

# Systematic Botany—a view from the Centre

Proceedings of the Australasian Systematic Botany  
Society Conference  
26–29 September, 2016—Alice Springs, Australia



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Journal of the Adelaide Botanic Gardens Supplement 4



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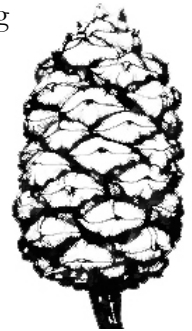
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## Forward

The bringing together of people at a conference is always an exciting, yet sometimes nerve wracking process. This is because you never know exactly what will emerge from the randomness of events that lead to the meeting. Fortunately the lead up to the 2016 Annual Conference of the Australasian Systematic Botany Society had by and large positive things occur, particularly the remarkable weather providing amazing botanical jewels to see throughout the region where we are meeting. We have attracted a diverse and exciting group of conference participants from across Australia, New Zealand and the world!

The program we have put together is interesting and includes the latest in systematics and taxonomy, sharing of regional knowledge from central and northern Australia and exploration of trans-Tasman research and collections. Many presentations have a global perspective and span the range of sub-disciplines including flora development, taxonomic key generation, molecular systematics, breeding system analysis of particular groups and taxonomic reviews. I am proud of the final result and applaud all our contributors and hope everyone enjoys the program.

A conference such as this cannot happen without a group of hard working individuals. The organising committee spanned the length (or should I say the 'height') of Australia from our local on-the-ground co-convenor in Alice Springs, Peter Jobson, to our Darwin herbarium colleagues, Ian Cowie and Donna Lewis, and the team in Adelaide, Ainsley Calladine, Bill Barker and myself, supported by Jessica Burdon and Jürgen Kellermann. An amazing level of support was provided by three people in particular: John Clarkson, whose able and effective handling of payments made that aspect of running this meeting not only seamless but most likely made the conference possible. Ainsley Calladine put in an amazing effort providing our website, wrangling registrations, abstracts and putting the proceedings together. Ainsley and John worked incredibly well together and they were the backbone of the business side of this meeting. Finally, and by no means least, Peter Jobson put together great venues and social events we will share together, in doing so he became a supreme 'deal-maker' and I am sure we will all enjoy our visit to his part of the world. Thanks MATE!



Next year, when the conference is in Adelaide, being run jointly with SASB, we hope to have as great a group there as we have here in the centre of Australia at this the 2016 ASBS Annual Conference.

*Michelle Waycott* Co-convenor

September, 2016

## Acknowledgements

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Tim & Sam of Milner Meat & Seafood

Rod Randall, Department of Corrective Services, for the use of the Alice Springs Correctional Centre BBQ

Ray Prunty, Manager General of Angkerle Aboriginal Corporation (Standley Chasm)

## Program—Monday

9:00	Welcome and Plenary	
09:00–10:45	Welcome	
	Plenary Talk—A modern view on polyploidy: studies of <i>Nicotiana</i> section <i>Suaveolentes</i> by <b>Mark Chase</b>	0–1
10:40–11:00	Morning Break	
11:00	Session 1: Problems and Systematics	
11:00–11:20	<b>John Clarkson</b> , It's not the snake in the grass you should be wary of!	1–2
11:20–11:40	<b>Matt AM Renner</b> , Nearly everything we thought we knew about Australian Plagiogchilaceae is wrong	1–3
11:40–12:00	<b>Gillian Brown</b> , <i>Archidendron</i> , are the east and west really that different?	1–4
12:00–12:20	<b>Robyn Barker</b> , The enigmatic and industrious Mr Schultz[e]	1–5
12:20–13:20	Lunch	
13:20	Session 2: Our Taxonomic Resources	
13:20–13:40	<b>James Clugston</b> , Conservation genomics of <i>Cycas calcicola</i> (Cycadaceae) in Australia	2–6
13:40–14:00	<b>Ilse Breitwieser</b> , State and future needs of New Zealand's nationally important taxonomic collections	2–7
14:00–14:20	<b>Ian Cowie</b> , Keys to the flora of the MacDonnell Ranges Bioregion of Central Australia: web enabling the MacFlora interactive keys	2–8
14:20–14:40	<b>Joel Collins</b> , Mobile field data collection: redefining possibilities	2–9
14:40–15:00	<b>Ryonen Butcher</b> , ALA: what's waiting in the wings?	2–10
15:00–15:30	Afternoon Break	
15:30	Session 3: Our Taxonomic Resources (continued)	
15:30–15:50	<b>Anthony Whalen</b> , The Australian Biological Resources Study—so where do we go to from here?	3–11
15:50–16:10	<b>Kevin Thiele</b> , The eFlora platform—ready and waiting for a Flora near you	3–12
16:30	ASBS AGM followed by ASBS business meeting	

## Program—Tuesday

09:00–10:30	Nancy T. Burbidge Medal Presentation and Address	
	Nancy T. Burbidge Medal Address	13
10:30–11:00	Morning Break and poster session	
11:00	Session 4: Evaluating Biodiversity	
11:00–11:20	<b>Daniel J Murphy</b> , Endemic areas and comparative biogeography of Australian plants	4–14
11:20–11:40	<b>WR (Bill) Barker</b> , How well do today's herbarium specimen data reflect the floristic diversity of a region?	4–15
11:40–12:00	<b>Hugh Burley</b> , Quantifying floristic beta-diversity of the Australian Wet Tropics using phylogenetic turnover	4–16 Student
12:00–12:20	<b>Nicholas Cuff</b> , Patterns of short range endemism in Top End <i>Typhonium</i> Schott illustrate the importance of taxonomic research to development planning and assessment	4–17
12:20–12:40	<b>Maarten J M Christenhusz</b> , Tiptoe through the tulips, a cultural history and phylogeny of <i>Tulipa</i> (Liliaceae)	4–18
12:40–13:40	Lunch	
13:40	Session 5: Systematics, Time and Evolution	
13:40–14:00	<b>Isaac A Kerr</b> , A <i>Ripogonum</i> look-alike from the Oligocene of New Zealand: a lesson in the importance of cuticle	5–19 Student
14:00–14:20	<b>Jessica Bruce</b> , <i>Reedia spathacea</i> F.Muell.: a study of phylogeography, population structure and co-occurrence	5–20 Student
14:20–14:40	<b>Rachael M Fowler</b> , <i>Eremophila</i> and tribe Myoporeae (Scrophulariaceae): phylogeny and biogeography based on high throughput sequencing	5–21 Student
14:40–15:00	<b>Ed Biffin</b> , Hybridisation between native and invasive <i>Carpobrotus</i> N.E.Br. (Aizoaceae) in South Australia—molecular and morphological insights	5–22
15:00–15:30	Afternoon Break	
15:30	Session 6: Insights into Biodiversity	
15:30–15:50	<b>Jürgen Kellermann</b> , Rhamnaceae—where art thou	6–23
15:50–16:10	<b>Kerry Lynne Gibbons</b> , <i>Mitrasacme</i> , morphology and the monsoon tropics	6–24
16:10–16:30	<b>Nick Kalfas</b> , Looking at the Big Pitcher: assessing the coevolution of <i>Cephalotus follicularis</i> and its associated wingless fly	6–25 Student
16:30–16:50	<b>Charles Foster</b> , Evaluating the impact of genomic data and priors on Bayesian estimates of the angiosperm evolutionary timescale	6–26 Student
16:50–17:10	<b>Timothy L. Collins</b> , Would you like a new species and a fertile hybrid with that? <i>Eucalyptus magnificata</i> is not just an endangered species	6–27 Student
17:10	Forum: Decadal Plan progress	
18:00	Conference Dinner	

## Program—Wednesday

9:00	Session 7: Systematics and Issues of Scale	
09:00–09:20	<b>Sarah Mathews</b> , Phylogenomics of seed plants	7–28
09:20–09:40	<b>Tanja M Schuster</b> , Using big data to answer large-scale questions in eucalypt systematics: analysis of chloroplast genomes does not support the monophyly of <i>Corymbia</i>	7–29
09:40–10:00	<b>Michael F. Fay</b> , Evolution of genome size in angiosperms	7–30
10:00–10:20	<b>Caroline Pannell</b> , Taxonomy, plant-disperser interactions, diversification and biogeography of the genus <i>Aglaia</i> (Meliaceae)	7–31
10:20–10:40	<b>Kristina Lemson</b> , Population variation in the seagrass <i>Halophila ovalis</i> (Hydrocharitaceae)	7–32
10:40–11:00	Morning Break	
11:00	Session 8: New Taxonomic Resources and Systematic Studies	
11:00–11:20	<b>Kevin Thiele</b> , Building a key to all Australian flowering plants—70% and counting	8–33
11:20–11:40	<b>Donna Lewis</b> , Flora NT—Northern Territory flora online	8–34
11:40–12:00	<b>Richard L. Boyne</b> , My time as a ‘Kewite’	8–35
12:00–12:20	<b>Yu Ito</b> , Molecular phylogeny of <i>Eriocaulon</i> (Eriocaulaceae)	8–36
12:20–12:40	<b>Kor-jent van Dijk</b> , Implications for conservation in the Mount Compass Swamp Gum <i>Eucalyptus paludicola</i> based on genome wide markers	8–37
12:40–13:40	Lunch	
13:40	Session 9: Systematics and Evolution of Species	
13:40–14:00	<b>Jennifer A Tate</b> , Diverse origins and evolution of sexual expression in Australasian Malveae (Malvoideae, Malvaceae)	9–38
14:00–14:20	<b>Melodina Fabillo</b> , The key problem in <i>Eremochloa</i> (Rottboelliinae: Poaceae)	9–39
14:20–14:40	<b>Trevor Wilson</b> , Are we splitting hairs? Resolving infrageneric relationships in the Australian <i>Plectranthus</i> (Lamiaceae)	9–40
14:40–15:00	<b>Heidi Meudt</b> , Species delimitation in Southern Hemisphere bracteate-prostrate forget-me-nots ( <i>Myosotis</i> , Boraginaceae) based on analyses of pollen and morphological data	9–41
15:00–15:30	Afternoon Break	
15:30–17:00	Conference handover and student awards	
17:30	Transport to Simpsons Gap BBQ	

## Associated events

### Sunday

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**Welcome–Registration** function, 17:00–19:00, open to all attendees and accompanying persons—there is an opportunity to register early and catch up with other delegates and friends. This event is at Yubu Napa, a studio and gallery specialising in local indigenous artworks. Located at 65 Hartley Street the gallery is close to a number of dining opportunities, around the corner from Todd Mall and about 2 km from the conference venue.

### Monday

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Apart from starting bright and early with our first presentation beginning at 9:00 there are no other events planned for today. Although the ASBS-AGM is at 16:30 following the last presentation.

### Tuesday

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**Conference Dinner at the Olive Pink Botanic Garden**, make your own way to the gardens, plan on a 18:00 departure, it's only a short walk from the Double Tree by Hilton and easily accessible from most of the nearby accommodation (but bring a torch to see your way). We are excited to offer you a taste of the outback with unique choices from local indigenous caterers Kungkas Can Cook. Dinner will be around 18:30.

### Wednesday

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**End of Conference BBQ**, 17:30 bus departure—what better way to end this year's conference than to have an informal BBQ at Simpsons Gap (20 km west of Alice Springs). Price includes food and transport to and from the conference venue. You are guaranteed to see the local rock wallaby population (as the sun sets) and we have organised to be shown some of the wildlife in the area.

### Thursday

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**Post-conference field trip to the MacDonnell Ranges**, 8:00 departure—the MacDonnell Ranges contain a staggering 750+ species with most of the endemics for the MacDonnell bioregion. You'll get a taste of some of the more easily accessible species. We will visit Standley Chasm and some of us will climb up onto the ridge. This climb is strenuous and you will need to wear proper footwear and we recommend you carry water with you. We also visit the chasm itself which is typical of a mesic gorge. If time permits, we will go to Ellery Big Hole to see a xeric gorge. This has a wonderful swimming hole, so bring swimmers and a towel. Return around 17:30.



# Field trip to Standley Chasm & Ellery Waterhole

Thursday, 29 September 2016

## Personal items to bring

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Hat, sunscreen, water, fly net, sunglasses, comfortable walking shoes, camera (optional: swim wear & towel for Ellery Waterhole)

## Itinerary

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- 8:00 Meet at entrance to Double Tree by Hilton.  
9:00 Arrive Jay Creek tributary (near Standley Chasm)—walk up dry gorge then over saddle to Standley Chasm kiosk. Optional side walk (steep) to lookout.  
11:30 Refreshment—tea/coffee, scone at kiosk  
12:00 Walk into Standley Chasm—mesic gorge  
13:00 Lunch  
13:45 Depart Standley Chasm  
14:45 Arrive Ellery Rock hole—xeric gorge & limestone flora, potential swim  
16:00 Depart Ellery Rockhole  
17:30 Return Double Tree by Hilton

## Species of interest

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### Jay Creek

<i>Acacia basedowii</i>	<i>Eucalyptus sessilis</i>
<i>Acacia comleana</i>	<i>Exocarpos sparteus</i>
<i>Acacia kempeana</i>	<i>Gastrolobium brevipes</i>
<i>Acacia mellodora</i>	<i>Grevillea striata</i>
<i>Acacia strongylophylla</i>	<i>Hibbertia glabberima</i>
<i>Acacia tenuisissima</i>	<i>Hydrocotyle trachycarpa</i>
<i>Amyema gibberulum</i>	<i>Indigofera basedowii</i>
<i>Callitris glaucophylla</i>	<i>Indigofera helmsii</i>
<i>Cheilanthes lasiophylla</i>	<i>Macrozamia macdonnellii</i>
<i>Corymbia aparrerinja</i>	<i>Olearia ferresii</i>
<i>Corymbia opaca</i>	<i>Olearia stuartii</i>
<i>Cyperus cunninghamii</i>	<i>Pandorea doratoxylon</i>
<i>Cyperus vaginalis</i>	<i>Sida phaeotricha</i>
<i>Dodonaea viscosa</i> subsp. <i>mucronata</i>	<i>Triodia hubbardii</i>

### Standley Chasm

<i>Actinotus schwartzii</i>	<i>Eucalyptus camaldulensis</i> subsp. <i>arida</i>
<i>Aponollstonia stirlingii</i> subsp. <i>aliciafontinalis</i>	<i>Macrozamia macdonnellii</i>
<i>Cremnothamnus thomsonii</i>	

### Ellery Waterhole

<i>Eucalyptus socialis</i> subsp. <i>eucentrica</i>	<i>Triodia longiceps</i>
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## Monday

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### Plenary Talk

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#### A modern view on polyploidy: studies of *Nicotiana* section *Suaveolentes*

0–1

Mark Chase

School of Plant Biology, The University of Western Australia, WA; Jodrell Laboratory, Royal Botanic Gardens, Kew, UK

Polyploidy was long viewed as an evolutionary dead end, but in the past 20 years this view has been completely reversed. A general review of polyploidy in seeds will be presented. All angiosperms have been shown to have experienced at least one round of polyploidy, and some, such as *Brassica*, have undergone more than 100 such episodes. Studies of isozymes, however, have for more than 40 years demonstrated that most angiosperms are diploid, in terms of numbers of coding loci for standard “house-keeping” genes. This apparent incongruence is resolved by the process of diploidisation, which takes several million years but results in a polyploid genome that has been stream lined, so that it appears to be diploid in terms of “house-keeping” genes. In contrast to the fate of these genes, transcription factors and other regulatory elements are retained during diploidisation. Polyploid lineages are not immediately evolutionarily successful (as measured by diversification). A lag between formation and diversification has been detected, and it is likely that during this several million-year period, diploidisation remodels the polyploid genome. The nearly exclusively Australian section *Suaveolentes* of *Nicotiana* will be used to illustrate how diploidisation proceeds.

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### Morning Break

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## Session 1: Problems and Systematics

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### It's not the snake in the grass you should be wary of!

1-2

John Richard Clarkson

Queensland Parks and Wildlife Service, Atherton, QLD

The term “high biomass grass” has been coined to describe a suite of invasive, exotic species that are often considerably taller and produce significantly more dry matter per hectare than native species. These grasses are usually, but not exclusively, of pastoral origin. They readily spread from places where they are introduced into relatively undisturbed plant communities. In the process they displace native species and form dense monospecific stands which can lead to serious declines in the biodiversity of both plants and animals. In some situations the changed fire behaviour brought about by the invasion of these grasses can lead to catastrophic changes in vegetation structure. While the full impact of some of these species has probably still to be realised, the ecological impacts observed to date are cause for much concern.

The success of any weed control program is often linked to how soon the problem is identified and control works commenced. The problem with exotic grasses is that, in many instances, land managers find them difficult to distinguish from native species. As a result they are often well established before the initial identification is made.

Systematic botanists can help tackle the problem of invasive grasses in many ways. These include the production of keys and other aids to identification and the maintenance of herbaria that house the comparative material essential to confirm identifications. Herbaria can also yield valuable information on distribution and rate of spread of these grasses. The genetic and molecular techniques, that have more recently become valuable tools of trade of modern systematists, might yield insights into the relationships within the grasses that may guide research towards the development of more effective selective herbicides.

Matt AM Renner<sup>1</sup>, Margaret M Heslewood<sup>1</sup>, Simon DF Patzak<sup>2</sup>, Alfons Schäfer-Verwimp<sup>3</sup> and Jochen Heinrichs<sup>2</sup>

<sup>1</sup>National Herbarium of New South Wales, Royal Botanic Gardens and Domain Trust, Sydney, NSW;

<sup>2</sup>Ludwig Maximilian University, Faculty of Biology, Department of Biology and Geobio-Center, Munich, Germany; <sup>3</sup>Herdwangen-Schönach, Germany

As a framework for revisionary study *Plagiochila* in Australia, we employed two methods for ‘objective’ species delimitation on molecular sequence data, General Mixed Yule Coalescence model (GMYC) and Automatic Barcode Gap Discovery (ABGD). A total of 265 individuals were newly sampled from Australia, New Zealand, and the Pacific, to capture as full a range of morphological and geographic diversity as possible. Overall grouping success for both methods varied between lineages, possibly reflecting underlying heterogeneity in the history of diversification within different lineages of *Plagiochila*. Our results suggest a minimum of 71 species are present in Australasia, 16 more than currently accepted for the region, comprising 8 (potentially) undescribed species and 8 (definite) synonyms requiring reinstatement. Despite modern taxonomic investigation over a four decade period, 1) real diversity is 29% higher than currently recognised; and 2) 12 of 22, or 39%, of currently accepted and previously untested Australasian species have circumscription issues, including polyphyly, paraphyly, and internal phylogenetic structure. These issues reflect the many challenges associated with grouping decisions based solely on morphological data in difficult plant lineages. We also tested the current infrageneric classification, and found it somewhat deficient. The unique difficulties associated with naming species within this globally distributed lineage will be considered.

Javier Aju<sup>1</sup>, Michael Bayly<sup>1</sup> and \*Gillian Brown<sup>1,2</sup>

\*Presenting; <sup>1</sup>School of BioSciences, University of Melbourne, VIC; <sup>2</sup>Queensland Herbarium, DSITI, Toowong, QLD

*Archidendron* is the largest group of Old World Ingeae (Leguminosae; Mimosoideae; Ingeae) occurring in Australian, New Guinean, and SE Asian lowland rainforests. It includes 94 species, at least 22 of these are listed as imperfectly known, which are placed into eight series. Preliminary phylogenetic results, based on limited sampling from tribal level studies, suggest that *Archidendron* is not monophyletic. Two geographic clades associated with Wallace's Line are identified and they are not closely related. Should this be one or two genera?

This study is the most comprehensive phylogeny of *Archidendron* attempted. We use the targeted amplicon next generation sequencing method to sequence 12 low copy nuclear, nuclear ribosomal and chloroplast DNA regions to critically evaluate taxon and series boundaries, the evolution of characters and identify historical biogeographic patterns within the SE Asian, Australian and Pacific region.

Robyn Barker

State Herbarium of South Australia, Adelaide, SA

Frederick Schultz spent almost two years as the naturalist of the Northern Territory Expedition to Port Darwin in 1869–70. In this time he and his son made numerous natural history collections and his praises were sung by those in charge of the expedition and those who received his collections in Adelaide. Today there is no sign of these collections in the South Australian Museum or the State Herbarium of South Australia, although at least a hundred of his 900 plant collections are type specimens. What do we know about Schultz and the present whereabouts of his plant collections?

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Lunch

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## Session 2: Our Taxonomic Resources

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

2–6

James Clugston<sup>1,2</sup>, Nathalie Nagalingum<sup>3</sup>, Richard Milne<sup>2</sup> and Gregory Kenicer<sup>1</sup>

<sup>1</sup>Royal Botanic Garden Edinburgh, Edinburgh, UK; <sup>2</sup>University of Edinburgh, Edinburgh, UK; <sup>3</sup>National Herbarium of New South Wales, Royal Botanic Gardens and Domain Trust, Sydney, NSW

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 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 south populations; recognise populations of conservation priority; and determine if botanic garden collections successfully represent existing genetic diversity found in the wild.

Ilse Breitwieser

Allan Herbarium, Landcare Research, New Zealand

In 2015, 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 report on the National Taxonomic Collections in New Zealand was published on 15 December 2015. The Panel recommended that a whole-of-systems approach must be taken to interconnect providers, custodians, practitioners, stakeholders, and end-users. Specific recommendations addressing system performance and investment were made.

Currently a conservation and environment science roadmap and a biosecurity roadmap are getting developed for New Zealand. Both are relevant to New Zealand's national taxonomic collections.

The New Zealand Budget 2016 brings a number of investments into a single new Strategic Science Investment Fund (SSIF). The SSIF will support underpinning research programmes and infrastructure of enduring importance to New Zealand. Although the changes will not get implemented until 1 July 2017, additional funding for Nationally Significant Collections and Databases (NSC&Ds) has already been allocated to CRIs with the largest responsibilities for NSC&Ds to support immediate cost pressures.

I will present an overview of the Royal Society of New Zealand report, the two roadmaps on conservation and environment science and on biosecurity, and the current operating environment for the National Taxonomic Collections in New Zealand.



## Keys to the flora of the MacDonnell Ranges Bioregion of Central Australia: web enabling the MacFlora interactive keys

2–8

Ian Cowie<sup>1</sup>, Donna Lewis<sup>1</sup> and Dave Albrecht<sup>2</sup>

<sup>1</sup>Northern Territory Herbarium, Flora and Fauna Division, Dept. of Land Resource Management, Darwin, NT; <sup>2</sup>Australian National Herbarium, CSIRO National Research Collections, Canberra, ACT

MacFlora is an online interactive system of identification keys to the flora of the MacDonnell Ranges Bioregion of Central Australia which covers approximately 1120 taxa of woody plants, petaloid monocots, ferns and aquatic plants. The product incorporates an introductory dichotomous html key to 21 plant subgroups, with interactive LUCID keys for seven of these subgroups. The largest of these separate LUCID keys are the Main Dicot key (1042 species), Eucalypts and Corymbias (20 species), Perianth Monocots (23 species) and Aquatics (17 species). The main dicot key makes extensive use of scoped or group-specific characters for individual genera. An important part of the project involved loading ancillary information such as identification notes and ethnobotanical information for many species into the Herbarium's HOLTZE specimen database for the Fact Sheets. Although originally designed as a static product on CD, web enabling the key allowed the product to be publicly released much sooner. Web enablement also provides a better pathway forward for the keys future development and for regular maintenance. The keys are linked to dynamically generated and custom-badged Flora NT Fact Sheets using data drawn from the NT Herbarium's HOLTZE specimen and flora information database. A Bush Blitz Applied Taxonomy Grant was essential to completing the web-enablement project.

The MacDonnell Ranges identification system is available at: <http://bit.ly/2bZcUbK> (eflora.nt.gov.au/dynamic?page=MacDonnellRanges&id=content)

Joel Collins

Eco Logical Australia, West Perth, WA

Embracing mobile field data collection technologies is the only way forward. While there have been the other mobile devices available to collect data, such as PDA's and Trimble, apps are a relatively new concept. With the current choice of tablets available, particularly rugged tablets designed to handle the field environment, the option to use data collection apps in the field is an exciting possibility. With existing apps being regularly updated and new apps being released on a regular basis, the question now that must be asked is why would you not use a mobile field data collection app for flora surveys?

These exciting technologies allow the user to improve efficiencies and save costs right through the project life cycle, from survey to reporting and data management. By replacing clipboards and pens with smart tablets you are able to redefine what is possible in the field while dramatically reducing the need for inefficient manual data entry which is prone to human error and inaccuracies.

There are many different apps available that are suitable for a range of purposes. The ArcGIS Collector app is an example that fulfils many of the requirements to effectively collect point and polygon shape files for ecological surveys. Survey and mapping projects that require the collection of specific data on a number of different species, such as weed species, across multiple sites is easily achievable when using Arc Collector. The efficiencies gained by using tablets is significant, particularly from reducing data handling. It is estimated that up to 30–40% of time can be saved on typical ecological survey and reporting projects, when comparing data collected in the field using the Arc Collector app compared to hard copies datasheets and hand drawn mapping. This presentation runs through some examples of the capabilities of the ArcGIS Collector.

Ryonen Butcher

Western Australian Herbarium, Perth, WA

The Atlas of Living Australia (ALA) has recently passed the milestone of 8 billion record downloads. Of these, 4.6 billion were classified as being for scientific or ecological research and c. 750 million for use in environmental assessment and conservation management. At its core, the ALA has 11.8 million preserved specimen records (19% of total), c. 6.3 million of which are plant or fungi records. Unlike observational data records (>75% of the ALA's total) the specimen-based records provided by the biological collections community (BCC) are authoritative, falsifiable, have longitudinal time series and can be used to extract further information, which can be stored, shared and re-used. The importance and utility of the records we provide for research in areas beyond taxonomy is duly recognised by the ALA, which considers the BCC to be a key partner in the delivery of value-added biodiversity data.

As such, in February 2016 the ALA hosted a two-day BCC roadmapping workshop in order to identify and plan priority activity areas where the community and the ALA might work together to our mutual benefit, and to assign timeframes and responsibilities for those activities. A list of key goals was drawn up by the ALA and potential activity areas to support those goals were distributed to participants to consider and prioritise. A series of questions related to community expectations and use of the ALA were also posed for discussion.

While the BCC and the ALA shared similar aspirations, core factors such as infrastructure maintenance, effective resource allocation and efficient bi-directional delivery of high-quality data were found to be of greatest importance to the BCC. Key priority areas included image management, digitisation of our collections, names management, duplicate handling, genomic data, annotation services and the eFlora. A 'fix-it' list was also drawn up, directed towards a range of technical issues and the ALA user interface.

This talk will summarise the outcomes of the roadmapping workshop and outline some recent developments in the ALA detailed in sprint reviews.

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## Afternoon Break

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## Session 3: Our taxonomic resources (continued)

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### The Australian Biological Resources Study—so where do we go to from here?

3-11

Anthony Whalen

Australian Biological Resources Study, Australian Government, Department of the Environment and Energy, Canberra, ACT

The Australian Biological Resources Study (ABRS) has supported Australian taxonomy and systematics for over forty years. Many botanists in this time have received ABRS grants to support writing treatments for the *Flora of Australia* book series (and other ABRS publications). In an age of new technologies and increasing connectivity, the ABRS is actively working to ensure it remains a relevant partner to Australasia's biological communities.

The *National Species Lists* initiative, the *Australasian eFlora platform* project and *Bush Blitz* species discovery program continue to build momentum, and will guide ABRS over the next few years. This presentation will outline current ABRS priorities and provide an update on delivering the flora of Australia on the eFlora platform. Discussion on the eFlora will include planned ABRS strategies for incorporating existing flora treatments from the book series and ways in which botanical authors will be able to actively contribute in the near future. The ABRS is keen to promote discussion with the botanical community about priorities around the flora of Australia.

Kevin Thiele

Eubio Consulting, Inglewood, WA

Under the auspices of the Council of Heads of Australasian Herbaria (CHAH) and the Australian Biological Resources Study (ABRS), the Atlas of Living Australia (ALA) is building an eFlora platform that will provide new opportunities to develop eFloras in Australia. The first project likely to be released on the new platform will be a renewed and refreshed Flora of Australia; it is expected that some Australian states will also commence significant Floras on the platform in the near future. This talk will provide an introduction to the functionality and opportunities of the eFlora platform, and discuss its advantages and strengths for building, deploying and maintaining online florae.

Tuesday

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Session 4: Evaluating Biodiversity

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Endemic areas and comparative biogeography of Australian plants

4–14

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Daniel J Murphy

National Herbarium of Victoria, Royal Botanic Gardens Victoria, Melbourne, VIC

Australia has been the subject of many historical biogeographic analyses of its flora. However, there is on-going difficulty in the definition of areas of endemism (biotic areas), or the description of biogeographic barriers within Australia. This may be due to the lack of sharp or abrupt barriers to define biotic areas or because the definition of biotic areas is inconsistent. In recent years there has been a focus on broad-scale ecologically-based biomes, which have been useful to investigate the recent evolution and assembly of floristic elements. For example, Northern Australia is dominated by a monsoon tropical savanna biome and the central parts of Australia form an arid biome. However, some studies and reviews have found multi-layered and complex historical distributional patterns of endemism of plants within these biomes, with recent (some human-mediated), pre-human and ancient (relictual) distributions recorded. To distinguish these complex recent evolutionary histories from historical biogeographic patterns, a return to a smaller scale of regionalisation of biotic areas has been necessary and a comparative approach using multiple lineages is required. In this talk I will review some of the main results, illustrate the broad ecological and historical patterns that are emerging, and discuss the value of a comparative approach to historical biogeography, using examples of iconic plant groups in Australia such as *Acacia* and *Adansonia*.

W R (Bill) Barker

State Herbarium of South Australia, Adelaide, SA

The State Herbarium of South Australia has more than a million specimens, with over 640 thousand vascular plant collections from its state. Such large numbers have led to two commonly held beliefs. For the best collected major group, the vascular plants, it is easy to believe that this a big enough sample for most taxonomic and floristic research. The second belief revolves around sampling methodology. Traditionally herbaria adopt an across-landscape approach to assembling a representative sample of collections covering the diversity of plants in a region, while ecologists interested in floristic mapping score and sampling taxa using plots – there is a view that the latter is cost-saving approach that services both branches of science well.

Two regions have been assessed using data from the State Herbarium collections and other Australian herbaria in order to test these beliefs. In Kangaroo Island and the Murray Mallee the earliest vascular plant collections in the two regions studied were made in the early and mid 1800s, respectively.

Kangaroo Island, 130 x 60 km in dimension, is probably the most diverse region in South Australia and one of the better collected, having had a strong history of institutional and individual collecting of herbarium specimens. Yet most taxa on Kangaroo Island are represented by few collections, many by one or two. This reflects the high degree of endemism on the island. Largely plot-based survey collections are not a surrogate for herbarium collections; they only cover half the species.

The Branch Broomrape Quarantine area in the Murray Mallee of South Australia, a polygon of c. 100 x 5–60 km, shows a steady accumulation of new records of taxa continuing almost to the present.

It is concluded that the vascular plant diversity of neither region can be considered to have been adequately sampled to this time. New records of taxa can be expected and samples of the distribution of many taxa are clearly inadequate. There is a strong case for continued general or directed collecting in each region and it is likely that this applies across the State generally.

For the purpose of strategic planning and promotion we might benefit from a set of indicators that similarly reflect the adequacy the coverage of Australasia's herbarium collections as regional samples of diversity of the major plant groups now and into the future.

# Quantifying floristic beta-diversity of the Australian Wet Tropics using phylogenetic turnover

4–16

Hugh Burley<sup>1</sup>, Shawn Laffan<sup>1</sup>, Darren Crayn<sup>2,3</sup>, Eda Adicott<sup>2</sup> and Andrew Thornhill<sup>4</sup>

<sup>1</sup>School of BEES, The University of New South Wales, NSW; <sup>2</sup>College of Marine and Environmental Sciences, Centre for Tropical Biodiversity and Climate Change, James Cook University Smithfield, QLD; <sup>3</sup>Australian Tropical Herbarium, James Cook University Smithfield, QLD; <sup>4</sup>University & Jepson Herbaria, University of California, Berkeley, CA, USA

The flora of the Wet Tropics of North Queensland (WT) is among the best studied globally, with a rich history of vegetation mapping. The original work of Webb and Tracey formed the basis of 1:100,000 scale maps, which delineated 23 main vegetation types for purposes of conservation and land use planning. These boundaries were primarily based on vegetation structure, the dominant species within each strata and major environmental features (Tracey, 1982). More recent 1:50,000 scale regional ecosystem maps (REM), based on analogous contemporary methods that incorporate remote sensing, recognise 35 Broad Vegetation Groups (BVGs) at the 1:1 million scale, and 16 BVGs at the 1:5 million scale. Greater accessibility to large genetic and spatial datasets coupled with methodological advances now enable the generation of phylogenetic turnover maps for entire floras at relatively fine spatial resolutions. Given the potential benefits for conservation planning applications, it could be insightful to test traditional taxonomic beta-diversity classified zones using phylogenetic approaches. Here we describe phylogenetic turnover patterns for the WT vascular flora. Phylogenetic turnover was generated using a phylogeny of more than 2500 vascular plants, based on 11 genetic markers sourced from GenBank. The phylogeny was combined with over 181,669 georeferenced plant specimens, sourced from Australia's Virtual Herbarium (AVH) and representing the broader WT region, to map the turnover of branch lengths between grid cells. We discuss potential methods for quantitatively comparing these genetic patterns with traditional species-level turnover classifications, such as the BVG vegetation units.

**Student Presenter**



## Patterns of short range endemism in Top End *Typhonium* Schott illustrate the importance of taxonomic research to development planning and assessment

4–17

Nicholas Cuff<sup>1</sup>, Matthew Barrett<sup>2</sup>, Ian Cowie<sup>1</sup> and David Liddle<sup>3</sup>

<sup>1</sup>Northern Territory Herbarium, Flora and Fauna Division, Dept. of Land Resource Management, Darwin, NT; <sup>2</sup>Kings Park Botanic Gardens, WA Botanic Gardens and Parks Authority, Perth, WA; <sup>3</sup>Species Conservation Unit, Flora and Fauna Division, Dept. of Land Resource Management, Darwin, NT

The Northern Territory Government has developed a set of predictive tools for threatened species to help development planning and assessment in the greater Darwin Region. This has highlighted the importance of both traditional taxonomy ( $\alpha$ -taxonomy) and molecular techniques (particularly DNA-barcoding and libraries— $\beta$ -taxonomy) in providing baseline species information for conservation, planning and land-use decision-making processes.

Specific examples are drawn from *Typhonium* Schott to illustrate the importance of simple, robust and reliable tools to help the decision-making process for short-range endemic taxa. Furthermore, these examples illustrate the importance of ongoing taxonomic research to the state of biodiversity information and the active role new taxonomic methods can play. For example, recent taxonomic studies suggest the existence of at least four entities within what was previously identified as *Typhonium praetermissum* giving rise to the development and implementation of new planning tools in the region.

Ongoing taxonomic research has highlighted the importance of the Darwin region as a centre of short range endemism in the Araceae: a pattern which is repeated in a number of other genera such as *Utricularia* L.

Land-use change and intensification will be an inevitable consequence of the renewed focus on development in northern Australia. Confident planning and decision-making needs to be underpinned by a rich information base, and a thorough understanding of plant diversity is integral to this. Flexible approaches utilising a combination of research methods will be essential to future risk assessment in remote and northern Australia where expertise and access limitations often severely hinder the adequacy and comprehensiveness of surveys. A flexible approach applying a variety of taxonomic techniques provides a pathway to strengthen the quality of outcomes and confidence in decision making processes.

Maarten J M Christenhusz

Royal Botanic Gardens, Kew and Plant Gateway, Hertfort, UK

Tulips (genus *Tulipa*, Liliaceae) have always triggered the imagination and been popular as garden plants for centuries. Garden tulips are hybrids and originated in Persia, probably when two or more species were brought together in a garden, where they crossed and this hybrid had more vigour and was easily shared. From there, they travelled along the Silk Route to Turkey, where they became a national symbol of the Ottoman Empire. As more tulips were collected from the wild and intentionally bred in gardens, special tulips received higher prices and soon prices were fixed by the Sultan. When they arrived in Europe through diplomatic means in the 16<sup>th</sup> Century, they became fashionable immediately. They achieved huge popularity in France and later in the Netherlands, where speculation on the bulb trade was responsible for the first major economic crash of modern times. However, classification and relationships in *Tulipa* have always been contentious, and new species were described from naturalised hybrid populations. The origins of wild tulips were often poorly documented, and species were largely described from cultivated sources. This convoluted taxonomic history mixes biological and horticultural taxonomy, and we have tried to tease the two apart to create a better understanding of the genus. We developed a molecular phylogenetic analysis of *Tulipa* in which four discrete clades can be recognised, corresponding to morphological characters. We resolved the issue of ‘neotulips’ and classified these into two cultivar groups. Two unplaced species (*T. regellii* and *T. sprengeri*) with confusing morphology, can now be placed. The origin and genetic background of garden tulips can be partially explained, but needs further research.

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Lunch

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### A *Ripogonum* look-alike from the Oligocene of New Zealand: a lesson in the importance of cuticle

5–19

Isaac A Kerr<sup>1</sup>, John G Conran<sup>1</sup>, Daphne E Lee<sup>2</sup>, Michelle Waycott<sup>1,3</sup>

<sup>1</sup>School of Biological Sciences, The University of Adelaide, Adelaide, SA; <sup>2</sup>University of Otago, Dunedin, New Zealand; <sup>3</sup>State Herbarium of South Australia, Adelaide, SA

A lauraceous *Ripogonum*-like macrofossil from the Pomahaka late Oligocene estuarine deposit in southern New Zealand is identified and described using macroscopic and cuticular characteristics as part of a phylogenetic study of many Ripogonaceae-like macrofossils from New Zealand Cenozoic deposits. Superficially, the morphology of the Pomahaka fossil closely resembles that of extant *Ripogonum* species and *Ripogonum* fossils from other southern NZ sites, for example from Hindon Maar, an early Miocene crater-lake. This is due to the presence of a superbasal secondary vein pair considered to be particularly characteristic of Ripogonaceae. However, cuticle from the Pomahaka fossil shows no abaxial cell wall sinuosity, the abaxial stomata are arranged in areoles and have prominent cuticular flanges, the hair bases have a clearly differentiated ring of associated cells and abaxial cell size is very small. These features are profoundly different from those associated with Ripogonaceae and instead suggest a possible affinity to Lauraceae. The triplinerved leaves resemble some members of genera such as *Cryptocarya*, *Cinnamomum*, *Daphnogene* and *Neolitsea*, as well as the Northern Hemisphere fossils from genus *Daphnophyllum*. However, because of the considerable difficulty in placing fossil Lauraceae leaves into modern genera, the fossil is described as a new species of *Laurophyllum*.

**Student Presenter**

Jessica Bruce

Edith Cowan University, Perth, WA

*Reedia spathacea* F.Muell is a declared rare species of sedge (Cyperaceae) found in the peat swamps of the Jarrah Forest and Warren Biogeographical Regions. *Reedia* has been identified as a Gondwanan relict species on the basis of (relatively little) morphological and genetic evidence. Characteristics of relictual taxa in the south-west include being of Gondwanan or Pangaeian origin, thus having become restricted to mesic habitat from a previously wider distribution and retaining some ancestral morphological states. They also are expected to have high interpopulational genetic diversity with relatively low intrapopulational diversity and be phylogenetically distinct from sister taxa. These criteria will be used to explore whether *R. spathacea* is a relictual taxon using chloroplast and microsatellite DNA analyses supported by morphological and phylogeographic evidence. These data will also allow for the detection of evolutionarily significant units or cryptic taxa. If this study supports the recognition of *Reedia* as a highly-restricted relict then the genetic consequences of historical population decline or extinction can be addressed. In a broader sense, our understanding of organisms that have become rare will be improved, in turn improving our understanding of the pressures that have caused contraction in ranges historically, and helping us to predict future trends in the face of a rapidly changing climate.

**Student Presenter**

# *Eremophila* and tribe Myoporeae (Scrophulariaceae): phylogeny and biogeography based on high throughput sequencing 5–21

Rachael M Fowler<sup>1</sup>, Michael J Bayly<sup>1</sup> and Daniel J Murphy<sup>2</sup>

<sup>1</sup>School of BioSciences, The University of Melbourne, VIC; <sup>2</sup>The National Herbarium of Victoria, Melbourne, VIC

*Eremophila* is a large Australian genus with over 200 described species and a growing number of newly discovered taxa. It is a significant component of the Australian arid zone flora, where members tolerate harsh, dry and saline conditions and provide food and shelter for a wide range of insect and bird species. The genus is placed in tribe Myoporeae, along with *Myoporum* (30 spp.), *Diocirea* (4 spp.) and a four monotypic genera (*Calamphoreus*, *Glycocystis*, *Bontia*, *Pentacoelium*). Relationships within Myoporeae, and particularly within *Eremophila*, are not clearly understood, and the current classification is based on morphology alone. We are using high throughput sequencing to study evolution of this group using large genomic datasets.

The aims of this study are: to discover the evolutionary relationships of *Eremophila*, in order to re-assess classification of the group using morphological and molecular data; to infer the biogeographic history of the group in arid Australia; and to investigate the relationships of *Eremophila* to other members of tribe Myoporeae, some of which are distributed outside of Australia. We have sampled ~98% of described *Eremophila* species from across Australia, and representatives from all six genera of Myoporeae, including species of *Myoporum* from across the Pacific region, *Bontia daphnoides* from the Caribbean and *Pentacoelium bontioides* from Taiwan. Using whole genome shotgun sequencing, we have assembled and aligned entire chloroplast genomes to reconstruct a well-supported phylogeny for a subset of taxa. We have also analysed high copy regions of the nuclear genome, including a section of nuclear ribosomal DNA stretching beyond the commonly used intergenic spacer regions (ITS/ETS), for comparison with chloroplast analyses.

**Student Presenter**

# Hybridisation between native and invasive *Carpobrotus* N.E.Br. (Aizoaceae) in South Australia—molecular and morphological insights

5–22

Ed Biffin<sup>1</sup>, Hellmut Toelken<sup>1</sup>, Korjent van Dijk<sup>1,2</sup>, Jürgen Kellermann<sup>1,2</sup> and Michelle Waycott<sup>1,2</sup>

<sup>1</sup>State Herbarium of South Australia, Adelaide, SA; <sup>2</sup>School of Biological Sciences, The University of Adelaide, Adelaide, SA

*Carpobrotus* is a genus of succulent plants that includes between 12 and 20 accepted species from southern Africa, Australia and America. Several species have been widely cultivated, including the African species *C. edulis* (L.) L.Bolus, which is a vigorous coloniser of sand dunes and is valued for erosion control and as an ornamental. In several regions, including the United States, New Zealand and the Mediterranean of France, *C. edulis* has reportedly hybridised with native or introduced *Carpobrotus* species and in some cases, the hybrids are considered invasive. In Australia, *C. edulis* is naturalised in several locations across the southern coastline and is frequently in sympatry with native *Carpobrotus*. We use molecular data to explore the occurrence of hybridisation between *C. edulis* and native *C. rossii* (Haw.) Schwantes in a region of co-occurrence near Adelaide, South Australia. These data indicate that hybridisation is common and widespread between the native and introduced species. Probabilistic genotype assignment tests suggest the presence of first generation (F1) hybrids along with backcrossing in the direction of both parental types. Given the invasive potential of *C. edulis* and its hybrids this first evidence of hybridisation within Australia forms the basis for ongoing research into the extent and dynamics of this system and its impact on coastal ecosystems.

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Afternoon Break

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Jürgen Kellermann

State Herbarium of South Australia, Adelaide, SA; School of Biological Sciences, The University of Adelaide, Adelaide, SA

Rhamnaceae is one of the major plant families in Australia and a well-known component of Australia's temperate and semi-arid environment, however the only treatment available to date is by Bentham (1863). With 25 genera and over 250 species, over one quarter of Rhamnaceae species worldwide are native to Australia; only four species are introduced.

In the last 15 years, several molecular phylogenies were published for the whole family and some tribes and genera. While there are still some issues at higher level, the situation in Australia is getting resolved.

The majority of taxa in Australia belong to the tribe Pomaderreae, which is almost exclusively distributed in Australia, only 8 species occur in New Zealand. The largest genera are *Cryptandra* Sm. (c. 60 spp.), *Pomaderris* Labill. (c. 75 spp.), *Spyridium* Fenzl. (c. 45 spp), *Stenanthemum* Rissek (c. 30 spp.) and *Trymalium* Fenzl (13 spp.). Smaller genera include *Blackallia* C.A.Gardner (1 sp.), *Papistylus* Kellermann *et al.* (2 spp.), *Polianthion* K.R.Thiele (4 spp.), *Serichonus* K.R.Thiele (1 sp.) and *Siegfriedia* C.A.Gardner (1 sp.).

The remaining genera belong to several tribes of Rhamnaceae, many of which with tropical to subtropical distributions, and are represented with only one or a few species in Australia: Paliureae (*Ziziphus* Mill., 4 spp. in Australia), Gouanieae (*Gouania*, 2 spp.), Rhamneae (*Dallachya* F.Muell., 1 sp.; *Rhamnus* L., 1 sp.; *Sageretia* Brongn., 1 sp.), Ventilagineae (*Ventilago* Gaertn., 3 spp.) and Colletieae (*Discaria* Hook., 2 spp.).

A few genera are still unplaced in the family, as relationships were not resolved in the molecular phylogenies: *Alphitonia* Rissek ex Endl. (5 spp.) and its sister genus *Granitites* Rye (1 sp.), *Colubrina* Rich. ex Brongn. (1 sp.), *Emmenosperma* F.Muell. (3 spp.) and *Schistocarpea* F.Muell. (1 sp.).

Rhamnaceae has only four naturalised species in Australia from the genera *Ceanothus* L., *Hovenia* Thunb., *Noltea* Rchb. and *Rhamnus* L.

Preparation of the *Flora of Australia* treatment was started in the 1990s and was on hold during the last few years, but will resume with the development of the new ALA eFlora platform. The revision of *Cryptandra* and *Spyridium* will need to be completed and several genera require up-dates.

Kerry Lynne Gibbons<sup>1,2</sup>, Barry John Conn<sup>1,2</sup> and Murray James Henwood<sup>1</sup>

<sup>1</sup>School of Biological Sciences, The University of Sydney, Sydney, NSW; <sup>2</sup>National Herbarium of New South Wales, Royal Botanic Gardens and Domain Trust, Sydney, NSW

*Mitrascme* (c. 55 spp., 50 in Australia) is the largest genus of Loganiaceae, an Australasian-Pacific tribe of the predominantly tropical Loganiaceae. The geographic distribution of *Mitrascme* extends north from southern Australia to Malesia and Asia, and east to New Caledonia, but it is most species-rich in the Australian Monsoon Tropics. *Mitrascme* is closely related to the southern Australian sclerophyll genera *Adelphacme* and *Phyllangium*, and the Australasian montane genus *Schizacme* – together these genera are referred to as the ‘*Mitrascme* alliance’. Using the chloroplast *petD* and nuclear ETS, we present the first species-level molecular phylogeny of the ‘*Mitrascme* alliance’. The monophyly of *Mitrascme*, and of the ‘*Mitrascme* alliance’, is strongly supported. *Mitrascme* subgenus *Plecocalyx* and *M.* subgen. *Schizogyne* are nested within the remainder of *Mitrascme*, rendering *M.* subgen. *Mitrascme* paraphyletic. Although many morphologically recognisable clades are resolved within *Mitrascme*, the nested patterns of morphological evolution and the high level of homoplasy currently preclude the recognition of a new subgeneric classification. Multiple morphological traits appear to have evolved in parallel many times within *Mitrascme*, but there is no clear morphological synapomorphy for the genus. Derived morphological character states and life history shifts appear to post-date a transition from an ancestral sclerophyll biome to a monsoonal biome. Ancestral character state analyses of selected morphological traits, life histories and biomes will be presented and compared.



## Looking at the Big Pitcher: assessing the coevolution of *Cephalotus follicularis* and its associated wingless fly

6–25

Nick Kalfas<sup>1</sup>, John Conran<sup>1</sup>, Michelle Waycott<sup>1,2</sup>, Kor-jent van Dijk<sup>1,2</sup>, Ed Biffin<sup>1,2</sup> and Terry Macfarlane<sup>3</sup>

<sup>1</sup>School of Biological Sciences, The University of Adelaide, Adelaide, SA; <sup>2</sup>State Herbarium of South Australia, Adelaide, SA; <sup>3</sup>Western Australian Herbarium, Perth, WA

The Albany Pitcher Plant (*Cephalotus follicularis*) is a carnivorous plant endemic to the south-west corner of Western Australia, and its jug-like traps are the only place the larvae of the wingless fly *Badisis ambulans* can be found. Little is known of both their individual ecologies and the relationship these two species share. The habitat *Cephalotus*, and therefore *Badisis*, is restricted to has become heavily fragmented which has led to the formation of multiple metapopulations. This allows the study of how a coevolved system is affected by such habitat fragmentation. The results of a preliminary study that will be presented has shown strong genetic structuring in *Cephalotus*, and a larger scale population genetic study utilising SNPs will be performed with both *Cephalotus* and *Badisis* in order to determine the extent of their coevolution. Studies of the life history of *Badisis*, the fire ecology of the system and the nature of the relationship the two species share will also be discussed.

**Student Presenter**

# Evaluating the impact of genomic data and priors on Bayesian estimates of the angiosperm evolutionary timescale

6–26

Charles Foster<sup>1</sup>, Hervé Sauquet<sup>2</sup>, Marlien van der Merwe<sup>3</sup>, Hannah McPherson<sup>3</sup>, Maurizio Rossetto<sup>3</sup> and Simon Ho<sup>1</sup>

<sup>1</sup>School of Life and Environmental Sciences, University of Sydney, Sydney, NSW; <sup>2</sup>Laboratoire Écologie, Systématique, Évolution, Université Paris-Sud, Orsay, France; <sup>3</sup>National Herbarium of New South Wales, Royal Botanic Gardens and Domain Trust, Sydney, NSW

The evolutionary timescale of angiosperms has long been a key question in biology. The oldest crown-group fossils date to the early Cretaceous (~140 Ma), yet fossils attributed to the angiosperm stem lineage date back to 247.2–242.0 Ma. Molecular estimates of the angiosperm evolutionary timescale have shown considerable variation, being influenced by differences in taxon sampling, gene sampling, fossil calibrations, evolutionary models, and choices of priors. However, a common theme in modern molecular dating studies is that the angiosperm crown age far predates the oldest fossils by a non-trivial amount of time, even by up to ~100 Ma. Did crown-group angiosperms really arise in the Triassic? Or are the substantially older molecular dating estimates a product of methodological biases? Here, we analyse a data set comprising 76 protein-coding genes from the chloroplast genomes of 195 taxa spanning 86 families, including novel genome sequences for 11 taxa, to evaluate the impact of models, priors, and gene sampling on Bayesian estimates of the angiosperm evolutionary timescale. Using a Bayesian relaxed molecular-clock method, with a core set of 35 minimum and two maximum fossil constraints, we estimated that crown angiosperms arose 221 (251–192) million years ago during the Triassic. Based on a range of additional sensitivity and subsampling analyses, we found that our date estimates were generally robust to large changes in the parameters of the birth-death tree prior and of the model of rate variation across branches. Under all calibration schemes other than highly informative gamma priors, we consistently found that the earliest divergences of angiosperm clades substantially predate the oldest fossils that can be assigned unequivocally to their crown group. Our results suggest that our understanding of the angiosperm evolutionary timescale is likely to improve through increased taxon sampling, significant methodological changes, and/or new information from the fossil record.

**Student Presenter**

Would you like a new species and a fertile hybrid with that?

*Eucalyptus magnificata* is not just an endangered species 6–27

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

School of Environment and Rural Science, University of New England, Armidale, NSW

Northern Blue Box, *Eucalyptus magnificata* L.A.S.Johnson & K.D.Hill (Myrtaceae) is listed as an endangered species in NSW, 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 NSW, and Dalveen in Queensland. Phytochemical and morphological data, and GBS SNP analysis of population genetic structure were used to determine whether these widely disjunct populations are actually a single species, or the Hillgrove populations (including the Type location) represent a gorge rim narrow endemic. Results provide strong evidence that: the Dalveen population of Northern Blue Box is a separate species; Tenterfield populations have been misidentified, and are *E. conica* H.Deane & Maiden; most trees thought to be *E. magnificata* in the Oxley Wild Rivers National Park are an undescribed fertile hybrid. These findings indicate *Eucalyptus magnificata s. str.* has a far more restricted distribution than previously realised and is poorly conserved in reserves, whilst the Dalveen Blue Box is also an endangered species with no known populations in conservation reserves. The fertile hybrid was found in several populations over a distance of 100 km on the Northern Tablelands. Further research is needed to understand the conservation status and evolutionary history of this undescribed entity.

**Student Presenter**

Wednesday

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Session 7: Systematics and Issues of Scale

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Phylogenomics of seed plants

7–28

Sarah Mathews

Australian National Herbarium, CSIRO National Research Collections, Canberra, ACT

Efforts to resolve relationships among living seed plant clades using molecular data are impeded by the high number of missing taxa due to extinction and by limits on the ability to model sequence evolution accurately. These challenges are exacerbated in analyses of phylogenomic data sets, which sometimes produce highly supported but erroneous topologies. Results will be presented from the exploration of nuclear (~850 loci) and plastid (~80 loci) phylogenomics data sets in an effort to determine the position of gnetophytes and to test the reciprocal monophyly of angiosperms and living gymnosperms. Insights from analyses of a new morphological matrix that includes a large number of living species as well as fossil seed plants will be considered in the discussion of results.

# Using big data to answer large-scale questions in eucalypt systematics: analysis of chloroplast genomes does not support the monophyly of *Corymbia*

7–29

Tanja M Schuster<sup>1</sup>, Sabrina D Setaro<sup>2</sup> and Michael J Bayly<sup>1</sup>

<sup>1</sup>The University of Melbourne, BioSciences 3, Parkville, VIC; <sup>2</sup>Wake Forest University, The Department of Biology, Winston-Salem, NC, USA

We used Next Generation Sequencing (NGS) to investigate the phylogenetic relationships of *Angophora*, *Corymbia* and *Eucalyptus*, particularly addressing the question of the monophyly of *Corymbia* (the bloodwoods). Chloroplast sequences were skimmed from NGS of genomic DNA. The dataset includes 121,228 base pairs of cpDNA for nine species of *Angophora*, 55 species of *Corymbia* (some with two accessions) and 31 species of *Eucalyptus*, with *Allosyncarpia* and *Stockwellia* as outgroups. Maximum Likelihood and Maximum Parsimony methods confirm that *Corymbia* and *Angophora* are related as one lineage. *Corymbia* is not monophyletic because *Angophora* is nested within it. Relationships among the bloodwoods are not all congruent with previous phylogenies or current infrageneric classification, though our results confirm outcomes from some previous analyses using fewer chloroplast and nuclear markers. These results frame a new working hypothesis for the evolutionary relationships of *Angophora*, *Corymbia* and *Eucalyptus*. Taxonomic changes await the future analysis of nuclear and mitochondrial data.

Michael F. Fay, Jaume Pellicer and Ilia J. Leitch

Royal Botanic Gardens, Kew, UK

Genome size in angiosperms ranges more than 2000-fold, but the vast majority of angiosperms have genomes at the low end of this range. Large genomes are phylogenetically clustered, with most of the species being members of the monocot orders Liliales and Asparagales. Before the development of next-generation sequencing techniques, it was not possible to study the constitution of the DNA in these genomes in sufficient depth to provide information about their evolution from the smaller ancestral genomes of their relatives. In recent years, however, these new technologies have made such studies possible, and examples of what we now know about the large genomes of some members of Liliaceae and Melanthiaceae will be presented.

Caroline Pannell

Department of Plant Sciences, University of Oxford, Oxford, UK; Queen's University Marine Laboratory, Queen's University Belfast, Pontaferry, UK

There can be no better 'natural laboratory' in which to study the evolution of interactions between plants and animals than the Indo-Australian-Pacific region. Widespread plant groups inhabit areas of radically different faunas. Recent work has improved our understanding of the movements of tectonic plates and the construction of this immensely complicated combination of sea, islands and continents. Fossils have been used to date molecular phylogenies of plant and animal groups and have shed light on the deep history of migrations and subsequent evolution of plants and animals through millions of years.

This presentation will focus on a case study spanning nearly four decades in which a monographic revision of *Aglaia*, the largest genus in the mahogany family, has been combined with field investigation of the biology of the interactions between different species and their vertebrate seed-dispersers. The biogeographical patterns exhibited by the genus, its colonisation of Australasia and southwestern Pacific islands during the last ten million years and the radiations of new species that followed establishment of the genus in these different faunal zones will be examined. The importance of refining species delimitations in a taxonomically intractable genus will be emphasised. If the many complex and variable species can be resolved into monophyletic species with improved distribution information, it will be possible to set conservation priorities more accurately, build informative molecular phylogenies and produce more detailed analyses of the historical biogeography of the genus. Since other plant groups have a similar biogeographical disjunction between the Sahul and Sunda shelves, a better understanding of *Aglaia* is likely to illuminate further our knowledge of the floristic interchange between these two continental shelves.

Kristina Lemson<sup>1</sup>, Kathryn McMahon<sup>1</sup>, Annette Koenders<sup>1</sup>, Kor-jent van Dijk<sup>2,3</sup>,  
Michelle Waycott<sup>2,3</sup> and Ainsley Calladine<sup>2,3</sup>

<sup>1</sup>School of Science, Edith Cowan University, Joondalup, WA; <sup>2</sup>School of Biological Sciences, The University of Adelaide, Adelaide, SA; <sup>3</sup>State Herbarium of South Australia, Adelaide, SA

The taxonomy of the diminutive but widely distributed Indo-Pacific seagrass *Halophila ovalis* (R.Br.) Hook.f. has been in constant flux. At various times and places, *H. ovalis* has been treated as a highly plastic single entity, a suite of subspecific taxa, or up to 11 distinct species. Molecular studies have recovered a monophyletic ‘*H. ovalis* complex’ that comprises three distinct clades; however single named taxonomic entities are frequently represented in two or more clades and nest among materials recognised as *H. ovalis*, suggesting that the delineation of species requires reconsideration.

Species in the *H. ovalis* group are morphologically simple and flowering is reportedly rare, so taxonomic works have emphasised leaf characters for diagnosis of identity. These include the shapes and absolute and relative dimensions of lamina and petiole, the numbers of pairs of cross-veins, the angles and extent of branching of cross veins, and the distance between blade margin and intra-marginal vein. Despite its wide application, recent description of multiple new taxa based on limited collections from narrow geographical ranges has highlighted a number of shortcomings in this approach. Pre-eminent among them are poor character definitions, use of highly correlated characters, recognition of species with overlapping morphological ranges, and lack of attention to within-population variability.

We therefore investigated the intra- and inter-population variation in key morphological features in eight Australian populations identified as *H. ovalis*. Two Western Australian populations were sampled intensively and scored for the diagnostic features. These were supplemented with less-intensively sampled populations from northern WA, Victoria and Queensland and one population of the closely related *H. australis*. Species identity was confirmed using established chloroplast and nuclear DNA markers. Our initial analysis indicates that within-population variation in *H. ovalis* is very wide and there is substantial within-individual variability. Critically, these forms of variation swamp any differences between populations, and within a single population one can find individuals that fall within the ranges of more than one described species or subspecies. Our findings support the contention that a review of morphologically-based species delimitations within the complex is warranted.



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## Session 8: New Taxonomic Resources and Systematic Studies

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### Building a key to all Australian flowering plants—70% and counting

8–33

Kevin Thiele

Eubio Consulting, Inglewood, WA

A project in KeyBase—the *Flowering Plants of Australia* project (<http://keybase.rbg.vic.gov.au/projects/show/1>)—has the ambitious aim to develop and maintain a nested set of keys to all flowering plant taxa in Australia and its island territories. While ambitious and aspirational (and perhaps even quixotic) this is eminently do-able. The first stage—gathering together in KeyBase all existing keys—is complete. The second stage—updating the taxonomy in existing keys by harmonising them with the Australian Plant Checklist (APC)—is largely complete. The next stage—creating new keys as required to cover the gaps—has commenced. Currently, the set of keys includes: an updated and improved key to all families; keys to genera for 97% of the 269 APC plant families; keys to species for 87% of the 2797 APC genera; and 14,937 (70%) of the 21,301 APC species. The project is thus within striking distance of completion, and could be completed within 3 years with suitable support and commitment from the community. A complete key to all flowering plant taxa will be of immense benefit to our community and our users including consultants, researchers, students and the general public, and will form an important component of the forthcoming *eFlora of Australia*. It also has the promise to be readily maintainable—once complete, an important goal for our community could be to ensure that appropriate keys are updated as a matter of course whenever a new taxon is described, to ensure that all Australian taxa are readily identifiable into the future.

Donna Lewis and Ian Cowie

Northern Territory Herbarium, Flora and Fauna Division, Dept. of Land Resource Management, Darwin, NT

FloraNT—Northern Territory flora online is an online system to search/browse the NT flora and access NT Herbarium specimen data. The first production release was November 2014 and is the first of its kind for the NT. FloraNT includes the ability for users to search/browse the entire NT flora and also the ability to view and extract threatened and introduced species information. FloraNT enables users to download flora checklists across user defined areas and by family/genus. Factsheets of plant species can be viewed and downloaded and includes flora descriptions, conservation status, ecological attributes, images and distribution maps. FloraNT has the ability to conduct spatial searches using mapping tools and various spatial layers. Identification keys for regional and ecological floras are also available for many families and genera. The content for FloraNT is maintained in the NT Herbarium's HOLTZE specimen database and will continue to be enhanced by adding new data and images, and improvements to overall functionality. FloraNT is available at <http://eflora.nt.gov.au/>

Richard L. Boyne

Royal Botanic Gardens, Kew, UK; Queensland Herbarium, DSITI, Toowong, QLD

From mid-2013 to early 2016 I was a digitisation officer for the herbarium at The Royal Botanic Gardens, Kew. The Herbarium contains about 7 million specimens collected since the 1700s and includes a large number of types from every floristic region on Earth.

My job was to make digital records and images of herbarium specimens for different projects. The purpose of this is to make the specimens accessible to a wider audience, facilitate the analysis of large datasets and to reduce the need for lending specimens to other institutions. The main projects were The Global Plants Initiative (type specimens) and Reflora (Brazilian specimens). There are plans to have 80% of the herbarium digitised by 2020, possibly in collaboration with other herbaria and using automated imaging equipment. The staff in the lab are also developing a workflow for digitising the microscope slide collection.

I participated in other activities for Kew while I was working there. I attended a field trip for the UK National Tree Seed Project that contributed to the Millennium Seed Bank. During London's Open House Day I led tours of the herbarium and talked about some of the historically significant collections. During the summer festival I talked about the history, phylogeny and biochemistry of spice plants and the work done by Kew in relation to them. These kinds of public engagement activities were valuable because they educated people about the importance of plant research and conservation, and raised Kew's public profile at a time of financial difficulties. Institutions in Australia could use these kinds of activities for the same purposes.

Yu Ito<sup>1</sup>, Norio Tanaka<sup>2</sup>, Anders [S.] Barfod<sup>3</sup>, Seong-Hyun Cho<sup>4</sup>, Stephan Gale<sup>5</sup>, Richard Jobson<sup>6</sup>, Young-Dong Kim<sup>4</sup>, Isabel Larridon<sup>7</sup>, Jie Li<sup>1</sup>, A. Muthama Muasya<sup>8</sup>, John Parnell<sup>9</sup>, Sylvia Phillips<sup>7</sup>, Amornrat Prajaksood<sup>10</sup>, Kotaro Shuto<sup>11</sup>, Phetlasy Souladeth<sup>12</sup>, Shuichiro Tagane<sup>13</sup>, Nobuyuki Tanaka<sup>2</sup>, Okihito Yano<sup>14</sup> and Mark Newman<sup>15</sup>

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<sup>2</sup>Tsukuba Botanical Garden, National Museum of Nature and Science, Tsukuba, Japan; <sup>3</sup>Department of Bioscience, Aarhus Universitat, Denmark; <sup>4</sup>Hallym University, South Korea; <sup>5</sup>Kadoorie Farm & Botanic Garden, Hong Kong, China; <sup>6</sup>Sydney Botanic Garden, NSW; <sup>7</sup>Kew Botanic Garden, England, UK;

<sup>8</sup>Department of Biological Sciences, University of Cape Town, Rondebosch, South Africa; <sup>9</sup>Trinity College Dublin, Dublin, Ireland; <sup>10</sup>Khon Kaen University, Thailand; <sup>11</sup>Fukushima University, Fukushima, Japan;

<sup>12</sup>National University of Laos, Laos; <sup>13</sup>Kyushu University, Fukuoka, Japan; <sup>14</sup>Okayama University of Science, Okayama, Japan; <sup>15</sup>Royal Botanic Garden Edinburgh, Edinburgh, UK

*Eriocaulon* is a genus of about 400 species of monocotyledonous flowering plants in the family Eriocaulaceae. The genus is widely distributed in the world, with the centres of diversity in tropical regions, such as tropical Asia and tropical Africa. A previous molecular phylogeny implied an African origin for *Eriocaulon* as a sister relationship between the genus and an African endemic one was recovered. The species of *Eriocaulon* primarily grow in wetlands while some inhabit shallow rivers and streams with an apparent adaptive morphology of elongated submerged stems. Polyploidy is known from the genus. In this talk, we provide preliminary results of our molecular phylogenetic analysis of the genus aiming to i) assess the biogeographic origin, ii) explore phylogenetic origins of submerged species, and iii) address the evolutionary role of polyploids.

# Implications for conservation in the Mount Compass Swamp Gum *Eucalyptus paludicola* based on genome wide markers

9–37

Kor-jent van Dijk<sup>1</sup>, Michelle Waycott<sup>1, 2</sup>, Joe Quarmby<sup>3</sup>, Doug Bickerton<sup>3</sup>, Ed Biffin<sup>2</sup> and Hugh Cross<sup>2,4</sup>

<sup>1</sup>Environment Institute and School of Biological Sciences, The University of Adelaide, Adelaide, SA; <sup>2</sup>State Herbarium of South Australia, Adelaide, SA; <sup>3</sup>Department of Environment, Water and Natural Resources, Adelaide, SA; <sup>4</sup>Norwegian Institute of Bioeconomy Research, Ås, Norway

*Eucalyptus paludicola* D. Nicolle, commonly known as Mount Compass Swamp Gum, Marsh Gum or Fleurieu Swamp Gum, is listed as an endangered species under the Commonwealth Environmental Protection and Biodiversity Conservation (EPBC) Act (1999). Populations of *E. paludicola*, and closely related species, *E. ovata* and *E. cosmophylla* were analysed using novel genetic markers developed using Next Generation Sequencing (NGS) to assess genetic diversity and phylogenetic relationships. NGS has facilitated the discovery of affordable management-informative markers that can be subsequently screened in species of conservation concern. A total of 410 samples were screened for 167 single nucleotide polymorphisms across 48 amplified DNA regions.

Initial population genetic analyses suggest significant signs of clonality in both *Eucalyptus paludicola* and *E. ovata*, 151 samples sharing one of 53 multilocus genotypes. The populations of Kangaroo Island did not show evidence of divergence of *E. paludicola* from mainland populations, as was expected. In fact, no genetic structure was observed for this species at all.

When genetic relationships of co-occurring species are considered, *Eucalyptus paludicola* demonstrates a genetic signature that contains elements of both *E. ovata* and *E. cosmophylla* suggesting a recent hybrid origin. Probabilistic hybrid analyses indicate they are usually first generation hybrids (F1) with rare back crosses to parents. These findings suggest *E. paludicola* is a rare case of natural inter-sectional hybridisation between *E. ovata* and *E. cosmophylla*. These results open a debate as to the conservation strategies that might be applied to this species including its status as endangered.

This study was a partnership with the Adelaide Mount Lofty Ranges and Murray Darling Basin National Resource Management organisations, the South Australian Department of Environment, Water and Natural Resources (DEWNR) and the University of Adelaide to test novel approaches to assess and refine the conservation status of threatened species.

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Lunch

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### Diverse origins and evolution of sexual expression in Australasian Malveae (Malvoideae, Malvaceae)

9–38

Jennifer A Tate<sup>1</sup>, Cynthia Skema<sup>2</sup> and WR (Bill) Barker<sup>3</sup>

<sup>1</sup>Institute of Fundamental Sciences, Massey University, Palmerston North, New Zealand; <sup>2</sup>Morris Arboretum of University of Pennsylvania, Philadelphia, PA, USA; <sup>3</sup>State Herbarium of South Australia, Adelaide, SA

Sexual dimorphism, with male and female functions separated in different flowers, has evolved repeatedly across the angiosperms. To address the origins and evolution of sexual dimorphism in a group of Australian/New Zealand Malvaceae, we used a phylogenetic approach analysing nuclear ITS and plastid (*rpl16* intron, *petL-psbE* and 3'*rps16*–5'*trnK*<sup>(UUU)</sup> spacers) sequence data and reconstructing the evolution of sex expression across the tree. Taxonomically, *Lawrenzia* is not monophyletic. *Lawrenzia berthae* occurs outside a core clade of *Lawrenzia* and is closely related to *Sida hookeriana*. Also, several species (e.g., *L. glomerata*) are not monophyletic as currently recognised. Sexual expression is varied amongst the species of *Lawrenzia* with multiple origins of some sexual types and reversions to the hermaphroditic state. On the evidence from collections within species and populations, the sexual state is almost always fixed in each species. A single, separate origin of dioecy unites Australian *Asterotrichion* and *Gynatrix* with *Plagianthus* from New Zealand and this clade is sister to *Hoheria* (endemic to New Zealand), which includes only hermaphroditic species. Our results indicate that sexual dimorphism can evolve repeatedly, even among closely related genera, and calls for further study of the plasticity of sex expression in these species.

Melodina Fabillo and Tanya Scharaschkin

Queensland University of Technology, Brisbane, QLD

*Eremochloa* is a genus of grasses, with approximately 12 species, found mainly in the open woodlands of Asia and Australia. *Eremochloa* is characterised by spikelets with lower glumes bearing apical wings and spiny keels. Other features of the spikelets of *Eremochloa* resemble other genera of the subtribe Rottboelliinae (e.g., *Mnesithea*, *Coelorachis*), leading botanists to place some species in these genera. Three species of *Eremochloa* occur in Australia and are also found in Asia. *Eremochloa bimaclata* and *E. ciliaris* are widely distributed in the eastern part of Australia, from north Queensland to New South Wales. There is only one record of *Eremochloa muricata* from Queensland (Cape Flattery, 1976) and one from New South Wales (Byron Bay, 1912). *Eremochloa muricata* has been declared an endangered species in Queensland. Due to the remoteness of Cape Flattery, where *E. muricata* was found in Queensland, some botanists suggest that human introduction of this “endangered” grass was unlikely. There are no phylogenetic studies that have established the monophyly of *Eremochloa*.

The objective of this study is to determine phylogenetic relationships of *Eremochloa*, with special reference to the Australian species. Preliminary observation of the gross morphology of Australian taxa show that the common species, *E. bimaclata*, exhibits infraspecific variation. Different morphological forms based on features of the spikelets have been identified. Gross morphological data obtained from the Cape Flattery and Byron Bay specimens of *E. muricata* are not consistent with description in grass keys. The Australian *E. muricata* specimens are, in fact, one form of *E. bimaclata*. Results of phylogenetic analyses of chloroplast sequence data (*matK*, *ndhF* and *trnL-F*) and leaf micromorphology will be presented. Findings of this study will contribute to establishing the phylogeny of the subtribe Rottboelliinae. These will also provide information that could assist in the identification of species of *Eremochloa*.

# Are we splitting hairs? Resolving infrageneric relationships in the Australian *Plectranthus* (Lamiaceae)

9–40

Trevor Wilson<sup>1,2</sup>, Paul Forster<sup>3</sup>, Barry Conn<sup>1,3</sup>, Maurizio Rosetto<sup>1</sup> and Murray Henwood<sup>3</sup>

<sup>1</sup>National Herbarium of New South Wales, Royal Botanic Gardens and Domain Trust, Sydney, NSW;

<sup>2</sup>Queensland Herbarium, DSITI, Toowong, QLD; <sup>3</sup>School of Life and Environmental Sciences, The University of Sydney, Sydney, NSW

Australia represents a high centre of species diversity for *Plectranthus* (Lamiaceae), a genus distributed across most of the old world tropics and well-known for its medicinal, agricultural and horticultural uses. The number of species descriptions for Australia has steadily increased over the past few decades, doubling in number since the last taxonomic revision of *Plectranthus*. Many of these species are found in close proximity, such as sharing similar but disjunct rock outcrop habitats, and they look extremely similar, as they are distinguished by subtle differences in morphology. Identification of these species can be extremely challenging due to a troublesome combination of phenotypic plasticity and morphological characters (e.g. corolla angle) that are easily distorted in pressed specimens; these problems, in combination with the subtlety of taxonomically useful characters such as trichomes (or ‘hairs’) and glands, have facilitated a high number of misidentifications. Currently there has been no phylogenetic study dedicated to *Plectranthus* and a careful integration of molecular and morphological data is necessary to test the utility of taxonomic characters and define a robust understanding of relationships. The systematics of *Plectranthus* will be explained along with the methods now being used to acquire a meaningful classification and phylogeny for the genus.



# Species delimitation in Southern Hemisphere bracteate-prostrate forget-me-nots (*Myosotis*, Boraginaceae) based on analyses of pollen and morphological data

9–41

Heidi Meudt<sup>1</sup> and Jessie Prebble<sup>1,2</sup>

<sup>1</sup>Museum of New Zealand Te Papa Tongarewa, Wellington, New Zealand; <sup>2</sup>Massey University, Palmerston North, New Zealand

Taxonomic revision is a high priority in New Zealand forget-me-nots (*Myosotis*, Boraginaceae), a genus in which approximately three of every four species is classified as threatened or at risk according to the New Zealand Threatened Classification System. The bracteate-prostrate group of forget-me-nots comprises 19 described species and varieties and nine tag-named entities, all endemic to New Zealand except *M. albiflora* (endemic to southern Chile and Argentina) and *M. antarctica* (also native to Chile). The main aim of the current study was to obtain taxonomically useful characters for delimiting species and species groups within the bracteate-prostrate group. To test species limits in this group, two different data sets were analysed: 1) pollen data set (16 pollen characters assessed using scanning electron microscopy [SEM] from 69 herbarium specimens), and 2) morphological data set (51 morphological characters from 266 herbarium specimens). The two data sets were analysed separately using Ward clustering, non-metric multidimensional scaling and Bayesian model-based clustering. *Myosotis* pollen is heterocolpate and variable, and analyses of the pollen data set recovered three significant clusters. Important pollen characters separating the clusters included number of apertures, presence of a polar cap, and shape. Pollen characters may be useful for taxonomy, particularly when combined with other data sets. Analyses of the morphological dataset recovered six significant clusters representing different habits. Important morphological characters included rosette leaf, calyx, corolla and nutlet characters, which support the recognition of several (but not all) described species. In addition, several of the tag-named entities may represent new species that will require formal description.

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Afternoon Break

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### Fruit mesocarp morphology of *Elaeocarpus* (Elaeocarpaceae): a phylogenetic survey

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Janet Gagul<sup>1,2</sup>, Andrew Rozefelds<sup>3</sup> and \*Darren Crayn<sup>1</sup>

\*Presenting; <sup>1</sup>Australian Tropical Herbarium, James Cook University, Cairns, QLD; <sup>2</sup>College of Science and Engineering, James Cook University, QLD; <sup>3</sup>Queensland Museum, Brisbane, QLD

Elaeocarpaceae, a moderately large family of trees and shrubs comprises about 550 species in 12 genera. Within Elaeocarpaceae, fruits are capsules (*Sloanea*, *Dubouzetia*, *Peripentadenia*), berries (*Sericolea*, *Aristotelia*) or drupes (*Aceratium*, *Elaeocarpus*). *Elaeocarpus* L., the largest genus (c. 360 spp.) in the family is well defined morphologically by the distinct fringed petals and drupaceous fruits, which often contain robust woody fruit stones. These woody stones (formed from inner mesocarps) are morphologically highly distinctive and vary in size, shape and ornamentation, providing useful characters to differentiate species. A rich fossil record of *Elaeocarpus* mesocarps exists.

Taxonomic studies on *Elaeocarpus* have been based largely on morphology, but few have included mesocarp morphology to support the classification. Phylogenetic studies, using morphological and molecular data, have resolved broad relationships within *Elaeocarpus* but none have incorporated fruit mesocarps extensively in a phylogenetic context. Consequently the evolution of fruit morphology and its value in taxonomy and interpreting the fossil record is poorly known.

In the present study, the mesocarp morphology of *Elaeocarpus* fruits will be interpreted for the first time in a phylogenetic context. A comprehensive survey of fruit mesocarp features such as size, shape, ornamentation and anatomy of the mesocarps will be undertaken. With the current strong molecular phylogenetic framework of the genus, which is built on c. 30% of species diversity, we aim to address the broad question: ‘what are the evolutionary patterns of fruit mesocarp morphology in the genus *Elaeocarpus*?’ The results will provide insights into species-level relationships and help us to understand the evolution of the genus.

## Leaf anatomy of invasive and non-invasive climbers: does it correspond with ecophysiological performance?

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Richard L. Boyne<sup>1,2,3</sup>, Olusegun O. Osunkoya<sup>2</sup> and Tanya Scharaschkin<sup>3</sup>

<sup>1</sup>Queensland University of Technology, Brisbane, QLD; <sup>2</sup>Biosecurity Queensland, Brisbane, QLD;

<sup>3</sup>Queensland Herbarium, DSITI, Toowong, QLD

An aspect of current research in invasion biology is the identification of characteristics that are common to invasive species that can be used to inform management and quarantine practices. This study was aimed at testing previous findings and inferences related to ecophysiological performance traits of invasive plants by examining the leaf anatomy of some invasive and non-invasive species of climber. It was found that the invasive species had traits consistent with a low construction cost and a higher carbon assimilation capacity than their non-invasive partners, but these traits were different for each family or functional group. The invasive species also exhibited higher phenotypic plasticity for most of the measured traits.

## There goes *Thecanthes*: molecular systematics expands the circumscription of *Pimelea* (Thymelaeaceae)

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Charles Foster<sup>1</sup>, David Cantrill<sup>2</sup>, Elizabeth James<sup>2</sup>, Anna Syme<sup>2</sup>, Rebecca Jordan<sup>2</sup>, Rachel Douglas<sup>2</sup>, Simon Ho<sup>1</sup> and Murray Henwood<sup>1</sup>

<sup>1</sup>School of Life and Environmental Sciences, University of Sydney, Sydney, NSW; <sup>2</sup>National Herbarium of Victoria, Royal Botanic Gardens Victoria, South Yarra, VIC

*Pimelea* Banks & Sol. ex Gaertn. is a genus of flowering plants comprising an estimated 90 species in Australia and approximately 35 species in New Zealand. The genus is economically important, with the inflorescences of some species having floricultural applications, and the presence of toxic compounds in several species proving poisonous to livestock. *Pimelea* grows in a variety of habitats ranging from arid to alpine, suggesting a complicated biogeographic history. The relationships within *Pimelea* remain largely uncertain, despite previous attempts at clarification using molecular phylogenetics. However, it is clear that *Pimelea* is closely related to *Thecanthes* Wikstr., with the two genera comprising the subtribe Pimeleinae. We used Bayesian and maximum-likelihood phylogenetic analyses of four plastid markers (*matK*, *rbcL*, *rps16*, *trnL-F*) and one nuclear ribosomal marker (ITS) to examine the evolutionary relationships within Pimeleinae, and place this group in the context of the broader subfamily Thymelaeoideae. We will discuss the implications of our results for the taxonomy of *Pimelea* and *Thecanthes*, and suggest necessary future directions to resolve further the relationships within Pimeleinae and Thymelaeoideae.

## Soil seed banks and the restoration of plant biodiversity in an arid zone habitat

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Duncan Mackay, \*Molly Whalen, Kieren Beaumont and Richard Davies

\*Presenting; School of Biological Sciences, Flinders University, Adelaide, SA

Predicting the response of native vegetation in Australia's arid rangelands to management actions such as changing grazing regimes is often hampered by a lack of knowledge regarding the nature of native plant biodiversity at a local scale. Simply measuring above-ground plant species richness can be quite misleading because in arid habitats a significant component of a site's plant diversity, particularly that of short-lived species, may be present as dormant seeds in the soil seed bank. We have investigated factors influencing variation in both above- and below-ground plant diversity in a large conservation reserve in arid South Australia. This reserve, "Witchelina", has a long history (c. 140 years) of pastoral use but was destocked in 2010 when it was purchased by the Nature Foundation of South Australia. Particular factors being investigated include variation among different habitats and effects of past grazing intensities. For example, we compared the diversity and composition of the seed banks and above-ground vegetation in areas close to watering points with a history of heavy grazing with those of areas more distant from watering points that have been less heavily grazed. Effects of past grazing in the two studied plant communities are reflected in changes in the cover, species richness and species composition of the above-ground vegetation. The soil seed bank contains a diverse array of plant species even after a long history of pastoral grazing.