
Entrance
Springs Road
Lincoln Township
Christchurch
Overflow Car Park Staff & Student Car Parking
Crescent Flats
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Commerce Building
Ivey Hall
Stewart Building
Union Car Park Staff & Student Car Parking
Recreation Centre
Tennis Courts
Bert Sutcliffe Oval
Burns Wing
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Staff Car Parking Only
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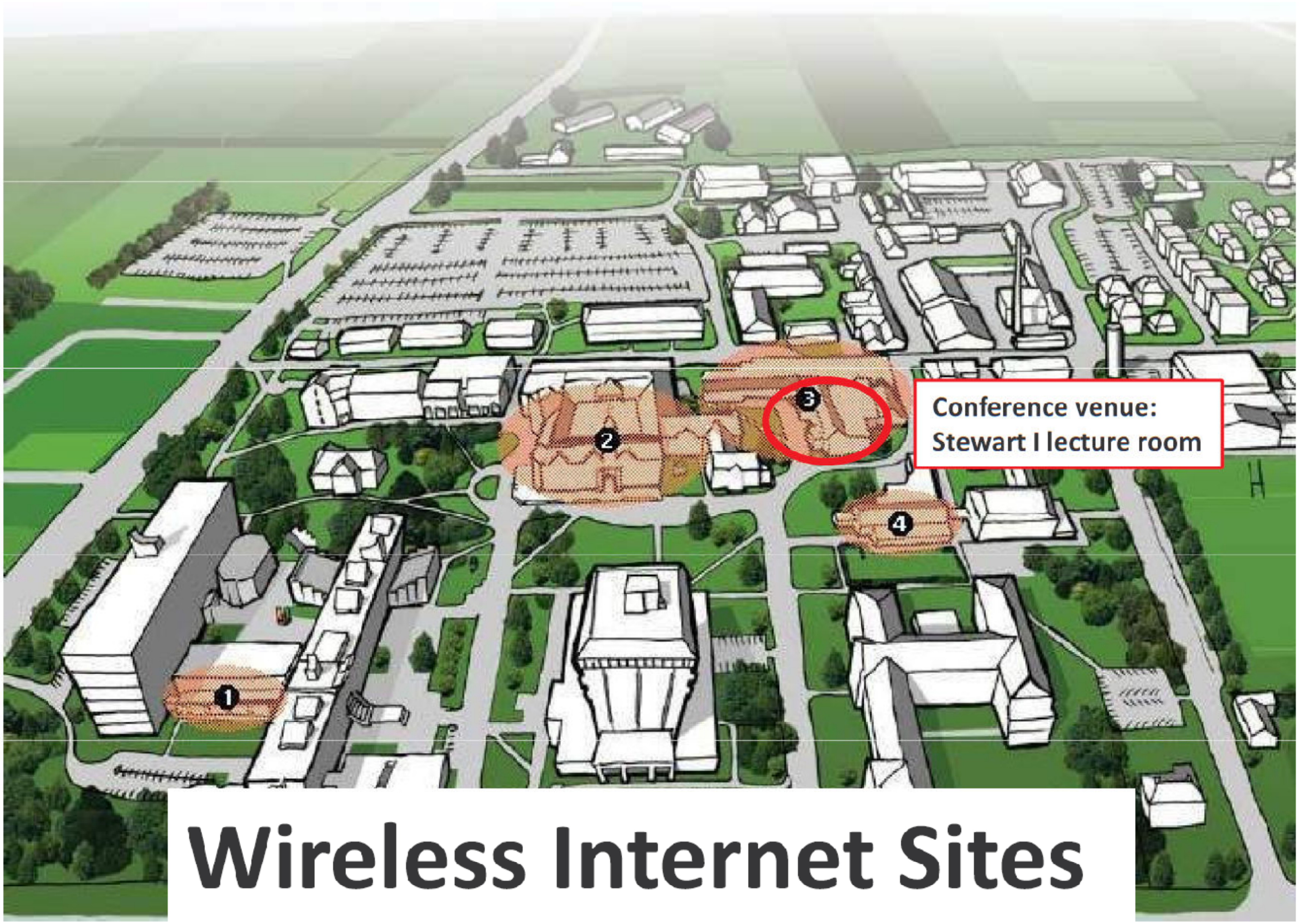

Wireless Internet Sites

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