Program and Abstracts

Australasian Systematic Botany Society Conference 2012

Local knowledge, global delivery

23–28 September, Perth, Western Australia

ASBS 2012
CONFERENCE PERTH

Front cover
Spine of a low unnamed range on Wyloo Station in the Pilbara bioregion
Image: Ryonen Butcher

Banksia meisneri
Drosera hyperostigma
Actinotus leucocephalus
Erichsenia uncinata
Images: Kevin Thiele

Verticordia grandis

The Scarlet Featherflower is an iconic Western Australian species endemic to the northern sandplains (or 'Kwongan') region in southern Western Australia. *Verticordia grandis* is one of several species named by colonial botanist James Drummond. With its prominent red flowers, large rounded leaves, and ability to resprout from a lignotuberous base, this species is a particularly striking element of post-fire habitats. This stunning species provided the inspiration for the ASBS 2012 Conference logo, designed by Lynne Whittle (Strategic Development and Corporate Affairs, Department of Environment and Conservation). Image: Kevin Thiele

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Australasian Systematic Botany Society Inc.
Web: www.anbg.gov.au/asbs
Email: asbs@anbg.gov.au

Published by the ASBS 2012 Perth Conference Committee

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Welcome from the ASBS 2012 Perth Conference Committee

Welcome to the 2012 Australasian Systematic Botany Society Conference and to the wonders of spring in the south-west of Western Australia.

The ASBS conference was last held in Perth in December 1999 and the local botanical community has since witnessed many changes, the most significant of which is undoubtedly the completion of a new State Herbarium within the Western Australian Conservation Science Centre at the Department of Environment and Conservation. With space for 1.2 million specimens and excellent research and curation laboratories, Western Australia finally has a facility that befits its extraordinary biodiversity. There has also been a dramatic improvement in our knowledge of the State's flora, with the description of more than 1,150 new vascular plant species since the last conference. The number of informally named taxa has also increased, from a little over 1,200 to 1,554, denoting the scale of taxonomic research that is still required to produce a baseline inventory of our State's flora. In 1999, FloraBase was in its infancy but has since grown to become the State's leading online botanical resource, receiving in the order of 3.5 million page views per year. This site now encompasses *Nuytsia*, the first Australian herbarium journal to embrace electronic publication following last year's landmark International Botanical Congress in Melbourne, where sweeping new changes surrounding the publication of new taxa were proposed.

In addition to the description of many new Western Australian species, there have been a significant number of changes to known taxa as researchers align classification with phylogeny. These include a plethora of familial name changes following the rearrangement of the collections at the Western Australian Herbarium to reflect the classification of the Angiosperm Phylogeny Group (APGIII), as well as generic-level changes such as the sinking of *Dryandra* into *Banksia*. The controversy generated by this particular change is the stimulus behind the session at this year's conference on the science and philosophy behind name changes, which aims to highlight some of the possible name-change events on the horizon. In keeping with our conference theme of *Local knowledge, global delivery*, we have two sessions dedicated to the delivery of taxonomic information to stakeholders, and we will also be showcasing research on new and innovative phylogenetic methods. As always, the conference will provide a fantastic snapshot of the wide variety of systematics research being conducted in the Australasian region. We're delighted that colleagues from New Zealand have been able to make the long and expensive journey to Perth, especially given that this is the first ASBS conference to be held since March 2011, when the society embraced its strong regional ties and became international in scope. We are also pleased to have so many students and early career scientists join us to present their research.

We acknowledge and thank all of the sponsors of ASBS 2012 Perth, for without their generous support this event wouldn't have been possible. We've been especially pleased by the positive response to this event by our local botanical consulting community, who share with us the understanding that close linkages between the research community and industry leads to improved conservation of Western Australia's remarkable biodiversity.

We thank you all for joining us for what we hope will be a fantastic event.

We thank these sponsors for their generous support

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Acknowledgments

Annette Wilson, Australian Biological Resources Study

ASBS Council, especially John Clarkson, Peter Weston and Frank Zich

Barbara Jamieson, Plant Biology, The University of Western Australia

David Gough, Strategic Development and Corporate Affairs, Department of Environment and Conservation

Julie Harrison, The University of Western Australia Club

Lynne Whittle and staff at Strategic Development and Corporate Affairs, Department of Environment and Conservation

The Botanical Artists Group of Western Australia, in particular Ellen Hickman

Staff at the Western Australian Herbarium

General Information

Tourist Information

Western Australian Visitor Centre

55 William St, (corner of Hay St), Perth 6000
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Perth After-hours GP Clinic

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Shop 14, City Station Concourse, 378 Wellington St (corner Wellington St and Barrack St), Perth
http://www.ccmc.net.au/Contact.html
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Police (non-emergency)

Phone: 131 444

Venues

Biodiversity Conservation Science Centre
Kings Park and Botanic Garden, Fraser Ave, West Perth, WA 6005

The University Club of Western Australia
Hackett Drive Entrance #1, The University of Western Australia, Crawley, WA 6009

Western Australian Conservation Science Centre
Department of Environment and Conservation, 17 Dick Perry Ave, Kensington, WA 6151

Events

Registration Mixer

Enjoy the wildflower extravaganza at the Kings Park Festival before catching up with old friends and meeting new ones over some light refreshments

Date: Sunday 23 September
Time: 4pm – 6pm
Location: Biodiversity Conservation Science Centre, Kings Park and Botanic Garden

ASBS Annual General Meeting

Date: Tuesday 25 September

Time: 4pm – 6pm
Location: Theatre Auditorium, The University Club of Western Australia

Conference Dinner

Pre-dinner drinks can be purchased at the UWA Club Cafe Bar following the AGM and prior to the dinner

Date: Tuesday 25 September
Time: 7pm – 11pm
Location: Banquet Hall, The University Club of Western Australia

DEC Sundowner

Refreshing beverages and a light supper will be provided

Date: Wednesday 26 September
Time: 5.45pm – 8pm
Location: courtyard, Western Australian Conservation Science Centre (DEC)

Mt Lesueur Field Trip

All meals provided

Date: Thursday 27 September – Friday 28 September

Lesueur National Park, *c*. 220 km north of Perth near the coastal town of Jurien Bay, has exceptional flora conservation values, supporting a large number of distinct, species-rich and endemic communities. The park has more than 900 species of vascular plants, including nine *Threatened* species and more than 100 locally or regionally endemic taxa. The vegetation is structurally diverse, consisting mostly of kwongan (low shrublands and heath) and woodlands interspersed in a complex mosaic. The region is also characterised by complex geological features and unusually rugged terrain. The fauna of Lesueur is also diverse, with at least 15 mammal, 124 bird, 52 reptile and nine frog species. The park is critically important to the survival of birds that nest in tree hollows, such as the endangered Carnaby’s Black Cockatoo. A new loop drive through the park has recently been completed providing panoramic views and ready access to a number of walk trails with stunning vistas. Part of the park was burnt in the summer of 2010, providing an opportunity for botanising in a post-fire habitat.

Botanical Artists Group of Western Australia

Exhibition and Sales

Date: Wednesday 26 September
Location: Western Australian Conservation Science Centre (DEC)

The Botanical Artists Group of Western Australia (more commonly known by their amusing acronym BAGs) play a significant role in investigating and celebrating Western Australia's globally renowned flora. The group has six practicing members—Philippa Nikulinsky, Katrina Syme, Pat Dundas, Margaret Pieroni, Penny Leech and Ellen Hickman—with Rica Erickson having sadly passed away in 2009 (aged 101). These highly specialised artists share an abiding wonder of the natural world that is captured in their exquisite works of art. They are a cherished part of the State's botanical community and it is extremely fitting that they are part of this year's ASBS conference.

Lechenaultia biloba and *L. formosa*
Illustrations: Ellen Hickman

Conference Program

Great Western Woodlands near Lake Johnston on the Hyden–Norseman Road
Image: Kevin Thiele

Chamaescilla corymbosa
Helichrysum macranthum
Goodenia coerulea
Trachymene grandis
Images: Kevin Thiele

Monday 24 September – The University Club of Western Australia, UWA

8.00–8.45 am	**Registration**
8.45–9.00 am	**Welcome and Acknowledgement**
	***Systematics sans frontièrs* (chair – Marco Duretto)**
9.00–9.30 am	**Keynote – David Mabberley** Whither Australian plant systematics? [p. 14]
9.30–9.45 am	**Darren Crayn** Plant dispersal across Wallace's line: dated molecular phylogenies reveal the dynamics of the Sahul-Sunda floristic exchange and assembly of the Australian tropical rainforest flora [p. 26]
9.45–10.00 am	**Michael Bayly** Genetic evidence for introgression and historical biogeographic patterns in *Correa* (Rutaceae) [p. 28]
10.00–10.15 am	**Tanya Scharaschkin** Phylogenetic placement and biogeographic history of the Australian Annonaceae [p. 39]
10.15–10.30 am	**Lyn Cook** Geographic range size and biodiversity hotspots: the SWAFR versus SE Australia [p. 25]
10.30–11.00 am	**Morning Tea**
	***Test tube taxonomy* (chair – Michelle Waycott)**
11.00–11.15 am	**Michelle Waycott** Dealing with those problematic taxonomic groups—introgressed, character reduced, polyploid, marginal habitat, recently evolved, clonal, disjunct 'species' [p. 48]
11.15–11.30 am	***Austin Brown** Taxonomic signatures in *Lachnagrostis* from AFLPs [p. 21]
11.30–11.45 am	***James Ingham** Integrative species delimitation of the *Macrozamia plurinervia* complex (Zamiaceae) [p. 32]
11.45–12.00 pm	***Lalita Simpson** Mind the gap: phylogeography and taxonomy of the *Dendrobium speciosum* complex (Orchidaceae) [p. 42]
12.00–12.15 pm	**Franck Stefani** An overview of species richness and phylogenetic relationships in *Cortinarius* (Fungi, Agaricales) from southern Australia [p. 43]
12.15–12.30 pm	**Kelly Shepherd** Good grief, what's happening to *Goodenia*? [p. 39]
12.30–1.15 pm	**Lunch**
	***Species boundaries under the microscope* (chair – Brendan Lepschi)**
1.15–1.30 pm	**Juliet Wege** Strategic taxonomy and revisionary taxonomy: two complementary approaches to reducing Western Australia's taxonomic backlog [p. 48]
1.30–1.45 pm	***Yumiko Baba** Systematics of *Elaeocarpus* (Elaeocarpaceae) in Australia: resolving the *E. obovatus* species complex [p. 18]
1.45–2.00 pm	***Margaret Stimpson** Instalment one in the resolution of the *Banksia spinulosa* complex (Proteaceae): *Banksia neoanglica* raised to species rank *comb. nov.* [p. 43]
2.00–2.15 pm	**Greg Keighery** Documenting and conserving local diversity in, within and beyond Perth [p. 33]
2.15–2.25 pm	***Julie Atkinson** A conservation perspective to species boundaries in *Grevillea* subgroup *floribunda*: exploring reproduction, population genetics and evolutionary trajectories [p. 18]
2.25–2.40 pm	***Bo-Kyung Choi** Systematics and evolution of *Melaleuca sens. lat.* (Myrtaceae): the status of *Melaleuca argentea* 'Ashburton biotype' [p. 23]
2.40–2.55 pm	***Todd McLay** Hard yacca: taxonomy and systematics of the Australian grass-tree genus, *Xanthorrhoea* [p. 35]
2.55–3.30 pm	**Afternoon Tea**
	***Systematics and diversity* (chair – Darren Crayn)**
3.30–3.45 pm	**Joanne Birch** Phylogeny of Australian Poaceae tribe Poeae focussing on the genus *Poa* [p. 20]
3.45–4.00 pm	**Peter Heenan** Classification of *Nothofagus* (Nothofagaceae): the past, the present, and the future [p. 31]
4.00–4.15 pm	***Sook-Ngoh Phoon** Re-evalution of the current infrageneric classification of the tropical rainforest tree genus *Elaeocarpus* (Elaeocarpaceae) in Australia and West Malesia [p. 37]
4.15–4.30 pm	***Nuttanun Soisup** Molecular systematics of the Australian endemic genera *Caulocystis* and *Acrocarpia* (Sargassaceae, Fucales, Phaeophyceae) based on ITS, *cox*1 and *rbc*L DNA sequences [p. 42]
4.30–4.45 pm	***Edward White** Are parasitic insects good plant taxonomists? Insights from gall-inducing scale insects feeding on Leptospermeae [p. 49]
4.45–5.00 pm	***Ken Mills** Myrmecochory is not all or nothing: comparative assessment of ant dispersal in a clonal sedge [p. 36]
5.00–5.15 pm	**Alexander Schmidt-Lebuhn** Monophyly and phylogenetic relationships of *Ozothamnus* and *Cassinia* (Asteraceae, Gnaphalieae) [p. 40]

***Student presentation**

Tuesday 25 September – The University Club of Western Australia, UWA

8.00–8.30 am	**Registration**
	Institutional data: use and abuse **(chair – Kevin Thiele)**
8.30–9.15am	**Keynote – Baden Appleyard** Implementing AusGOAL and supporting good science [p. 14]
9.15–9.30 am	**Ilse Breitwieser** Flora of New Zealand: development of a dynamic resource [p. 20]
9.30–9.45 am	**Murray Dawson** Interactive keys to the New Zealand flora: trans-Tasman connections [p. 27]
9.45–10.00 am	**Bryan Simon** Grasses online – Scratchpads for Poaceae [p. 41]
10.00–10.15 am	**John Huisman** Smoke and mirrors: are Australian seaweed communities retreating? [p. 32]
10.15–10.30 am	**John Hosking** Herbaria need better funding to encourage collection of vouchers and to allow for their retention by herbaria [p. 31]
10.30–11.00 am	**Morning Tea and Poster Session**
	Methods to our madness **(chair – Joe Miller)**
11.00–11.05 am	Introduction
11.05–11.20 am	**Brent Mishler** Phylogenetic measures of biodiversity and endemism, with an example using Australian bryophytes [p. 36]
11.20–11.35 am	**Joseph Miller** Phylogeny and endemism of *Acacia* [p. 35]
11.35–11.50 am	**Andrew Thornhill** Eucalypts and orchids: a phylogenetic and spatial analysis of two of Australia's largest plant groups [p. 46]
11.50–12.05 pm	**Alexander Schmidt-Lebuhn** Spatial distribution of species richness, phylogenetic diversity and collecting activity in the Australian native daisies (Asteraceae) [p. 40]
12.05–12.20 pm	**Carlos González-Orozco** Phylogenetic Niche Modelling (PhyNM): exploring the evolutionary history of Australia in a new way [p. 30]
12.20–12.35 pm	**Nunzio Knerr** Biodiversity research data cleaning and visualisation methods [p. 34]
12.35–1.25 pm	**Lunch**
	It's character building **(chair – Kristina Lemson)**
1.25–1.40 pm	**Caroline Puente-Lelievre** Is pollen morphology useful to define monophyletic genera in the epacrids? [p. 38]
1.40–1.55 pm	***George Plunkett** Systematic studies in eastern Australian *Lepidosperma* (Cyperaceae): identifying novel characters and data sources [p. 38]
1.55–2.10 pm	***Melodina Fabillo** Does inflorescence morphology warrant taxonomic revision in the Australian native grass *Tripogon loliiformis*? [p. 28]
2.10–2.25 pm	**John Thompson** New genera or just variation? A preliminary perspective on some new Queensland grass taxa [p. 45]
2.25–2.40 pm	**Katharina Schulte** Assembling the bigger picture: phylogenetic relationships and character evolution in Dendrobiinae (Orchidaceae) [p. 41]
2.40–3.00 pm	**Afternoon Tea**
	Evolutionary perspectives **(chair – Jϋrgen Kellermann)**
3.00–3.15 pm	**Michael Crisp** Can directional bias in evolutionary transitions be inferred from phylogenies? An investigation using Australian pea-flowered legumes [p. 47]
3.15–3.30 pm	**Marco Duretto** Molecular phylogeny of *Boronia* and *Boronella* (Rutaceae) using chloroplast and nuclear markers [p. 19]
3.30–3.45 pm	**Michael Bayly** Chloroplast genome sequencing across the eucalypt clade: *Allosyncarpia*, *Stockwellia*, *Angophora*, *Corymbia*, *Eucalyptus* (Myrtaceae) [p. 46]
3.45–4.00 pm	**Daniel Murphy** Divergence dating of *Acacia* [p. 37]
4.00–6.00 pm	**ASBS AGM**

***Student presentation**

Wednesday 26 September – Western Australian Conservation Science Centre, DEC

8.00–8.20 pm	**Registration**
8.20–8.30 pm	**Acknowledgment**
	***iPlants* (chair – Ilse Breitwieser)**
8.30–9.15 am	**Keynote – Brent Mishler** A new era for natural history collections: the impact of digitization and phylogenetics on analysis of biodiversity data [p. 36]
9.15–9.30 am	**Kevin Thiele** KeyBase – an interactive dichotomous key to all Australia's plants [p. 33]
9.30–9.45 am	**Frank Zich** Online delivery and use of Australian Tropical Rainforest Plants identification tool [p. 50]
9.45–10.00 am	**Paul Gioia** Atlas of Living Australia: where to now for State-based online systems? [p. 29]
10.00–10.15 am	**Judy West (pre-recorded)** Flora of Australia online [p. 45]
10.15–10.30 am	**Alex Chapman** Protologues, Floras and taxon profiles – how many descriptions do we need? [p. 23]
10.30–11.00 am	**Morning Tea**
	***Western focus* (chair – Rachel Meissner)**
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11.30–11.45 am	**Ryonen Butcher** Tackling *Tephrosia* (Fabaceae) in north-Western Australia [p. 22]
11.45–12.00 pm	**Neil Gibson** The ultramafic flora of Western Australia [p. 29]
12.00–12.15 pm	**Russell Barrett** Documenting the Kimberley flora: a never-ending story? [p. 19]
12.15–1.20 pm	**Lunch**
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1.35–1.50 pm	**Margaret Byrne** Conservation of refugia and their evolutionary lineages [p. 22]
1.50–2.05 pm	**Chris Dunne** Biosecurity for natural ecosystems: a case study of the introduction of *Phytophthora* species into the native plant communities of south-west Western Australia [p. 27]
2.05–2.20 pm	**Colin Crane** Influence of climate on canker disease in the Proteaceae of the Southwest Australian Floristic Region [p. 26]
2.20–2.35 pm	**Mark Harvey** Short-range endemism amongst the Australian fauna: patterns, problems and prospects [p. 30]
	***Is bigger better?* (chair – Kevin Thiele)**
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2.50–3.05 pm	**Peter Weston** Contested, uncontested and potentially controversial taxonomic changes in the Proteaceae: how do they differ? [p. 49]
3.05–3.35 pm	**Afternoon Tea**
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3.50–4.05 pm	**Mark Clements** Robert Brown's *Caladenia* (Orchidaceae) revisited: updated interpretation based on results of multigene phylogenetic analyses inferred from plastid and nuclear loci [p. 24]
4.05–4.20 pm	**Karen Wilson** *Carex sens. lat.* (tribe Cariceae, Cyperaceae): an international initiative [p. 50]
4.20–4.35 pm	**Barbara Briggs** Aligning classification with phylogeny in Restionaceae, Centrolepidaceae and Anarthriaceae (the restiid clade of Poales) [p. 21]
4.35–4.50 pm	**Lyn Cook** They are all bottlebrushes: should they all be *Melaleuca*? [p. 25]
4.50–5.20 pm	**Nancy Burbidge Medal Presentation**
5.20–5.45 pm	**Student Prizes and Conference Wrap**

***Student presentation**

Posters Monday 24 – Wednesday 26 September

10.30–11.00 am Tuesday 25	**Informal Poster Session**
***Ben Anderson**	A revision of *Rhynchotechum* (Gesneriaceae) [p. 52]
Matt Buys	BRAHMS: music to a cyber-taxonomist's ears [p. 52]
Karina Knight	Water fire suppression system to protect a valuable Herbarium collection – is this folly or the future for herbaria? [p. 53]
Kristina Lemson	Untangling inflorescence structures in epacrids (Ericaceae: Epacridoideae) [p. 53]
Claire Micheneau	Selection of candidate DNA regions for use on closely related orchid species: a case study from African angraecoid orchids (Vandeae, Epidendroideae, Orchidaceae) [p. 54]
Michaele Milward-de-Azevedo	Taxonomy and evolutionary relationships in a section of the genus *Passiflora* (Passifloraceae), contribution of pollen, morphological and molecular characters [p. 54]
***Chrissie Prychid**	It's character building – systematic implications of silicon and stomata in mapaniid sedges [p. 55]
***Lalita Simpson**	What is at risk? Phylogeography and taxonomy of orchids endemic to Queensland's mountaintop biodiversity hotspots [p. 55]
Udani Sirisena	Seed morphology in *Thysanotus* and related genera of Asparagaceae, Lomandroideae, Cordylineae [p. 56]
Ghadir Taheri	Assessment of genetic diversity in Rhubarb (*Rheum ribes*, Polygonaceae) [p. 56]
Ghadir Taheri	A revision of *Trisetum* (Poaceae, Aveneae) in Iran [p. 57]
Karen Wilson	Understanding the big genera of tribe *Schoeneae* (Cyperaceae) [p. 57]

***Student poster**

Keynote abstracts

Acacia papyrocarpa mass flowering over *Maireana sedifolia* and *Austrostipa plumigera,* Great Victoria Desert Nature Reserve

Image: Rob Davis

Stylidium dichotomum
Drosera microphylla
Marsilea mutica
Melaleuca undulata

Images: Kevin Thiele

Implementing AusGOAL and supporting good science

Baden Appleyard

Australian Governments’ Open Access and Licensing Framework (AusGOAL)
Email: b.appleyard@ausgoal.gov.au

The natural environment is vital to our wellbeing and that of future generations. Our landscapes, oceans, water, atmosphere and biodiversity play an important role in the economy—from agriculture and mining to energy production and tourism—and are fundamental to our Australian identity and way of life. To manage this natural capital responsibly, governments, industry and the community need comprehensive, trusted and timely environmental information. Good information is essential for us to make sound decisions, individually and collectively, about the major issues affecting our natural assets. AusGOAL is a glimpse into the future of management and sharing of this publicly funded information. It foreshadows exciting and daunting issues around how publicly funded information can be re-used in a legally appropriate way. I will describe how AusGOAL works and provide some insights into the data-rich future; how the open access licensing regimes affects institutional information management and how governments, the research and innovation sector, and the community may benefit.

Whither Australian plant systematics?

David J. Mabberley

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A brief review of the history of the discipline of plant systematics in Australasia is presented. The questions as to the importance to society of this endeavour through time are addressed—why the activity is pursued and who pays or should pay for it. The global position of Australasian work is assessed with regard to what society now expects of plant systematists. What are the ‘big questions’? The importance of determining priorities with regard to taxonomic groups and biological phenomena studied, on the one hand, and the different niches of workers in universities, research institutes and botanic gardens, on the other, are highlighted. The obligations of Australasian plant systematics with regard to neighbouring countries are outlined and justification for funding of these and domestic priorities is explored.

A new era for natural history collections: the impact of digitisation and phylogenetics on analysis of biodiversity data

Brent D. Mishler

University and Jepson Herbaria, and Department of Integrative Biology, University of California,
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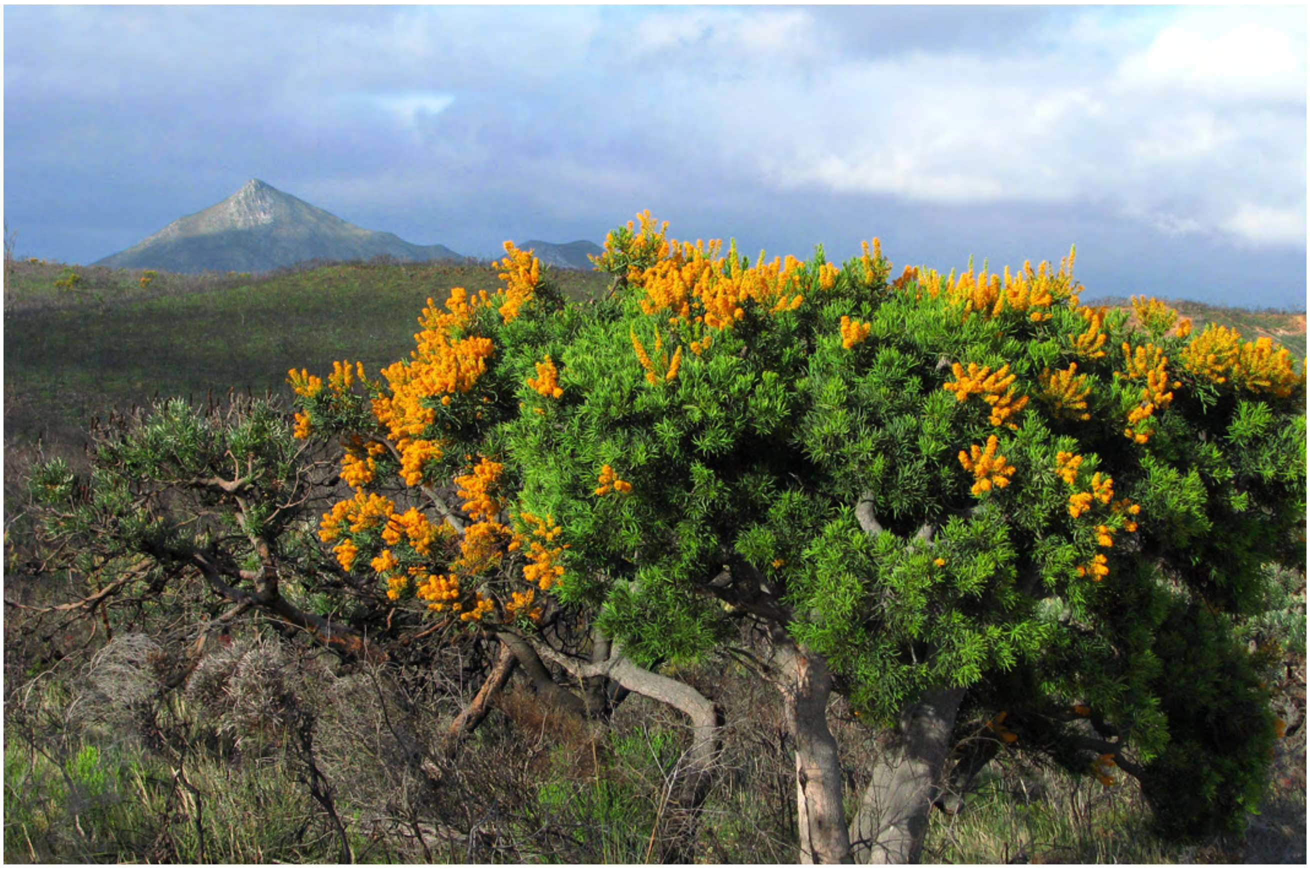
Digitisation is rapidly making specimen data available to the public, via increasingly advanced bioinformatics. Inexpensive DNA sequencing and rapid advances in computational methods for both tree building and tree using have eclipsed previous limits on the scope of phylogenetic investigations and phylogenetic systematics. Natural history collections are the nexus where it all comes together; specimens and their associated meta data are the ground truth for all biodiversity studies. Specimens are essential DNA vouchers, fundamental phylogenetic, geographic, evolutionary and ecological data points, sole resolvers of taxonomic issues, and primary evidence for global change and other human-caused modifications of the environment. I will present examples of new uses for specimen data, drawing mainly from two places with an advanced state of herbarium digitisation, Australia and California, but also from other efforts around the world. The many uses of collection databases include important practical applications, taking advantage of temporal aspects of collection data, such as: 1) climate change modelling; 2) spatial ecology/mapping historical habitats and landscapes; 3) tracking the introduction of pathogens and invasive species; and 4) phenology estimates through time, as well as scientific applications, such as: 1) identification of under-collected areas (targeted exploration) and other collection biases; 2) production of floras and identification tools; 3) discovery of previously undescribed taxa; 4) reconstructing assembly of communities; 5) biogeography and diversification studies; and 6) assessing biodiversity and endemism using new phylogenetic approaches.



Oral Presentation Abstracts

Fitzgerald River National Park, with *Nuytsia floribunda* in full bloom and West Mount Barren in the background
Image: Steve Dillon

Oligarrhena micrantha
Nuytsia floribunda
Pogonolepis stricta
Diplolaena obovata
Images: Kevin Thiele

A conservation perspective on species boundaries in *Grevillea* subgroup *floribunda*: exploring reproduction, population genetics and evolutionary trajectories

Julie L. Atkinson, Susan E. Hoebee and Trevor J. Edwards

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Morphology, reproductive and genetic characteristics, and environmental constraints all influence species boundaries. The study complex *Grevillea* subgroup *floribunda* consists of ten species, widely distributed from Queensland to Victoria. Floral divergence is evident within and among taxa but all are thought to be primarily bird pollinated. Boundaries between the three Victorian members of this subgroup (*G. alpina*, *G. celata* and *G. chrysophaea*) are taxonomically unclear. For example, numerous informal subspecific forms have been suggested for two of the species, both sexual and asexual reproduction are reported, and *G. celata* is potentially of hybrid origin with the other species as its putative parental lineages. These species present an interesting scenario in which to study the processes promoting divergence and the scale at which species function. We propose to examine this subgroup using a hierarchical approach based upon: 1) construction of a phylogeny using ITS, *mat*K, *rbc*L and *waxy*, to assess the monophyly of the species, subspecies and forms; 2) exploration of diversity within and among the Victorian species and evidence of gene flow using microsatellites (SSRs); and 3) floral phenology, floral traits, visual and olfactory cues, as well as pollinator observations, as evidence for morphological and functional divergence among groups identified from the SSR analyses. Together these will allow us to tease apart the relative importance of different traits that underpin the evolution of elements within this subgroup.

Systematics of *Elaeocarpus* (Elaeocarpaceae) in Australia: resolving the *E. obovatus* species complex

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Elaeocarpus, the largest genus in Elaeocarpaceae is predominantly distributed in the Old World tropics and subtropics, and usually found in well-developed rainforests. The Australian species of *Elaeocarpus* were last revised by Coode nearly 30 years ago with 27 species and one subspecies recognised. Since then few taxa have been described. Despite this thorough morphological revision, there remain taxonomic problems to be addressed. *Elaeocarpus obovatus* exhibits morphological variation that appears to be continuous with that of two other entities*: E. arnhemicus* and *E.* sp. Mt Bellenden Ker (L.J.Brass 18336). As a result there is significant confusion in the circumscription of these closely related entities. Coode identified seven variants within the group but systematic investigation of this morphological variation and an assessment of the appropriate taxonomic status of the constituent groups has not been undertaken until now. This project aims to define species boundaries within the *E. obovatus* species complex, using a combination of cytogenetics, population genetics and morphometric techniques. A Principal Component Analysis with selected quantitative characters identified boundaries of the entities. The genetic structures and distances, and ploidy levels within the complex also revealed congruence with the kinship determined from the morphometric analysis. Diagnostic characters distinguishing the newly circumscribed taxa and taxonomic ranks will be discussed.

Documenting the Kimberley flora: a never-ending story?

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Despite an increase in exploration of the Kimberley region in recent decades, the plant diversity is still considered to be poorly known. In 1992, the *Flora of the Kimberley Region* recorded just over 2,000 plant species in the region. Since then, that number has climbed to 3,000 species and continues to grow. Even in regions considered well known and close to towns such as Broome and Kununurra, new species continue to come to light. The largest number of new species are being found on the sandstone plateaux of the north-west Kimberley, in the high rainfall zone (1,000–1,400 mm p/a). Many of these species are wet season ephemerals, and are completely missed by dry season visitors. We have utilised helicopters, remote bush camps and station homesteads to survey many remote parts of the Kimberley in search of unknown plants. Not all of the new discoveries are small or annuals, with new acacias and the occasional new eucalypt still coming to light. We suggest that there are still hundreds of new species awaiting discovery in the region, most of which are likely to be endemic and deserve protection through conservation measures. We will take you well beyond the Gibb River Road to present highlights of our discoveries and the incredible landscapes of the region. From the world's only non-carnivorous carnivorous plant, to dead-horse lilies, and a mock orange that was 'lost' for 180 years, the Kimberley flora is very unique. We will show how this flora compares to the remainder of Australia and discuss the threats currently facing the region.

Molecular phylogeny of *Boronia* and *Boronella* (Rutaceae) using chloroplast and nuclear markers

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As currently circumscribed, *Boronia* (Rutaceae) is a large Australian genus of 149 species distributed across all States and mainland Territories. It is particularly diverse in south-western Western Australia, with minor centres of diversity in south-eastern Australia, the Top End of the Northern Territory and the Kimberley. *Boronella* is confined to New Caledonia and contains six species. The two genera have a complicated taxonomic history, with various accounts indicating they should be combined or moved to different tribes. Recent molecular phylogenies indicate the genera are closely related, though isolated from the other genera traditionally placed in tribe Boronieae, and more closely related to Australian rainforest genera. To test the relationships of the two genera and of the sections in *Boronia* a phylogeny was produced using chloroplast (*trn*L-*trn*F) and nuclear (ITS, ETS) DNA sequences. Results indicate that *Boronella*, *Boronia* sections *Algidae*, *Valvatae* and *Cyanothamnus*, and series *Pedunculatae* (section *Boronia*) are monophyletic. Section *Boronia* is paraphyletic; nested in it are *Boronella*, section *Algidae* and the monotypic sections *Alatae* and *Imbricatae*. Series *Boronia* is polyphyletic and a number of more natural groups were identified. These results are congruent in part with previous studies using morphological data and indicate a broader concept of *Boronia* is required. A key implication of the study is that a narrower circumscription of section *Boronia* is necessary and that both *Boronella* and *Boronia* series *Pedunculatae* require recognition at the sectional level. The status of the three remaining small sections and several species currently placed in series *Boronia* requires clarification.

Phylogeny of Australian Poaceae tribe Poeae focusing on the genus *Poa*

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Poaceae tribe Poeae includes some of the most economically and environmentally important native and introduced pasture grasses in Australia, including *Poa* (Tussock-grasses), *Festuca* (Fescues) and *Lolium* (Ryegrasses). Poeae is represented by 19 genera and 94 species in Australia and is dominated in species numbers by the genus *Poa*, which contains 46 described species. Native Australian *Poa* species are placed in a large clade, subgenus *Poa* supersection *Homalopoa*, within which little phylogenetic resolution has been achieved. In previous studies determination of relationships has proven challenging due to low levels of sequence divergence in both chloroplast and nuclear markers, intraspecific variability within nuclear markers, and incongruence between chloroplast and nuclear datasets. Resolution of relationships within Australian *Poa* is critical for our understanding of the morphological complexity of the genus, and for clarifying taxonomic boundaries, including possible cryptic species that may exist in known species complexes. With this aim, investigation of Australian Poeae relationships has been undertaken as part of a broader DNA barcoding project into the tribe. Sequence data from three chloroplast (*rbc*L and *mat*K genes and the *rpl32-trn*L intergenic spacer) and two nuclear (ITS, ETS) markers have been generated for phylogenetic reconstruction of the genus using maximum parsimony, maximum likelihood and Bayesian search criteria. Evolutionary relationships are discussed and congruence of the relationships inferred from chloroplast and nuclear sequence data will be assessed.

Flora of New Zealand: development of a dynamic resource

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The electronic *Flora of New Zealand* was launched at the ASBS meeting in Lincoln in December 2010. We have the goal to deliver the next generation of New Zealand Floras as a dynamic resource that is up-to-date and engages a wide range of users. This requires changing the Flora creation process to develop an information system that allows integration of data from a range of sources, and extending the concept of a Flora to include its delivery via a variety of tailored products—the first being a version delivered over the internet. Central to this are processes that allow capture and analysis of granular, highly linked data which are up-to-date. It also creates a number of technical challenges, such as efficiency of processes that capture specimen-linked data and the development of processes to analyse them, as well as the social and legal challenges of changing working practices of scientists and recognition of authorship and copyright. We will present our experiences in developing this new electronic *Flora of New Zealand*, our planning processes, some of the difficulties we encountered, how work processes of our taxonomists have changed, the lessons we learned, what we have achieved so far, and some of our plans.

Aligning classification with phylogeny in Restionaceae, Centrolepidaceae and Anarthriaceae (the restiid clade of Poales)

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Restionaceae are among the many plant groups where DNA-based phylogenetic studies are leading to changes at the upper taxonomic levels. With small wind-pollinated flowers, reduced leaves and homoplasious changes in stem anatomy, their classification has been problematic, making them a prime candidate for molecular studies. *Ecdeiocolea* and *Anarthria* had already been lost on anatomical grounds when DNA sequencing began; *Anarthria* stayed in the restiid clade but *Ecdeiocolea* subsequently gained unexpected fame as likely sister-group to the grasses. *Lyginia* and *Hopkinsia* were next excluded since they formed a clade with *Anarthria* and joined Anarthriaceae *s.l.,* or the small families Lyginiaceae and Hopkinsiaceae. Change continued when four eastern Australian species were found to be embedded in *Chordifex,* despite their geographical distribution and different stem anatomy; so we said goodbye to the small genera *Acion*, *Guringalia* and *Saropsis*. Then came a clearer view of the main clades of the family, with the African genera forming subfamily Restionoideae, the Australasian members comprising Sporadanthoideae and Leptocarpoideae, together with evidence that a fourth subfamily, Centrolepidoideae, should replace Centrolepidaceae. Meanwhile, in Africa, *Restio* and *Elegia* were enlarged at the expense of five formerly recognised genera. Now it is time to deal with some Australasian clades that are monophyletic and readily characterised but embedded in other such clades. In our attempt to give morphologically definable, monophyletic groups, we expect to see *Leptocarpus* and *Lepidobolus* enlarged and to lose *Meeboldina* and *Stenotalis*, as well as *Coleocarya*, *Desmocladus*, *Harperia*, *Kulinia* and *Onychosepalum*.

Taxonomic signatures in *Lachnagrostis* from AFLPs

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The presence vs absence of amplified fragment length polymorphisms (AFLPs) was used to examine genetic relationships among Australian species and subspecies of *Lachnagrostis* (blown-grasses). AFLPs were obtained from 3–9 individual plants of multiple accessions of 80% of the current species. Samples were distributed across six 96-well extraction plates, so that most plates had representatives of most taxa and accessions. Amplicons of restriction fragments were analysed through Peak ScannerTM v1.0 using a minimum peak-height (florescence intensity) of 20 and scoring fragments sized from 50–255 base pairs. Despite variation between plates in DNA amplification and difficulties in scoring peaks of extremely variable height and definition, more than 200 variable fragment lengths were useable for analysis. Furthest-neighbour joining (complete-linkage method in R) was used in a preliminary cluster analysis of the data. Clustering varied according to the plate analysed but some results were consistent. For example, the rare and restricted *L. limitanea* and *L. leviseta* were clustered with *L. aemula*, while *L. scabra* was most closely related to *L. robusta*. For many taxa, all individuals and accessions were clearly clustered within species, while within some species, such as *L. aemula* and *L. adamsonii*, sub-clustering into potential new subspecies was evident and supported by morphological characters. The widespread *L. filiformis* showed a considerable amount of variation, occurring across a range of sub-clusters, and suggested that further taxonomic examination is warranted. Although further analysis refinement is required, evidence to date indicates that AFLPs can be useful in unravelling the complex taxonomy of this genus.

Tackling *Tephrosia* (Fabaceae) in north-Western Australia

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Tephrosia (Fabaceae) is a globally-distributed genus with >400 species, concentrated in Africa–Madagascar, northern and central Australia, and Central and tropical North America. Its taxonomy is far from resolved—within Australia there are *c*. 136 taxa (46% informally named), with 60 taxa (38% informally named) currently recognised in the Eremaean and Northern Botanical Provinces of Western Australia (WA). Studied by Les Pedley (BRI) and Ian Cowie (DNA) for many years, focussed taxonomic investigation of *Tephrosia* in WA was initiated in 2011 through mining industry offset funding. A key aim of the project has been to improve the accuracy of specimen identifications by all stakeholders. Improvement of the PERTH collection (and hence FloraBase) as an ID tool has been facilitated by the return of >750 annotated sheets from loan, a research visit from Cowie, ongoing specimen curation, including an overhaul of the reference herbarium collection, subsequent taxonomic research and timely communication of findings to the consultancy community. Ongoing research and collaborations have led to eight new names and four pre-existing names being recognised on the State plant census, two names being removed and 12 informal synonyms reconciled between PERTH, DNA and BRI. As a result, the status and distribution of many taxa are better understood; however, further new questions have been raised. In addition to developing identification tools and preparing new taxon descriptions for *Tephrosia* in WA, current research is focused on the *T. supina* complex, which contains a number of different orange- and pink-purple-flowered taxa across Australia. An International Barcode of Life (iBOL) DNA barcoding study has also been undertaken, which aims to assess the utility of different-aged herbarium specimens as sources of DNA for barcoding, and the utility of those barcodes (*rbc*L and *mat*K) for the identification and differentiation of taxa.

Conservation of refugia and their evolutionary lineages

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The evolutionary history of the Australian biota has been significantly influenced by Pleistocene climatic oscillations, which ranged from warm, wet interglacial conditions to cool, dry environments during glacial maxima, and that became more extreme from the mid-Pleistocene with increasing aridity. Genetic signatures reveal multiple levels of divergence and complex geographical structuring in both arid and mesic environments. In arid environments the effects of increased aridity may have been less significant than in mesic environments, where increased aridity would be expected to lead to major contraction of the biota. These genetic signatures of high diversity and endemism indicate persistence of the biota through climatic oscillations over multiple glacial cycles as a major response to changing climatic conditions. There is growing interest in understanding the role of historical refugia in facilitating persistence through the Pleistocene, and their potential role in conservation of the current biota under future climate variability. While many species show patterns consistent with multiple localised refugia throughout species' distributions, areas of more major refugia are likely to have facilitated persistence and recolonisation. Proposed areas that would act as refugia during arid conditions include buffered coastal areas, ranges and granite outcrops. Several recent studies have revealed genetic patterns identifying these areas as refugia in south-west and north-west Australia. Presence of refugia and areas of localised persistence highlight the importance of dynamic evolutionary processes and a mosaic of habitats in heterogeneous landscapes for species persistence though changing environmental conditions.

Protologues, floras and taxon profiles: how many descriptions do we need?

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Textual taxon descriptions, illustrations, images and keys are perhaps the most widely used and valuable syntheses of botanical knowledge. As the number of systematists declines, the number of web portals delivering taxon profiles increases, usually cannibalising previous, static, publications. In 21st century Australia how might the capture and maintenance of taxon profiles develop to ensure data currency and maximum reusability so that local knowledge can be delivered globally?

Systematics and evolution of *Melaleuca sens. lat.* (Myrtaceae): the status of *Melaleuca argentea* 'Ashburton biotype'

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Melaleuca s.l. (tribe Melaleuceae; 380 spp.) is found in all biomes and diverse habitats throughout Australia and extends to surrounding landmasses. It is characterised by bottlebrush-shaped inflorescences and persistent fruits, and species are sclerophyllous shrubs to trees. *Melaleuca s.s.* (290 spp.) excludes nine or ten genera such as *Callistemon* and *Calothamnus* and lacks a morphological synapomorphy or a combination of characters that is diagnostic. Previous phylogenetic analyses using molecular, or both molecular and morphological, data showed *Melaleuca s.s.* is not monophyletic with one study suggesting that all the genera in Melaleuceae should be placed in *Melaleuca*. This study aims to: 1) construct a more complete phylogeny of Melaleuceae using more taxa and DNA regions, and a re-evaluation of the morphological characters; 2) investigate the evolution of the high species diversity within *Melaleuca s.l.* and the relationship between rates of diversification and historical changes in environmental parameters, such as climate; and 3) determine whether gall insects have co-speciated with *Melaleuca*. The first part of my project is on *Melaleuca argentea* 'Ashburton biotype', which occurs in the Pilbara of Western Australia. *Melaleuca argentea* is distributed across northern Western Australia, the Northern Territory and Queensland but DNA sequence data indicate that *M. argentea* 'Ashburton biotype' is genetically distinct from other populations, bringing its taxonomic status into doubt. Five species of the *M. leucadendra* group occurring in Western Australia are being compared with the Pilbara taxon. About 30 morphological characters are measured using herbarium specimens in preparation for morphometric analysis.

Robert Brown’s *Caladenia* (Orchidaceae) revisited: updated interpretation based on results of multigene phylogenetic analyses inferred from plastid and nuclear loci

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Robert Brown’s *Caladenia* (Orchidaceae: Caladeniinae) is revisited based on multigene analyses using nuclear ribosomal ITS and plastid regions from species representing all major taxonomic groups within Caladeniinae. Nuclear ITS trees were very similar to those previously published. However, trees based on chloroplast plastid data alone differed significantly from previously published accounts where: 1) both *Cyanicula* and *Caladenia* subgenus *Phlebochilus* were not monophyletic; and 2) *Cyanicula s.s.* was sister to a combined *Glossodia* and *Elythranthera* clade. Our combined analysis reveals support for the recognition of only three genera, *Leptoceras*, *Praecoxanthus* and *Caladenia,* where all remaining taxa align in a strongly supported, monophyletic group containing a number of subgroups. Analyses of characters and character states historically used to delimit taxa revealed that there is strong morphological synapomorphic support for these three genera. Conversely, most characters used to support recognition of the genera *Arachnorchis*, *Cyanicula*, *Drakonorchis*, *Ericksonella*, *Jonesiopsis*, *Petalochilus*, *Pheladenia* and *Stegostyla*, as previously proposed, are homoplasious. Significantly, these studies suggest that *Glossodia* and *Elythranthera* are specialist groups embedded within *Caladenia*. Based on our results, none of the current systems of classification of the subtribe are satisfactory and a new system of classification akin to Lindley’s 1840 interpretation of *Caladenia*, but with *Glossodia* included, is proposed.

The role of genetics in defining taxonomic boundaries and conservation units

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Identification of appropriate taxonomic and population units for protection and management is essential for the conservation of biological diversity. To be effective, conservation strategies should not only aim to preserve current levels of species diversity, but also consider intraspecific variation and the evolutionary and ecological processes associated with its generation and maintenance. Genetic principles and methods for species identification and classification are relatively well developed, although biologists and wildlife managers are still faced with ongoing debates concerning species and taxon delimitation. Within species the identification and characterisation of genetically distinct local populations or conservation units, based on population genetic structure and phylogeographic patterns, provides an important basis upon which more specific strategies can be developed for the conservation of genetic diversity and evolutionary processes. Furthermore, the local population is often considered the functional unit in ecosystems. However, like species delimitation, defining conservation units can be controversial, as is evident in the various views expressed when identifying Evolutionarily Significant Units (ESUs). These issues are discussed in the context of a number of Western Australian examples that highlight the use of molecular genetic approaches in assessing taxonomic boundaries and delimiting populations as conservation units.

Geographic range size and biodiversity hotspots: the SWAFR versus SE Australia

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Geographic range size and range overlap are important factors shaping biodiversity. Areas of high biodiversity occur through species having smaller ranges (tighter packing), more range overlap, or both. Here, we compare these spatial patterns of biodiversity in the Southwest Australian Floristic Region (SWAFR) with those in south-eastern Australia (SEA) using the endemic pea genera *Daviesia* and *Bossiaea*.

They are all bottlebrushes: should they all be *Melaleuca*?

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The Myrtaceae tribe Melaleuceae currently comprises nine or ten genera, depending on whether or not the 2006 synonymy of *Callistemon* with *Melaleuca* is accepted. Previous genus-level taxonomic decisions for the tribe have been strongly biased towards recognising differences among groups of species and, as a consequence, many species-poor genera are now recognised. A further outcome of erecting genera for autapomorphic clades has been that there is no synapomorphy, or even a combination of characters, that allows recognition of the largest genus in the tribe – *Melaleuca*. Recent studies using DNA sequences have found that *Melaleuca* is not monophyletic and that all other genera of Melaleuceae are nested within it. Assuming that additional DNA markers add support to the current relationships, then rather than splitting out even more genera, some of which have no obvious morphological synapomorphies, it seems preferable to synonymise all other genera with *Melaleuca*. Bottlebrush flowers, persistent woody fruit, and non-showy (inconspicuous) petals make it relatively easy, even for the casual bushwalker, to recognise a member of *Melaleuca s.l.*

Influence of climate on canker disease in the Proteaceae of the Southwest Australian Floristic Region

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The incidence and severity of plant canker diseases caused or associated with fungi and other endophytes has been steadily increasing worldwide. Climate change is seen as the driving force in the apparent emerging pathogenicity of these normally minor diseases. The contribution of canker to stem and branch death in the Southwest Australian Floristic Region (SWAFR) is poorly documented and understood. *Banksia verticillata* and *Lambertia orbifolia*, both *Threatened* and endemic to the SWAFR, are currently being severely impacted by canker disease. Transects were established in populations of *B. baxteri*, *B. coccinea, B. verticillata* and *L. orbifolia* populations to quantify and monitor canker severity and impact, with 1,620 individuals assessed across 32 sites. Climate as interpolated rainfall, temperature, humidity, and actual temperature and humidity data for sites covering the northern and southern rainfall extremities were used for comparison against canker impact scores in an attempt to develop predictive ability in climate change scenarios. The most frequently isolated pathogenic canker fungi were in the *Botryosphaeria* complex, a putative *Zythiostroma*, *Cryptodiaporthe* and *Cytospora* spp. respectively. All except *Cytospora* spp. have been isolated at a low level from healthy asymptomatic tissue suggesting that they have some degree of benign endophytic role and that the environment is shifting the host-pathogen relationship to a more aggressive one. Co-occurrence of several of the pathogens in single canker lesions demonstrates a synergism in canker disease expression that will impact the distribution of some proteaceous species in the SWAFR. Systemic fungicides were also investigated as control options for the four main canker fungi as part of an integrated pest management approach.

Plant dispersal across Wallace's line: dated molecular phylogenies reveal the dynamics of the Sahul-Sunda floristic exchange and assembly of the Australian tropical rainforest flora

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The origins and evolution of the Australian tropical flora and its relationship with Asian floras have fascinated botanists for over 150 years. Nineteenth to mid-twentieth century notions of Australian tropical rainforests as depauperate samples of south-east Asian floras, and therefore 'alien and invasive', gave way to hypotheses that they are unadulterated remnants of an ancient Gondwanan flora. More recently, the idea of a significant post-Miocene interchange between the Indo-Malesian (Sunda shelf) and Australian (Sahul shelf) floras after a long period of separation has become well established. However, the historical dynamics of this exchange are poorly understood owing to a paucity of relevant fossil data. Dated molecular phylogenies (chronograms) offer unprecedented power to evaluate competing hypotheses of lineage origins. In this study we employed a meta-analysis of published molecular chronograms to investigate the historical dynamics (rate and polarity) of the Sunda-Sahul floristic exchange and interpret it in the context of earth history. Results indicate that the Sunda-Sahul floristic exchange commenced in earnest about 18 Ma when the two landmasses had drawn to within *c*. 100 km of each other. The exchange rate increased through the Tertiary. A strong directional bias in the exchange is evident, with immigration of Sunda lineages into Sahul outweighing the reverse by a factor of about four. Almost all the lineages which successfully dispersed across Wallace's line possess adaptations for zoochory.

Interactive keys to the New Zealand flora: trans-Tasman connections

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Since *c*. 2000, Landcare Research and our collaborators have been developing online interactive keys for efficient identification and management of the New Zealand flora. We will provide an overview of ten keys that we have created, or are developing, including keys for identifying pest plants, grasses, native orchids and native and naturalised flowering plant genera. These New Zealand projects are created using Australian-developed Lucid™ software and are compared and contrasted with related initiatives in Australia.

Biosecurity for natural ecosystems: a case study of the introduction of *Phytophthora* species into the native plant communities of south-west Western Australia

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The application of biosecurity in Australia is largely focussed on preventing the introduction of pathogens, pests and weeds that impact the agricultural industry. However, similar standards and hygiene procedures are required to protect Australian natural ecosystems from the introduction and subsequent spread of a number of identified invasive species. The introduction of *Phytophthora cinnamomi* with European settlement and its spread into the native plant communities of south-west Western Australia demonstrate the significant impacts that can occur as a result of poor biosecurity practices. However, more concerning is that a number of other *Phytophthora* species have also been introduced into Western Australia's native ecosystems as recently as the past few decades. Unless there is a significant increase in application of hygiene procedures then other pests, pathogens and weeds will continue to become established within the natural ecosystems of Western Australia. This presentation will cover a range of simple standards and hygiene procedures that you can implement when entering native ecosystems that will significantly reduce the risk of introducing or spreading invasive species.

Does inflorescence morphology warrant taxonomic revision in the Australian native grass *Tripogon loliiformis*?

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Tripogon loliiformis is the only described species of *Tripogon* in Australia among the *c*. 40 species in the genus. It is a desiccation-tolerant grass occurring throughout Australia. It exhibits extensive morphological variation across its geographic range, especially in inflorescence structure, leading some to suggest that it might consist of more than one species. Plants occurring in the central and western parts of Australia have short and dense inflorescences with overlapping, relatively small spikelets, whilst those from the eastern part have longer and less dense inflorescences with slightly overlapping to widely spaced, relatively large spikelets. This morphological variation may also correlate with the variation in habitat type where plants from this species are found. Variation in inflorescence morphology of *T. loliiformis* will be compared against the criteria used for species delimitation in taxonomic revisions of other species of *Tripogon* from different regions of the world. This work forms part of a larger systematic study of the genus *Tripogon*, using both morphological and molecular data, and will contribute to subsequent decisions supporting or rejecting the need for a taxonomic revision of *Tripogon* in Australia.

Genetic evidence for introgression and historical biogeographic patterns in *Correa* (Rutaceae)

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Correa (11 species, 32 accepted varieties) occurs in eastern Australia, with one species extending to Western Australia. Morphological accounts suggest hybridisation between some species has been common and a recent molecular study showed incongruence between nuclear and cpDNA gene trees, which was inferred to be a product of introgression. In the current study we aimed to further examine genetic patterns in *Correa*, using expanded population sampling, to document incongruence between molecular markers and taxonomy, to resolve patterns of geographic variation, and to understand biogeographic history. Samples of known provenance (87 localities in Queensland, South Australia, Tasmania and Victoria) were genotyped using two chloroplast loci (*trn*L-*trn*F; *trn*K intron) and ITS regions of nrDNA. Two closely related species, *C. lawrenceana* and *C. bauerlenii*, hold an isolated position in the genus, and share unique cpDNA and nrDNA lineages. Among the other species there are geographically-based lineages of both cpDNA and nrDNA. Widespread sharing of divergent lineages between species is consistent with widespread regional introgression. The deepest divergences in both cpDNA and nrDNA datasets involve the differentiation of distinctive South Australian lineages from more widespread ones. Geographic distributions of genetic lineages are consistent with divergence caused by historical vicariance across the Murray basin, followed by subsequent dispersal and re-connection of populations across this area.

The ultramafic flora of Western Australia

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Ultramafic lithologies are known to host very significant proportions of plant biodiversity in places such as Cuba (1,400 taxa – 66% endemic), New Caledonia (1,844 taxa – 69% endemic) and California (650 taxa – 24% endemic). Comparative figures for Western Australia have not previously been compiled. Data from 1:500,000 geology maps, >600,000 herbarium records and >54,000 survey records indicates an ultramafic flora of 1,355 taxa in Western Australia, but only 14 (1%) appear to have their distributions largely restricted to ultramafic substrates. The small number of restricted taxa is similar to that reported for the ultramafic areas of Queensland, Tasmania and Witwaterstand in South Africa, but contrasts greatly with the well known untramafic floras of Cuba, New Caledonia and California. Of the 14 ultramafic taxa found in Western Australia, nine are restricted to the Ravensthorpe Range. Five of these are restricted to one location, which is also the site of the major laterite nickel mine. The Ravensthorpe Range has long been recognised as a centre of diversity with over 60 taxa largely restricted to it. In general, the lack of clear differentiation between ultramafic and adjacent substrates across Western Australia may have resulted from both the long period of weathering of these ancient soils and the complex nature of the regolith acting to ameliorate the harsh edaphic conditions often associated with ultramafic substrates.

Atlas of Living Australia: where to now for State-based online systems?

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State-based agencies have expended millions of development hours over decades building systems to make local biodiversity information publicly visible and accessible. Examples in Western Australia include FloraBase and NatureMap, flagship systems for the Department of Environment and Conservation (DEC) that are widely used within research, environmental impact assessment and conservation planning. More recently, the Atlas of Living Australia (ALA) received funding to build capabilities for aggregating and publishing biodiversity data. With the funding and development cycle for ALA largely over, where does this leave State-based publishing systems? What assumptions, if any, have been made about data availability and maintenance? This talk explores options and strategic directions that may benefit and impact on DEC, similar jurisdictions, and the ALA itself.

Phylogenetic Niche Modelling (PhyNM): exploring evolutionary history of Australia in a new way

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Understanding evolutionary history of plants and their environment requires innovative analyses of environmental niches, of not only species, but also taxa on deep nodes of a phylogeny. Traditional phylogenetic methods that explore such aspects often reconstruct ancestral character states of morphological or environmental traits on the nodes of a phylogenetic tree. Only rarely have character traits been directly modelled on these same nodes. Our Phylogenetic Niche Modelling (PhyNM) uses Maxent modelling to measure environmental trait niche changes or shifts directly on all nodes of a phylogeny. We used an Australian hornwort phylogeny and a variety of environmental traits at continental scale to test it. Our results identify PhyNM as an efficient method to complement current phylogenetic approaches that use ancestral state reconstruction to measure niche shifts. Direct modelling of nodes identified additional niche shifts, unrecognised by the reconstructed methods. It appears that Australian hornworts have undergone non-conservative evolution of their fundamental environmental niche, leading to divergence among nodes in traits. PhyNM is a promising technique to better understand the evolutionary history of the Australian flora.

Short-range endemism amongst the Australian fauna: patterns, problems and prospects

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In 2002 the expression ‘short-range endemic’ (SRE) was used to characterise certain species with a natural range of less than 10,000 km^2. These species were mainly invertebrate animals but many plant species that have similar distributional patterns have also been documented. The invertebrate animals used to exemplify the SRE concept mostly had very similar life histories, including a lack of any significant dispersal abilities, were confined to certain micro-habitats such as moist gullies or subterranean environments, were highly seasonal, and had low reproductive potential. The history of SRE research over the past ten years in Western Australia is reviewed, with an overview of the main groups of terrestrial SRE animals. The discovery of significant radiations of subterranean organisms in the Western Australian arid zone is also highlighted. SRE surveys have become a preferred mechanism for government agencies to assess the impact of infrastructure developments on invertebrate assemblages, without the need to undertake surveys of all invertebrate groups. Finally, the use of molecular methods to elucidate species and their distributions is shown to be the way of the future, avoiding the need for lengthy surveys to collect the suitable life stage or sex to provide an accurate, species-level identification.

Classification of *Nothofagus* (Nothofagaceae): the past, the present, and the future

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The genus *Nothofagus* is well-represented in the Cretaceous and Tertiary fossil record and the extant species are an exemplar for Southern Hemisphere biogeographic studies. Classifications in the mid-19th century reflected Northern Hemisphere taxonomic perspectives and in the mid-20th century classifications conflicted based primarily on 1) pollen of fossil and extant species, and 2) leaf and fruit characters of extant species. DNA sequence analyses during the last two decades support the classification based on pollen. We present a synthesis of taxonomic characters in *Nothofagus*, including morphologies of leaves, pollen, flowers and fruit, and DNA sequence data. Data from the cpDNA *rbc*L gene for Nothofagaceae and other families of the Fagales is presented, with emphasis on between- and within-genus genetic variation. Morphological characters used in generic circumscription of families of the Fagales are reviewed. The outcome of these studies is a recommendation for a revised classification for Nothofagaceae.

Herbaria need better funding to encourage collection of vouchers and to allow for their retention by herbaria

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A comparison is made between current plant names and those published in 1998 for a study by Hosking and James of species found in the North Western Slopes botanical region of New South Wales, upstream of the junction of the Peel and Namoi Rivers. The 1998 publication listed 1,041 taxa. Of these, 65 were misidentified and a further 129 are now known by another name. Many of the name changes are due to revision of genera and species complexes and can only be determined because vouchers were collected. Most voucher specimens for this study are housed at the National Herbarium of New South Wales (NSW) or at the University of New England's N.C.W. Beadle herbarium (NE). From 1992 to the present time duplicate specimens have also been lodged at the National Herbarium of Victoria (MEL) and the Australian National Herbarium (CANB). Since the original study the number of plant taxa recorded in the area has increased to 1,170. Differences between plant names used in the 1998 study and those used now point to the importance of collection and storage of voucher specimens. Such vouchers also prove invaluable to future taxonomic revisions. Clearly a funding regime that permits and encourages (if not demands) the collection and retention of vouchers is needed across Australia.

Smoke and mirrors: are Australian seaweed communities retreating?

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A recent publication by Wernberg *et al.* (2011, *Current Biology* 21: 1828–1832) used historical herbarium specimen records sourced from Australia's Virtual Herbarium to suggest that the distributions of numerous seaweed species were shifting southward, purportedly as a response to climate change. I contend that the paper is fatally flawed for several reasons: an inappropriate interpretation of herbarium records, a failure to check the underlying data relating to crucial records, the absence of ground-truthing to confirm actual extirpation, and an incorrect interpretation of collection effort. The major assumptions of the paper are that herbarium records from a particular period are equivalent to a species' distribution in that period, and that the absence of a herbarium specimen from subsequent periods is evidence for the species' local extinction. No effort, however, has been made to validate these assumptions. Herbarium specimens are not collected in a systematic way, geographically or otherwise. Collectors are often selective in their taxonomic coverage, and there has never been a program of extensive seaweed collection over a defined period. Collections are often built up *ad hoc*, as opportunities and funding arise. Thus the absence of a herbarium record is potentially due to any number of factors, the least likely being a local extinction. Moreover, none of the results were tested by revisiting sites and checking for the presence of supposedly locally extinct species. To compound the problems, the locality data of crucial specimens were not checked. I also suggest that the claimed northwards collection effort bias, used in support of the conclusions, is grossly oversimplified. When examined in detail the collection effort is actually skewed southward, and potentially the underlying cause for the perceived range contractions.

Integrative species delimitation of the *Macrozamia plurinervia* complex (Zamiaceae)

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Establishing meaningful measures of biodiversity and subsequent environmental management policies is dependent upon objectively defining species boundaries and species relationships. Species complexes, in which species boundaries (usually based on morphology) are unclear, represent groups that require taxonomic investigation. The *Macrozamia plurinervia* species complex consists of six species of cycad (*M. conferta*, *M. cranei*, *M. machinii*, *M. occidua*, *M. plurinervia* and *M. viridis*) currently described on subtle differences in morphology. Because four species are listed as threatened (EPBC Act 1999), an understanding of the evolution of these plants is crucial for assessing conservation status and designing effective conservation management schemes. However, previous attempts to assess species limits using isozymes or chloroplast DNA have revealed little or no differentiation between species. In the present study, we assess the current species limits by comparing morphometric and genetic clustering analyses. Plants were scored for a suite of morphological characters and clustered using morphometric analyses. Approximately 80 individuals per species were genotyped for 12 novel microsatellite markers to discriminate species, test alternative explanations of chloroplast sharing, and investigate the pattern of divergence within the *M. plurinervia* complex.

Documenting and conserving local diversity within and beyond Perth

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Several decades of detailed floristic study of the Swan Coastal Plain biogeographic region (including Perth) have revealed a wealth of new, often rare and poorly known biodiversity at all levels. Description and conservation of this diversity involves reporting at a variety of levels, including cabinet briefings, whole of Government plans, court cases, statutory plans, scientific papers and reports, and verbal presentations in the field on bushland walks or inspections for international, national, state and local groups. Several examples of these will be briefly mentioned. While work aimed at conservation has progressed, the delineation of new taxa recognised during these studies has continued in the background, including the naming of obvious new taxa and the recognition of significant populations. Other species contain numerous variants that extend beyond the Swan Coastal Plain and to understand the limits of these taxa requires the redescription of all populations to define those that are potentially rare and/or restricted. Species complexes of note include such well known, recently reviewed and common species such as *Grevillea thelemanniania*, *Hovea trisperma*, *Bossiaea eriocarpa* and *Samolus repens*. Variation within *Melaleuca systena*, a coastal taxon revised in 1999, extending from Shark Bay to Albany, will be described as the main example. The 'species' as we currently understand it consists of six closely related taxa, two widespread taxa—one from Dongara to Albany and the other from Kalbarri to Shark Bay—and four other restricted taxa—one restricted to the Burma Road area, another to the eastern Wheatbelt, and two highly restricted and endangered species from limestone soils (Muchea limestones, near Bunbury, and massive hills north of Perth) of the Swan Coastal Plain.

KeyBase – an interactive dichotomous key to all Australia's plants

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Keys to plants are an essential part of Australia's botanical infrastructure. Dichotomous keys in particular, however, have been a rather poor cousin in the modern informatics landscape. Partly, this is because they have been regarded as a bit old-fashioned. However, with appropriate technology and a flexible web delivery system, dichotomous keys will be an important component of the emerging eTaxonomy platform we're building in Australia. This talk will discuss KeyBase*, a new and marvellous web-based platform for handling and delivering dichotomous keys for plants, and launch a new initiative to compile and build a dichotomous key to the entire Australian flora.

*Keybase may not be the final name of the system, as it is already taken as a brand name by a number of US financial and IT firms, and a job training provider in South Africa! Final name to be announced.

Biodiversity research data cleaning and visualisation methods

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Online access to biological specimen data now enables spatial biodiversity analyses to be conducted on large datasets at continental scales. These analyses include addressing questions of phylogenetic diversity and phylogenetic endemism as well as environmental niche modelling of taxonomic diversity. Unfortunately the data contained in these databases, such as Australia's Virtual Herbarium, often contain errors. Correcting these errors, such as geocodes and names, improve the results for spatial analyses. This talk covers the common problems faced in preparing data for biodiversity analyses, tools to aid in the data cleaning process and software for conducting biodiversity analyses and visualising the results. For example our protocol includes the use of Google Refine software to quickly update taxonomy and correct spatial errors. This streamlining has enhanced our ability to analyse large datasets of the Australian flora for biodiversity analysis and Maxent niche modelling.

Flora and vegetation of the Burrup Peninsula and some indigenous usage

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The Burrup Peninsula is located off the Pilbara coast in north-west Australia, 1,500 km north of Perth, and is the only large peninsula between the North-West Cape and the Kimberley. It was once an island, which may have been accessible on a low tide, but is now connected to the mainland by a causeway and embankments for salt ponds. The Burrup Peninsula is formed of prominent rocky hills with extensive areas of boulder scree, steep-sided valleys, coastal plains and high plateaux, and falls into the Abydos Plain physiographic unit previously described by Beard; however, the hilly terrain of the Burrup and surrounding islands differs markedly from the extensive flat to gently sloping quaternary alluvium of the majority of the coastal parts of the granitic plain. The rock outcrop presents as jumbled rock and boulder piles, ridges and slopes, with the predominant rock types being granophyres and gabbro with some granitoid, estimated to be some 2.7 billion years old. The Burrup's size, location and climate make it the ideal meeting place for Eremaean, coastal and Kimberley species. The highly varied topography and the mix of coastal and inland habitats results in numerous micro-niches that support a great diversity of flora and vegetation quite distinct from that found on the adjacent Pilbara mainland. This talk describes characteristics of the Burrup vegetation and flora and discusses some indigenous use of the species found there.

Hard yacca: taxonomy and systematics of the Australian grass-tree genus, *Xanthorrhoea*

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The grass trees, genus *Xanthorrhoea* (Xanthorrhoeaceae subfamily Xanthorrhoeoideae), are striking components of the Australian flora. They are characteristic members of heathlands, heathy woodlands and dry sclerophyll forests in eastern and south-western Australia. Twenty-eight species and five subspecies were recognised in the last generic revision, 22 in eastern and 11 in south-western Australia. In many respects, *Xanthorrhoea* is taxonomically ‘difficult’, as vegetative characters vary greatly within species, reproductive characters are only sporadically produced in some taxa, and hybridisation blurs species boundaries. Geography is often relied on to identify species but the distributions of some are poorly understood, and populations in areas where ranges overlap can be difficult to assign. Using a combination of nuclear and chloroplast markers, we aim to produce a molecular phylogeny of *Xanthorrhoea* in order to interpret relationships and the evolutionary history of the genus. The molecular phylogeny will then serve as a foundation for a taxonomic revision of the genus, using morphological and anatomical characters. Taxa within the global biodiversity hotspot of south-west Western Australia will be a focus of this research. This will inform conservation activities and will provide insight into the biogeographical history of Western Australian taxa.

Phylogeny and endemism of *Acacia*

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We present a multi-gene phylogeny of over 650 species of *Acacia*. The phylogeny, which contains over 2,000 terminal taxa, was built as a supertree containing 14 compartments (major clades) ranging in size from seven to 400 species. We combine this phylogeny with an analysis of over 170,000 spatial records from Australia’s Virtual Herbarium to perform a detailed phylogenetic and spatial analysis of the Australian *Acacia*. We used a species-based turnover metric (βsim) to identify five major *Acacia* bioregions. These are generally similar to the bioregions for the entire flora: south-west temperate, south-east temperate and monsoonal tropics, but the arid Eremaean is divided into two regions, north and south. By combining the phylogeny and spatial data we identified areas of neo- and paleo-endemism in *Acacia*. Paleo-endemic areas, which contain species on long branches not found elsewhere in Australia and are potential refugia, were found in the Wet Tropics in northern Queensland, central alpine areas of Tasmania, south-western Western Australia and scattered areas throughout the arid interior. Neo-endemic areas, containing species on short branches not found elsewhere and representing potential areas of high speciation, were found in the Kimberley region, the Flinders Ranges and several areas in eastern Australian including the Greater Sydney Basin. The metric also identified areas that combine both paleo- and neo-endemism, particularly in portions of south-western Western Australia.

Myrmecochory is not all or nothing: comparative assessment of ant dispersal in a clonal sedge

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Many Australian plants are myrmecochorous—their seeds or fruits are dispersed by ants, which are attracted by an oil-rich food body, the elaiosome. Ants involved in myrmecochorous dispersal are usually generalist foragers, and a small number of uncommon species, particularly of the genus *Rhytidoponera*, have been identified as the main dispersers in Australia. Sedges of the genus *Lepidosperma* (Cyperaceae) produce fruit which bear scales at the base which have been shown to function as elaiosomes in two eastern Australian species. We conducted experiments to determine whether diaspores of *L. gladiatum* are ant-dispersed, and to compare their attractiveness to ants to that of a co-occurring species of *Acacia*. Ants removed significantly more dispores of *A. cochlearis* than *L. gladiatum*, which we conclude is only mildly myrmecochorous. Its capacity for rapid clonal reproduction may have allowed selection against resource investment in elaiosome production to occur, reducing the effectiveness of sexual reproduction.

Phylogenetic measures of biodiversity and endemism, with an example using Australian bryophytes

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Understanding spatial patterns of biodiversity is critical for conservation planning, particularly given the need to prioritise efforts in the face of rapid habitat loss and human-induced climatic change. Biodiversity and endemism are typically measured using species; however, investigation of patterns of species distributions alone misses out on both the full richness of patterns that can be inferred using the full tree of life, and the analytical power that comes from a phylogenetic approach. Here we show that the application of phylogenetic methods, particularly the new measures Relative Phylogenetic Diversity (RPD) and Relative Phylogenetic Endemism (RPE), greatly enhances our knowledge of the distribution of biodiversity across both space and time. Our results demonstrate that the RPE metric allows a clear, quantitative distinction between areas of neo- and paleo-endemism. These methods are valuable in the conservation decision-making process. Conservation reserve design can be guided by assessment of phylogeny rather than species counts alone and can identify complementary areas of biodiversity that have unique evolutionary histories and processes in need of conservation. Bryophytes are three separate lineages—liverworts, mosses, and hornworts—each monophyletic but paraphyletic when taken together. The bryophytes are a diverse group that shares a grade of organisation and physiology that resembles in many ways the lifestyle of the earliest plants on land, and occupy a spectrum of habitats across Australia. They demonstrate centres of neo- and paleo-endemism that are sometimes similar to, but other times different from, those evident in other plant groups.

Divergence dating of *Acacia*

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As a ubiquitous and highly diverse element of the flora, Australian *Acacia* make an ideal candidate for molecular divergence dating aimed at examining multiple questions about the evolution of the flora of continental Australia. In the past, such efforts have been hampered by a lack of well-supported phylogenies and by a relatively poor macrofossil record, which probably reflects the depositional environment in which *Acacia* species are predominantly found. However, the broader sub-family Mimosoideae offers a number of reliably age-constrained fossils for use in divergence dating analyses. The microfossil pollen record of *Acacia* is relatively rich, and provides a good age constraint for the entire *Acacia* clade, although its taxonomic resolution for constraining subclades within the *Acacia* lineage is limited. This is an issue of broad significance for molecular divergence dating: how to reliably undertake divergence dating on a fossil-poor lineage within a fossil-rich clade? By using multiple, reliable fossil contraints to cross-validate age constraints and diagnostic synapomorphies for clades, we applied a combination of primary and secondary calibration points to produce the most comprehensive divergence dating study of *Acacia* and related mimosoid legumes so far undertaken. Previous dating studies included very small sample sizes of the diversity of Australian *Acacia* and experienced difficulties in applying appropriate age constraints for the lineage, leading to considerable variation in their results. We now provide estimates of divergence dates for all major clades in Australian *Acacia* and for related lineages across subfamily Mimosoideae.

Re-evalution of the current infrageneric classification of the tropical rainforest tree genus *Elaeocarpus* (Elaeocarpaceae) in Australia and West Malesia

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It has been difficult to delimit with confidence natural infrageneric groups within the tropical rainforest tree genus *Elaeocarpus* (Elaeocarpaceae), due to a paucity of sets of characters whose distributions among taxa corroborate one another. In order to determine which of these characters reflect phylogenetic relationships, it is necessary to test them critically against an independent dataset (such as DNA sequences). Those characters shown to be phylogenetically informative could then be used to develop a stable, natural infrageneric classification of *Elaeocarpus*. As *Elaeocarpus* is species-rich (*c*. 290 species), we aim to test the monophyly of the Australian and West Malesian groups, and the relationships between them, using a range of plastid and nuclear markers. There are nine informal infrageneric groups (*c*. 35 species) in Australia, and six in West Malesia (*c*. 100 species). Our preliminary results revealed that parts of Group V and Group XI in Australia are probably monophyletic, while the *Coilopetalum* and *Elaeocarpus* groups in West Malesia are probably not. Our analyses for the West Malesian groups revealed that the embryo shape (straight or curved), which is a diagnostic character in the current system, is possibly homoplasious.

Systematic studies in eastern Australian *Lepidosperma* (Cyperaceae): identifying novel characters and data sources

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Lepidosperma (Cyperaceae) is a morphologically distinct genus, but can be taxonomically difficult at the species level: few obvious characters differentiate between species and intra-specific variation is often high. Consequently, various species complexes remain unresolved, particularly in eastern Australia (*c*. 12 species). At a minimum estimate there are also 200 undescribed species. To provide a sound assessment of biodiversity within this predominantly Australian genus, it is clear that more informative characters, denser sampling and an integration of anatomical and molecular data are needed. Variation in the morphologies of perianth and culm/leaf margin are taxonomically informative but hard to characterise under low magnification. Our work using high-resolution LM and SEM has allowed better visualisation of novel micro-morphological and anatomical characters. These characters have been added to phenetic analyses to delimit new taxa, such as the western Tasmanian endemic *Lepidosperma* sp. Eldon Bluff. A preliminary phylogeny has been constructed which identifies major clades in the genus that will be the subject of more intensive research. To resolve the more difficult groups, particularly the *L. laterale* complex, we plan to supplement morphological data with data from next generation sequence multiplexing. This will also allow the construction of a robust phylogeny which can be used to map the evolution of selected morphological characters and gain insight into structure-function relationships. Outputs of our study of eastern Australian *Lepidosperma* will include online floras, interactive identification and contributions to eMonocots.

Is pollen morphology useful for defining monophyletic genera in the epacrids?

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The fleshy-fruited epacrids (tribe Styphelieae, Epacridoideae, Ericaceae) comprise more than 350 species. The group is highly diverse in southern Australia with several endemic genera and more than 50 undescribed species. They are regarded as an important component of the Australian flora, particularly in heaths. Styphelieae are atypical in Ericaceae with regards to their pollen structure. Even though the pollen grains are shed in tetrads as in the majority of the family, they present patterns of variable sterility from full normal tetrads to pseudomonads (three aborted cells), including triads and dyads, or more rarely, nullads. Although the ontogeny of the pollen types has been well studied, their origin and evolution in the tribe are unclear and assumptions of homology remain untested. The latest hypotheses require reinterpretation, as variable sterility may be underreported in the subfamily and the taxonomy within Styphelieae is under reconsideration. We conducted the first comprehensive pollen survey using SEM within the *Styphelia-Astroloma* clade of Styphelieae, with the aims of characterising the diversity of pollen morphology and its homology (assessed against molecular phylogenetic trees) as a basis for determining the taxonomic utility. Preliminary results show that pollen morphology is variable within the *Styphelia-Astroloma* clade and broadly congruent with the lineages revealed in molecular cladograms. Accordingly, pollen morphological characters are potentially useful to support the diagnosis of monophyletic genera. We discuss the evolution of external morphological characters in a phylogenetic framework and the implications for understanding the biology of the group.

Phylogenetic placement and biogeographic history of the Australian Annonaceae

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The Annonaceae is a tropical flowering plant family consisting of *c*. 250 genera and approximately 2,500 species. Forty-eight species were described in a taxonomic revision of the Annonaceae in Australia, with a large number of species, and some genera, considered to be Australian endemics. The monophyly and taxonomic placement of all Australian Annonaceae are investigated using a comprehensive sampling of both Australian and non-Australian representatives from the same or closely-related genera. The results are used to evaluate biogeographic scenarios for a Gondwanan and/or Malesian origin for the Australian Annonaceae. The phylogenetic placement of the Australian taxa is consistent with studies on individual genera. The high level of species endemism seen in Australian Annonaceae is indicative of speciation subsequent to arrival from Asia, due to one or more dispersal or range extension events.

Good grief, what's happening to *Goodenia*?

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A recent cpDNA phylogenetic analysis of monophyletic Goodeniaceae supported two large clades—the smaller 'LAD' group comprising *Lechenaultia*, *Anthotium* and *Dampiera*, and the 'Core Goodeniaceae' including the monotypic *Brunonia australis* as sister to *Goodenia s.l*. and *Scaevola s.l*. Core Goodeniaceae are characterised by the presence of free anthers and an indusium with a protruding stigma. *Goodenia s.l*. includes *Velleia*, *Verreauxia*, *Coopernookia*, *Selliera*, monotypic *Pentaptilon*, and *Scaevola collaris*, and is much more variable in floral morphology than *Scaevola s.l*. The majority of *Goodenia s.l*. have bilabiate flowers but it is clear that fan flowers and intermediate floral symmetries have evolved multiple times across the group. In contrast, the iconic fan flower floral symmetry is almost ubiquitous within *Scaevola s.l*., with the notable exception of embedded monotypic *Diaspasis filifolia*, which has pseudo-actinomorphic flowers. Preliminary phylogenetic analysis of nrITS sequences corroborate cpDNA analyses and indicate that *Goodenia s.s*. resolves into three major clades with varying levels of support. Currently it appears that no morphological features unite *Goodenia s.l*., and that most of the included smaller genera are both monophyletic and morphologically well-defined. It is deemed likely that the recognition of new genera from within *Goodenia s.s*. will be the better course of action, rather than subsuming all included taxa into an expanded genus of more than 190 taxa; however, broader taxon sampling, further cpDNA and nrDNA sequencing, and a re-evaluation of morphological synapomorphies for each new taxonomic entity are required before a formal revision of this charismatic group can be made.

Monophyly and phylogenetic relationships of *Ozothamnus* and *Cassinia* (Asteraceae, Gnaphalieae)

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The shrubby everlastings of *Ozothamnus*, *Cassinia* and their small satellite genera represent about 100 species and *c.* 10% of the Australian daisy flora. Generic delimitations in the group have long been controversial and subject to revision. In the current circumscription, the two large genera are differentiated based on the presence or absence of paleae and the shape of the phyllaries, although several exceptions exist. It has been suspected that at least the more heterogeneous *Ozothamnus* is not monophyletic, and that several of the smaller genera in the group may constitute apomorphic segregates (defined merely by, for example, loss of the pappus), but no comprehensive phylogenetic study had been undertaken. We have produced a molecular phylogeny based on very broad sampling and using nuclear ITS, ETS and chloroplast *psb*A-*trn*H, *mat*K-*psb*A and *ycf6*-*psb*M sequence regions. We have tested the monophyly of the two main genera with Templeton and K-H-Rell tests, by statistical comparison of phylogenies from constrained analyses against the best trees from unconstrained analysis. We found *Ozothamnus* is not monophyletic even in a very narrow circumscription, i.e. after the removal of non-shrubby section *Hebelaena* and several divergent species. *Cassinia*, on the other hand, probably is monophyletic. Nuclear data suggest that *Calomeria*, *Cassinia*, *Haeckeria* and *Odixia* are nested in *Ozothamnus*; chloroplast data provide poorer resolution and a somewhat contradictory topology but the results of the constraint tests are identical for both datasets.

Spatial distribution of species richness, phylogenetic diversity and collecting activity in the Australian native daisies (Asteraceae)

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Australia is home to *c*. 1,000 native species of daisies (Asteraceae) found in all biogeographic areas. Their large number, wide distribution, ease of recognition and attractiveness to plant collectors make them an ideal group to examine spatial patterns of diversity. Based on specimen data from Australia's Virtual Herbarium, we analysed the distribution of species richness at the 1° scale to identify hotspots, using three different approaches: 1) direct use of specimen records; 2) Chao 1 estimator of species richness; and 3) sums of species distribution models. To identify geographical biases in collecting activity and areas in need of additional, targeted collecting, we visualised the spatial distribution of sampling activity and calculated completeness indices (% of estimated species that have already been recorded). Inferred hotspots of species richness are broadly consistent between our three estimates, but the model-based approach provides patently unrealistic completeness scores. Hotspots are inferred nearly exclusively in the south-east. Botanical collecting activity is biased towards the vicinity of the largest cities and Alice Springs/Uluru, in the latter case leading to an over-perception of relative local diversity compared with estimated values. We also produced a genus-level molecular phylogeny of 159 of the 164 currently accepted native genera and used it to study the spatial distribution of phylogenetic diversity and phylogenetic endemism. Phylogenetic diversity is particularly high in the south-east and Victoria, while phylogenetic endemism is highest in the tropical north, the south-west, the Alps and the Queensland/NSW border ranges.

Assembling the bigger picture: phylogenetic relationships and character evolution in Dendrobiinae (Orchidaceae)

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The Dendrobiinae is a morphologically highly diverse subtribe within the largest and taxonomically most challenging orchid subfamily, the Epidendroideae. In its traditional circumscription, the majority of species belong to the genus *Dendrobium s.l.* (1,200+ species), one of the three orchid mega-genera, with distribution across the Indo-Asian, Australasian and Pacific regions. In the past, highly divergent taxonomic concepts of *Dendrobium* have been proposed, and the monophyly of many of the discerned taxonomic entities remains to be tested. Robust molecular evidence is urgently needed to elucidate phylogenetic relationships and evaluate the taxonomic value of morphological characters that delineate natural groups. Here we will present the first broad scale phylogeny of Dendrobiinae, with a representative sampling including over 500 taxa, and discuss major clades and evolutionary trends within the subtribe. For the Australasian clade, a refined phylogeny with an increased taxon sampling and additional molecular markers will be presented and discussed.

Grasses online: Scratchpads for Poaceae

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Scratchpads are social networking applications that enable groups of researchers to build, manage, share and publish taxonomic data online. Sites are hosted free at the Natural History Museum London for any biologist applying for registration. Key features of Scratchpads include tools to manage classifications, phylogenies, bibliographies, images, specimen records, documents and maps. Two Scratchpads are dedicated to Poaceae, providing information and identification for this economically important family. One has global coverage at species level (GrassWorld http://grassworld.myspecies.info/) with 12,096 species. Menu Items include descriptions of all world grass species in four languages (English, French, German and Spanish), TDWG global distribution maps, checklists of world grasses, a classification section including issues related to generic circumscription, historic literature, a list of published grass illustrations and images, world grass floras and references. Useful Links list 32 connections to websites that have information on grasses in a global scale. It is anticipated GrassWorld will become a primary website to access grass information online, either for information located there or through its links; in March 2012 it was accessed in 92 countries. The other Scratchpad is designed specifically for Australian users (AusGrass2 http://ausgrass2.myspecies.info/), with information on all species and infra-specific taxa (last count 1,616 entities). It is an update of AusGrass (2002) and is emended as new information comes to hand. Menu Items include characters, classification, common names, dichotomous keys, fact sheets of genera, species and infra-specific taxa that include bibliography, morphology, biogeography, distribution maps, glossary, references, synonyms and Useful Links (7). Interactive identification of taxa from both Scratchpads will be placed on IdentifyLife http://www.identifylife.org/.

Mind the gap: phylogeography and taxonomy of the *Dendrobium speciosum* complex (Orchidaceae)

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The phylogeography of the *Dendrobium speciosum* complex, a taxonomically contentious Australian orchid group, was investigated using the DNA fingerprinting method Amplified Fragment Length Polymorphisms (AFLPs). One hundred individuals from within the complex were sampled from across the known distribution along Australia's east coast, and the congruence of phylogeographic patterns with known geographic barriers and previous taxonomic treatments were assessed. Cladistic, NeighbourNet and Bayesian clustering analyses revealed phylogeographic structure within the complex, identifying distinct northern and southern groups. The geographic barrier separating the two main groups was identified and the genetic structure was found to be consistent with past contractions and expansions of Australia's mesic biome. The taxonomic implications of the results will be discussed.

Molecular systematics of Australian endemic genera *Caulocystis* and *Acrocarpia* (Sargassaceae, Fucales, Phaeophyceae) based on ITS, *cox1* and *rbc*L DNA sequences

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Two Australian endemic brown algae genera, *Acrocarpia* and *Caulocystis*, were reassessed based on three molecular markers: *cox1*, *rbc*L and ITS2. Two species of *Acrocarpia* clustered together in *cox1* and *rbc*L trees with high support values while the ITS2 dataset could not clarify the phylogenetic relationship of two *Acrocarpia* species. Two species of *Caulocystis*, *C. cephalornithos* and *C. uvifera*, were separated by the shape of pneumatocysts. However, pneumatocyst shape is a continuous character and delimiting *Caulocystis* species based on pneumatocyst shape was vague. The results from *cox1*, *rbc*L and ITS2 markers indicated that *Caulocystis* specimens from variant shape of pneumatocyst were in the same clade with high support values. Hence, two species of *Caulocystis* were conspecific and the name *C. cephalornithos* has priority. Within the *Caulocystis* clade of *cox1* and *rbc*L trees, a phylogeographic signal was detected between two regions, South Australia and south-east Australia (Victoria, New South Wales and Tasmania), while the geographic pattern was not shown in the ITS2 tree. In this study, *cox1*, *rbc*L and ITS2 markers can delimit species boundaries in *Caulocystis*, however, only *cox1* and *rbc*L can specify phylogenetic relationships within *Acrocarpia* and reveal geographic patterns within the *Caulocystis* species.

An overview of species richness and phylogenetic relationships in *Cortinarius* (Fungi, Agaricales) from southern Australia

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Cortinarius, the largest genus within the Agaricales (mushrooms), includes numerous species in Australia that remain poorly documented, despite their important ecological roles as ectomycorrhizal partners of forest trees. Traditional morphological taxonomy using fruiting-bodies has limited power to identify *Cortinarius* to species level. The aim of this study is to characterise the species richness of *Cortinarius* from southern Australia. Firstly, the effectiveness of ITS as a barcode has been established by comparison of this region and five protein coding genes on a subsample of 86 specimens belonging to subgenus *Dermocybe*. Secondly, the ITS region has been sequenced for a wider sample of more than 400 specimens from field surveys performed in southern Australia, including ecological monitoring programs such as FORESTCHECK in south-western Western Australia. Using an ITS intra-specific distance of 2%, results show 150 putative species of *Cortinarius*, among which the vast majority are new to science. Morphologically cryptic species are common. The contribution of southern hemisphere collections to the global phylogenetic diversity of *Cortinarius* and the importance of utilising herbarium specimens to uncover new species awaiting identification and description are discussed.

Instalment one in the resolution of the *Banksia spinulosa* complex (Proteaceae): *Banksia neoanglica* raised to species rank

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Named subspecies/varieties in the *Banksia spinulosa* complex (Proteaceae) have populations with sympatric, parapatric or allopatric distributions and unclear or disputed taxonomic boundaries. Our hypothesis is that, under biological, phenetic and diagnosable species concepts, each of the currently named taxa within the *B. spinulosa* complex is a separate species. In an initial study, we undertook detailed morphological study of new collections and of herbarium specimens in BRI, CANB, CNS, MEL, NE and NSW, including phenetic analysis (semi-strong multidimensional scaling and UPGMA clustering) of 23 morphological characters (11 quantitative, 5 binary, and 7 multistate) for 89 specimens. Ordination and cluster analysis resulted in individuals (OTUs) grouping strongly, allowing recognition of distinct groups consistent with separate species. Additional morphological analysis was completed on all specimens using leaf, flower, fruit and stem morphology, providing clear-cut diagnosable groups and strong support for the elevation of *B. cunninghamii* subsp. A, *B. cunninghamii* subsp. B and *B. cunninghamii* subsp. *cunninghamii* to species rank. A broader study of the complex is planned.

Who’s afraid of a giant *Phyllanthus* (Phyllanthaceae)?

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Recent molecular phylogenetic analyses have shown that the genera *Glochidion* (*c*. 350 spp.), *Synostemon* (42 spp.) and *Breynia* (*c*. 60 spp.) render *Phyllanthus* paraphyletic. A giant *Phyllanthus* of *c*. 20 subgenera, *c*. 1,300 species, subsuming the nested clades, has been proposed. Before disruptive decisions are made, an expanded phylogeny of tribe Phyllantheae with much denser taxon sampling (currently less than 10%) and intensive study (total evidence) of poorly known groups are essential. Based on morphological, palynological, and some molecular evidence we predict *c*. 20 monophyletic, morphologically recognisable genera (the proposed subgenera within a giant *Phyllanthus*) will emerge and would be more informative and workable, causing less disruption to nomenclature in regions of greatest generic/species numbers: south-east Asia, Malesia and Australia.

Taxonomy and its users—do we need to keep changing the names of large and/or iconic groups of plants?

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Biological taxonomy—the science and practice of naming—is an odd and rather unique discipline. We are a science, but (perhaps more than many sciences) will always have an element of subjectivity. We provide an underpinning framework that virtually every other biological discipline—and many a non-biological one—depends on. Importantly, and unlike most other taxonomies, we provide names to many non-scientists. Our user groups amongst other disciplines and in the broader community sometimes get annoyed when we change the names of organisms in response to growth in knowledge and understanding. How should we as practicing scientists and taxonomists handle this annoyance? This talk will explore the sociology of name changes from the personal perspective of someone responsible for a controversial and, to some people, inconvenient name change, and the intersection with changes (and lags in) our own and our users’ understandings of exactly what it is that we do, and why.

Flora of Australia Online

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The recent National Species List (NSL) project funded by the Atlas of Living Australia (ALA) has paved the way for an open and shared Flora of Australia Online (FOA) system. The infrastructure developed as part of NSL includes an open biodiversity services layer which enables the ALA to reuse names from the Australian Plant Names Index (APNI) and concepts from the Australian Plant Census (APC) as contributions to ALA web products. APNI/APC provides a robust and defensible taxonomy built on a thorough and complete nomenclator—the backbone of a Flora and modern biodiversity information system. The FOA project will further develop the NSL infrastructure, providing for incremental change, removal of duplication of effort, and reusability of data. This will enable the FOA to be used to populate other websites (e.g. FloraBase for species profiles), and in turn for the FOA to pull treatments from external sources. Development of a public editing interface with a registered logon will be developed, along with an editorial process for incoming data. Open access to APNI will provide for the first steps in the contribution of a species treatment. As its core, the NSL services will allow the FOA to link dynamically to the Australian Plant Census for taxon information, the Australian Plant Image Index for images, Australia's Virtual Herbarium for dynamic maps, and to pdfs of the original Flora of Australia publication.

New genera or just variation? A preliminary perspective on some new Queensland grass taxa

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The presentation will be an illustrated outline of a group of nine Queensland panicoid grass taxa, five of which are new, that have both chasmogamous and cleistogamous spikelets arranged in axillary and terminal inflorescences. Historically three genera have been recognised, *viz*. *Calyptochloa*, *Cleistochloa* and *Dimorphochloa*, but *Dimorphochloa* is currently in synonymy with *Cleistochloa*. Examination of the morphology of the group, based on field work, examination of herbarium specimens and cultivation trials, reveals enough characters to intuitively allocate the taxa to five different genera, of which two may be new, and including resurrection of *Dimorphochloa*. Information on characters that may indicate a phylogenetic signal are being assembled to undertake a morphological cladistic analysis. Material has also been collected for molecular analysis of the group, using a marker other than *ndh*F. Recent work using *ndh*F placed the cleistogamous group together with non-cleistogamous Australian endemic genera (*Ancistrachne*, *Neurachne*, *Thyridolepis* and *Paraneurachne*).

Eucalypts and orchids: a phylogenetic and spatial analysis of two of Australia's largest plant groups

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The eucalypts (7 genera, *c*. 900 species) and orchids (*c*. 200 genera, *c*. 1,300 species) are two of the largest plant groups in Australia. Their taxonomies have often been controversial and there have been many different classifications in the past. Using a concatenated multiple gene alignment for each group, we created two large phylogenies, a species-level for eucalypts, containing around 800 taxa, and a genus-level for orchids, containing around 200 taxa. Spatial data from Australia's Virtual Herbarium were downloaded and cleaned to reflect the natural range of each taxon. Phylogenetic diversity and endemism were then calculated by combining the phylogenetic and spatial data. The presentation will present the results for these two groups and contrast and compare the patterns that are obtained from two widespread groups of Australian plants, at different taxonomic levels.

Chloroplast genome sequencing across the eucalypt clade: *Allosyncarpia*, *Stockwellia*, *Angophora*, *Corymbia*, *Eucalyptus* (Myrtaceae)

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The eucalypts, including *Eucalyptus*, *Corymbia* and *Angophora*, dominate the Australian landscape and are highly significant both ecologically and economically. Molecular and morphological phylogenetic analyses have made considerable progress in determining genetic relationships (including among rainforest genera such as *Allosyncarpia* and *Stockwellia*), but further resolution of clades remains a challenge. We have commenced a comparative genomic study based on Illumina next-generation sequencing. We report here complete chloroplast genomes of 39 species (41 accessions) sampled broadly across the phylogeny of the eucalypts to maximise divergence among major lineages. These sequences provide 7,046 variable characters, excluding indels, and maximum parsimony analysis produced one fully resolved tree that is largely congruent with existing generic and infrageneric groups, and on which most nodes have 100% bootstrap support. Chloroplast genomes range from 159,527 bp in *Eucalyptus obliqua* to 161,071 bp in *E. spathulata*. Gene structure and order is highly conserved across the group. Length mutations, especially frame shift mutations, are rare in protein coding regions. Comparisons across chloroplast genomes allow identification of variable DNA regions for use in further phylogenetic analyses. However, decreasing sequencing costs make whole genome studies increasingly feasible on a broad scale, and this approach provides more data, by orders of magnitude, than traditional amplicon-based methods.

Can directional bias in evolutionary transitions be inferred from phylogenies? An investigation using Australian pea-flowered legumes

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Reconstructing morphological change through time using a phylogeny can give us insights about ancestral morphology and direction of evolutionary change. When rates of transition between morphological states are asymmetrical, reconstruction methods can incorporate unequal transition rates. However, because these models depend on the distribution of trait states at the tips of the tree, they can perform poorly when there is an unequal distribution of tip states. We show that choice of reconstruction method affects selection of transition rate model and might lead to erroneous rejection of plausible histories. When applied to reconstructions of the evolution of bee- and bird-pollination syndromes in Australian egg-and-bacon peas, maximum likelihood (ML) modelling favoured an asymmetrical transition model, with higher reverse rates (bird- to bee-pollination syndrome), over an equal rates model. However, simulation tests showed that the preference for an asymmetrical rates model was driven by unequal numbers of extant putative bee- and bird-pollinated taxa. We argue that the higher estimated rate of reverse transitions compared with forward transitions (asymmetrical transition model) results from the assumption in the ML method that rates remain constant over the tree. This assumption seems unlikely to be true, given that changes in selection pressure are likely to occur with changing environments and the evolution of differing species-species interactions over time. This study demonstrates the general difficulty in inferring directionality of evolutionary transitions from phylogenies alone.

There's more to the Pilbara than just iron

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The flora of the Pilbara has not been comprehensively documented despite the region having one of the longest botanical collecting histories in Australia, dating back to 1699, and now arguably being the most intensively surveyed of any bioregion in Western Australia, as a consequence of sustained resource development. New species to the region, State and not surprisingly to science continue to be recorded, even in what could be considered well known groups like the wattles. The Pilbara flora is diverse, being dominated by arid and tropical elements, although many mesic and rainforest elements persist in refugial habits. The juxtaposition of arid and tropical elements, as highlighted by the phytogeographically important *Acacia-Triodia* line with evolutionarily significant refugia, has consequence on floristic diversity that we are only now gaining some insight into. Over the last 25 years the Pilbara species list has increased by over 55% to be in the vicinity of 1,700 species. Approximately 150 taxa are of conservation significance; although the overwhelming majority of these are poorly known and ongoing survey is required to assess their status. As many of these species are in poorly known or taxonomically challenging groups (130 undescribed), ongoing taxonomic investigation is essential. While unsustainable pastoral practices, mining and land clearing for development pose substantial threats, the primary landscape-wide threatening processes impinging on the flora are altered fire regimes and transforming environmental weeds. Addressing the threatening processes and securing the floristic diversity of the region, in an inventory-deficient and taxonomically uncertain setting, presents both an opportunity and a challenge for conservation.

Dealing with those problematic taxonomic groups—introgressed, character reduced, polyploid, marginal habitat, recently evolved, clonal, disjunct ‘species’

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In this age of rapid and relatively easy molecular genetic analysis, systematic studies sometimes result in what are seemingly disconnected outcomes when comparing taxonomy and molecular phylogenetics. In fact, the differences between the core business of taxonomists in defining taxonomic groups for public consumption and the complexities of molecular genetic evidence that may be generated, may lead to confusion and conflict as to what is the ‘right’ answer. This is no more prevalent than with taxonomic groups that exhibit a range of what might be seen globally as unusual traits: inter-taxon introgression; highly reduced or modified morphological traits; polyploidy and various forms of aneuploidy; association with highly stressful habitats; rapid radiations and recently evolved lineages; extreme longevity and clonality; populations that are highly disjunct. The Australian flora presents numerous examples of these features, across diverse taxonomic groups. Interestingly, these features represent some of the more interesting and unusual stories of evolutionary adaptation. For example, widespread, diverse genera such as *Solanum* exhibit variable ploidy, clonality and apparently unresolved radiations in several Australian lineages. In another example, plasticity and reduction in morphology, clonality and specialised niche occupancy in many aquatic plant groups has lead to confusion in species concepts in several important cases. In this presentation I will discuss examples from Australian plant groups that allow exploration of the utility, and confusion, that molecular genetic analyses bring. I will discuss the need for a pragmatic, unambiguous application of taxonomy that accommodates, or is not in conflict with, these datasets. Moves toward the incorporation of genomic data in systematic analysis highlight need for the development of tools enabling the effective use of more diverse data types into the consideration of taxonomic boundaries.

Strategic taxonomy and revisionary taxonomy: two complementary approaches to reducing Western Australia’s taxonomic backlog

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In 2006, a strategic taxonomy initiative was implemented in Western Australia to reduce the State’s taxonomic backlog by expediting the publication of undescribed taxa of conservation concern, especially those at risk from mining activity. The project also had a tactical regional focus, targeting new taxa on Banded Iron Formation Ranges of the Yilgarn as well as the Ravensthorpe Range and Bandalup Hill. A major early outcome of the project was the publication of a special issue of *Nuytsia* (Volume 17)—a national collaboration in which 95 new taxa (of which 78 are *Threatened*, geographically restricted or poorly known) were formally described. With the assistance of several complementary external grants, this project has retained momentum, successfully combining a highly targeted approach with regional work (e.g. the Swan Coastal Plain, Ravensthorpe Range and Burrup Peninsula) and broader revisionary research encompassing taxa of high conservation significance (most notably on *Androcalva*, *Commersonia*, *Leucopogon* and *Stylidium*). In the six years of the initiative, 78 papers have been published, descriptions for 317 taxa have been generated (including 155 published descriptions of new or reinstated taxa), and more than 7,000 PERTH specimens have been annotated. Despite these taxonomic gains, the number of undescribed vascular plants in Western Australia remains unacceptably high (*c*. 1,600 taxa). Even more alarmingly, the number of undescribed conservation-listed taxa has increased from 520 in 2006 to 652 in 2012, emphasising the extraordinary rates of species discovery across the State and the threats posed to this biodiversity. An approach that combines strategic taxonomy with revisionary taxonomy will be most effective in tackling our State’s enormous taxonomic backlog.

Contested, uncontested and potentially controversial taxonomic changes in the Proteaceae: how do they differ?

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Scientific knowledge consists of hypotheses (models that simulate reality) that have survived empirical tests. Various kinds of models have been proposed as the basis for forming higher taxa, including arbitrarily circumscribed groups, conveniently circumscribed sectors of ‘natural variation’, clades, ‘adaptive zones’ and phenetic clusters. Three decades of intense debate (1960–1990) resulted in the great majority of biological systematists agreeing that only clades were real, predictive and testable entities suitable for recognition as higher taxa. Numerous changes to the higher-level classification of the Proteaceae have been proposed since publication of the treatment of this family in the *Flora of Australia*, most notably in a paper that Nigel Barker and I published in 2006. All of these proposals were motivated by the goal of recognising only clades as higher taxa. With one exception (the sinking of *Dryandra* into *Banksia*), these changes have been uncontroversial and have been used in numerous other studies of evolution and biogeography. Why the inconsistent reaction to an enlarged *Banksia*? That proposal involved changes to the generic name of a large number (93) of species with showy flowers, admired by a group of enthusiasts who are understandably reluctant to change the names they use. Are these good reasons to abandon a generally agreed, consistent relationship between phylogeny and biological classification? The circumscription of *Persoonia* will also have to be altered in response to improved knowledge of phylogeny but this will be minor compared to the changes to generic limits needed in the subtribe Hakeinae.

Are parasitic insects good plant taxonomists? Insights from gall-inducing scale insects feeding on Leptospermeae

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Australia’s myrtaceous flora is relatively well known. In contrast, many of the insects that consume and parasitise members of the family Myrtaceae are yet to be described. One insect-plant interaction that typifies this disjuncture is the gall-inducing scale insects that feed on members of the Leptospermeae. Leptospermeae is a clade consisting of at least seven distinct plant genera, including *Agonis*, *Asteromyrtus*, *Homalospermum*, *Kunzea*, *Leptospermum*, *Neofabricia* and *Pericalymma*. *Eremococcus* (Hemiptera, Sternorrhyncha, Coccoidea, Eriococcidae) is a genus of gall-inducing scale insects that feed only on members of Leptospermeae. There are currently three described species: *E. turbinata*, *E. pirogallis* and *E. rugosus*. However, many undescribed gallers have been collected from a diverse range of Leptospermeae, including species of *Agonis*, *Kunzea*, *Leptospermum* and *Neofabricia*. Based on a molecular phylogenetic analysis of two nuclear gene regions (18S and Dynamin), we identify at least eight distinct species groups (three described, five previously undescribed), from two distinct and monophyletic lineages of gallers feeding on Leptospermeae: *Eremococcus s.s*. and a previously undescribed sister group. From this analysis we also reassess the classification of a previously described Leptospermeae galler, *Ascelismelaleucae*. The evolution of *Eremococcus* (and its relatives) is discussed with reference to recent phylogenetic assessments of Leptospermeae.

Carex sens. lat. (tribe Cariceae, Cyperaceae): an international initiative

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Carex s.l. (*c*. 2,100 species) is one of the four most speciose genera of flowering plants. It is ecologically important in habitats ranging from tundra to alpine meadows, arid creek-lines, heathlands, swamps and tropical wetlands. It is the largest genus of the temperate zone, particularly speciose in the Northern Hemisphere (Australia has only *c*. 50 native spp., New Zealand *c*. 80 spp.). The other ('caricoid') genera in the tribe are *Cymophyllus* (1 sp.), *Kobresia* (*c*. 40 spp.), *Schoenoxiphium* (*c*. 20 spp.) and *Uncinia* (*c*. 60 spp.). Of these, only *Uncinia* occurs in Australasia. Recent phylogenetic studies show that the tribe is monophyletic, with four main clades. *Carex* as traditionally circumscribed is paraphyletic: the four 'caricoid genera' are embedded in it. Based on the present state of knowledge, the best option is to enlarge *Carex* to include these four genera. A BioSynC workshop in 2011 brought together 30 cyperologists to plan a global revision of the tribe. A Scratchpad site, Sedges of the World (http://cyperaceae.e-monocot.org), has been set up, with funding from BioSynC (the synthesis arm of Encyclopedia of Life) and in collaboration with eMonocot and ViBRANT /Scratchpads. It is a virtual research tool for cyperologists and will gradually become a portal to authoritative Cyperaceae data for all users. In the next few years, the group aims to: create a phylogenetic framework for sectional revision of Carex; assemble a traits database to test diversification patterns, with the help of school students; and create an evolving online monograph, cyber-infrastructure for ongoing collaboration, and training ground for the next generation of taxonomists.

Online delivery and use of Australian Tropical Rainforest Plants identification tool

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Australian Tropical Rainforest Plants, or RFK as it is commonly known, has been the primary identification tool and information system for Australian tropical rainforest plants in its various forms since the first edition in 1971. Each edition has optimised use of available technology from card keys to computers and the internet. The latest edition was released on the internet in December 2010, and includes 2,554 species of plants excluding ferns and cryptogams. Deployment over the internet enabled ready access to the system for users across Australia and the world, either directly from the home page or through search engines. Monitoring has provided various insights into aspects of the online use of the system, including tracking the local and global uptake. A new collaborative project has recently been initiated to develop an interactive identification system for the Australian tropical 'savannah' flora to complement the RFK and Flora products, and the opportunities and challenges of such a project will be compared with the RFK experience.

Poster Abstracts

Sandplain country at Coolcalalaya Station, east of Kalbarri National Park
Image: Neil Gibson

Baeckea sp. Darling Range (R.J. Cranfield 1673)
Sarcostemma viminale
Calytrix carinata
Tribulus suberosus
Images: Kevin Thiele

A revision of *Rhynchotechum* (Gesneriaceae)

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Rhynchotechum (Geserneriaceae) comprises a group of typically understory subshrubs occurring from India east to China and Japan, south through Thailand into Sumatra, west to Papua New Guinea and north into the Philippines. They are recognised by their sub-regular flowers with short corolla tubes in cymose inflorescences, four fertile stamens, anthers with confluent pollen sacs that dehisce by a valve, and white berries. A morphological revision of the genus based on the examination of herbarium specimens has identified 16 species, including three new species (from Burma, north-east India and Vietnam) and one new combination. Specimen location data was used to evaluate geographic range, which was correlated with precipitation seasonality and precipitation in the driest quarter. This suggests the species inhabit areas with a distinct dry season but require a minimum amount of precipitation in that period.

BRAHMS: music to a cyber-taxonomist's ears

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BRAHMS is a powerful database management system empowering botanical researchers and herbaria. It provides wide-ranging and innovative functionality to gather, edit, analyse and publish botanical data, optimising its use for the widest possible range of curation services and research outputs. Recently implemented at the National Forestry Herbarium, New Zealand, a brief overview of the main functions in BRAHMS is presented. Some of the main features illustrated pertain to:

- Taxonomic information system—dictionaries of taxonomic and people names, the ability to link synonyms to accepted names, to record determination histories for specimens, to link images to any record;
- Collection management—creating and managing traditional as well as online image-based loans, the latter with the ability to edit determinations online;
- Taxonomic outputs—linking synonyms and type specimens to accepted names, the ability to produce complex formatted voucher-based checklists, protologues, citation lists or any other custom report, and transfer distribution data to Google Earth and other GIS software;
- Online presence—inbuilt functionality to design a web homepage and transfer online a fully searchable database;
- Internet toolbar links—a host of online services (e.g. IPNI, The Plant List, Taxonomic Name Resolution Service, TROPICOS, New Zealand Plants, ePIC etc.) are all a click away;
- Diversity calculations—calculate and display data about the distribution of taxa and optionally summarise indicators (species richness, Chao 2 etc.) per area. Data can be style-set and mapped directly from BRAHMS to Google Earth and other GIS software;
- Export in specialised exchange formats—XML, DARWIN CORE and HISPID.

Water fire suppression system to protect a valuable herbarium collection—is this folly or the future for herbaria?

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In 2012, the Western Australian Herbarium (PERTH) completed its move to a modern purpose-built facility. In an unusual step for a modern herbarium, a water-based fire suppression system was installed to protect the collection. The justification behind this decision, the novel approaches PERTH has taken to protect specimens from water damage in the event of a fire, and other benefits gained from this approach are discussed.

Untangling inflorescence structures in epacrids (Ericaceae, Epacridoideae)

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Inflorescence characters have been used repeatedly in phylogenetic analyses of Styphelioideae, but characters based on traditional concepts—e.g. flower position or bract and bracteole number and position—have generally emerged as homoplastic. Architectural concepts offer one alternative to using traditional descriptors and can provide a clear analytical framework for comparing complex structures with different components. I applied this approach to understanding homologies among units across Epacridoideae, characterising inflorescences in terms of basic units such as: apical meristems, metamers, shoot units (SU); timing of development of SUs and flowers; spatial organisation of components; and hierarchical relationships between axes. My work shows that previous studies have compared units that are not homologous. 'Traditional' descriptions confound groups of flowers derived from a single SU (apical meristem) with groups that include many sequentially produced SUs. Neither do they differentiate between monopodially and sympodially-derived axes. The 'bracts' and 'bracteoles' in various groups are also not homologous, and may form at different points in the branching hierarchy. They may be caducous, and may or may not differ from 'normal' leaves. Lastly, shoot dimorphism occurs in at least some taxa (e.g. *Lysinema*, *Dracophyllum s.s.* and *Richea*). It is therefore highly probable that high levels of homoplasy exhibited in phylogenetic analyses of the epacrids and of the Ericaceae *in toto* result at least in part from using non-homologous character states, and that the concept of 'inflorescence' should be reassessed across the entire family.

Selection of candidate DNA regions for use on closely related orchid species: a case study from African angraecoid orchids (Vandeae, Epidendroideae, Orchidaceae)

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Recent molecular studies have shown that *Angraecum*, the most diverse genus of angraecoid orchids, is polyphyletic. There is a clear-cut phylogenetic pattern of species distribution, with some occurring exclusively in continental Africa, and others in Madagascar and the nearby islands of the western Indian Ocean. This situation makes interpretation of evolutionary patterns within the genus particularly difficult, especially for sections that encompass species in both regions. Our study was conducted on species occurring in tropical Africa, and belonging to sections *Dolabrifolia* (African continent exclusively) and *Pectinaria* (African continent and Indian Ocean islands). To investigate the systematics and biogeography of these continental orchids, phylogenetic relationships were inferred from five plastid DNA regions (*mat*K, *rps*16, *trn*C-*pet*N, *trn*L-*trn*F and *ycf1*), and the nuclear rDNA internal transcribed spacer (ITS). Parsimony analyses conducted on each marker separately provided identical patterns of relationships: 1) sections *Dolabrifolia* and *Pectinaria* form a well-supported clade, from which Malagasy-Mascarene species of section *Pectinaria* are excluded; and 2) within the African clade, both sections are monophyletic, each receiving a high bootstrap support in all analyses. We further discuss the potential of the target candidate DNA regions to: 1) discriminate closely related species; 2) detect new species; and 3) clarify the unclear taxonomy of this orchid group, in which few vegetative/floral characters have been historically used for species delimitation.

Taxonomy and evolutionary relationships in a section of the genus Passiflora (Passifloraceae): contribution of pollen, morphological and molecular data

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Passiflora subgenus *Decaloba* supersection *Decaloba* section *Xerogona* is a tropical and subtropical group of 14 species, occurring in Latin American, Tropical and Atlantic Forests. The section is characterised by a herbaceous vine habit, eglandular petioles, leaf blades without ocelli, the absence of bracts and capsular fruits. This study analyses palynotaxonomy and phylogeny of section *Xerogona* based on pollen in combination with vegetative and reproductive morphological data and molecular sequences, contributing to the characterisation, circumscription and delimitation of the section and species within it. The pollen grains were acetolysed, measured, described and illustrated using light microscopy and scanning electron microscopy. Phylogenetic relationships among species based on plastid intergenic spacers *trn*L-*trn*F and the nuclear ribosomal DNA internal transcribed spacers (ITS) were evaluated, to examine the consistency of the section. The pollen grains are large or medium, isopolar, prolate-spheroidal, prolate, oblate-spheroidal, spheroidal or subprolate, 12-colpate, 6-colporate or 12-colporate, with a heterobrochate exine. A key for species identification based on pollen characteristics was generated. Phylogenetic trees based on morphological and molecular data indicate that section *Xerogona* is monophyletic. Pollen morphology makes a valuable contribution to understanding the taxonomy of section *Xerogona*, allowing a reassessment of circumscription and arrangement of infra-generic categories currently in place and, consequently, a better understanding of phylogenetic lineages.

It’s character building — systematic implications of silicon and stomata in mapaniid sedges

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Cyperaceae subfamily Mapanioideae includes taxa with a bizarre floral architecture, and is represented in Australia by eight out of the 11 genera in the subfamily. As part of a project integrating data on phylogeny, developmental morphology and genetics to understand the origins and diversity of the mapaniid floral form, we aim to reconstruct mapaniid evolutionary relationships via combined multigene and morphological analyses. As part of the ‘Local Knowledge, Global Delivery’ theme, we highlight how our work impacts on large scale phylogenetic analyses. We will present preliminary studies in these genera of two of the apomorphic micromorphological characters of the commeliniid clade, namely the presence of the biomineral silicon dioxide, and stomatal development by non-oblique cell division. We showcase new forms of silicon deposition in subfamily Mapanioideae and a diagnostic synapomorphy for the tribe Chrysitricheae, the presence of stomata on fruits. *Silicon*: conical cellular inclusions of silicon are found in Arecales and Zingiberales, where they are located internally in silica cells (stegmata) overlying sclerenchymatous vascular bundle sheaths. In these groups, stomata are absent from the epidermis. In Poales this silica form has only been recorded in Cyperaceae, predominantly in the Cyperoideae, where it occurs in epidermal cells adjacent to underlying fibres. Silicon records within mapaniid genera remain enigmatic, with contradictory data and reports of unusual forms. A new family-wide survey is presented and the results optimised onto a family phylogeny. *Stomata*: micromorphological characters related to the formation of the embryo, fruit and seed are of particular significance for familial relationships in the Poales clade. However, data for Mapanioideae are lacking, and interpretations of the fruit remain controversial. Our study showed the presence of paracytic stomata on the outer fruit walls of members of tribe Chrysitricheae but not in tribe Hypolytreae, subfamily Cyperoideae, Juncaceae or Thurniaceae. The data support the recognition of tribes Hypolytreae and Chrysitricheae and an earlier transfer of *Exocarya* and *Capitularina* from the former tribe to the latter.

What is at risk? Phylogeography and taxonomy of orchids endemic to Queensland’s mountaintop biodiversity hotspots

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The mountaintops of Australia’s Wet Tropics and the Cape York Peninsula are important biodiversity hotspots, harbouring a unique flora with high levels of endemism. Recent climate-change scenarios indicate that this specialised montane flora is highly vulnerable to global warming, as the predicted upward altitudinal changes in species’ ranges leave them nowhere to go. In order to support efficient, evidence-based biodiversity conservation and management decisions, comprehensive baseline data that help determine exactly what is at risk are required urgently. Epiphytic mountain top specialists are sensitive indicators for environmental and climate change. In the present study we use epiphytic orchid groups characterised by high levels of endemism on Queensland’s tropical mountain tops as a suitable model group to provide a clearer picture of the relationship between genetic diversity, climatic niche and taxonomy. The project will focus on the phylogeography of groups within the *Bulbophyllum* and *Dendrobium* alliance, which include several taxa confined to high elevation habitats characterised by high humidity and colder temperatures. Currently, there are no baseline data that provide information about the genetic diversity of the orchid populations on Queensland’s mountain tops, the extent of gene flow between them, and the putative locations of past refugia. Furthermore, species delimitation in these groups is often problematic and needs to be re-evaluated based on robust molecular evidence.

Seed morphology in *Thysanotus* and related genera of Asparagaceae: Lomandroideae: Cordylineae

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The limited literature on seed morphology in Asparagaceae subfamily Lomandroideae indicates that, although taxonomically useful, seed characters are largely unknown for *Thysanotus* and related genera. Although there are two clear tribal lineages within subfamily Lomandroideae—Lomandreae and Cordylineae—only the former are morphologically readily recognisable. Accordingly, seed morphology in *Thysanotus* and related members of Cordylineae was investigated in order to determine which characteristics may have systematic and/or phylogenetic value. Seed patterns were phylogenetically informative and observed variation in seeds distinguished different species and different groups of species; for example, angular seeds were unique to most of the annual climbing *Thysanotus* species, while elongated seeds with long-stalked arils were restricted to all 3-staminate *Thysanotus* species. All studied Cordylineae (including *Thysanotus*) shared numerous common seed morphological features, such as polygonal epidermal cells and convex periclinal walls. In particular, *Murchisonia* and *Thysanotus* possessed a large number of common seed characteristics, supporting recent molecular results that show *Murchisonia* to be polyphyletic and nested within *Thysanotus.*

Assessment of genetic diversity in rhubarb (*Rheum ribes*, Polygonaceae)

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Rhubarb (*Rheum ribes*) is a cool season vegetable and an important traditional medicine plant. However, the wild resource has been declining. In order to design appropriate conservation methods for the species across its natural distribution, it is important to characterise its genetic diversity. In this study, I isolated salt soluble globulins and alcohol soluble prolamines from 33 populations of rhubarb from 13 geographically distinct populations in Iran, and resolved them by SDS-PAGE. I also used genomic DNA-based AFLPs from fresh leaves of greenhouse-cultivated plants. Genetic distance between populations was calculated using Euclidian Distance Efficiency. The globulin proteins were very similar in their polypeptide profiles and hence offered little promise of ecotype identification; however, SDS-PAGE analysis of prolamines effectively differentiated the rhubarb ecotypes on the basis of presence or absence of a unique polypeptide. Results of this study indicate that different ecological conditions affected genetic diversity, and SDS-PAGE analysis of alcohol soluble prolamins and AFLPs are reliable methods for identification of rhubarb populations.

A revision of *Trisetum* (Poaceae: Aveneae) in Iran

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In order to clarify taxonomic questions concerning the species belonging to *Trisetum*, I performed an in-depth survey based on herbarium and field investigations. The outcomes of this study allowed me to recognise several taxa that are well differentiated from the morphological, chorological, and ecological viewpoints. A taxonomic treatment of *Trisetum* in Iran is given. Three species and two subspecies are recognised. Two species represent a Euro-Siberian element (*T. sibiricum* and *T. flavescens*) and *T. rigidum* is an Irano-Turanian element. *Trisetum sibiricum* was newly recorded in Iran.

Understanding the big genera of tribe Schoeneae (Cyperaceae)

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Tribe Schoeneae (family Cyperaceae) includes about 30 genera as currently delimited, with most of the 700 species found in Australia and in southern Africa. *Lepidosperma* and *Schoenus* are the two biggest genera in the tribe, and they will increase in size when the full range of variation and ecological niches in eastern and western Australia is investigated further. *Lepidosperma* has 73 named species but the number may more than double. About 120 species, some unnamed, are currently recognised in *Schoenus*; more are expected to be found, particularly in south-western Australia. Recent studies by us and collaborators in South Africa and Europe have shown that several genera in the tribe are not monophyletic. *Lepidosperma* is monophyletic if *L. aphyllum* is removed. In the case of *Schoenus*, several groups of species need to be moved. Our studies to date (including two ABRS grants, one post-doc and two PhD projects) have improved knowledge of the limits and phylogeny of these two genera and their known species, using morphological, molecular and anatomical datasets. Nomenclatural and taxonomic papers will be published soon to clarify names to be used in future papers, Floras and online resources such as the Atlas of Living Australia and eMonocots. Our studies provide a framework for investigating finer phylogenetic relationships in these groups, looking at character evolution and biogeographic patterns and further refining generic limits, infrageneric taxa and various species complexes.

List of Participants

Limestone heathlands at Toolinna Cove in Nuytsland Nature Reserve on the Great Australian Bight
Image: Andrew Brown

Dioscorea hastifolia
Hypocalymma sp. Cascade (R. Bruhn 20896)
Exocarpos aphyllus
Wurmbea tenella
Images: Kevin Thiele

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Back cover

Lomandra preissii
Thysanotus manglesianus
Clematicissus angustissima
Pembertonia latisquamea
Images: Kevin Thiele

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