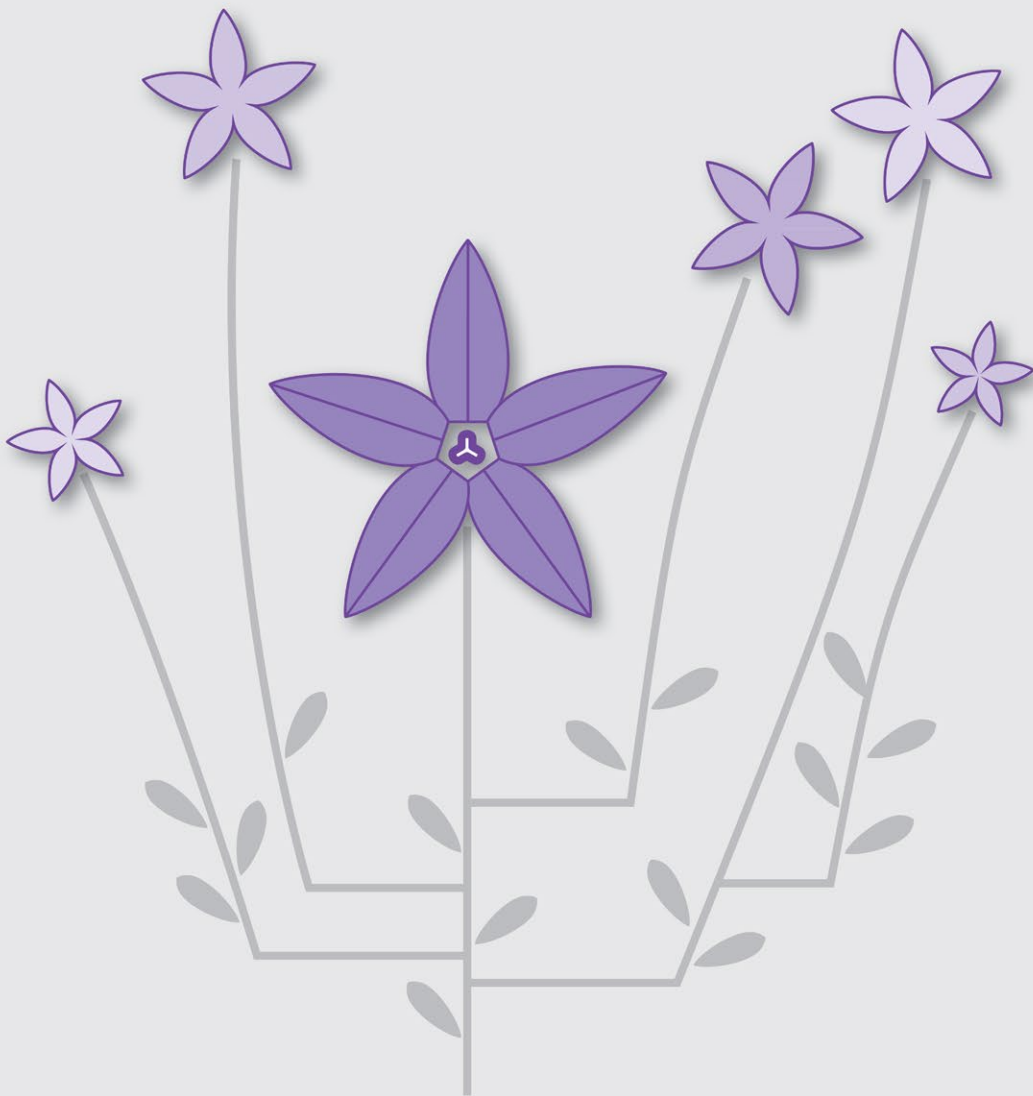


AUSTRALASIAN SYSTEMATIC BOTANY SOCIETY

Annual Conference  Canberra 2015



Building Our Botanical Capital

PROGRAM AND ABSTRACTS

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Conference website:

<http://www.asbs.org.au/cbr2015>

Notes

AUSTRALASIAN SYSTEMATIC BOTANY SOCIETY CONFERENCE

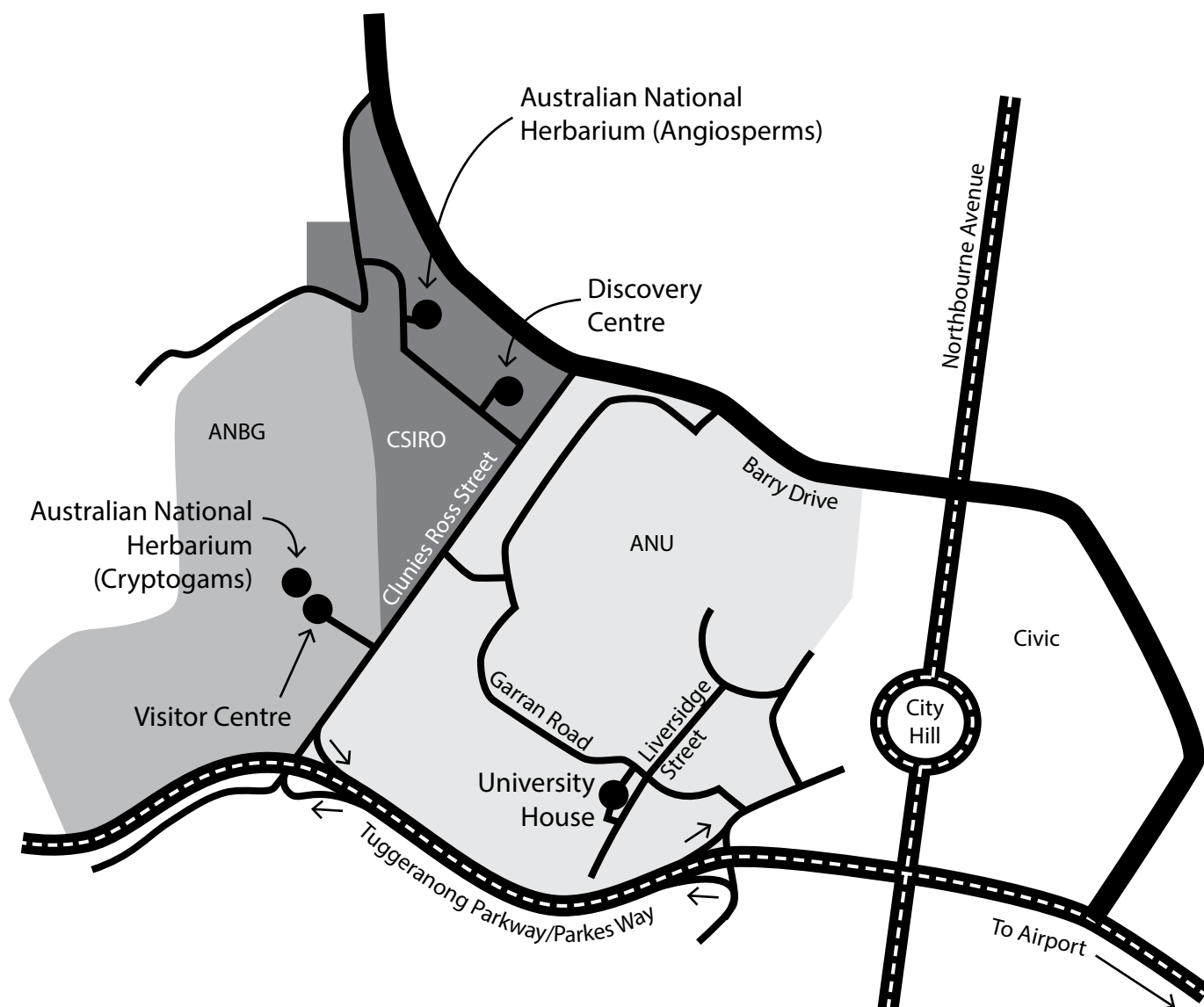
Building Our Botanical Capital

29 November–3 December 2015

Canberra, Australia

Venues & Map

The main conference venue is the CSIRO Discovery Lecture Theatre on the CSIRO's Black Mountain site, with the Discovery link room being used for displays and sales by various exhibitors. Associated events will be held elsewhere on the CSIRO Black Mountain site, at the Australian National Botanic Gardens (ANBG), and The Australian National University (ANU) campus.



Notes

Sponsors

The ASBS 2015 Conference Organising Committee would like to acknowledge the following organisations for their generous support of the “Building Our Botanical Capital” conference and associated events.

Atlas of Living Australia	http://ala.org.au
Australian Biological Resources Study	http://www.environment.gov.au/abrs
Australian Network for Plant Conservation	http://www.anpc.asn.au
Bush Blitz	http://www.bushblitz.org.au
Centre for Biodiversity Analysis	http://cba.anu.edu.au
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CSIRO Publishing	http://publish.csiro.au
CSIRO's National Research Collections of Australia	http://www.csiro.au/en/Research/Collections
Transport by George!	http://www.transportbygeorge.com.au

Conference Organising Committee

- Logistics and Communications: Christine Cargill, Jim Croft, Brendan Lepschi, Anna Monro and Cath Reed
- Science Committee: Lydia Guja, Sarah Mathews and Alexander Schmidt-Lebuhn

Booklet Credits

- Layout by Brigitte Kuchlmayr (Australian Biological Resources Study) and Anna Monro
- Proof-reading by Catherine Davis (Department of Agriculture and Water Resources), Brendan Lepschi and Anna Monro
- Cover design and map by Brigitte Kuchlmayr
- Conference logo design by Alexander Schmidt-Lebuhn

PROGRAM OVERVIEW

	Sunday 29 November	Monday 30 November
MORNING		<p>Symposium:</p> <ul style="list-style-type: none"> • Collections-based science <p>Keynote Speaker: Vicki Funk</p>
AFTERNOON		<p>Symposia:</p> <ul style="list-style-type: none"> • Assembly and visualisation of morphological data • Species delimitation, new species, and cryptic diversity <p>ASBS AGM</p>
EVENING	<p>Pre-conference registration and mixer</p> <p>"Interface" art exhibition launch</p>	<p>Public Forum:</p> <ul style="list-style-type: none"> • Effective transition from science to policy?

Tuesday 1 December	Wednesday 2 December	Thursday 3 December
<p>Symposium:</p> <ul style="list-style-type: none"> • Genomic data in plant systematics <p>Keynote Speaker: Craig Moritz</p>	<p>Symposium:</p> <ul style="list-style-type: none"> • Integrated floras, eFloras, and online keys <p>Keynote Speaker: Ilse Breitwieser</p>	<p>Field trip</p> <p>Workshops</p>
<p>Poster session</p> <p>Symposia:</p> <ul style="list-style-type: none"> • Phylogenetics • Decadal Plan for Australasian Biodiversity Science 	<p>Burbidge Medal presentation</p> <p>Symposium:</p> <ul style="list-style-type: none"> • Phylogenetics (continued) <p>Student award presentations Conference close</p>	
<p>Conference Dinner</p>	<p>Memorial Ceremony for Hansjörg and Marlies Eichler</p>	<p>Free</p>

CONFERENCE PROGRAM

Monday 30 November 2015

8:00–8:45	Registration/Set-up	
8:45–9:00	Welcome and Opening Remarks	
9:00–10:15	Collections-based science	
	9:00–9:45	KEYNOTE PRESENTATION Vicki Funk, Collections in a phylogenomic era: more important than ever
	9:45–10:00	Gill Brown, Crowd sourcing data entry at the University of Melbourne Herbarium
	10:00–10:15	Liqin Wu, The measurement and source apportionment of Australian atmospheric lead depositions in archived lichen and fungi (1885–2010)
10:15–10:45	Morning tea	
10:45–12:15	Collections-based science (continued)	
	10:45–11:00	Robyn Barker, Tales from the Type bay
	11:00–11:15	Sarah Mathews, Global hotspots of conifer diversity
	11:15–11:30	Peter Heenan, Biodiverse analyses reveal hotspots of endemism in the vascular flora of the New Zealand archipelago
	11:30–11:45	Joe Miller, Spatial phylogenetics of the Australian flora at different scales
	11:45–12:00	Peter Jobson, Botanical contributions of the Hermannsburg missionaries: then and now
	12:00–12:15	Elisabeth Bui, Soil geochemistry patterns explain richness patterns of the Australian flora
12:15–13:15	Lunch	
13:15–14:30	Assembly and visualisation of morphological data	
	13:15–13:30	Kelly Shepherd, Exploring floral diversity in the core Goodeniaceae
	13:30–13:45	Nathalie Nagalingum, Semi-automated generation of morphological matrices: examples using the cycads
	13:45–14:00	Peter Weston, A database of variation in floral characters in the Proteaceae, and implications for key questions in floral evolution
	14:00–14:15	Matt Renner, Lobule shape evolution in <i>Radula</i> (Jungermanniopsida): one rate fits all?
14:15–14:30	Joe Miller, The evolution of <i>Acacia</i> traits through space and time	
14:30–15:00	Afternoon tea	

15:00–16:30	Species delimitation, new species, and cryptic diversity	
	15:00–15:15	Russell Barrett, The tangled web of Australian spider flowers: a multifaceted approach to understanding the evolution of the Australian <i>Cleome</i> clade
	15:15–15:30	Ian Telford, Morphological and molecular data show <i>Synostemon trachyspermus</i> (Phyllanthaceae: Phyllanthaeae) to be a heteromorphic species assemblage
	15:30–15:45	Karen Muscat, Phylogeny, biogeography and classification of <i>Dianella</i> (Xanthorrhoeaceae) — insights into global biogeography and new species for the genus
	15:45–16:00	Melodina Fabillo, How many species of <i>Tripogon</i> in Australia — resurrecting or laying to rest an old debate?
	16:00–16:15	D. Christine Cargill, The liverwort genus <i>Riccia</i> (Ricciaceae): building relationships to capitalise on Australian species
	16:15–16:30	Ryan Phillips, Mismatch in the distribution of floral ecotypes and pollinators: insights into the evolution of sexually deceptive orchids
16:30–16:45	Break	
16:45–17:45	ASBS AGM	
17:45–18:00	Break	
18:00–19:00	Public panel discussion: Effective transition from science to policy?	

Tuesday 1 December 2015

8:30–9:00	Registration/Set-up	
9:00–10:15	Genomic data in plant systematics	
	9:00–9:45	KEYNOTE PRESENTATION Craig Moritz, Opportunities and challenges in next-gen molecular systematics
	9:45–10:00	Todd McLay, Evolution of the Australian grass trees, <i>Xanthorrhoea</i> , using multiple next-generation sequencing techniques
	10:00–10:15	Benjamin Anderson, Using genotyping by sequencing to resolve evolutionary relationships in a species complex of Australian arid zone grasses (<i>Triodia</i>)
10:15–10:45	Morning tea	
10:45–12:00	Genomic data in plant systematics (continued)	
	10:45–11:00	Ed Biffin, Cryptic diversity and hybridisation in the sea grass genus <i>Halodule</i> (Cymodoceaceae) revealed by high throughput sequencing
	11:00–11:15	James Clugston, Conservation genomics of <i>Cycas calcicola</i> (Cycadaceae) in Australia
	11:15–11:30	Rachael Fowler, The genus <i>Eremophila</i> (Scrophulariaceae, Myoporeae) in Australia's arid zone: phylogeny and biogeography using the chloroplast genome
	11:30–11:45	Bo-Kyung Choi, Identification of phylogenetically useful loci for a shallow level phylogeny
	11:45–12:00	Marlien van der Merwe, Can we use phylogenomics to date plant community assembly?
12:00–13:00	Lunch	

13:00–14:15	Phylogenetics	
	13:00–13:15	Juliet Wege, Triggering new insights into a remarkable genus: the <i>Stylidium</i> phylogeny and pollination project
	13:15–13:30	Endymion Cooper, Resolving ancient phylogenetic relationships in green plants
	13:30–13:45	Cécile Gueidan, Molecular phylogeny of the tropical lichen family Pyrenulaceae: contribution from dried herbarium specimens and FTA card samples
	13:45–14:00	Tanya Scharaschkin, Phylogenetics of Rottboelliinae (Andropogoneae: Panicoideae: Poaceae) using sequence data, with emphasis on the Australian taxa
	14:00–14:15	Katharina Schulte, The <i>Dendrobium</i> alliance revisited: Examining macroevolutionary patterns in Dendrobiinae (Orchidaceae)
14:15–15:00	Afternoon tea and poster session	
15:00–16:15	Phylogenetics (continued)	
	15:00–15:15	Alexander Schmidt-Lebuhn, Species checklists and a supermatrix approach in the study of biogeography at a global scale
	15:15–15:30	Janet Gagul, Molecular phylogenetics of <i>Elaeocarpus</i> (Elaeocarpaceae) with a focus on New Guinea species
	15:30–15:45	Xénia Weber, Papery problems: resolving generic boundaries of <i>Leucochrysum</i> and <i>Waitzia</i> (Asteraceae: Gnaphalieae)
	15:45–16:00	Charles Foster, Molecular systematics and biogeography of <i>Pimelea</i> (Thymelaeaceae)
	16:00–16:15	Lalita Simpson, Endemism in mountain-top plant communities of Australia's Wet Tropics: Past, present and future
16:15–16:30	Break	
16:30–18:00	Decadal Plan for Australasian Biodiversity Science	
	16:30–16:45	Ilse Breitwieser, Royal Society of New Zealand Panel on National Taxonomic Collections in New Zealand
	16:45–17:00	Michelle Waycott, Progress towards a Decadal Plan for Australasian Biodiversity Science — an update
	17:00–18:00	Decadal Plan Discussion
18:00–18:30	Break	
18:30–22:00	Conference Dinner	

Wednesday 2 December 2015

8:30–9:00	Registration/Set-up	
9:00–10:15	Integrated floras, eFloras, and online keys	
	9:00–9:45	KEYNOTE PRESENTATION Ilse Breitwieser, Electronic Floras — integrating the best of the past with the possibilities of the future
	9:45–10:00	Zoe Knapp, Gaps and priorities for the Flora of Australia: where to next?
	10:00–10:15	Kevin Thiele, This changes everything — an eFlora platform for Australasia
10:15–10:45	Morning tea	
10:45–12:00	Integrated floras, eFloras, and online keys (continued)	
	10:45–11:00	Michelle Waycott, Reinvigorating an already well-used electronic flora: 5 th Edn Flora of South Australia
	11:00–11:15	Frank Zich, Ongoing development of the “Australian Tropical Rainforest Plants” Interactive Identification Tool
	11:15–11:30	David Cantrill, That’s not a flora... This is a flora
	11:30–11:45	Russell Barrett, Keys to the Kimberley Flora: transitioning from hardcopy to e-floras
11:45–12:00	Leon Perrie, Untangling New Zealand’s tangle ferns for eFloraNZ	
12:00–13:00	Lunch	
13:00–14:00	Burbidge Medallist presentation and lecture	
14:00–14:30	Afternoon tea	
14:30–15:30	Phylogenetics (continued)	
	14:30–14:45	Darren Crayn, A detailed phylogenetic classification of Ericaceae: are we there yet?
	14:45–15:00	Jennifer Tate, Widespread morphological parallelism in <i>Korthalsella</i> mistletoes (Viscaceae)
	15:00–15:15	Matt Buys, <i>Metrosideros</i> : a contribution to the ongoing quest to decipher the phylogeny and phylogeography of a complex group
15:15–15:30	Peter Wilson, Phylogeny of the tribe Leptospermeae (Myrtaceae)	
15:30–16:30	Student Award Presentations and Closing Remarks	
16:30–17:00	Break	
17:00–18:00	Memorial Ceremony for Hansjörg and Marlies Eichler (Australian National Botanic Gardens)	

ABSTRACTS

Abstracts for both oral and poster presentations are listed alphabetically by the surname of the presenter. Where a presentation or poster has multiple authors the presenter is indicated in **bold** text.

Oral Presentations

Using genotyping by sequencing to resolve evolutionary relationships in a species complex of Australian arid zone grasses (*Triodia*)

Benjamin Anderson^{1,2}, Matthew Barrett^{1,2}, Pauline Grierson², Siegy Krauss^{1,2} & Kevin Thiele^{1,3}

Tuesday 1 December, 10:00–10:15

¹ School of Plant Biology, University of Western Australia, Crawley, WA 6009, Australia

² Kings Park and Botanic Garden, Fraser Avenue, Kings Park, WA 6005, Australia

³ Western Australian Herbarium, Department of Parks and Wildlife, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia

The application of next generation sequencing (NGS) technologies to systematics is still an emerging area of research, and systematists are increasingly faced with the challenge of interpreting the massive data sets associated with NGS. Genotyping by sequencing (GBS) is one of a number of NGS approaches based on the digestion of genomic DNA by restriction enzymes, and it can be applied to non-model systems. The *Triodia basedowii* species complex comprises two named taxa, five informally-named taxa and at least two additional taxa awaiting recognition. Morphological overlap between taxa and variability within taxa make identifications challenging, and previous sequencing of ITS was unable to clearly distinguish between some taxa. We applied GBS to samples from the *T. basedowii* complex using a commercial service through ANU. We used STACKS and PyRAD to demultiplex sequences and assemble them into loci for calling single nucleotide polymorphisms (SNPs). As part of this process, we optimised assembly parameters using replicate samples and genetic distances within populations. We analysed concatenated loci using RAxML, and used hierarchical clustering and PCA on distance matrices based on called SNPs. Our preliminary results reveal strong support for previously recognised taxa and distinction between taxa that were indistinguishable using ITS.

Tales from the Type bay

Robyn Barker

Monday 30 November, 10:45–11:00

State Herbarium of South Australia, Hackney Road, Adelaide, SA 5001, Australia

Today for any new species we designate a holotype and list the isotypes and where they can be found and so there is usually no question about the identity and location of any type material. However, this is a relatively recent practise and for older names the location and identification of type specimens is a much more challenging process.

Most herbaria will have already made at least one pass through their collections to set aside their types and, in the case of AD, assigned them to their red folders and placed them in the type bay. Once in the type bay they are readily identified and are then available to be worked on by visiting scientists or for loan. The advent of the Global Plants Initiative type digitisation project has led to these types being revisited and scrutinised before their images are captured and made available to the world through the web. What are we learning from this process?

Keys to the Kimberley Flora: transitioning from hardcopy to E-floras

Russell Barrett

Wednesday 2 December, 11:30–11:45

Australian National Herbarium, Centre for Australian National Biodiversity Research,
National Research Collections Australia, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia

Over 20 years in preparation, a new set of keys to the vascular flora of the Kimberley region of Western Australia is nearing completion. The keys will be published in traditional hard copy, but also made available as an open-access PDF, under a Creative Commons Copyright licence, to allow the content to be freely incorporated into existing online databases (KeyBase and the Australian Plant Name Index). The background to these keys will be presented, along with the rationale for publishing them in this format. It is hoped that publication of the keys will stimulate the production of a revised regional flora in an electronic format. Preparation of taxonomic identification tools is very time consuming. Publishers often have very specific formats that they require for the final hardcopy version. With the development of interactive electronic identification tools and large-capacity PDAs, users will increasingly be looking to access the information that systematists produce in electronic form. We need to consider the way we publish taxonomic descriptions with e-floras in mind.

The tangled web of Australian spider flowers: a multifaceted approach to understanding the evolution of the Australian *Cleome* clade

Russell Barrett^{1,2}, Kym Ottewell³, Margaret Byrne³, David Coates³ & Kevin Thiele¹

Monday 30 November, 15:00–15:15

¹ Western Australian Herbarium, Department of Parks and Wildlife, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia

² Australian National Herbarium, Centre for Australian National Biodiversity Research,
National Research Collections Australia, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia

³ Science and Conservation, Department of Parks & Wildlife, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia

Australian members of Cleomaceae form a monophyletic clade that has speciated across tropical Australia, presumably from a single dispersal event to the continent. Contrasting patterns of morphological and molecular variation have been identified using a combination of micromorphology, nuclear and plastid sequence data and phylogenomic analyses. The highest diversity of Australian *Cleome* species is in the Kimberley region and the “Top End” of the Northern Territory. *Cleome viscosa* has spread through south-east Asia, and more recently become weedy in central America. Morphological variation has suggested that additional taxa should be recognised, but taxon boundaries remain unclear. SEM studies of seed morphology complemented by phylogenetic and phylogenomic data allow relationships and taxon limits to be re-evaluated. Concordant phylogenetic data allow the significance of individual morphological characters to be established. A number of novel, geographically restricted lineages have been identified that may be of conservation significance.

Cryptic diversity and hybridisation in the sea grass genus *Halodule* (Cymodoceaceae) revealed by High Throughput Sequencing

Ed Biffin¹, Michelle Waycott^{1,2} & Kor-Jent van Dijk²

Tuesday 1 December, 10:45–11:00

¹ State Herbarium of South Australia, Hackney Road, Adelaide, SA 5001, Australia

² School of Earth and Environmental Sciences, University of Adelaide, Adelaide, SA 5001, Australia

Using molecular data, several studies have highlighted unexpected levels of diversity within and among species groups. In lineages with low morphological complexity species delimitation has always been challenging and a sole focus on morphology may underestimate the true extent of diversity. Here, we use an AFLP sequencing approach to investigate diversity in the seagrass genus *Halodule*. Phylogenetic analysis supports the monophyly of the Old World (*H. uninervis*, *H. pinifolia*) and New World (*H. wrightii*) lineages. Phylogenetic, Bayesian clustering and ordination analyses were used to investigate genetic structure within each of these groups. We find evidence for divergent genetic lineages within both clades. Within the “*uninervis*” clade, three largely sympatric lineages show greater connectivity across their distributional range than was observed on a local geographic scale. Two genetic groups were identified within the “*wrightii*” clade and are incongruent with existing taxonomic concepts. In both the “*uninervis*” and “*wrightii*” clades we identified admixed individuals consistent with hybridisation amongst each of the genetic groups. While conventional morphological concepts provide little indication of the level of complexity harboured within *Halodule*, our genetic evidence forms a powerful basis for *a posteriori* investigation to clarifying the systematics and evolution of *Halodule*.

Electronic Floras — integrating the best of the past with the possibilities of the future

Keynote Presentation

Ilse Breitwieser, Aaron Wilton & Peter Heenan

Wednesday 2 December, 9:00–9:45

Allan Herbarium, Landcare Research, PO Box 69040, Lincoln 7640, New Zealand

Floras are an authoritative summation of taxonomic knowledge for a given region at a given time. Traditionally Floras are books, but because of the considerable time and resources required to compile and produce a Flora, these books are often out of date as soon as the Flora is printed. Developments in biodiversity informatics make it now possible to use different approaches to create Floras, and worldwide there are numerous “next generation Flora” projects underway. These range from digitisation of existing Floras to development of novel information systems that replace or extend traditional Floras. Such systems variously include tools to address different parts of the Flora writing process from accumulating and synthesising data through to generating products to meet specific audience needs. These new approaches lead to different work processes for systematists and different possibilities of engagement with a much wider Flora user community. We will provide an overview of integrated and electronic Flora developments but will focus particularly on our own experiences in New Zealand and the development of our electronically-based Flora of New Zealand.

Royal Society of New Zealand Panel on National Taxonomic Collections in New Zealand

Ilse Breitwieser

Tuesday 1 December, 16:30–16:45

Allan Herbarium, Landcare Research, PO Box 69040, Lincoln 7640, New Zealand

The challenges and needs of New Zealand's national biological collections have been around for many years. In February 2015, in the face of concern over the extent to which strategic guidance was being provided over this "backbone" of necessary research infrastructure, the Royal Society of New Zealand Council convened a panel of leading experts to assess the state and future needs of New Zealand's nationally important biological collections.

The Panel was chaired by Dr Wendy Nelson FRSNZ, and included Dr Ilse Breitwieser, Professor Ewan Fordyce FRSNZ, Dr Janet Bradford-Grieve FRSNZ, Dr David Penman, Dr Nick Roskrige, Dr Tom Trnski, Dr Susan Waugh, and Dr Colin Webb FRSNZ.

The focus of the panel was to identify the significance of New Zealand's national taxonomic collections; review the value being gained from them now and the potential value possible in the future; evaluate taxonomic training in New Zealand and any impediments; and provide recommendations on the most effective process for supporting, developing and managing our taxonomic collections, databases, information systems and research for the future.

I will present a short overview on the work of the Panel and the report.

Crowd sourcing data entry at the University of Melbourne Herbarium

Gill Brown & Erin Batty

Monday 30 November, 9:45–10:00

University of Melbourne Herbarium, School of BioSciences, University of Melbourne, Vic 3010, Australia

We used crowd sourcing to database specimens from our Burnley Horticultural Collection, through the DigiVol portal on the Atlas of Living Australia. This was a test project for the Australian herbarium community with CHR being the only other Australasian collection to previously use the portal. We have run two expeditions and the data from these have been fed into AVH. We hope to use it in the future as a teaching tool, as well as providing opportunities for undergraduate students to increase their botanical knowledge and learn about herbaria and specimen curation through volunteering.

The Burnley Horticultural collection comprises c. 6,000–7,000 specimens that are predominantly horticultural and invasive plant species but also includes native plants. It was originally used for teaching and research at the (now) University of Melbourne's Burnley campus and was donated to MELU in 2007, where it has sat awaiting curation and cataloguing.

Soil geochemistry patterns explain richness patterns of the Australian flora

Elizabeth Bui

Monday 30 November, 12:00–12:15

CSIRO Land and Water, GPO Box 1666, Canberra, ACT 2601, Australia

The National Geochemical Survey of Australia (NGSA) has reported 68 elemental concentrations at 1315 georeferenced point measurements across the continent at two depth intervals (TOS, 0–10 cm, and BOS, 60–80 cm), for two size fractions (<2 mm and <75 µm). In addition the pH and electrical conductivity (EC) on 1:5 soil:solution extracts from bulk samples at the same locations was reported. This is a low-density survey (1 site/5500 km²) but is suitable to capture geochemical composition and variability at the continental scale.

Using geostatistics we can use this sparse dataset in biodiversity studies. For example we have used ordinary kriging to predict the major elemental concentrations (aluminium (Al), calcium (Ca), iron (Fe), magnesium (Mg), manganese (Mn), phosphorus (P), potassium (K), sodium (Na), sulphur (S), silicon (Si), all in mg kg⁻¹), pH1:5, and EC1:5 for the <2 mm fraction at the two depth intervals (TOS and BOS) at sites with *Acacia* (127,259), eucalypt (153,164), and Proteaceae (149,361) presence recorded in the Australia's Virtual Herbarium (AVH) database (<http://avh.chah.org.au>).

Combining these records with climate data has enabled us to establish that where species richness is high, geochemistry plays as important a role as climate in explaining *Acacia*, eucalypt, and Proteaceae species assemblages in biodiversity hotspots of southwest and eastern Australia.

Acacias are responding to pH, EC, Na, P, and Al whereas Proteaceae are responding to P, pH, Si, Na, and Ca. In the west, eucalypts as a whole are responding to Ca and Na whereas in the east they are responding more to EC, Fe, and pH but different groups of eucalypts respond to different variables.

***Metrosideros*: a contribution to the ongoing quest to decipher the phylogeny and phylogeography of a complex group**

Matt Buys¹ & Brent Berger²

Wednesday 2 December, 15:00–15:15

¹ National Forestry Herbarium, NZ Forest Research Institute (Scion), New Zealand

² Department of Biology, St. John's University, USA

To begin to explore the modern paradigm of biogeography as it pertains to volcanic islands, we investigated the genus *Metrosideros* (Myrtaceae) across its South Pacific distribution and utilised molecular data and fossil evidence to provisionally time the initial spread of the genus across the Pacific, focusing on non-Hawaiian species. Using three plastid (*matK*, *psbA-trnH*, *rps16*) and two nrDNA (ITS, ETS) regions, we find strong support for the monophyly of tribe Metrosidereae. While the backbone of the phylogeny is largely unresolved indicating a rapid radiation, we do find support for *Metrosideros* subg. *Metrosideros*, *Metrosideros* subsect. *Crassinervis*, the monophyly of *Carpolepis*, and a sister relationship between the South American *Tepualia stipularis* and the South African *M. angustifolia*. Divergence time estimates suggest an origin of *Metrosideros s.l.* (including *M. angustifolia* and *Tepualia stipularis*) ~25 Ma during the Oligocene. Our data indicate that the initial diversification invokes a southern Gondwana signal with an Australasian, South American, South African split. *Metrosideros s.s.* likely dispersed from New Guinea to New Zealand during the Miocene with subsequent LDDE events between New Zealand and New Caledonia occurring at least three times, with additional LDDE to the Kermadec Islands, the Lord Howe Islands, and the Bonin Islands occurring more recently.

That's not a flora... This is a flora

David Cantrill, Frank Udovicic & Niels Klazenga

Wednesday 2 December, 11:15–11:30

Royal Botanic Gardens Victoria, Birdwood Avenue, Private Bag 2000, South Yarra, Vic 3141, Australia

The *Flora of Victoria* was published in four volumes between 1993 and 1999. Rebranded as VicFlora it has been available online since early 2015 and incorporates the Census of the Vascular Plants of Victoria. We are currently in the middle of a three-year project to generate taxon descriptions for over one thousand taxa that are needed to get the flora up-to-date and complete, and intend to keep it up-to-date into the future. At the Royal Botanic Gardens Victoria, six botanists are involved in bringing and keeping VicFlora up-to-date, as well as three other staff and two volunteers who take care of the infrastructure and the images. For sustainable long-term management of the content of VicFlora, VicFlora will be managed in the National Species Lists, new treatments will be born-APNI and VicFlora will run almost entirely on ALA services. VicFlora currently has about 100 users on any weekday. It is used by land managers and rangers, as well as many interested amateurs, in Victoria and is being used for teaching at universities in Melbourne.

The liverwort genus *Riccia* (Ricciaceae): building relationships to capitalise on Australian species

D. Christine Cargill¹, Will C. Neal², Ish Sharma, Karen Beckmann & Cécile Gueidan¹

Monday 30 November, 16:00–16:15

¹ Australian National Herbarium, Centre for Australian National Biodiversity Research,
National Research Collections Australia, GPO Box 1600, Canberra, ACT 2601, Australia

² University of Melbourne, School of BioSciences, Vic 3010, Australia

A number of Australian *Riccia* taxa have been sequenced for the first time, with the majority from the monsoon tropics of the Northern Territory, north of 18° latitude. This allowed the investigation of a number of infrageneric groupings within the genus as well as morphological species concepts. Molecular data from three chloroplastic and nuclear markers support the genus as a monophyletic group, however, the monophyly of the two largest subgenera, *Riccia* and *Ricciella* are not supported, with the latter well nested within subg. *Riccia*. A number of widespread and common species such as *R. inflexa* and *R. lamellosa* were found to be polyphyletic. A second tree reconstruction using only *trnL-F* sequences allowed the inclusion of a number of extra-Australian material. Results from this study indicated congruence between material of some Australian and extra-Australian taxa, with further research required to determine the taxonomic placement of remaining taxa.

Identification of phylogenetically useful loci for a shallow level phylogeny

Bo-Kyung Choi^{1,2}, Lyn G. Cook³, Alicia Toon³, Robert D. Edwards³, Michael D. Crisp¹ & Carsten Külheim¹

Tuesday 1 December, 11:30–11:45

¹ Research School of Biology, Australian National University, Canberra, ACT 0200, Australia

² Australian National Herbarium, Centre for Australian National Biodiversity Research,
National Research Collections Australia, GPO Box 1600, Canberra, ACT 2601, Australia

³ The University of Queensland, School of Biological Sciences, Brisbane, Qld 4072, Australia

Identifying informative loci has been a challenge for phylogenetic studies. The aim of our study was to find informative loci to create a phylogeny of recently diverged taxa within the Myrtaceae. We aimed to find orthologous loci with low copy numbers from several target species. This task has been made easier through the number of annotated genomes across various organisms that have become available online. We introduce a method using an annotated genome of one target species together with transcriptome and shot gun genome sequences of three other species. Our target groups are *Eucalyptus* and *Melaleuca*. We performed a de-novo assembly from RNAseq reads of *M. quinquenervia*

and then mapped shot-gun genome sequence reads from *M. bracteata* and *M. leucadendra* against the assembled transcriptome. We selected transcripts that showed the expected shot-gun coverage and searched for orthologous loci in *E. grandis* using a blast search in the phytozome database. If a single ortholog was found, we compared the copy numbers of the gene across the plant kingdom. We identified 200 loci totalling 200 kb in length. This method is applicable to other groups of organisms with unresolved phylogenies.

Conservation genomics of *Cycas calcicola* (Cycadaceae) in Australia

James A.R. Clugston^{1,2} & Nathalie S. Nagalingum¹

Tuesday 1 December, 11:00–11:15

¹ Royal Botanic Garden Sydney, Mrs Macquaries Road, Sydney, NSW 2000, Australia

² The University of Edinburgh Darwin Building, The King's Buildings, Max Born Crescent, Edinburgh EH9 3BF, UK

Many cycads exist in small populations, and so understanding the genetic variation in cycads is imperative to help conserve the remaining populations, thus ensuring their survival. Genetic data plays a fundamental role in identifying and conserving multiple genotypes and populations with the highest levels of genetic diversity. Although Australia represents a significant biodiversity hotspot for cycads, the genetic diversity of *Cycas* in Australia has yet to be explored. This research applies next generation sequencing (NGS) technologies for cycad conservation genetics. More specifically, we are using restriction associated DNA sequences (RADseq) to produce thousands of small stretches of the genome, which can be used for population genotyping by identifying potentially thousands of polymorphisms. Our target species is *Cycas calcicola*, a species endemic to the Northern Territory, Australia and which occurs in disjunct populations between the Litchfield National Park and the Katherine region. The RADseq data generated for this species will be used to: understand genetic variation in and between populations; identify genetic differences between northern and southern populations; recognise populations of conservation priority; and determine if botanic garden collections successfully represent existing genetic diversity found in the wild.

Resolving ancient phylogenetic relationships in green plants

Endymion Cooper

Tuesday 1 December, 13:15–13:30

School of Biological and Chemical Sciences, Queen Mary University of London, London E1 4NS, UK

Identifying the closest living relatives of land plants and resolving the sequence of earliest divergences amongst major embryophyte groups are fundamental to our understanding of the origins and diversification of the terrestrial flora. Yet, despite considerable effort to resolve these parts of the green plant tree of life, considerable uncertainty remains. It is clear that these ancient divergences present significant challenges. Whilst the focus has been on obtaining the best supported topologies, low confidence and ambiguity have been considered the enemy to be vanquished. However, in the uncertainty there lies valuable information for resolving not just the topology, but also the patterns of gene and genome evolution that accompanied the major adaptive changes that facilitated the transition to land. In this talk I discuss the processes that erode phylogenetic signal and consider how, by attempting to reconstruct these processes, we might be able to overcome the challenges they create. I emphasise that without an understanding of these processes we cannot accurately estimate branch lengths and, consequently, divergence times. These issues have broad implications for resolving the tree of life.

A detailed phylogenetic classification of Ericaceae: are we there yet?

Caroline Puente-Lelievre¹, Michael Hislop², Benjamin Potter³, Andrew Thornhill⁴, Will Freyman⁴, Kathy Kron⁵ & **Darren Crayn**⁶

Wednesday 2 December, 14:30–14:45

- ¹ Department of Botany, National Museum of Natural History, Smithsonian Institution, Washington DC 20013-7012, USA
- ² Western Australian Herbarium, Department of Parks and Wildlife, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia
- ³ School of Biological Sciences, University of Auckland, Auckland 1010, New Zealand
- ⁴ University and Jepson Herbaria, Department of Integrative Biology, University of California - Berkeley, Berkeley, CA, 94720-2465, USA
- ⁵ Department of Biology, Wake Forest University, Winston-Salem NC 27109-7325, USA
- ⁶ Australian Tropical Herbarium, James Cook University, PO Box 6811, Cairns, Qld 4870, Australia

Ericaceae is a large angiosperm family of more than 120 genera and 4000 species. The ericaceous flora of Australasia is distinct, being dominated and characterised by subfamily Epacridoideae (>35 genera and 550 spp.). We present advances in the phylogenetic systematics of Ericaceae on two fronts (1) a supermatrix approach to resolving a densely sampled family phylogeny, and (2) systematics of the Styphelieae (fleshy-fruited epacrids), the largest of the seven tribes in Epacridoideae. For the former we analysed a supermatrix of published and unpublished DNA sequences (16 markers, 1200+ taxa) to draft by far the most comprehensively sampled Ericaceae phylogeny to date. For the latter we analysed sequences from four plastid (*rbcl*, *matK*, *trnH-psbA*, *atpB-rbcl*), and one nuclear (ITS) marker for 207 taxa (many only phrase-named). The results corroborate the polyphyly of the genera *Astroloma*, *Leucopogon* and *Styphelia* and resolve twelve robust clades. Of these, two can be distinguished by unique morphological features and another six by different character combinations. The remaining groups are morphologically heterogeneous and inconsistent and not readily distinguishable, and a number of species remain ungrouped. We discuss the nomenclatural options and conclude that expanding *Styphelia* to include *Astroloma sensu stricto*, *Coleanthera*, *Croninia*, and much of *Leucopogon* best serves nomenclatural stability and predictability.

How many species of *Tripogon* in Australia — resurrecting or laying to rest an old debate?

Melodina Fabillo & Tanya Scharaschkin

Monday 30 November, 15:45–16:00

School of Earth, Environmental and Biological Sciences, Queensland University of Technology (QUT), Brisbane, Qld 4000, Australia

Tripogon loliiformis, the only described species of *Tripogon* in Australia, exhibits extensive morphological variation across its geographic range, leading to the suggestion of it being multiple species. The gross morphological variability of *T. loliiformis* is covered in its 13 syntypes. Gross vegetative and reproductive characters were commonly used in previous taxonomic studies of *Tripogon*. However, micromorphological descriptions remain unknown. This study describes and compares the leaf and inflorescence micromorphology of multiple accessions of *T. loliiformis*, including the 13 syntypes. Leaf and inflorescence materials were collected in the field and from herbarium vouchers. Light and scanning electron microscopy were undertaken. Notable surface features of the leaf and inflorescence that were studied include long cells, bulliform cells, subsidiary cells, micro-hairs, macro-hairs, prickles and papillae. In general, the micromorphology of *T. loliiformis* indicates features typical of chloridoid grasses. Despite gross morphological variability, *T. loliiformis* shows uniform micromorphological features across its geographic range. These findings support our phylogenetic study using sequence data showing that there is no basis for splitting the different gross morphological forms into multiple species. This is the first report on the leaf and inflorescence micromorphology of *T. loliiformis*. This new knowledge opens up pathways for future areas of study, for example, those involving the desiccation tolerance of *T. loliiformis*.

Molecular systematics and biogeography of *Pimelea* (Thymelaeaceae)

Charles Foster, Simon Ho & Murray Henwood

Tuesday 1 December, 15:45–16:00

School of Biological Sciences, University of Sydney, Sydney, NSW 2006, Australia

Pimelea (rice flowers) are important members of Australia's diverse biomes, with most species found nowhere else. The nature of the relationships between them, and other plants in the same family (Thymelaeaceae), are unknown. Resolving these relationships is crucial to prioritising the conservation of *Pimelea*, since many are known to be endangered under the EPBC Act List of Threatened Flora. We will take a molecular phylogenetic approach to solve this problem, using high-throughput sequencing technology to obtain informative molecular markers. We will then amplify these markers for a large proportion of Australian and New Zealand species of *Pimelea* to improve our understanding of the evolutionary relationships among these species. Ultimately, this will tell us when and how they diversified, and provide insight into how they responded to climate change, and which ecological factors might have driven their evolutionary success.

The genus *Eremophila* (Scrophulariaceae, Myoporeae) in Australia's arid zone: phylogeny and biogeography using the chloroplast genome

Rachael Fowler

Tuesday 1 December, 11:15–11:30

The University of Melbourne, School of BioSciences, Vic 3010, Australia

Eremophila is a large Australian genus with over 200 described species and a growing number of newly discovered taxa. *Eremophilas* are a significant component of the Australian arid zone flora, where they tolerate harsh, dry and saline conditions and provide food and shelter for a wide range of insect and bird species. To date our understanding of species relationships in *Eremophila* are based solely on morphological characters, but with the advancement of next generation sequencing methods we now have the opportunity to understand this group from a comprehensive molecular perspective.

The aims of my PhD research are to discover the evolutionary relationships of *Eremophila* species, in order to re-assess classification of the group using morphological and molecular data, and to infer the biogeographic history of the group in arid Australia. I am also exploring the relationships of *Eremophila* to other members of the tribe Myoporeae. To address these research aims I have trialled an "in-house" library preparation protocol followed by whole genome shotgun sequencing for a small subset of species. This approach, though not without challenges, has proven successful in allowing for entire chloroplast construction and preliminary analyses.

Collections in 21st Century Science: more important than ever

Keynote Presentation

Vicki Funk

Monday 30 November, 9:00–9:45

Smithsonian Institution, PO Box 37012, Washington, DC 20013-7012, USA

The 19th Century ushered in a new age as naturalists undertook large-scale collecting expeditions leading to field observations and preserved specimens in the short term, and to major scientific advances in the long term. Notable among these were the founding of Physical Geography, Meteorology, Ecology (Humboldt), Biogeography (Hooker), and the theory of Evolution (Darwin, Wallace). In the 20th Century collections were central to paradigm shifts, including theories of Continental Drift (Eigenmann) and Phylogenetic Systematics (Hennig, Brundin). Past expeditions provided tissues for all the cladograms as the era of Phylogenetics took over biological thought. Will this tide of collections-based scientific advancement continue? In the first 15 years of the 21st Century we have seen tree-thinking pervade the life sciences, leading to the emergence of Evolutionary Ecology, Evolutionary Medicine, and new Food Safety methods, and collections data increasingly are used for climate change studies. Collections are a gold mine of information and are now leading the way to advances in three main areas: collections contain vast quantities of genomic data accessible through Next-Generation Sequencing techniques and phylogenomics, allowing us to address big evolutionary questions such as the frequency of gene duplication and its role in species diversification; open access to specimen data, allowing us to model changes in diversity through time; and estimating extinction risk and conservation priorities, by linking collections and climate data with phylogenies. Our “grand challenge” is to determine where we want to be with collections-based research in 2050 and plan a strategy to get there.

Molecular phylogenetics of *Elaeocarpus* (Elaeocarpaceae) with a focus on New Guinea species

Janet Gagul^{1,2,4}, Darren Crayn^{1,3} & Lars Nauheimer¹

Tuesday 1 December, 15:15–15:30

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³ Centre for Tropical Biodiversity and Climate Change, James Cook University, Cairns, Qld 4878, Australia

⁴ Biological Sciences, University of Papua New Guinea, Port Moresby, Papua New Guinea

Elaeocarpus is the largest genus in Elaeocarpaceae comprising approximately 360 species of trees and shrubs distributed throughout tropical and subtropical zones from Asia to the Pacific region, with outliers in Madagascar. The genus is distinguished from other Elaeocarpaceae by the possession of fringed petals and drupaceous fruits.

New Guinea is a major centre of *Elaeocarpus* diversity with approximately 97 taxa.

However, with a few exceptions the phylogenetic relationships of the New Guinea taxa are unknown due largely to the difficulty experienced to date in obtaining suitable material for molecular phylogenetic studies.

Our study builds on recent work on the genus that has resolved, using a sample of c. 30% of the species diversity, the main lineages, their phylogenetic relationship, and aspects of their historical biogeography. We aim to address the New Guinea sampling gap together with increasing taxon representation from other under sampled areas such as Sulawesi. Plastid *trnL-F*, *trnH-psbA* and *trnV-ndhC* sequence data will be analysed using a range of phylogenetic tree reconstruction and biogeographical analysis methods to better understand the relationships, biogeography and evolutionary history of the genus.

Molecular phylogeny of the tropical lichen family Pyrenulaceae: contribution from dried herbarium specimens and FTA card samples

Cécile Gueidan¹, André Aptroot², Marcela Eugenia da Silva Cáceres³ & Quoc Binh Nguyen⁴

Tuesday 1 December, 13:30–13:45

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³ Departamento de Biociências, Universidade Federal de Sergipe, CEP: 49500-000, Itabaiana, Sergipe, Brazil

⁴ Vietnam Academy of Science and Technology, Vietnam National Museum of Nature, Department of Biology, 18 Hoang Quoc Viet Street, Cau Giay, Hanoi, Vietnam

The family Pyrenulaceae is one of the main components of the epiphytic lichen flora in tropical rainforests. This family mainly comprises corticolous species and *Pyrenula*, the most species-rich genus (about 200 species), is typically found on smooth, shaded bark. Although a world key is available for the currently accepted species of *Pyrenula*, recovering molecular data from these tropical taxa has proven to be challenging. As a result, generic and species concepts have not been tested and little is known about phylogenetic relationships between species of Pyrenulaceae. A recent attempt to investigate phylogenetic relationships within Pyrenulaceae using material from Sri Lanka highlighted the presence of two main well-supported monophyletic groups. However, the number of taxa for which sequences were generated in this study was still low, mostly due to the difficulty to recover enough genomic DNA from dry herbarium specimens collected more than a year before DNA extraction. A new method of DNA collection and storage was therefore investigated in this study. Because the genomic DNA of corticolous crustose tropical lichens seems to degrade rapidly, often before reaching the laboratory, we investigated the use of FTA Classic Cards (Whatman) to collect and transport DNA samples of our lichen material. These chemically treated matrix cards lyse cell membranes on contact, physically bind the DNA, and protect it from UV damage and microbial degradation. In this study, several fieldtrips to South-East Asia (Vietnam, Thailand and Laos) and to Brazil allowed us to collect fresh specimens for various species of Pyrenulaceae and recover genomic DNA from both freshly collected material and FTA card samples. Sequences generated give us a new insight into generic and species concepts in Pyrenulaceae.

Biodiverse analyses reveal “hotspots” of endemism in the vascular flora of the New Zealand archipelago

Peter Heenan, Tim Millar, Aaron Wilton, Rob Smissen, Matt McGlone & Ilse Breitwieser

Monday 30 November, 11:15–11:30

Landcare Research, PO Box 69040, Lincoln 7640, New Zealand

Herbarium specimen records are increasingly available electronically and considerable DNA sequence data exists as a result of systematics research. Along with the development of new software programmes such as Biodiverse we can now undertake comprehensive analyses of endemism. In a “proof of concept” project, we used Biodiverse to analyse georeferenced data for the indigenous fern, conifer and flowering plant genera and species from the entire New Zealand archipelago of over 700 islands. We also developed an rbcl phylogeny showing relationships of all genera in the New Zealand flora so that phylogenetic metrics could be analysed in conjunction with the spatial data.

The results confirmed previously identified areas of endemism with greater accuracy and detail than previous studies and also revealed important new centres and patterns of endemism. Some of these “hotspots” are poorly protected but this new evidence should enable more targeted use of limited conservation resources and enable conservation initiatives to be focused on the most important areas.

Botanical contributions of the Hermannsburg missionaries: then and now

Peter Jobson

Monday 30 November 11:45–12:00

Northern Territory Herbarium, Alice Springs, PO Box 1120, Alice Springs, NT 0870, Australia

The Lutheran mission at Hermannsburg was established by Kempe and Schultz in June 1877, with Schultze joining them the next year. These three men were the first Europeans to extensively collect in the MacDonnell Ranges, sending their material to Mueller in Melbourne. Often their specimens were the first records of species that reside in the species-diverse West MacDonnell Ranges. Kempe published two papers (1880, 1882) on the floristics of the region. Re-establishing the mission in October 1894, Strehlow would send his specimens to Pritzel in Germany, increasing the knowledge of the region. All four missionaries are honoured with species epithets, or with their specimens representing type material. Using AVH and current knowledge of plant distributions, a selection of species are compared. These species represent those of subsequent reduced distribution, of conservation significance, or at limits of their known range.

Gaps and priorities for the *Flora of Australia*: where to next?

Zoe Knapp, Patrick McCarthy & Joanne Nathan

Wednesday 2 December, 9:45–10:00

Australian Biological Resources Study, Department of the Environment, GPO Box 787, Canberra, ACT 2601, Australia

The Australian Biological Resources Study and the Council of Heads of Australasian Herbaria have partnered with the Atlas of Living Australia to develop an online Australasian eFlora platform to support collaborative and more flexible creation and delivery of online floras. One of the benefits of moving to an online platform is the ability to publish various treatments without waiting for a whole volume to be completed. This means our focus can shift to gradually filling gaps and working to harmonise the *Flora of Australia* with the Australian Plant Census, rather than prioritising treatments in order of volumes.

But what are the gaps and future priorities for the *Flora of Australia*? This presentation will provide an overview of current gaps, and highlight some possible future priorities for updating the *Flora of Australia*. These priorities include continuing to publish high quality manuscripts received for inclusion in planned, but unpublished, volumes. Since the *Flora of Australia* is a national collaborative resource, the ABRS seeks input from the botanical community in deciding on future priorities.

Global hotspots of conifer diversity

Leslie Andrew¹ & Sarah Mathews²

Monday 30 November, 11:00–11:15

¹ Department of Ecology and Evolutionary Biology, Brown University, Providence, Rhode Island, USA

² Australian National Herbarium, Centre for Australian National Biodiversity Research, National Research Collections Australia, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia

We used a comprehensive dataset of conifer geographic data, comprising ~37,000 records from vetted herbarium specimens of all 615 species. The data were combined with data from GBIF and previously published expert range maps and were used to create approximate range maps for every living species. The range maps were then mapped onto a global network of 100 km by 100 km grid cells. Principal components analyses of five variables were used to characterise the physical environment of every grid cell: mean annual temperature, annual precipitation, temperature variability, precipitation variability, and topographic heterogeneity. Conifer diversity in grid cells was characterised by estimating species richness (SR), evolutionary distinctiveness (ED), and the net relatedness index (NRI). ED and NRI were calculated in conjunction with an updated dated phylogeny of 572 species. Areas of high conifer diversity (≥ 17 species per grid cell) were found in

14 regions of the world, with a greater number of these occurring at lower latitudes. Globally, climate and topography play an important role in determining where hotspots occur, and climatic factors influence whether a hotspot combines high ED with low NRI (is museum-like) or low ED with high NRI (is cradle-like).

Evolution of the Australian grass trees, *Xanthorrhoea*, using multiple next-generation sequencing techniques

Todd McLay¹, Stephen Doyle², Heroen Verbruggen³, Josquin Tibbits⁴, Andrew Drinnan¹ & Mike Bayly¹

Tuesday 1 December, 9:45–10:00

¹ School of BioSciences, University of Melbourne, Vic 3010, Australia

² Parasite Genomics Group, Wellcome Trust Sanger Institute, Hinxton, Cambridge, UK

³ Algal Biology Lab, School of BioSciences, University of Melbourne, Vic 3010, Australia

⁴ Department of Primary Industries, AgriBio, Vic 3086, Australia

The potential of next-generation sequencing to produce very large datasets of sequence information is promising for studying evolutionary questions in difficult to resolve groups, but application of the technology is still in its infancy, and sequencing costs can be prohibitive. Here I will present the results from several different library preparation methods for Illumina sequencing in order to identify genetic variation in *Xanthorrhoea*, the Australian grass trees.

Firstly, a targeted amplicon sequencing approach was used to infer phylogeographic patterns in *Xanthorrhoea*, using GenBank data as a resource to identify short chloroplast amplicons. Secondly, double digest RAD sequencing was used to obtain population level genetic information for delimitation of Western Australian taxa. Finally, I developed a PCR-based reduced representation library preparation method to resolve the phylogeny of *Xanthorrhoea*. These different methods display the utility of next-generation sequencing in obtaining large amounts of sequence variation, at an affordable cost per sample, for testing hypotheses in a group with low molecular variation.

Spatial phylogenetics of the Australian flora at different scales

Joe Miller^{1,2}, Andrew Thornhill³, Carlos González-Orozco⁴, Shawn Laffan⁵, Nunzio Kner⁶ & Brent Mishler³

Monday 30 November, 11:30–11:45

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⁵ School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney 2052, Australia

⁶ Australian National Herbarium, Centre for Australian National Biodiversity Research, National Research Collections Australia, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia

Biodiversity is usually measured by examining changes in the number of species across a region to identify areas of high species diversity, endemism and turnover. Our research group is applying a novel suite of spatial phylogenetic tools including two new metrics, Relative Phylogenetic Diversity (RPD) and Relative Phylogenetic Endemism (RPE), and a new method called Categorical Analysis of Neo- And Paleo-Endemism (CANAPE) to measure biodiversity. CANAPE searches for centres of endemism, and classifies them by the branch lengths of the rare taxa within them, allowing, for the first time, a clear, quantitative distinction between centres of neo- and paleo-endemism across an area. Spatial phylogenetic analyses of the eucalypts and the Australian flora at the genus level were undertaken to investigate patterns at multiple scales. As expected the areas of significant endemism change depending on the phylogenetic scale of terminals that are used. Areas of endemism also vary over time and when different components of the flora are analysed. Understanding the patterns of biodiversity on the landscape is important for conservation planning, given the need to prioritise efforts in the face of rapid habitat loss and human-induced climate change.

The evolution of *Acacia* traits through space and time

Joe Miller^{1,2}

Monday 30 November, 14:15–14:30

¹ National Science Foundation, 4201 Wilson Avenue, Arlington VA, USA

² National Research Collections Australia, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia

Acacia is an important Australian plant clade in many respects: economic, taxonomic, ecological and cultural. Recent advances have generated large datasets such as phylogenies, taxonomic traits embedded in the Wattle plant identification key and *Flora of Australia*, climatic and soil data layers in the Atlas of Living Australia as well as detailed spatial occurrence datasets in the Australian Virtual Herbarium. When embedded within the taxonomic framework of the Australian Plant Census it provides an opportunity to integrate data to investigate evolutionary questions and to provide data for conservation planning. During this talk we will investigate the evolutionary patterns of inflorescence, seed mass and phyllode evolution in *Acacia* from a phylogenetic perspective. The results will be visualised using PhyloLINK and will include linkages to spatial and environmental data. Patterns of seed mass correlate with temperature and phylogeny at small scales while patterns of leaf type correlate with precipitation and phylogeny at larger scales but less so at smaller scales. Visual interrogation of integrated data provide a powerful opportunity for generating specific hypotheses for evolutionary studies.

Opportunities and challenges in next-gen molecular systematics

Keynote Presentation

Craig Moritz

Tuesday 1 December, 9:00–9:45

Centre for Biodiversity Analysis, Australian National University, Canberra, ACT 0200, Australia

The recently attained ability to generate sequence data across hundreds to thousands of loci in any taxon of choice is both an opportunity and challenge for molecular systematics. This creates the opportunity to reinvigorate the nexus between population divergence, speciation and macroevolution, including a deeper understanding of divergence/reticulation processes. At the same time, we are now able to generate datasets well beyond the computational limits of many model-based analytical methods, which itself is an exciting challenge to computational biologists. For many problems in species delimitation and phylogenetics, a modest number of informative loci, properly analysed, will suffice. Thus, emphasis on thorough sampling of populations/taxa, on data quality and connectivity, and on selecting appropriate analysis methods remains crucial. While biologically fascinating, the prevalence of reticulation and polyploidy in plants provides challenges in both bioinformatics and inference with nextgen sequencing approaches.

Phylogeny, biogeography and classification of *Dianella* (Xanthorrhoeaceae) — insights into global biogeography and new species for the genus

Karen Muscat

Monday 30 November, 15:30–15:45

The University of Melbourne, Parkville, Vic 3010, Australia

The genus *Dianella* (flax lilies) is a group of petaloid monocots (c. 60 taxa) that mostly occur in Australia (more than half of the species), throughout South-East Asia, in New Zealand and the Pacific (east to Hawaii), and across to the Indian Ocean to Madagascar. Current infrageneric and species-level classification is based on morphology without detailed molecular phylogenetic analyses.

The first detailed global phylogeny of *Dianella* and closely-related genera will be presented, based on chloroplast and nuclear DNA markers. Sampling includes the majority of Australian *Dianella* taxa and extra Australian species from New Zealand, New Caledonia, Papua New Guinea, Norfolk Island, Lord Howe Island, Hawaii, Japan, Taiwan, Brunei, Malaysia, Bangladesh, Madagascar and Mauritius.

Results show a good correlation between morphological patterns and molecular relationships. Biogeographic patterns across the global range and within Australia are identified, particularly an early divergence between eastern and western Australian lineages. The study also identifies new species of Australian and extra-Australian *Dianella*.

Semi-automated generation of morphological matrices: examples using the cycads

Nathalie S. Nagalingum¹, Lorena Endara² & J. Gordon Burleigh²

Monday 30 November, 13:30–13:45

¹ National Herbarium of New South Wales, Royal Botanic Gardens and Domain Trust, Mrs Macquaries Road, Sydney, NSW 2000, Australia

² Department of Biology, University of Florida, Gainesville, FL 32611, USA

With the ease of obtaining molecular datasets improving considerably, we have witnessed a decrease in the use of morphological datasets. However, morphology has much to offer phylogenetic analyses, ranging from the inclusion of fossils to sorting out poorly resolved relationships. To obtain a morphological matrix, we are using a newly developed methodology that scans species descriptions from floras, converts them into characters, and scores the characters. We have obtained two morphological matrices for the cycads using this method. After reviewing the matrices, they were analysed alone or combined with molecular data and yielded well-resolved phylogenies. These results indicate that morphological datasets can be relatively straightforward to generate, and can potentially help to address interesting phylogenetic questions.

Untangling New Zealand's tangle ferns for eFloraNZ

Leon Perrie & Patrick Brownsey

Wednesday 2 December, 11:45–12:00

Museum of New Zealand Te Papa Tongarewa, PO Box 467, Wellington 6011, New Zealand

The Gleicheniaceae is one of several fern families for which we have recently published treatments in the electronic Flora of New Zealand (eFloraNZ). The eFloraNZ is a relatively new initiative to provide revised floristic information online (<http://www.nzflora.info>). Challenges and opportunities with this platform will be discussed from an author's perspective. For the Gleicheniaceae itself, the number of species recognised in New Zealand has increased from five to 11 in the last 20 years, with new and reinstated species, and new records. Taxonomic problems remain, particularly with the pan-tropical *Dicranopteris linearis* and the Australasian *Gleichenia dicarpa*. The latter appears to be a complex of species in New Zealand, but determining their correct names depends on resolving the taxonomy in Australia.

Mismatch in the distribution of floral ecotypes and pollinators: insights into the evolution of sexually deceptive orchids

Ryan Phillips & Rod Peakall

Monday 30 November, 16:15–16:30

Research School of Biology, Australian National University, Canberra, ACT 0200, Australia

Plants are predicted to show floral adaptation to geographic variation in the most effective pollinator, potentially leading to reproductive isolation and genetic divergence. Here, we investigate *Drakaea concolor*, which attracts two sexually deceived pollinator species. Using pollinator choice tests, we detected two morphologically similar ecotypes within *D. concolor*. The common ecotype only attracted *Zaspilothynnus gilesi*, whereas the rare ecotype also attracted an undescribed species of *Pogonothynnus*. The rare ecotype occurred at populations nested within the distribution of the common ecotype, with no evidence of ecotypes occurring sympatrically. Surveying pollinators at 100 sites revealed that ecotype identity was not correlated with wasp availability, with most orchid populations only attracting the rare *Z. gilesi*. Using microsatellites, genetic differentiation among populations was very low regardless of ecotype, suggestive of frequent gene flow. Taken together, these results may indicate that the ability to attract *Pogonothynnus* has evolved recently, but this ecotype is yet to spread. The nested rather than allopatric distribution of ecotypes illustrates that in sexually deceptive orchids, pollinator switching could occur throughout a species' range, resulting from multiple potentially suitable but unexploited pollinators occurring in sympatry. This unusual case of sympatric pollinators highlights *D. concolor* as a promising system for understanding pollinator switching from ecological, chemical and genetic perspectives.

Lobule shape evolution in *Radula* (Jungermanniopsida): one rate fits all?

Matt Renner

Monday 30 November, 14:00–14:15

Royal Botanic Gardens and Domain Trust, Mrs Macquaries Road, Sydney, NSW 2000, Australia

Four approaches to measuring the evolutionary rate of lobule shape, a quantitative, multidimensional character, return four different assessments of that trait's history. Significant rate variation between lineages was identified by Adams' Q-mode analysis, with the fastest subgenus evolving 23 times more quickly than the slowest. Species of subg. *Volutoradula* and subg. *Metaradula* are apparently over-dispersed throughout lobule morphospace according to Sidlauskas' method; morphometric branch lengths and hypervolumes in other subgenera can be explained by a stochastic process. In contrast, Bayesian analysis of macroevolutionary mixtures (BAMM) identified a single evolutionary rate as having the highest posterior probability. Sometimes it's better to ignore all of your results and just tell a great story about your plants, so I'll spend most of the 12 minutes doing this. Convergent lobule shapes result from convergent lobule ontogenies and are correlated with bipinnately branched shoot systems and robust primary stems. Maybe structural requirements for light interception have driven some lobule shape evolution via porous growth regulatory mechanisms. Lobules themselves, however, may be a key innovation facilitating radiation into microsities devoid of or depauperate in fungal endophytes.

Phylogenetics of Rottboelliinae (Andropogoneae: Panicoideae: Poaceae) using sequence data, with emphasis on the Australian taxa

Tanya Scharaschkin & Melodina Fabillo

Tuesday 1 December, 13:45–14:00

School of Earth, Environmental and Biological Sciences, Queensland University of Technology (QUT),
Brisbane, Qld 4000, Australia

Rottboelliinae is one of six subtribes in the grass tribe Andropogoneae. The number of genera recognised varies with taxonomic treatments, ranging from 12 to 19. Taxonomic instability in the subtribe is mainly due to variability in gross morphological characters used to delimit genera and the lack of a comprehensive taxonomic sampling in previous phylogenetic studies. In Australia, Rottboelliinae is represented by 20 species in six genera that occur mainly in mesic eucalypt woodlands and savannahs. Seven of these species are endemic to Australia and some of them are rare and threatened species. The number of species may, however, be an under-representation of the diversity. *Hemarthria uncinata* var. *uncinata* and *H. uncinata* var. *spathacea* show great, but continuous, morphological diversity, raising the question as to whether *H. uncinata* includes cryptic species or is a single variable species. Preliminary results, based on phylogenetic analyses of chloroplast sequence data (*matK*, *ndhF*, *rbcl* and *trnL-F*) will be presented. Some genera and a few species appear to be non-monophyletic.

Species checklists and a supermatrix approach in the study of biogeography at a global scale

Christiana McDonald-Spicer¹, Nunzio Knerr² & **Alexander Schmidt-Lebuhn**²

Tuesday 1 December, 15:00–15:15

¹ Australian National University, Canberra, ACT 0200, Australia

² Australian National Herbarium, Centre for Australian National Biodiversity Research,
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With an estimated 20–30,000 species, the Asteraceae (daisy family) account for one in ten flowering plants. They occur on all continents except Antarctica and in a wide range of habitats. Semi-arid to arid environments and mountain ranges are generally considered to be their centres of diversity, but no quantitative spatial study has been conducted to date. Exploring patterns of diversity in such a large, globally distributed group ideally requires high quality occurrence data. Unfortunately, specimen databases show significant geographical biases and are insufficiently complete for large parts of the world. We therefore used a unique resource for Asteraceae, the expertly curated Global Compositae Checklist database, as the basis of spatial and biogeographic analysis. We will discuss the advantages and the challenges of using checklists and political areas instead of occurrence point data in large scale spatial studies. We also constructed a supermatrix approach to infer the presently most complete genus level phylogeny of the family and used it to explore patterns of phylogenetic diversity and to infer ancestral areas.

The *Dendrobium* alliance revisited: examining macroevolutionary patterns in Dendrobiinae (Orchidaceae)

Katharina Schulte¹, Claire Micheneau¹, Ashley Field², Peter Weston³, Darren Crayn¹ & Mark Clements⁴

Tuesday 1 December, 14:00–14:15

¹ Australian Tropical Herbarium & Centre for Tropical Biodiversity and Climate Change, James Cook University, Cairns, Qld 4878, Australia

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The Dendrobiinae are a morphologically highly diverse subtribe within the largest and taxonomically most challenging orchid subfamily, the Epidendroideae. In the traditional circumscription of Dendrobiinae the majority of species belong to the genus *Dendrobium s.l.* (1200+ species), one of the three orchid mega genera, with a distribution across the Indo-Malayan, Australasian and Pacific regions.

We reconstructed phylogenetic relationships of Dendrobiinae based on plastid and nuclear markers (*matK*, *ycf1*, ITS, *Xdh*). In total, 650 samples representing 430 species of the subtribe and all genera and sections recognised in previous taxonomic treatments were included in the analyses. Ancestral character state reconstructions were conducted which provide insights into the evolution of key morphological characters within Dendrobiinae. Molecular clock analyses were carried out under the lognormal relaxed molecular clock model using secondary and fossil calibrations and model-based ancestral area analyses were conducted based on the dispersal extinction cladogenesis model. Our study provides novel insights into macroevolutionary patterns in Dendrobiinae, and provides a phylogenetic framework for a taxonomic revision of the group.

Exploring floral diversity in the core Goodeniaceae

Andy Gardner¹, Kelly A. Shepherd², Eden Johnson¹, John Menz¹, Pryce Michener¹, Jonathan N. Fitz Gerald¹, Veronica Thompson³, Aedric Lim³, Dianella Howarth³ & Rachel Jabaily¹

Monday 30 November, 13:15–13:30

¹ Department of Biology, Rhodes College, Memphis, TN, USA

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³ St John's University, Queens, New York, USA

The core Goodeniaceae, comprising *Brunonia* and sister clades *Scaevola s.l.* (*Scaevola s.s.* with *Diaspasis*) and *Goodenia s.l.* (*Goodenia s.s.*, *Cooperookia*, *Velleia*, *Verreauxia*, *Pentaptilon* and *Selliera*), display diverse patterns of floral symmetry (bilabiate, fan-shaped and pseudo-radial flowers). We hypothesise this evolutionary lability may have been one of the key drivers of diversification in the family; however, before a clade-wide comparative phylogenetic study of floral form can be done discrete, objective, symmetry bins need to be determined. This was achieved using geometric morphometrics. Front-on flower images from 45 species were digitally landmarked and then a Procrustes transformation and principal components analysis undertaken to extract quantitative information. Almost all members of *Scaevola s.l.* have fan-flowers, evocative of the ligulate floret of some Asteraceae. While *Goodenia s.l.* exhibits greater variation in floral shape, all three of its major clades exhibit independent shifts to fan-flower symmetry, indicating potential convergent selection for the fan form. Each of these shifts in morphospace also sets up potential hypotheses about gene regulation of symmetry. The majority of interspecific floral variation was encompassed by landmarks on dorsal and lateral petals and preliminary results examining CYC gene expression in flower-bud petals provides early evidence that these genes do play a role in floral transitions.

Endemism in mountain top plant communities of Australia's Wet Tropics: Past, present and future

Lalita Simpson¹, Mark Clements², Darren Crayn¹, Craig Costion³, Pertina Pert⁴, Monica Carlsen³, John Kress³ & Katharina Schulte¹

Tuesday 1 December, 16:00–16:15

¹ Australian Tropical Herbarium, James Cook University, Cairns, Qld 4878, Australia

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In Australia's Wet Tropics bioregion the highest diversity of endemic species occurs within the mountain top habitats. In this talk we present two lines of research that consider the origins and future of endemic species in these mountain top communities: in the first we assessed the impact of climate change on endemic plant diversity by modelling the distribution of suitable climate niches under future climate scenarios. Herbarium records of 19 mountain top endemic species and fine scale Wet Tropics climate data were analysed using MAXENT. The results predict drastic declines in the distribution of suitable climate under three climate scenarios by 2080. In the second line of research we examined the phylogeny, evolution and historical biogeography of endemic mountain top orchids of the Australian Wet Tropics (*Bulbophyllum* sect. *Adelopetalum*) as a case study to explore the origin of endemic species in these communities. Using a dataset of three molecular markers we inferred divergence times using BEAST and reconstructed ancestral areas using LaGrange. The results provide insights into the spatio-temporal evolution of this mountain top endemic plant group of the Australian Wet Tropics.

Widespread morphological parallelism in *Korthalsella* mistletoes (Viscaceae)

Jennifer Tate¹, Amir Sultan², Sofie Pearson¹, Vaughan Symonds¹ & Alastair Robertson³

Wednesday 2 December, 14:45–15:00

¹ Institute of Fundamental Sciences, Massey University, Palmerston North 4410, New Zealand

² National Herbarium (Stewart Collection), Plant Genetic Resources Institute, National Agricultural Research Centre, Park Road, Islamabad, Pakistan

³ Institute of Agriculture and Environment, Massey University, Palmerston North, New Zealand

Korthalsella (Viscaceae) is a genus of about 30 scale-leaved mistletoe species with cylindrical or flattened stems and diminutive unisexual flowers. The species are distributed widely across the Indo-Pacific region with mainland Australia, the Hawaiian Islands, Malesia and Madagascar having the highest levels of species richness. As with many other parasitic groups, identifying useful taxonomic characters has been challenging given the highly reduced and specialised nature of the plants and this has led to conflicting taxonomic circumscriptions. Here we present the results of a phylogenetic study of the genus that expands on a previous study that did not sample key biogeographic areas of the genus. The phylogenetic results suggest widespread morphological parallelism among species that are geographically disparate. In general, geographic proximity is a better indicator of phylogenetic relatedness. We also present the results of a population genetic study that aims to address the nature of host specificity in the New Zealand endemic, *K. salicornioides*.

Morphological and molecular data show *Synostemon trachyspermus* (Phyllanthaceae: Phyllanthaeae) to be a heteromorphic species assemblage

Ian R. H. Telford¹, Kanchana Pruesapan², Peter C. van Welzen^{3,4} & Jeremy J. Bruhl¹

Monday 30 November, 15:15–15:30

¹ School of Environmental and Rural Science, University of New England, Armidale, NSW 2351, Australia

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⁴ Institute of Biology Leiden, Leiden University, PO Box 9505, 2300 RA Leiden, The Netherlands

Morphological studies of species previously, intuitively placed in *Synostemon* (Phyllanthaceae: Phyllanthaeae), corroborated by phylogenetic analysis using DNA sequence data, show *Synostemon trachyspermus*, as currently applied, to be a heterogeneous species assemblage of five species: *Synostemon trachyspermus* s. str., *Phyllanthus rhytidospermus*, *Sauropus hubbardii*, *S. lissocarpus* (including *Phyllanthus arnhemicus*) and *Sauropus* sp. A Kimberley Flora (T.E.H. Aplin *et al.* 1929) (= *Synostemon judithae* ined.). The “Trachyspermus clade” retrieved by phylogenetic reconstruction includes *Sauropus salignus* and *Synostemon umbrosus* ined. from the Kimberley as predicted by morphology, but surprisingly also the “leafless” *Synostemon hamersleyensis* and *Sauropus aphyllus*.

This changes everything — an eFlora platform for Australasia

Kevin Thiele

Wednesday 2 December, 10:00–10:15

Western Australian Herbarium, Department of Parks and Wildlife, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia

The *Flora of Australia* is one of the most important projects facing the Australian botanical community — finishing the Flora is a core task for us. Similarly, State-based floras are crucially important at regional levels. The development and near-completion of an online, flexible electronic editing and deployment platform for eFloras substantially changes the way in which we can both construct and manage floras, and make our knowledge widely available and accessed. It may also (at least potentially) substantially change the way we do our work, and think about our information, its management, and the ways in which we can help our users. This talk will explore some of the implications of the eFlora platform for taxonomy, systematics, and the world.

Can we use phylo-genomics to date plant community assembly?

Marlien van der Merwe¹, Hannah McPherson¹, Juelian Siow¹, Simon Ho², Charles Foster² & Maurizio Rossetto¹

Tuesday 1 December, 11:45–12:00

¹ National Herbarium of New South Wales, Royal Botanic Gardens and Domain Trust, Mrs Macquaries Road, Sydney, NSW, 2000, Australia

² School of Biological Sciences, University of Sydney, Sydney, NSW 2006, Australia

The history of the Australian rainforest can be traced back to the Late Cretaceous, and fossil records suggest that some of the extant lineages have been around since the Paleocene. Molecular phylogenies have been used to infer origins (Sunda vs Sahul) and dates of particular components of the Australian rainforests, however environmental changes over the last 15mya have had a great impact on rainforest species distribution and assembly. Here we discuss our results from a study using multiple samples from multiple species to investigate Rainforest evolution. We assembled and annotated full chloroplast genomes from over 70 Australian rainforest species using whole genome shotgun sequencing data. These species are representative of most major Angiosperm clades. After extracting and aligning seventy six chloroplast genes, molecular phylogenetic methods and several fossil calibrations were used to obtain substitution rates across the phylogenetic tree. These species specific substitution rates could then be applied to within-species data to infer times of diversification of extant taxa. We use this data to investigate relative ages of rainforest communities within New South Wales, and assess continental divergences.

Progress towards a Decadal Plan for Australasian Biodiversity Science — an update

Kevin Thiele¹, William R. Barker², Darren M. Crayn³, **Michelle Waycott**^{2,4}, Ailsa Holland⁵, Ilse Breitwieser⁶, Peter Lockhart⁷, Mike Bayly⁸, Peter H. Weston⁹ & Katharina Schulte³

Tuesday 1 December, 16:45–17:00

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⁵ Queensland Herbarium, Department of Science, Information Technology and Innovation, Toowong, Qld 4066, Australia

⁶ Allan Herbarium, Landcare Research, PO Box 69040, Lincoln 7640, New Zealand

⁷ Institute of Fundamental Sciences, Massey University, Palmerston North 4410, New Zealand

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⁹ National Herbarium of New South Wales, Royal Botanic Gardens and Domain Trust, Mrs Macquaries Road, Sydney, NSW 2000, Australia

The “Decadal Plan for Australasian Biodiversity Science” (Decadal Plan) is an attempt by the Australasian systematics community to provide a well-argued, rigorous and persuasive case for continued and increased support for plant taxonomy and systematics in Australia and New Zealand, as well as a clearly outlined roadmap for Australasian biodiversity science over the next decade. The Decadal Plan is aimed at Australian and New Zealand governments at different jurisdictional levels, and is developed in consultation with the Australasian systematics community and our diverse stakeholders in science, government, non-governmental organizations, and the wider community.

In this talk we will report on the progress made over the past year in conceptualising the Decadal Plan, and will present some ideas and options on how to shape the future of systematics and taxonomy in Australasia over the next ten years and beyond.

Reinvigorating an already well-used electronic flora: 5th edition *Flora of South Australia*

Michelle Waycott & Juergen Kellermann

Wednesday 2 December, 10:45–11:00

State Herbarium of South Australia, Hackney Road, Adelaide, SA 5001, Australia

The *Flora of South Australia* is undergoing its fifth complete revision. Previous editions date back to 1922–29 (Black), 1943–52 (Black & Robertson) and 1965 (supplement; Eichler), 1978 (Monocots, Jessop) and 1986 (Jessop & Toelken, eds).

Since 1998 an online version has been available (<http://www.flora.sa.gov.au>), known as the Electronic Flora of South Australia or eFloraSA. This provides a number of services; up-to-date information from the Census of South Australian Plants, Algae and Fungi database, dichotomous keys to the vascular flora, species fact sheets, mapping capabilities based on herbarium specimens and some identification tools. The dichotomous keys and fact-sheets use the text and illustrations from the 4th edition of the Flora (Jessop & Toelken 1986) but they are delivered with updated (current) regional distribution data from the Census and current distribution maps generated directly from the State Herbarium specimen database.

The 5th Edition is principally intended as an electronic resource. Currently each family or large genus, such as *Eucalyptus*, is published in pdf form as they are completed. A content management system is used in preparation of these and we intend to utilise the new eFlora platform to reinvigorate the process and develop wider audiences.

Papery problems: resolving generic boundaries of *Leucochrysum* and *Waitzia* (Asteraceae: Gnaphalieae)

Xénia A. Weber¹ & Alexander N. Schmidt-Lebuhn²

Tuesday 1 December, 15:30–15:45

¹ Fenner School of Environment and Society, Australian National University, Canberra, ACT 0200, Australia

² Australian National Herbarium, Centre for Australian National Biodiversity Research, National Research Collections Australia, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia

Many of the Australian-New Zealand Gnaphalieae (Asteraceae) are characterised by a distinctive set(s) of papery involucre bracts, however within this ecologically diverse clade many phylogenetic relationships remain unresolved. A previous study suggested that the genus *Leucochrysum*, as currently circumscribed, may not represent a monophyletic group. This was confirmed by our examination into the morphological and molecular phylogeny of fourteen species and six infraspecific taxa within the genus and closely related *Anemocarpa* and *Waitzia*. Chloroplast (*psbA-trnH*) and nuclear ribosomal (ITS, ETS) genetic markers, along with morphological data scored from the examination of herbarium specimens, produced congruent trees confirming *Waitzia* as a monophyletic group, but both *Anemocarpa* and *Leucochrysum* as polyphyletic. Our results support earlier findings from hybridization trials, morphological examination and preliminary genetic analyses. To resolve the current lack of monophyly we propose generic recircumscription and the new combination of one species. These small and delicate endemic paper daisies have yielded interesting insights into their true phylogenetic relationships and demonstrate the benefits of combining morphological and genetic characters in phylogenetic analyses.

Triggering new insights into a remarkable genus: the *Stylidium* phylogeny and pollination project

Juliet Wege¹, W. Scott Armbruster², Sian Evans³, Steve Wagstaff⁴ & Felix Forest³

Tuesday 1 December, 13:00–13:15

¹ Western Australian Herbarium, Department of Parks and Wildlife, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia

² School of Biological Sciences, University of Portsmouth, UK

³ Royal Botanic Gardens, Kew, UK

⁴ Landcare Research, PO Box 69040, Lincoln 7640, New Zealand

The triggerplant genus *Stylidium* (Stylidiaceae) contains over 300 taxa, the vast majority of which are endemic to Australia. The genus is remarkable not only for its touch-sensitive floral column, which transfers pollen to and from insect visitors in one of the most rapid plant movements known, but also for its diverse array of floral morphologies. Our current research program, which includes classical taxonomy and micromorphology, molecular phylogenetics and pollination ecology, is providing novel insights into evolutionary relationships within the genus, the evolution of key traits, the broad spectrum of insect pollinators, and the intricacies of its extraordinary pollination mechanism. An overview of this research is presented, including a preliminary phylogeny of 135 taxa based on cpDNA sequence data (*matK*, *trnL-trnF*, *trnQ-rps16* and *rpl32-trnL*).

A database of variation in floral characters in the Proteaceae, and implications for key questions in floral evolution

Peter Weston¹, Elisabeth Reyes² & Hervé Sauquet²

Monday 30 November, 13:45–14:00

¹ National Herbarium of New South Wales, Royal Botanic Gardens and Domain Trust, Mrs Macquaries Road, Sydney, NSW 2000, Australia

² Laboratoire Écologie, Systématique, Évolution, CNRS UMR 8079, Université Paris-Sud, Orsay, France

A set of 58 characters, describing variation in inflorescences and flowers of the Proteaceae, was assembled. States for these characters were scored for 237 species, representing all 81 currently recognised genera of Proteaceae plus selected outgroup species. Data were entered and managed using PROTEUS, an international collaborative database of plant morphological traits. PROTEUS was used in preference to matrix-management programs such as Mesquite because of several advantages, including that each cell in a matrix is the union of one or more observation records, each of which must be linked to an explicit reference (e.g. cited literature or specimens). The data were used, in conjunction with a chronogram for the species, to test several hypotheses of floral evolution in the family, using parsimony and maximum likelihood methods. How many times did zygomorphy evolve? Did the evolution of zygomorphy pre- or post-date the evolution of diagonal carpel orientation in the tribe Embothrieae? Did grevilleoid flower pairs evolve by reduction from a paniculate inflorescence or by floral doubling in a raceme? Our analyses support 16 origins of zygomorphy and multiple reversals, an early origin of zygomorphy in the Embothrieae and floral doubling in the Grevilleoideae.

Phylogeny of the tribe Leptospermeae (Myrtaceae)

Peter G. Wilson & Margaret M. Heslewood

Wednesday 2 December, 15:15–15:30

National Herbarium of New South Wales, Royal Botanic Gardens and Domain Trust, Mrs Macquaries Road, Sydney, NSW 2000, Australia

An earlier phylogenetic analysis of tribe Leptospermeae showed that the persistent-fruited species of the genus *Leptospermum*, which include the type, form a well-supported monophyletic group sister to *Homalospermum*. We sampled the predominantly non persistent-fruited taxa extensively, using both chloroplast and nuclear markers, to investigate their phylogenetic position, particularly in relation to *Neofabricia* and *Kunzea*. We also reassessed Thompson's proposed subgroups of *Leptospermum*. Taxonomic implications are considered.

The tribe is strongly supported as monophyletic and the non persistent-fruited taxa fall into four subclades in a larger clade that includes *Neofabricia* and *Kunzea*. Analyses to constrain taxa with hemitropous ovules (*Asteromyrtus* and *Agonis sens. lat.*) result in almost equally parsimonious trees that resolve all the non persistent-fruited taxa plus *Neofabricia* in a single clade. We favour the simpler generic circumscription of *Leptospermum* which resurrects the name *Leptospermopsis* for all the non persistent-fruited members, including *Neofabricia*.

The measurement and source apportionment of Australian atmospheric lead depositions in archived lichen and fungi (1885–2010)

Liqin Wu¹, Mark Patrick Taylor¹, Heather K. Handley² & Michael Wu³

Monday 30 November, 10:00–10:15

¹ Department of Environmental Sciences, Macquarie University, Sydney, NSW 2109, Australia

² Department of Earth and Planetary Sciences, Macquarie University, Sydney, NSW 2109, Australia

³ Inorganic Section, National Measurement Institute, North Ryde, NSW 2113, Australia

Archived lichens (*Cladonia* and *Usnea*) and fungi (*Trametes*) sampled from various herbaria were used as reliable biomonitors of atmospheric lead pollution throughout the Greater Sydney area (New South Wales, Australia). Lead concentrations and their isotopic compositions were determined for the lichens and fungi that had been collected and archived over the past 120 years. Median lead concentrations rise during the late 20th century in line with the increased industrial emissions of lead and then decrease 74% in *Cladonia* and drop more than 90% in *Usnea* in the 2000s due to the removal of lead in petrol. Lead isotope data of lichens and fungi indicated that the most likely sources of atmospheric lead pollution were natural background lead, leaded gasoline combustion and industrial lead emissions, inter alia other secondary sources.

Ongoing development of the “Australian Tropical Rainforest Plants” Interactive Identification Tool

Frank A. Zich^{1,2}, Raelee A. Kerrigan^{1,2}, Ashley R. Field^{1,3}, Christopher J. Quinn¹ & Darren M. Crayn¹

Wednesday 2 December, 11:00–11:15

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² National Research Collections Australia, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia

³ Queensland Herbarium, Department of Science, Information Technology and Innovation, Brisbane Botanic Gardens, Mt Coot-tha road, Toowong, Qld 4066, Australia

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. The latest edition was released on the internet in December 2010, and includes 2554 species of plants excluding ferns and cryptogams. Since then additional modules have been developed — an orchid module published in 2010, and a fern module currently in beta testing.

A new project has recently been initiated to extend the RFK to include the eastern Central Queensland region which will “close the gap” between the current extent of the RFK which ends at Townsville and the south-eastern “Rainforest Plants of Australia” system which extends from Rockhampton to Victoria.

Posters

Phylogeny of *Hibiscus* species (Malvaceae) from Egypt Based on Chloroplast and Nuclear Sequences

Mohamed O. Badry Barbary & Jennifer A. Tate

Tuesday 1 Decembaer (poster session 14:15–15:15)

Institute of Fundamental Sciences, Massey University, Private Bag 11222, Palmerston North, 4442, New Zealand

This study presents preliminary results on the phylogenetic relationships among *Hibiscus* species in the Egyptian flora, following the recent discovery of *Hibiscus diversifolius* subsp. *diversifolius* in Egypt. To investigate the placement of the Egyptian taxa within *Hibiscus*, new DNA sequences were generated for six *Hibiscus* species (three from Egypt and three from New Zealand), combined with 81 Hibisceae taxa from GeneBank. Six data sets were generated: five plastid regions (*ndhF*, *rpl16* intron, 3'*matK-trnK* intron; *psbA-trnH* and *trnLUAA-trnFUAG* spacers) and the internal transcribed spacer regions (ITS1, 5.8S, and ITS2) of the nuclear ribosomal repeat. Analysis of the different data sets indicated that the available Egyptian taxa fall into two primary clades, one consisting of representatives from sect. *Furcaria* and the other of sect. *Trionum*.

Rare and Peculiar Hornworts: *Notothylas javanica* and *Notothylas orbicularis*, new records for Australia

D. Christine Cargill

Tuesday 1 December (poster session 14:15–15:15)

Australian National Herbarium, Centre for Australian National Biodiversity Research,
National Research Collections Australia, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia

The hornwort genus *Notothylas* and species *Notothylas javanica* and *N. orbicularis* are newly recorded for Australia. Both present a peculiar and new phenomenon whereby the sporogone grows from the ventral surface of the gametophore rather than from the dorsal surface. This is known only to occur in Australian populations and is reported and illustrated here for the first time.

Scanning electron microscope studies on the spores of Microsoreae from Taiwan

Chi-chuan Chen

Tuesday 1 December (poster session 14:15–15:15)

Department of Biosciences, University of Helsinki, Rasinkatu 20 A 001, 01360, Vantaa, Finland

Spore morphology of five genera and 13 species of Taiwanese ferns in the tribe Microsoreae (Polypodiaceae) were studied with light and scanning electron microscopy. Microsoreae spores were ellipsoidal and monolete; with spore ornamentation verrucate, echinate, globule, rugate and undulate. Based on spore characters, Microsoreae were not internally consistent.

What's in the Blue Box? Phytochemistry and species limits in *Eucalyptus magnificata*

Timothy L. Collins, Rose L. Andrew & Jeremy J. Bruhl

Tuesday 1 December (poster session 14:15–15:15)

School of Environmental and Rural Science, University of New England, Armidale, NSW 2351, Australia

Northern Blue Box, *Eucalyptus magnificata* (Myrtaceae) is listed as an endangered species in New South Wales, threatened by land clearing, grazing impacts, disturbance from roadworks, and dieback. Northern Blue Box has been recorded for three widely separated locations: Hillgrove and Tenterfield in New South Wales, and Dalveen in Queensland. Extensive field sampling of putative *E. magnificata* populations indicates that the Tenterfield collections have been misidentified, and are actually *Eucalyptus conica*. There is additional uncertainty about the species limits of the Hillgrove population of *E. magnificata*, which is found on or close to the gorge rim, and the Dalveen population that occurs on level tablelands far from any gorge country. Molecular sequence, phytochemical and morphological data are being collected and analysed to determine whether these widely disjunct populations are actually a single species, or the Hillgrove populations represent a gorge rim narrow endemic. Here we present initial phytochemical analysis of leaf oils by GC-MS using a modified method of solvent extraction. This method drastically reduces sample and solvent volumes, with potential to be applied across plant groups using dried herbarium specimens.

Genome sequencing of *Fraxinus* species to identify loci relevant to ash dieback and emerald ash borer

Endymion Cooper, Elizabeth Sollars, Laura Kelly, David Swarbreck, Bernardo Clavijo, Jasmin Zohren, David Boshier, Jo Clark, Steve Lee, Jennifer Koch, John Carlson, Erik Kjaer, Lene Nielsen, Will Crowther, Stephen Rossiter, Anika Joecker, Sarah Ayling, Mario Caccamo & Richard Buggs

Tuesday 1 December (poster session 14:15–15:15)

School of Biological and Chemical Sciences, Queen Mary University of London, London E1 4NS, UK

Fraxinus (ash) species are highly threatened by emerald ash borer (EAB) in North America and ash dieback (ADB) in Europe. Their future may depend on genomically assisted breeding for low susceptibility to these threats. We have produced a *de novo* reference genome from a low-heterozygosity British *F. excelsior* (European ash) tree (N50 = 99Kbp, Total length = 875Mbp; see <http://www.ashgenome.org>), and sequenced 38 further trees from this species across Europe, including a Danish tree with low susceptibility to ADB, which we are comparing. We are now sequencing the genomes of 35 other *Fraxinus* species from around the world. Genome size in *Fraxinus* varies from 750Mbp to 4Gbp (1C-values), encompassing diploid, tetraploid and hexaploid taxa. Preliminary evidence suggests that Asiatic *Fraxinus* species have low susceptibility to EAB and ADB: we are testing this with genus-wide experimental EAB inoculation experiments in Ohio, and genus-wide field exposure to ADB in Britain. We aim to identify loci relevant to low susceptibility to ADB and EAB by identifying loci in the genus *Fraxinus* that have phylogenies incongruent with the typical genus phylogeny, but congruent with patterns of low susceptibility among species. We hope that this method will be applicable to other tree pest/pathogen interactions.

Evolutionary relationships of *Heimioporus* and *Boletellus* (Boletales), with an emphasis on Australian taxa

Nigel Fehner¹, Roy E. Halling², Mitchell Nuhn³, Todd Osmundson⁴, Kasem Soyong⁵, David Arora⁶, Manfred Binder⁷ & David Hibbett³

Tuesday 1 December (poster session 14:15–15:15)

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Boletellus and *Heimioporus*, two genera of Boletaceae with ornamented basidiospores, are shown to be distinct genera on the basis of phylogenetic analyses of nuclear ribosomal large-subunit and translation elongation-factor 1 α DNA sequences. Comparison of spore ornamentation type is further evidence for distinction *viz.* longitudinally ribbed in *Boletellus* vs punctate, alveolate-reticulate in *Heimioporus*. Analyses of multiple accessions from the Americas, Asia and Australia support the monophyly of *Heimioporus* and a “core *Boletellus*” clade, containing the type species, *B. ananas*, and approximately seven additional species. Tests of alternative phylogenetic topologies could not reject monophyly of a more inclusive group containing the core *Boletellus* clade and six other species.

Estimating the evolutionary timescale of flowering plants using complete chloroplast genome sequences

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Tuesday 1 December (poster session 14:15–15:15)

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The origins and evolution of flowering plants (Angiospermae) have been major topics of research interest in phylogenetics. In particular, the evolutionary timescale of angiosperms has proven to be a source of considerable attention, although most studies have been based only on a small number of loci and/or taxa. However, the application of high-throughput sequencing techniques has produced substantial amounts of genetic data, with many chloroplast genome sequences now being available.

We estimated the evolutionary timescale of angiosperms by analysing sequences of whole chloroplast genomes. Our data set comprises published sequences from GenBank as well as novel data produced by collaborators at the Royal Botanic Garden, Sydney. In total, our data set comprises full chloroplast genomes from 195 taxa. We analysed this data set using a Bayesian phylogenetic relaxed-clock approach in MCMCTREE, which incorporates a fast algorithm designed for molecular dating of genome-scale data sets. Our analysis included a large number of fossil-based age constraints. We also investigated the robustness of our estimates by varying a number of parameters, including the number of independent molecular clocks, and the gamma priors for overall rates and rate variation across branches. Additionally, we investigated the effects of taxon sampling and gene sampling on date estimates for the angiosperm evolutionary timescale. Our analysis provides the most comprehensive and reliable estimate of the timescale of angiosperm evolution to date.

Pollinator-mediated cryptic speciation in the warty hammer orchid complex and implications for the conservation of cryptic species

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Tuesday 1 December (poster session 14:15–15:15)

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Sexually-deceptive orchids provide a unique opportunity to investigate the mechanism of pollinator-mediated speciation due to their high degree of pollinator specificity and prevalence of pollinator switching. We investigate the process and extent of speciation in the sexually-deceptive *Drakaea livida* complex (Orchidaceae), which was found to attract different pollinator species across its range. Analysis of biologically active orchid volatiles revealed the presence of three discrete chemical profiles. These chemical profiles correlated with the pollination results, in that orchids of each chemical profile exclusively attracted a different pollinator species, indicating the existence of three allopatric reproductively isolated orchid ecotypes. For one ecotype, picked flowers presented outside their natural distribution attract the pollinator of another ecotype. Intriguingly, this pollinator is also present within the distribution of the first ecotype, where it does not visit flowers. In all other translocations, foreign ecotypes were ignored by local pollinators. The three ecotypes cannot be distinguished using multivariate morphometric analysis, indicating that chemical shifts alone may drive speciation. Conservation of the three entities could be severely hampered by this inability to identify them using morphological traits. The introduction of floral chemical analysis as a tool to identify cryptic species of sexually-deceptive orchids is proposed.

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