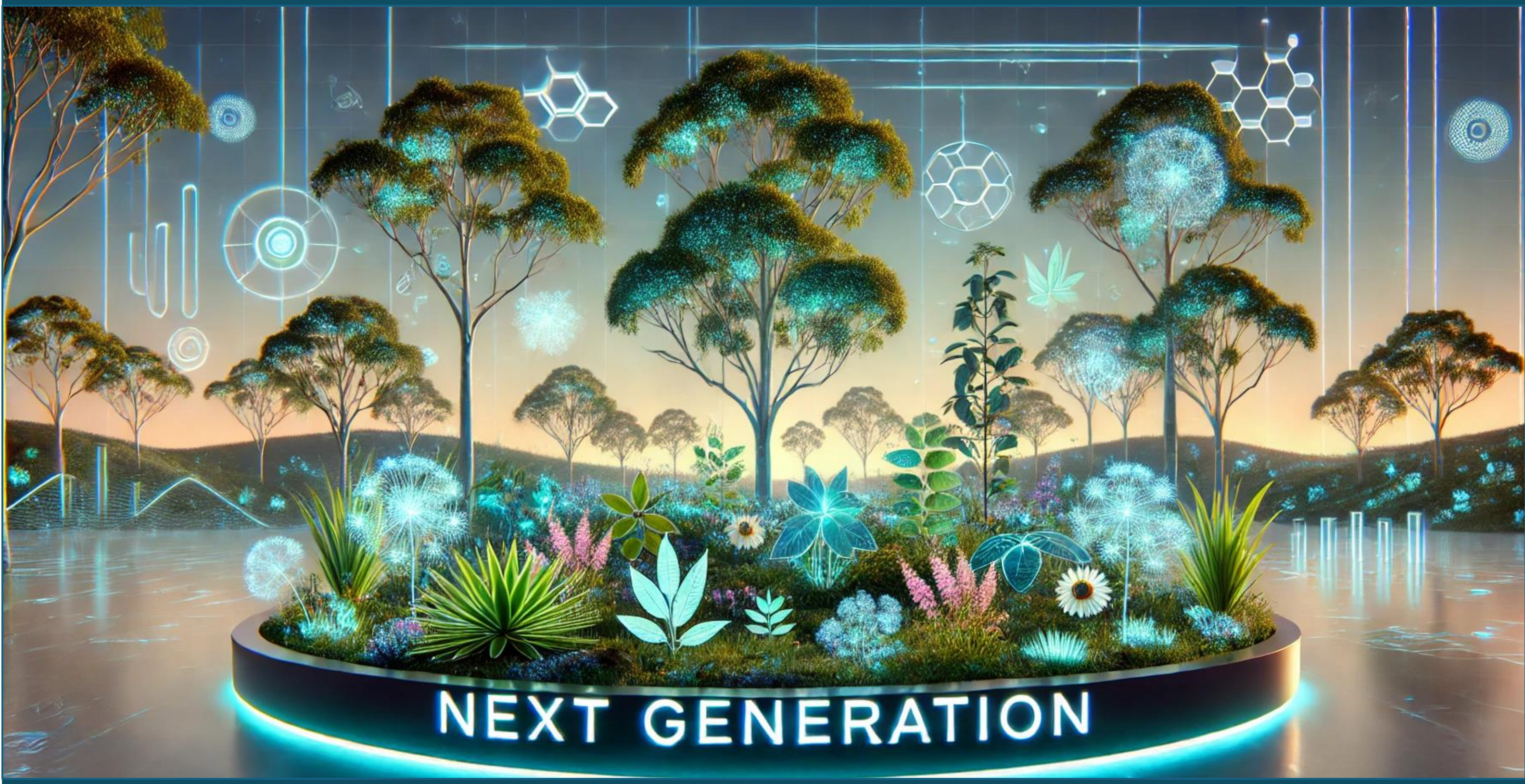
Australasian Systematic Botany Society 2025 Conference

Next Generation Botany

2nd– 6th November, UNE, Armidale



Conference website

https://asbs.org.au/conferences/asbs-2025-conference/

Conference contacts

conference.asbs@gmail.com

Social media ASBS Facebook #ASBS2025
https://www.facebook.com/groups/434955569922530/

If you have any questions, or if problems arise during the conference, please speak to a conference organiser or ASBS Council Member.

ASBS 2025 conference organising committee

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Conference banner & logo design by Andrew Thornhill using AI.

Contents

Welcome

Welcome to the 2025 ASBS Conference at the University of New England, Armidale, NSW. UNE Botany has a rich history of over 80 years of research and teaching in plant systematics, supported by the N.C.W. Beadle Herbarium.

The conference theme, **Next Generation Botany**, provides inspiration for a range of talks focusing on new techniques and discoveries covering aspects of Australasian plant taxonomy, systematics, phylogenetics, genomics, biogeography, palaeobotany, and conservation.

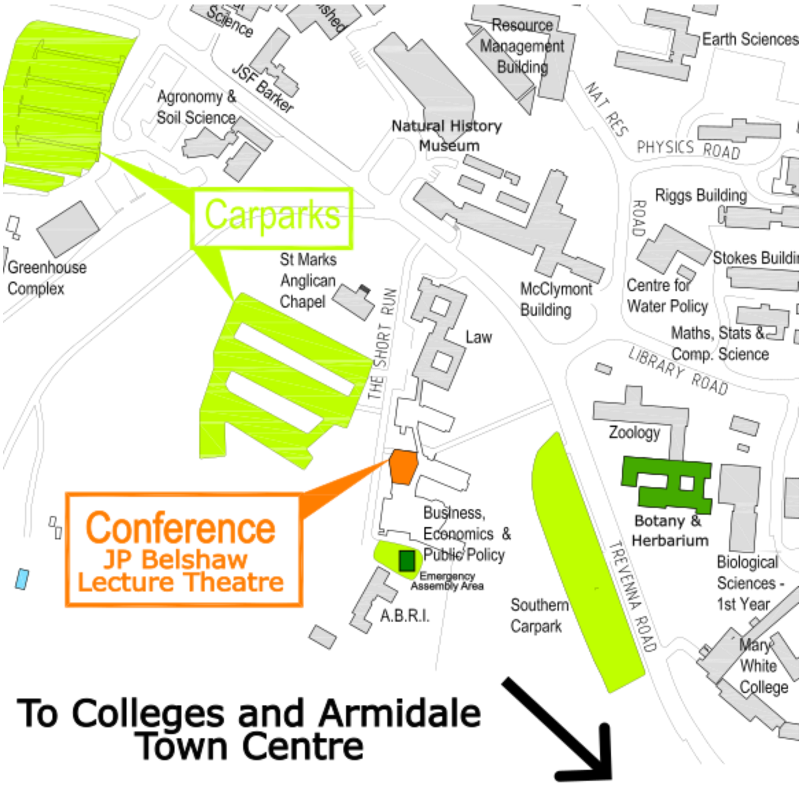
A highlight of this conference will be the launch of the **Palaeobotany and Palynology Chapter**, with special sessions on Monday, the 3rd of November.

Conference venue

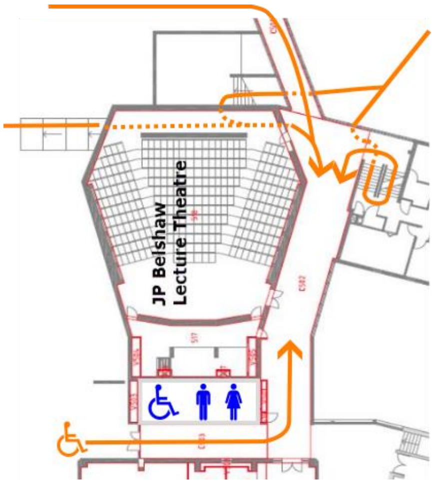
The conference will be in the EBL Building (Economics, Business and Law). Talks will be in the **JP Belshaw Lecture Theatre** (LT1) on the main floor of the Economics wing (W40), which is continuous with the walkway from the Law wing (W39). Follow the signs to get there from the Eucalypt Lawn or the EBL carpark.

Please be aware that some parts of the University grounds and carparks are still closed due to snow damage. Don't ignore taped-off areas.

Building and location map



Floor and access map



For more maps, see https://www.une.edu.au/maps or https://studentvip.com.au/une/armidale/maps

Registration

Registration will be available at the following times and locations.

- Sunday 8 am for workshop attendees.
- Sunday evening from 5 pm at the Registration mixer at Welder's Dog Brewery
- Monday-Wednesday from 8 am in the Conference Foyer.

Food & Beverages

All catering breaks during the conference (morning tea, lunch, and afternoon tea) will be held in the foyer outside of the Belshaw Lecture theatre in the EBL Building. Please refrain from eating food that is labelled with particular dietary requirements, unless you have selected a particular option on your registration.

Toilets & Accessibility

The toilets closest to the lecture theatre are in the entryway off the foyer. There is also another set of toilets over the walkway in W39 to the north of the Belshaw Lecture Theatre.

Wheelchair access is from a drop-off zone on the Short Run road (see maps above). An accessible toilet is available in the entryway off the foyer, near the external door.

Emergency Evacuation

In case of an emergency, please leave the building and gather at the Emergency Assembly Area in the carpark to the south of the EBL building.

Parking

Parking is free of charge at UNE in blue or purple zones. The nearest carpark is behind St Mark's Chapel.

Quiet Spaces

A dedicated quiet room will be available for this conference: Lecture Theatre 3, immediately downstairs from the Belshaw Lecture Theatre. There is also a less private quiet area in the main foyer, continuous with the catering area.

Smoking

UNE is a non-smoking environment. All types of smoking including electronic smoking devices are not permitted in or near buildings.

Internet Access

Connect your PC, tablet or smart phone to WiFi network "**UNE-Guest"**.

Enter the access key below.

Access Key: ASBS-2025
Your ID: Australasian Systematic Botany Society 2025

Transport

A shuttle bus will run each day between UNE campus and the Armidale Post Office, with extra services for evening events.

Daily, Monday the 3rd to Wednesday the 5th of November

- Armidale Post Office – Pickup at 8:10 am, 8:35 am
- UNE to Armidale Post Office – Pickup at 5:10 pm

Palaeo & ECR events, Monday the 3rd of November

- UNE to Great Hops for– 5.45 pm
- Great Hops to UNE and Armidale Post Office – 8 pm, 8:45 pm

Conference Dinner, Tuesday the 4th of November

- UNE to NERAM via Armidale Post Office – 5:30 pm
- Armidale Post Office to NERAM – 5:50 pm
- NERAM to UNE via Armidale Post Office – approx. 9:45 pm, 10 pm

Annual General Meeting, Wednesday the 5th of November

- UNE to Armidale Post Office – approx. 6 pm

Other transport options include regular buses (Edwards Coaches, https://edwardscoaches.com.au/) and taxis (Armidale Taxis, https://armidaletaxis.com.au/).

Visiting the Herbarium

The N.C.W. Beadle Herbarium houses > 100,000 land plant specimens. If you wish to visit the Herbarium, please contact the Director, Dr Andrew Thornhill (andrew.thornhill@une.edu.au).

Oral Presentations

Themed sessions follow the morning lectures and keynote talks Monday-Wednesday. Oral presentation slots are either 15 minutes long (10–12 minute presentation plus 3 minutes for questions and transition to the next speaker) or 7 minutes long (5 minute presentation plus 2 minutes for questions and transition). A rule of thumb is to plan to have approx. 1 slide per minute, with a total of up to 12 slides or 5 slides respectively. You will be “oinked” off stage if you go over your allotted time.

A remote slide advancer with laser pointer, lectern, several microphone options, and a monitor screen for the speaker will be available. Talks will also be simultaneously presented online for online registrants.

Talks must be a PowerPoint presentation submitted to Submit PowerPoint to Dropbox by the day before https://www.dropbox.com/scl/fo/9qz5gycouot7ee48zpuuo/AJpxRA4fV5LpZ2YdFgN_IcY?rlkey=e2qaxto0g2887c5sn3n0jbn7c&st=051x0vw2&dl=0

If you need help loading your presentation during the conference, please look for Tareg Shaldoom, who has kindly volunteered to organise slides.

Student Prizes

Student talks will be eligible for prizes supported by CSIRO Publishing and the journal Australian Systematic Botany.

- Pauline Ladiges Award for best student talk (full talk) - $500
- Prize for best student speed talk - $250
- Runner up prize for best student talk (full talk) - $250

Annual General Meeting

The ASBS AGM is an update on Society business and an opportunity for members to participate in decision-making. All ASBS members are welcome to attend, including students and other ECRs.

SUMMARY PROGRAM

Workshop – SUNDAY 2 Nov	
9:00 – 16:30	**Wiki for Botanists workshop** Armidale City Bowling Club, 92–96 Dumaresq St, Armidale
17:00 – 19:00	**Registration mixer** Welder's Dog Brewery Brew Bar & Entertainment Centre, 101 Beardy St, Armidale

DAY 2 – MONDAY 3 Nov		**DAY 3 – TUESDAY 4 Nov**		**DAY 4 – WEDNESDAY 5 Nov**	
8:15 – 8:50	Registration	8:15 – 8:50	Registration	8:15 – 8:50	Registration
9:00 – 9:45	**Welcome to Country & Opening Address**	9:00 – 9:45	**2024 N.T. Burbidge Medal** presentation and address: Karen Wilson	9:00 – 9:45	**2025 N.T. Burbidge Medal** presentation and address: To be announced
9:45 – 10:30	**Keynote I:** Hervé Sauquet	9:45 – 10:30	**Keynote II:** Francis Nge	9:45 – 10:30	**Keynote III:** Helen Kennedy
10:30 – 11:00	**Morning Tea**	**10:30 – 11:00**	**Morning Tea**	**10:30 – 11:00**	**Morning Tea**
11.00 – 12.35	**Session 1:** Phylogenomics I	11.00 – 12.30	**Session 4:** Phylogenomics II	11.00 – 12.15	**Session 7:** Non-flowering plants and fungi
12:35 – 13:30	**Lunch**	**12:30 – 13:30**	**Lunch**	**12:15 – 13:15**	**Lunch**
13:35 – 14:55	**Session 2:** Palaeobotany I Palaeo Keynote I: Andrew Rozefelds	13.30 – 15.15	**Session 5:** Speed talks	13.15 – 14:30	**Session 8:** Methods
15:00 – 15:30	**Afternoon tea**	**15:15 – 15:50**	**Afternoon tea**	**14:30 – 15:00**	**Afternoon tea**
15:30 – 17:00	**Session 3:** Palaeobotany II Palaeo Keynote II: Vera Korasidis	15:50 – 17:00	**Session 6:** 10-Minute updates	15:00 – 16:15	**Session 9:** Population genetics and taxonomy
18:00–22:00	**ECR Student Catch up/Palaeo Welcome Dinner**	**18:00–22:00**	**Conference Dinner**	**16:15–17:15**	**ASBS AGM**

Field Trip – THURSDAY 6 Nov	
8:00 – 17:00	Field Trip to Crystal Shower Walk at Dorrigo National Park meet at UNE Botany car park

FULL PROGRAM

Day 1 - Monday 3rd November

08:15–8:50	Registration	
9:00–9:45	**Welcome to Country & Opening Address** Uncle Colin Ahoy and UNE Vice Chancellor, Professor Chris Moran	
9:45–10:30	**KEYNOTE I: Hervé Sauquet** Angiosperm macroevolution: embracing the unknown (and the unknowable)	
10:30–11:00	**Morning tea**	
	Session 1: Phylogenomics I Chair: Rose Andrew	
11:00–11:20	1.1	Dan Murphy **Next Generation systematic botany in Australasia: looking back, looking forward**
11:20–11:35	1.2	Lalita Simpson **Exploring target sequence capture for multi-scale conservation genomics of Australian orchid species complexes**
11:35–11:50	1.3	Mike Bayly **The ABC of eucalypts: (another) phylogeny of *Angophora*, *Blakella* and *Corymbia***
11:50–12:05	1.4	Jessie Prebble **Genetic characterisation and conservation of New Zealand *Pimelea***
12:05–12:20	1.5	Matthew Renner **Species at the edge of evolution: a population-level assessment of species delimitation in *Pterostylis* section *Parviflorae* (Orchidaceae)**
12:20–12:35	1.6	Heidi Meudt **Forget-me-not phylogenomics: improving the resolution and taxonomy of a rapid island and mountain radiation in Aotearoa New Zealand (*Myosotis*; Boraginaceae)**
12:20–13:30	**Lunch**	
	Session 2: Palaeobotany I Chair: Jessie Prebble	
13:35–13:55	2.1	Palaeo Keynote 1: Andrew Rozefelds **Born of Fire – The sub-basaltic silcrete floras of eastern Australia and the role for volcanism in shaping the modern Australian flora**
13:55–14:10	2.2	Anne-Marie Tosolini **Eocene-Oligocene Floras from Fildes Peninsula, King George Island, Antarctic Peninsula**
14:10–14:25	2.3	Miriam Slodownik **The Austral Antarctic Forest during the Early Eocene Climatic Optimum – biogeography, diversity and the fate of polar lineages**
14:25–14:40	2.4	Greg Jordan **Extreme greenhouse climate events drive major restructuring of floras**
14:40–14:55	2.5	David Cantrill **Malvaceae (Sterculioideae) inflorescences with *in situ* pollen preserved by nanophase goethite from the Miocene of Australia**
15:00–15:30	**Afternoon tea**	
	Session 3: Palaeobotany II Chair: Anne-Marie Tosolini	
15:30–16:05	3.1	Palaeo Keynote 2: Vera Korasidis **New techniques for reconstructing ancient atmospheres and fire intensities**
16:05–16:20	3.2	Jeremy Wyman* **Comparative rhizotaxy of fossil and living isoetalean rhizomorphs reveals development through rootlet intercalation within a triangular lattice**

16:20–16:35	3.3	Maria Paulsen **Anglesea amber from Australia as new archive for Eocene liverwort and moss species**
16:35–17:00	3.4	Nunzio Knerr **Pannotator: transforming ecological field surveys using 360-degree camera imagery**
18:00–21:00	**ECR student catch up/Palaeo Welcome Dinner**	

*Student talks

Day 2 – Tuesday 4th November

08:15–8:50	Registration	
9:00–9:45	**2024 N.T. Burbidge medal address: Karen Wilson**	
9:45–10:30	**KEYNOTE II: Francis Nge** Flora-wide trends in macroevolution: Australia and beyond	
10:30–11:00	**Morning tea**	
	Session 4: Phylogenomics II Chair: Matthew Renner	
11:00–11:15	4.1	Ryan O'Donnell* **Population genomics provides molecular support for morphological species hypotheses and hybridisation among sexually deceptive greenhood orchids (*Pterostylis*; Pterostylidinae)**
11:15–11:30	4.2	Emily Rose Hoskin* **Into the Depths – Investigating the species identity of tree roots in the Naracoorte Cave Systems**
11:30–11:45	4.3	Consolata Nanjala* **Phylogenomics provides insights into the diversification and range evolution of the mega genus *Bulbophyllum* (Orchidaceae)**
11:45–12:00	4.4	Stephanie Goedderz* **Plastid genome evolution in Australasian mycoheterotrophic orchid genus *Danhatchia***
12:00–12:15	4.5	Andrew McDougall* **Phylogenetic and population level analyses of South Australian *Caladenia patersonii* and *C. reticulata* spp. complexes**
12:15–12:30	4.6	Robb Eastman-Densem* **Exploring phylogenetic relationships and discordance in the paper-fruited bloodwoods (*Blakella* sect. *Blakella*)**
12:30–13:30	**Lunch**	
	Session 5: Speed talks Chair: Dan Murphy	
13:30–13:38	5.1	Tareg Shaldoom* **Morphological insights into species delimitation within the *Phebalium glandulosum* complex (Rutaceae)**
13:38–13:46	5.2	Thomas Carter* **A newly discovered diatomite fossil flora from Barraba, NSW**
13:46–13:54	5.3	Rinchen Yangzom* ***Pedicularis bhutanica ined.* (Orbanchaceae), a new species from Bhutan and taxonomic clarification of *P. heydei* Prain and *P. pheulpinii* Bonati**
13:54–14:02	5.4	Millicent Oulo* **Phylogenomics and evolutionary reconstruction of *Lepidosperma* (Cyperaceae): An Integrative Approach**
14:02–14:10	5.5	Millard Uy **The taxonomic status of the Oceanian species of *Carex* section *Indicae* (Cyperaceae)**
14:10–14:18	5.6	Miriam Slodownik **The Witness Tree Project: Long-Term Plant Monitoring for a Changing Climate and Urban Pollution**

14:18–14:26	5.7	Patrick Fahey **A new classification of mallee-boxes (Myrtaceae: *Eucalyptus* ser. *Subbuxeales*) from south-eastern Australia**
14:26–14:34	5.8	Tim Hammer **A comparison of two universal angiosperm bait sets and the phylogenomics of Alismatales**
14:34–14:45	**Break**	
14:45–15:00	5.9	Harvey Orel* **On the effect of chimeric assemblies in target capture studies: investigating the evolution of *Flindersia* (Rutaceae) using a novel method for chimera detection**
15:00–15:15	5.10	Peter Pemberton* **Morphological analysis reveals additional new *Homoranthus* (Myrtaceae: Chamelaucieae) species in the Northern New England Tableland Bioregion**
15:15–15:50	**Afternoon tea**	
	Session 6: 10 minute updates Chair: Helen Kennedy	
15:50–16:00	6.1	Peter Jobson **Creating a new Census for the Flora of New South Wales**
16:00–16:10	6.2	Melinda Laidlaw **Update from the Queensland Herbarium 2025**
16:10–16:20	6.3	Siobhan Leachman **Botanists in the Wikiverse - planting the seeds of open data enrichment and reuse**
16:20–16:30	6.4	Tim Collins **Doing what we can for the ones we love: delivering data to inform assessments of extinction under the Red List**
16:30–16:40	6.5	Tim Hammer **Introducing FloraSA – the new electronic flora for South Australia**
16:40–16:50	6.6	Katarina Nargar **Update from Taxonomy Australia on Discovering Biodiversity: A Decadal Plan for Taxonomy and Biosystematics in Australia and New Zealand 2018–2027**
16:50–17:00	6.7	Niels Klazenga **KeyBase: Interactive online identification keys**
18:00–22:00	**Conference Dinner**	

*Student talks

Day 3 – Wednesday 5th November

08:15–8:50	Registration
9:00–9:45	**2025 N.T. Burbidge medal address:** TBA
9:45–10:30	**KEYNOTE III: Helen Kennedy** Stewardship in Botany: Taking Care for the Next Generation
10:30–11:00	**Morning Tea**
	Session 7: Non-flowering plants and fungi Chair: Ryan O'Donnell
11:00–11:15	7.1 Frances Guard* ***Marasmius*: an Australian Perspective**
11:15–11:30	7.2 Yuqun Du* **Uncovering cryptic diversity and biogeographic history of *Dictyosphaeria* (Siphonocladaceae, Cladophorales)**

11:30–11:45	7.3	Ryan O'Donnell* **Long-read whole genome sequencing reveals novel lineages and genomic divergence thresholds in *Rhizoctonia* (Ceratobasidiaceae; Cantharellales)**
11:45–12:00	7.4	Sapphire McMullan-Fisher **Pretty in pink, purple and orange: fungal fans in *Crepidotus***
12:00–12:15	7.5	Lyn Cook **A coming of age story: population structure and dynamics in *Macrozamia***
12:15–13:15	**Lunch**	
	Session 8: Methods Chair: Andrew Thornhill	
13:15–13:30	8.1	Shawn Laffan **Biodiverse, a tool for the spatial analysis of diversity, version 5**
13:30–13:45	8.2	Jo Birch **Harnessing artificial intelligence to accelerate digitisation of biodiversity data on natural history collection specimens**
13:45–14:00	8.3	Benjamin Anderson **Using Angiosperms353 to address taxonomic questions of conservation significance**
14:00–14:15	8.4	Russell Barrett **A pilot phylogenomics project and plan to construct the New South Wales Plant Tree of Life (NSWPTOL)**
14:15–14:30	8.5	Brent Mishler **New developments in spatial phylogenetics, a global discipline with Australian roots**
14.30–15:00	**Afternoon tea**	
	Session 9: Population genetics and taxonomy Chair: Patrick Fahey	
15:00–15:15	9.1	Alexander Schmidt-Lebuhn **What species of fleabanes (*Erigeron*, Asteraceae) have been introduced to Australia?**
15:15–15:30	9.2	Austin Brown **Blown away by the taxonomic utility of DArTseq for *Lachnagrostis* (Poaceae)**
15:30–15:45	9.3	Brendan Lepschi **Camouflaged by the obvious: a revision of *Goodenia connata* and allies**
15:45–16:00	9.4	John Clarkson ***Erythroxylum* no longer an enigmatic genus in Australia**
16:00–16:15	9.5	Prizes announced and conference close
16:15–17:15	**ASBS AGM**	

ABSTRACTS

Benjamin M. Anderson[1] & Rachel M. Binks

WA Department of Biodiversity, Conservation and Attractions
Biodiversity and Conservation Science, Department of Biodiversity, Conservation and Attractions, Kensington, Western Australia
[1]Email: benjamin.anderson@dbca.wa.gov.au

Using Angiosperms353 to address taxonomic questions of conservation significance

Many of us have been using the widely adopted Angiosperms353 (A353) bait set for target sequence capture and phylogenetic work. For those unfamiliar with it, the bait set allows researchers to sequence up to 353 nuclear genes from plant samples, including older herbarium material. The potential to work with herbarium specimens makes sampling for research on Australian plants much more achievable given how difficult and expensive it is to access remote areas and how variable weather patterns are for ensuring flowering material is present, especially in the arid zone. Another advantage to using A353 is that our datasets become more comparable and reusable across plant groups, allowing the incorporation of distant relatives and previously sequenced samples in our studies. In this talk, I will highlight examples of how we are using A353 genes in studies of herbarium specimens to inform conservation of plants in Western Australia. One of the main ways larger datasets like A353 inform conservation decisions is through the improved taxonomic framework they support, allowing decision makers to better assess whether taxa are rare and threatened. In particular, deciding whether older and more remote specimens are conspecific with known species helps to establish whether they need separate treatment and what the geographical distributions of taxa are. Our examples will illustrate the use of specimens that are (1) geographically widespread and relatively inaccessible and (2) old (> 40 years) for answering conservation questions. I will also discuss approaches (target capture, genome skimming) and lessons learned when using these datasets.

Russell L. Barrett[#,1,2,5], Amy R. Tims[#,3], Carolyn L. Connelly[1], Alexandra S. Dayde[1], Natalie Karbowiak[1], Michael Elgey[4], Lesley Elkan[1], Marie-Benedicte Foyard[1], Margaret M. Heslewood[1], Peter C. Jobson[1], Richard W. Jobson[1], Patricia Lu-Irving[1], Seanna F. McCune[1], Francis J. Nge[1], Andrew E. Orme[1], Matthew A.M. Renner[1], Catherine Wardrop[1], Simon Ho[3], Hannah McPherson[1], Hervé Sauquet[1, 2] & Trevor C. Wilson[1]

[1]National Herbarium of New South Wales, Botanic Gardens of Sydney, Australian Botanic Garden, Mount Annan, NSW, Australia; [2]Evolution & Ecology Research Centre, School of Biological, Earth and Environmental Sciences, UNSW Sydney, Sydney, NSW, Australia; [3]Molecular Ecology, Evolution, and Phylogenomics Laboratory, University of Sydney, Camperdown, NSW, Australia; [4]Horticulture and Living Collections, Botanic Gardens of Sydney, Australian Botanic Garden, Mount Annan, NSW, Australia
[#]equal first authors
[5]Email: Russell.Barrett@botanicgardens.nsw.gov.au

A pilot phylogenomics project and plan to construct the New South Wales Plant Tree of Life (NSWPTOL)

A pilot project has been undertaken to assess the feasibility of creating a comprehensive genomics-based New South Wales Plant Tree of Life (NSWPTOL). We utilised living collections of native plant species growing in the Australian Botanic Garden at Mount Annan, with verified herbarium vouchers, to create a pilot Tree of Life for the New South Wales (NSW) flora with Angiosperms 353 target capture methods. Target Capture methodology was highly successful in generating genomic libraries for 278 angiosperm species (*c.* 4% of the NSW angiosperm flora). A broad cross-section of the flora is represented, with denser sampling for *Acacia* and Eucalypts. When combined with available data from the PAFTOL and GAP projects, >10% of the NSW flora now has A353 data available. We outline the steps necessary to complete the NSWPTOL.

Mike Bayly[1, 5], Harvey K. Orel[1], Rachael M. Fowler[2], Todd G.B. McLay[3], Donald C. Franklin[4], Daniel J. Murphy[2] & David J. Cantrill[2]

[1]School of BioSciences, The University of Melbourne, Parkville, Victoria; [2]National Herbarium of Victoria, Royal Botanic Gardens Victoria, South Yarra, Victoria;[3]National Biodiversity DNA Library, CSIRO, Parkville, Victoria; [4]Ecological Communications, Herberton, Queensland
[5]Email: mbayly@unimelb.edu.au

The ABC of eucalypts: (another) phylogeny of *Angophora*, *Blakella* and *Corymbia*

Molecular phylogenies of eucalypts have unanimously supported the grouping of *Angophora*, *Corymbia* and the recently recognised genus *Blakella* as a clade. However, relationships between as well as within these groups have been poorly supported, prompting taxonomic debate and limiting understanding of their evolution. Using target-capture data from a eucalypt-specific bait set (568 genes) and whole plastome sequences, we conducted the largest phylogenomic investigation of the genera to date (97 species, 168 accessions), with greatest sampling in *Blakella* and *Corymbia*, aiming to clarify evolutionary relationships, characterise patterns of phylogenetic discordance, and infer temporal patterns of diversification. Although analyses of nuclear DNA show strongest support for *Blakella* as sister to *Angophora* + *Corymbia*, we found extensive phylogenomic discordance among nuclear gene trees and striking incongruence between nuclear and plastid phylogenies. Analyses of nuclear data inferred persistently high levels of incomplete lineage sorting (ILS) through time, with signals of introgression concentrated at particular branches. A combination of ILS and introgression likely accounts for the substantial cytonuclear discordance, and comparison of nuclear and plastid trees, including separate divergence dating of each, provides insight into their temporal and spatial patterns. Our results improve understanding of eucalypt diversification, provide a solid basis for comparing competing generic classifications, and further highlight the complexity of eucalypt evolution.

Joanne Birch[1,3], Emily Fitzgerald[2] & Robert Turnbull[2]

[1]School of BioSciences, The University of Melbourne; [2]Melbourne Data Analytics Platform, The University of Melbourne
[3]Email: joanne.birch@unimelb.edu.au

Harnessing artificial intelligence to accelerate digitisation of biodiversity data on natural history collection specimens

Biodiversity data on natural history collection specimens comprise a significant global data resource. However, natural history collections face a massive task to mobilize, through transcription, these high-value biodiversity data. While investment in digitization has significantly increased the generation of digital specimen images over the last decade, transcription rates have remained flat. Reliance on human-mediated data transcription is a major impediment to the increased availability and reuse of these biodiversity data. A rate shift is needed to extract data from specimen images efficiently, moving beyond human-mediated transcription.

Advanced computer vision, text-based machine learning, and large language models hold the potential to provide this rate shift. A multi-disciplinary team at the University of Melbourne has developed ‘Hespi’ (HErbarium Specimen sheet PIpeline) that applies advanced computer vision techniques to extract data from the primary specimen labels and parses those data into output files suitable for upload into collection management systems. Hespi integrates two object detection models: the first detects the components of the specimen sheet and the second detects targeted data fields on the primary specimen label. Handwritten or typed text within those fields is extracted, taxon names are checked against authoritative taxon databases (Plants of the World Online and Australian National Species List), and data are refined using a multimodal Large Language Model (LLM). Outputs are presented in an interactive report, enabling manual correction of the derived text by comparison with cropped images of the label or field. Output files (csv, json, and html files) contain the extracted data and match scores from data correction. The pipeline achieves accurate results for the target data fields on test datasets, which included specimens from Australian and international herbaria.

Hespi holds the potential to be applied to any collection objects with labels or text-based data for which digital images are available. Work is underway to expand functionality of the pipeline, including its application to museum specimens.

Austin J Brown[1], Tara Hopley, Laura Simmons, Elizabeth A James

Royal Botanic Gardens Victoria
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Blown away by the taxonomic utility of DArTseq for *Lachnagrostis* (Poaceae)

DArTseq was utilised for genomics of the endangered, endemic Victorian grass, *Lachnagrostis adamsonii*: a grass restricted to saline habitats in moderate annual rainfall (500–700 mm) regions of Western Victoria. In order to test the distinctiveness of the species and its subspecies, additional *Lachnagrostis* taxa (Blown-grasses) growing in sympatry or parapatry with *L. adamsonii* were also genetically tested. This included the more widely distributed *L. robusta*, *L. billardierei*, *L. filiformis* and *L. aemula*, and the narrow endemics, *L. leviseta*, *L. deflexa* and *L. ×contracta*. DNA sequence analyses confirmed *L. adamso nii* subspp. *adamsonii*, *ampla* and *limosa* to be distinct, although hybridisation was apparent between subspp. *adamsonii* and *ampla* at one site and between subspp. *adamsonii* and *limosa* at a second site. Results suggest that there may be at least one undescribed subspecies within *L. adamsonii*. Genetic examination of *L. ×contracta* found that, contrary to original speculation, which involved *L. adamsonii* as a parent, it has proved to be an intergeneric hybrid of *L. deflexa* and *Polypogon monspeliensis*, with the possible inclusion of a third unknown species at one site. Although *L. robusta*, *L. billardierei* and *L. leviseta* lacked evidence of subspeciation, at least three separate lineages, that may represent new taxonomic entities, were observed in *L. filiformis sensu lato* and possibly two new entities in both *L. aemula sensu lato* and *L. deflexa*. Further genetic study is required across the broader distribution of *L. robusta*, *L. billardierei*, *L. filiformis* and *L. aemula*, for which DArTseq appears to be a useful technique in unravelling taxonomic questions among closely related taxa. In the meantime, detailed morphological examination is underway in the search for characters that may serve as diagnostic features to support potential new taxa raised by the DNA evidence.

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Malvaceae (Sterculioideae) inflorescences with *in situ* pollen preserved by nanophase goethite from the Miocene of Australia

A Miocene (11 to 16 Ma) waterbody in central New South Wales preserves in remarkable detail fish, insects, spiders, and plants. Here we describe small flowers consisting of a fused five-partite perianth attached to paniculate inflorescence axes that were found in the hundreds at the McGraths Flat deposit. The flowers contain more than ten sessile anthers clustered apically on an androgynophore. Pollen contained within the anthers are prolate, isopolar and tricolporate with lalongate apertures. Fine ultrastructural details of the pollen wall layers are preserved as internal and external casts by the iron oxide-hydroxide mineral goethite. We place the material within the Sterculioideae subfamily of the Malvaceae and close to the genera *Brachychiton*, *Agyrodendron* and *Franciscodendron*. This further adds to our understanding on the deposit that contains a mixture of sclerophyll and rainforest elements.

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A newly discovered diatomite fossil flora from Barraba, NSW

New fossil finds from a Diatomite Mine near Barraba NSW will be described. The 18-million-year-old deposit, part of the Miocene Nandewar Shield Volcanics, has so far yielded 50 fossils, many of which are eucalypt leaves. The fossil flora also consists of rare *Syzygium* and *Nothofagus* leaves, a *Gymnostoma* fruit and flower of *Ceratopetalum* (Cunoniaceae). The fossils suggest a time of change in the Australian flora, with sclerophyll and less commonly rainforest elements. The fossils are of relevance in understanding the early evolution and diversification of the eucalypts that currently dominate the Australian flora.

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Erythroxylum no longer an enigmatic genus in Australia

Erythroxylum is a pantropic, predominantly tropical American genus of about 250 species. Until relatively recently, three species were known to occur in Australia. Field work and herbarium studies have doubled this number and shown the misapplication of a name used for a north Queensland rainforest species for over 95 years. Where studied, the Australian species have been shown to have a rich leaf chemistry but none produce cocaine or cocaine derivatives. Correct nomenclature has implications for Australian drug misuse legislation.

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New universal genetic tools for determining management units and conserving Australia's imperilled cycad species

Cycads (Cycadales) are among the most evolutionarily distinct and globally threatened groups of plants, with over 70% of species considered threatened with extinction. Despite their evolutionary and conservation importance, the genetic resources available for cycads have remained limited. This has constrained our ability to define species boundaries, assess genetic variation, detect hybridisation, and develop effective conservation strategies. A key obstacle has been the absence of universal, repeatable genomic tools suitable for genotyping and population-level analysis, which are essential for standardising genomic reporting in cycads. More importantly, species are routinely listed as threatened with extinction, without understanding genetic relationships across populations or within similar species. Determining management units based on genetic divergence is crucial to ensure that the correct conservation units are targeted for actions. Defining conservation management units is essential for identifying which individuals and landscape locations to prioritise for conservation interventions and for developing ex-situ conservation assurance colonies.

To fill this gap, we have developed the first universal cycad marker set, comprising 629 universal and 129 genus-specific single-copy nuclear genes. These markers were selected based on capture efficiency and low paralogy, ensuring applicability across all existing cycad lineages and broader gymnosperms. Designed towards population-level and genotyping studies, these markers offer a scalable approach also for phylogenomics. The maker set will not only be used to clarify species boundaries, but also to examine genetic diversity, structure, and connectivity across landscapes. This includes detecting signs of local adaptation and understanding demographic processes shaping conservation-significant cycad species. Such data will directly inform species recovery plans and provide evidence for conservation policy and legislation. This work has significant forensic applications, enabling the identification of specimens in trade and supporting efforts to curb the illegal collection and trafficking of cycads, a major global and Australian threat.

In Australia, this marker set will support a comprehensive conservation genomics program, focused on defining real-world management units. Initial efforts will target species in the horticulturally sought-after cycad species complex, *the Cycas cairnsiana* group from Northern Queensland. A species group which includes *C. brunnea*, *C. cairnsiana*, *C. couttsiana*, *C. cupida*, *C. distans*, *C. desolata*, and *C. platyphylla*. Species in this group are morphologically plastic and are mostly differentiated based on geographic boundaries or localities. The new marker set, we will characterise genetic variation within and between species and populations, reconstruct evolutionary relationships, and test for hybridisation and introgression. Genotyping will also help to establish conservation management units, which are vital for guiding he management of wild and ex-situ populations.

By combining a universal cross-species marker set with an Australia-centred conservation genomics program, this work will mark a significant advance in cycad conservation and management. It will create a reproducible genomic framework for cycads that can be scaled globally, while delivering immediate conservation benefits for Australian taxa. Ultimately, this work aims to ensure that decisions about the protection, management, and potential recovery of Australian cycads are based on solid genomic evidence, helping to ensure that the correct management units are conserved.

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Doing what we can for the ones we love: delivering data to inform assessments of extinction under the Red List

Taxonomic studies inform and ultimately underpin conservation and the management of threatened species. Taxonomic uncertainty can lead to an underestimation of the threats to a species or the misallocation of resources in conservation programs.
The International Union for Conservation of Nature (IUCN) Red List of Threatened Species applies quantitative data to assess the extinction risk of species under criteria such as population size, rate of decline, geographic range, and degree of population fragmentation. Species are categorised into groups like Least Concern, Vulnerable, Endangered, and Critically Endangered.

All states and territories in Australia have agreed to determine extinction risk using a common assessment method based on the IUCN Red List.

Field observations can add impact to taxonomic outputs. As field botanists we routinely record information on habitat and associated species, plant phenology, morphology that cannot be inferred from the preserved specimen such as flower or leaf colour, height of mature plants, and descriptions of bark. Additional information such as demographics of a population, timing and effects of past disturbances, abundance or population sizes, and observed threats are less often recorded.

Inclusion of quantitative estimates of population size, the proportion of seedlings and mature plants in populations, and evidence of any impacts due to threats, are data that can directly inform threat assessments using the IUCN approach. These data can increase outputs and impact to the herbarium specimens, taxonomy and systematics of the species we love.

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A coming of age story: population structure and dynamics in *Macrozamia*

Cycads represent some of the most endangered and vulnerable plants globally, yet we still know relatively little about their population genetic structure and life histories that might be critical to help conserve them. Within southeast Queensland, there are species of *Macrozamia* that have small geographic ranges and others that are widespread. Here, we compare and contrast summary statistics and population genetic structure of several of these species, including *M. conferta*, *M. moorei*, *M. lucida* and, from central Australia, *M. macdonnellii*.

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Uncovering cryptic diversity and biogeographic history of *Dictyosphaeria* (Siphonocladaceae, Cladophorales)

The green macroalgal genus *Dictyosphaeria* (Siphonocladaceae, Cladophorales) is widespread across tropical and subtropical coasts, where it plays an important role in nearshore ecosystems. However, its species-level diversity and evolutionary history remain poorly understood, hampered by limited molecular sampling. In this study, we integrate DNA barcoding with high-throughput sequencing (HTS) to comprehensively assess global diversity, reconstruct phylogenetic relationships, and explore the historical biogeography of the genus. From 105 specimens collected across the Atlantic, Indo-Pacific, and Australasian regions, we delimit 15 species, revealing substantial cryptic diversity. The Indo-Pacific harbors the greatest species richness, highlighting its role as a center of diversity. In Australia, three distinct species were identified, including *D. sericea*, a deeply divergent and phylogenetically isolated lineage. This suggests long-term isolation and supports the hypothesis of regional endemism within the Australasian marine flora. Full-length nuclear ribosomal DNA cistrons were assembled from HTS data, providing a robust multilocus backbone for phylogenetic inference across *Dictyosphaeria* and related taxa. Divergence time estimation using PhyloBayes, calibrated with node age of Pithophoraceae and Cladophoraceae, suggests that

Dictyosphaeria diverged from its sister genus *Valoniopsis* during the Cretaceous, indicating a deep evolutionary history. Ancestral range reconstruction was conducted through BioGeoBEARS, supporting a scenario in which the Atlantic clade arose through long-distance dispersal, with subsequent divergence likely driven by vicariance associated with the closure of the Tethys Seaway. The Australasian clade, by contrast, likely formed through tectonic isolation and long-term geographic stability, contributing to lineage persistence in this region.

Our study provides new insights into the diversification of *Dictyosphaeria* at both global and regional scales. The use of complete nuclear ribosomal DNA sequences enhances phylogenetic resolution, offering a framework for future taxonomic revisions. Notably, the discovery of a deeply divergent lineage in Australia underscores the evolutionary distinctiveness of the Australasian region, aligning with broader efforts to document and understand regional endemism and biodiversity. While *Dictyosphaeria* is globally distributed, its Australasian representatives exemplify the impacts of ancient geologic processes on modern marine diversity—an area of ongoing interest in Australasian botanical and phycological research.

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Exploring phylogenetic relationships and discordance in the paper-fruited bloodwoods (*Blakella* sect. *Blakella*)

The paper-fruited bloodwoods are a section from the newly recognised eucalypt genus *Blakella*, and includes several iconic ghost gum species. With a distribution encompassing Australia's monsoonal tropics, as well as parts of the arid zone and Papua New Guinea, *Blakella* sect. *Blakella* is an ideal group to explore questions concerning the biogeography, taxonomy, and evolutionary ecology of flora from northern Australia. Unfortunately, despite several phylogenomic studies applying contemporary sequencing and bioinformatic approaches, well-supported evolutionary relationships within this group remain elusive due to high levels of Incomplete Lineage Sorting and introgression creating phylogenetic discordance. Using a combination of cutting-edge and traditional phylogenomic approaches, we have attempted to better resolve species relationships within the paper-fruited bloodwoods and explore this discordance further, providing a framework for taxa where clear phylogenetic insights continue to be difficult.

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A new classification of mallee-boxes (Myrtaceae: *Eucalyptus* ser. *Subbuxeales*) from south-eastern Australia

We propose a new taxonomy for the mallee-boxes in *Eucalyptus* series *Subbuxeales* from south-eastern Australia, based on biogeographical, morphological and molecular evidence. Under this new taxonomy the lineage is reduced to four species – *E. albopurpurea*, *E. froggattii*, *E. odorata* with five subspecies, and *E. viridis* with two subspecies. *Eucalyptus cajuputea*, *E. polybractea* and *E. wimmerensis* are reduced to subspecies of *E. odorata*, while a novel fifth subspecies of *E. odorata* is described based on *E. viridis* var. *latiuscula* Blakely. The five subspecies of *E. odorata* form a geographical replacement pattern, and while they are variably distinguishable genetically, they have no reliable, non-overlapping distinguishing morphological features. *Eucalyptus aenea* is reduced to a geographic subspecies of *E. viridis* from which it differs morphologically only in vegetative traits. All other taxa within the complex are placed into synonymy or recognised as hybrids.

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Plastid genome evolution in Australasian mycoheterotrophic orchid genus *Danhatchia*

Fully mycoheterotrophic plants have lost the ability to photosynthesise and rely entirely on their fungal partners for nutrition. As a result of this shift, their plastid genomes (plastomes), which encode essential genes for photosynthesis, often exhibit structural rearrangements and extensive gene loss due to relaxed selective pressure on photosynthetic functions. Comparative analysis of plastomes in mycoheterotrophic plant lineages provide valuable insights into plastome evolution and reveal the genomic consequences of transitioning away from photosynthesis to a fully heterotrophic lifestyle.

Danhatchia Garay & Christenson is a fully mycoheterotrophic orchid genus and has long been considered monospecific and endemic to New Zealand, comprising only *Danhatchia australis* (Hatch) Garay & Christenson. In 2010, the genus was discovered in Australia for the first time. Since then, four populations have been discovered in New South Wales and Queensland, for which two species have been described for the Australian flora: *Danhatchia novaehollandiae* D.L. Jones & M.A. Clem. and *D. copelandii* D.L. Jones & M.A. Clem. Thus, the genus provides the opportunity to investigate plastome degeneration among closely related species.
So far, only one representative, *D. australis* from New Zealand, has been studied, providing an initial insight into plastome structure in the mycoheterotrophic genus. However, comparative

phylogenetic analyses within *Danhatchia* have not yet been conducted. This study addressed this gap by examining plastome degeneration among closely related species in *Danhatchia* within a phylogenomic context. Complete plastomes were de novo assembled and annotated for Australian and New Zealand *Danhatchia*, representing all described species within the genus, as well as a putative novel species from Australia's east coast.

The comparative assessment of plastome structure in *Danhatchia* revealed the extent of plastome degradation within the genus. Moreover, our molecular phylogenetic analysis provided first insights into genetic divergence between Australian and New Zealand species in *Danhatchia*.

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***Marasmius*: an Australian Perspective**

Marasmius is a large genus (700–900 species) of mainly saprotrophic fungi occurring worldwide. It is especially diverse in the tropics and subtropics. Five years ago, there were 2 confirmed species described from Australia (*M. elegans* & *M. crinisequi*), one exotic (*M. oreades*), and several named as European species, some of which are no longer accepted as being in the genus. Morphological, molecular and ecological data were used to examine three species groups in different series within *Marasmius*. After the examination of over 250 fresh collections and scores of herbarium specimens, several cryptic species groups have been disentangled, resulting in 25 species being described and named. In addition, we have untangled the historic nomenclatural mess of the aerial rhizomorph net-forming *Marasmius crinisequi*, the horsehair fungus. This included selecting an epitype, discounting its pathogenicity, and discovering at least two look-alikes in the tropics, one of which is widespread and may have pathogenic potential in overseas occurrences. In the *M. haematocephalus* complex, seven new species were defined – none of which are *M. haematocephalus s.s.* from Brazil. Five of these species are Australian endemics, one may be an introduced species, and one is probably widespread across the globe. The endemic Australasian species, *M. elegans*, is morphologically very variable across its broad distribution with sporing bodies that are significantly larger the further from the equator it occurs. Molecular data suggests this species remains almost identical across its range, but the Western Australian specimens are genetically distinct. Four other species in the same series (*Luteoli*) have been described, *M. pseudoelegans, M. dilkusha, M. leppii* and *M. durifagus*. One look-alike, *M. multicystidiatus* is micro-morphologically and genetically distinct and has been placed in a new series, *Multicystidiati,* with its sister from the USA, *M. sullivantii*. Some species of fungi form tangles of aerial rhizomorphs (litter traps) in the understory of subtropical rainforest (STRF), capturing falling litter for their nutrients. DNA analysis of collections from Mary Cairncross Reserve shows they are from at least three genera (*Marasmius, Crinipellis* and *Gymnopus*). Litter traps are widespread in STRF at this site, often small, (unlike tropical rainforest traps), relatively long-lived, with many lasting over three years, and sporadically fruiting. A strong relationship between horsehair fungi and birds has been observed. The rhizomorphs are sought out by rainforest birds for nest material, up to 75% of small bird nests from the reserve containing rhizomorphs, as either suspension fibres, wall material or nest lining. We have confirmed that the rhizomorphs are living and help bind other nesting material. Benefits to the birds are multiple. From our broader morphological and DNA analyses, Australia is now known to be home to at least 50 species of *Marasmius*. We believe there are many more yet to be discovered in Australia. There is also more work to do on the ecology of all the species.

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A comparison of two universal angiosperm bait sets and the phylogenomics of Alismatales

High throughput sequencing of hybridisation capture libraries provides an efficient approach for assembling large scale phylogenomic data. These include universal bait sets that aim to generate comparable data from any lineage within the taxon of interest. Here, we present the OzBaits v2 bait set, which targets a set of low copy nuclear loci for angiosperms. Using published genomic data, we design a set of RNA baits targeting a single exon in each of 98 putatively orthologous nuclear protein coding genes. We tested the efficiency of this bait set for a diverse range of angiosperms and recovered, on average, 93 (95%) genes per sample. As a component of the Genomics for Australian Plants initiative, we undertook to improve the data availability for a difficult aquatic plant lineage and to evaluate the resolution of the data generated for order-to-species level phylogenetic diversity. We compared a common set of samples for the monocot order Alismatales enriched using OzBaits and the Angiosperms353 (A353) bait set, a widely used universal probe set targeting up to 353 nuclear genes in angiosperms. Gene recovery was, on average, c. 1.7 times higher for OzBaits relative to A353. Using proxies for signal and bias to rank gene alignments by their phylogenetic usefulness, we found that on average, the OzBaits data had higher phylogenetic utility. Both data sets resolved largely congruent, well-supported phylogenies for Alismatales although measures of internal discordance where higher for the A353 data. We discuss the implications of these findings for the design universal baits sets.

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Introducing FloraSA – the new electronic flora for South Australia

FloraSA represents the next generation of the electronic Flora of South Australia, building upon decades of botanical research and data collation led by the State Herbarium of South Australia. The previous platform, eFlora (SA), once provided an authoritative resource for plant, algae, fungi, and lichen information across the state but was retired when its outdated technology could no longer securely or effectively deliver content. FloraSA replaces this system with a modern, robust platform designed to meet contemporary technical, practical, and cyber-security requirements while enhancing accessibility and functionality for users. The development of FloraSA (2025) involved an extensive process of technical analysis, information integration, and system redesign. Multiple authoritative datasets and published resources were consolidated, and a new content management system was implemented to handle the complexity of the information while enabling ongoing updates. The result is a platform that not only preserves the scientific integrity of South Australia's botanical data but also makes it more user-friendly and visually engaging, with a growing repository of images and supporting resources.

At its core, FloraSA presents the state's flora in alignment with the most current taxonomic concepts, as reflected in the Census of South Australian Plants, Algae, Fungi and Lichens. Taxonomic names, synonymy, and related attributes form the foundation of the platform, ensuring scientific accuracy and consistency. Future iterations will incorporate additional layers of information, including trait data and regional conservation status—resources already integral to threatened species assessments and fire management strategies employed by South Australian government agencies. By consolidating generations of taxonomic expertise, FloraSA aims to be the most comprehensive, authoritative, and dynamic flora resource for the state.

In this talk, we will introduce the new FloraSA website, highlighting its key features, such as the improved user interface, integrated datasets, and expanding image library. We will also outline the ongoing and anticipated work to enhance the platform, including the systematic review and updating of taxon profiles, the incorporation of additional multimedia content, and the maintenance of current nomenclature and taxonomic concepts in line with global and regional standards. Finally, we will discuss how FloraSA will continue to evolve as both a scientific resource and a public-facing tool for conservationists, land managers, educators, and the broader community.

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Into the Depths – Investigating the species identity of tree roots in the Naracoorte Cave Systems

Naracoorte Caves World Heritage Area preserves globally important vertebrate fossil material however, not everything within the caves is fossilised, and live plants roots occur in many places within the caves. The identity of these roots is unknown and the relationship between the above-ground flora and below-ground roots has been unresolved. Elsewhere in the world, studies have utilised DNA analysis methods to identify the potential identity of unknown roots present within caves. However, previous published studies have not combined the use of modern, target capture DNA analysis techniques with a comparative analysis of species diversity of plants living above ground. Next-generation sequencing of chloroplast DNA has grown in popularity with the advent of more cost-effective tools. In addition, the ability to screen multiple loci simultaneously from potentially mixed DNA samples is an approach not yet applied to cave roots and in general where there have been limited studies on cave floras overall. In this study a target capture chloroplast DNA analysis approach was utilised where the relationship between the species of roots present in caves and the vegetation above caves was tested. This study developed successful methods of extracting high quality sequences from cave root material, which was sequenced, and the results were compared to custom reference DNA sequence databases created for the Naracoorte sampled sites and the region. Successful identification of roots was completed when DNA sequences generated across multiple gene regions were compared to the custom reference databases. The results found that vegetation associated with cultivated areas (garden vegetation) exhibited the highest species diversity of living roots in the caves. Overall, the most common roots found among all the samples analysed across the 8 different Naracoorte caves were eucalypt and acacia species reflecting the above ground vegetation that was present at each site. Future research will benefit from the reference library data generated and the improved collecting, DNA analysis and bioinformatic techniques applied set a standard for additional studies.

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Creating a new Census for the Flora of New South Wales

New South Wales has not published a formal census of its flora since 1981. As the legislated authority for accepted plant names in New South Wales, the National Herbarium of New South Wales has a responsibility to maintain current names and track changes. In order to increase transparency, and facilitate timely updates to PlantNet, the public face of name changes, we here present the process we have gone through to create a new checklist. This will provide a baseline to track future name changes and additions to the Flora of New South Wales, and assist curation updates. To supplement this checklist, we also propose an annual publication of updates to names in PlantNet to facilitate communication of changes to our broad user group.

Kale Sniderman[1], **Greg Jordan**[2,4] & Chris Mays[3]

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Extreme greenhouse climate events drive major restructuring of floras

This talk presents analyses of changes in pollen and spore assemblages over the last 100 million years in southeastern Australia, northeastern Africa and the Neotropics. Using methods that allow for differences in sampling effort, we looked at changes in standing diversity, and rates of originations and extinctions. We also developed local climate curves for the relevant regions. Standing diversity, originations and extinctions peaked together in the two warmest periods of the last 100 million years (the Cenomanian-early Turonian of the early late Cretaceous and the Palaeocene-Early Eocene of the early Cenozoic). Furthermore, these peaks were synchronous in flowering plants, gymnosperms and free-sporing plants, and at high and low latitudes. This is clear evidence that peak greenhouse climates promote major turnover in floras,and challenges some well-established views on the diversification of angiosperms.

Helen Kennedy (Keynote III)

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Stewardship in Botany: Taking Care for the Next Generation

Botany and herbaria in Australasia are extraordinary — dynamic archives of our natural world and testaments to generations of curiosity and care. Yet their value is not always recognised beyond our community, as economic and ideological pressures favour what is new, fast, and profitable. In these uncertain times of climate change, biodiversity loss, and global instability, stewardship — the deliberate care of collections, people, and knowledge — provides a guiding principle for sustainable practice in our field. This talk explores stewardship through three interconnected lenses: herbaria, caring for collections in the age of digitisation; community, the achievements of ASBS, CHAH, and ABRS and approaches to sustaining their impact; and research, designing projects that prioritise care for biodiversity and people. By reflecting on what we value most as botanists and intentionally nurturing it, we can help ensure that 50 years from now, another generation of systematic botanists will be debating, discovering, and shaping the future of our field.

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KeyBase: Interactive online identification keys

KeyBase was developed 14 years ago to manage identification keys for emerging Flora projects, in particular VicFlora, and to make the dichotomous keys from taxonomic papers and printed Floras work on the web. KeyBase has always remained a proof of concept and, while it never really fell over, at the end of 2023 the home page was defaced and we had to disable login and editing, because the security of KeyBase fell way short of what is required in today's cyber security landscape. Because there is still strong interest in the functionality KeyBase provides, we are now redeveloping KeyBase into a production-ready web application, with support from five Australian herbaria.

The redevelopment that is underway completely focuses on KeyBase itself, especially the editorial part. So, the editor interface has a complete CRUD (Create, Read, Update, Delete) form system, with contributor, manager (for projects) and administrator (for the entire system) roles. Login will be using ORCID, which provides Multi-Factor Authentication (MFA). The new KeyBase will support subkeys and will handle reticulations, i.e. more than one lead leading to the same couplet, differently.

The public interface will get a face lift too and will have a modern mobile-first design with light and dark mode.

On the other hand, at this stage we are not spending a lot of time on making KeyBase work with external applications, like the Flora of Australia and VicFlora. So, the new KeyBase will keep supporting the old API (Application Programming Interface) and plugin. The reason for this is partly triage, but just as importantly that replacing the API and plugin will break the existing implementations, as the architecture of the new tools will be radically different. This will be picked up next year when VicFlora will be upgraded and the new Flora of Australia will be developed.

We hope to complete the redevelopment of KeyBase by the end of 2025. At the time of ASBS 2025 we will be in the UAT (User Acceptance Testing) phase, so this presentation will include a demo.

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Pannotator: transforming ecological field surveys using 360-degree camera imagery

In a rapidly changing world, there is a growing need for tools that enable fast and efficient collection of ecological field data. Fortunately, the development of affordable, high-resolution 360-degree cameras now provides not only the ability to capture survey data on landscape scales, but also a means of permanently recording ‘snapshots’ of ecological systems over time for longitudinal analysis. Our new open-source software package ‘pannotator’ and associated workflows provide a powerful, scalable and repeatable platform for collecting and extracting ecological data from 360-degree imagery, delivering maximum impact for minimal effort. In this presentation, I demonstrate how pannotator can be applied across a wide array of use cases, including biodiversity mapping, invasive species detection, and environmental monitoring, with examples ranging from the Daintree to Uluru in the Red Centre.

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New techniques for reconstructing ancient atmospheres and fire intensities

Plant microfossils hold tremendous potential for revealing ancient vegetation and environments because they are so common. We are currently developing two new methods, one that uses fossil pollen to reconstruct the isotopic composition of CO_2 in the ancient atmosphere and another that uses fossil charcoal to estimate the intensity of ancient wildfires.

The stable isotopic composition of CO_2 in the ancient atmosphere ($\delta^{13}C_{CO2}$) is an important tool for geological studies of the carbon cycle, but can be difficult to reconstruct in continental settings because many factors influence the δ13C of terrestrial organic matter. We conducted an experiment in which we grew Ginkgo biloba trees under varying CO_2 concentrations (~420 to ~1000 ppm) and $\delta^{13}C_{CO2}$ (-9.5‰ to -40‰), then measured the carbon isotopic composition of their pollen ($\delta^{13}C_{pollen}$). We found that $\delta^{13}C_{CO2}$ is the first-order determinant of $\delta^{13}C_{pollen}$ (r^2=0.97, p= <0.0001), though the difference between $\delta^{13}C_{CO2}$ and $\delta^{13}C_{pollen}$ (discrimination $\delta^{13}C$) varied among individual plants by as much as ~5.5‰. Surprisingly, these differences in $\delta^{13}C$ were poorly correlated with environmental factors including pCO_2, temperature, vapour pressure deficit and soil moisture. The $\delta^{13}C$ of Ginkgo biloba pollen can be used to infer $\delta^{13}C_{CO2}$, with a 95% prediction interval of ~3.7‰ ($\delta^{13}C_{CO2} = 0.8955 \times \delta^{13}C_{pollen} + 10.3001$). The error of the estimate is large enough that some geologically significant carbon isotope excursions would be difficult to detect with a small number of fossil pollen samples, however, by using $\delta^{13}C_{pollen}$ from a single taxon, and through analyzing dispersed pollen from multiple individuals, it is likely that unwanted individual variation could be reduced and more precise estimates of $\delta^{13}C_{CO2}$ made. The lack of correlation between $\delta^{13}C_{pollen}$ and environmental factors in the experiment suggests $\delta^{13}C_{pollen}$ may be a poor proxy for pCO_2, temperature and water stress.

Our second study involves developing new methods to quantify whether rising global temperatures resulted in increased fire intensity during previous intervals of elevated CO_2. The Palaeocene–Eocene Thermal Maximum (PETM) was the largest early Cenozoic hyperthermal event, one of a series of carbon cycle and climate perturbations marked by massive releases of carbon into the atmosphere and spikes in global temperature. Previous studies have documented major changes in the composition of terrestrial plant and animal communities during the PETM. Here, we examine possible changes in fire intensity during the PETM in the Bighorn Basin (BHB), Wyoming, USA. To do so, we generated charcoal under controlled fire intensities using a custom-designed gas flame burner. We generated charcoal from the palms *Sabal palmetto*, *Sabal minor* and *Serenoa repens* because these resemble the macroscopic charcoal recovered from the BHB after scanning electron microscopy examination and the nearest living relatives of pollen recovered from the same sites. This generated charcoal was subsequently analyzed using Fourier Transformed Infrared (FTIR) spectroscopy to examine the optical absorption features of the charcoal structure, revealing the effects of increasing fire intensity. We also analyzed PETM macroscopic charcoal derived from the Bighorn Basin using FTIR. Through analogue matching we are investigating whether fire regimes, including intensity, changed during the PETM.

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Biodiverse, a tool for the spatial analysis of diversity, version 5

Biodiverse is a tool for the spatial analysis of diversity, supporting a wide range of taxon and phylogenetic indices through spatial moving window and cluster analyses. Hypothesis testing is supported through a range of null models that can be spatially configured and constrained. Spatial windows and constraints can be defined using arbitrarily complex conditions.

Biodiverse can be used through a graphical user interface or through user defined scripts, with an R interface in development.

Biodiverse has been under active development for twenty years. Version 5, released this year, contains a completely rewritten graphical engine that greatly enhances the ability of users to interact with and explore their data. This enables a more thorough understanding of how the results in a location were obtained. In this talk I will demonstrate some of the new functionality and visualisations in Biodiverse version 5.

Melinda Laidlaw

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Update from the Queensland Herbarium 2025

The Queensland Herbarium and Biodiversity Science unit is a hub for science, research and information on Queensland's ecosystems and biodiversity. Our mission is to gather, synthesise, and disseminate information and knowledge on Queensland's species and ecosystems to inform planning, management and the conservation of Queensland's biodiversity both now and into the future. Our team of expert botanists, ethnobotanists, mycologists, geneticists, ecologists and collection management specialists strive to ensure that we have the best understanding of Queensland's plant and fungal diversity possible. The baseline information that we curate underpins important biodiversity data products and decisions in our state impacting threatened and priority species, land use planning, conservation and protected area management. We also connect with herbaria across Australia and worldwide to improve our understanding of the tree of life and the place of Australian biodiversity within it. Our collaborative Tropical Indigenous Ethnobotany Centre (TIEC) is managed by and works closely with Traditional Owners to document and preserve traditional biocultural knowledge. We also partner with Queensland's Department of Primary Industries to host the Weed Spotters Network, Queensland's largest and oldest biosecurity citizen science project focused on the early detection of new and emerging weeds. This presentation with provide an update on the current priority systematics projects underway at the Queensland Herbarium, and highlight collaborative opportunities on our horizon.

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Botanists in the Wikiverse - planting the seeds of open data enrichment and reuse

This presentation will summarise the motivations, organisational logistics and implementation of the WikiProject International Botanical Congress (IBC) 2024, a project to engage with and upskill attendees of the XX IBC held in Madrid, Spain. Our team delivered a free, full-day, multilingual Wikidata workshop to botanists aiming at improving their knowledge of Wikidata. We bookended the in-person workshop with two shorter online Zoom workshops as onboarding and follow-up sessions. We "wikified" the conference thereby boosting the richness of open data in Wikidata about IBC organisers and presenters. This included creating and improving their Wikidata items, and linking them to their publications, institutions, and identifiers. We also ensured ORCiD identifiers for the organisers and presenters, where available, were linked to their herbarium collection contributions via Bionomia.net. Finally, our team presented a Wikidata related poster.

As a result of this poster our team was invited by associate editors of the Annals of Botany to submit a paper to that journal. We will explain the logistics of managing our multinational collaboration across time zones to write, submit and publish this Open Access paper. We will give a summary of the content of the paper including the reuse of Wikidata items and their open data in digital tools such as the Wikidata Query Service, Bionomia, Scholia, TL-2 and Expeditia, as well as our call to action to the botanical community.

As a result of this initiative, we have continued our outreach efforts at the ASBS 2025 Conference by offering a more general, free, full-day pre-conference “Wiki for Botanists” workshop. Our goal was to collaborate with attendees to empower improvements to their digital outreach skills, and to harness their research expertise to enrich the Wikiverse – one of the world’s most comprehensive open knowledge platforms – with more Australasian botanical content. This workshop covered editing not only the data repository Wikidata, but also the online encyclopaedia Wikipedia and the image repository Wikimedia Commons. We will share some initial outcomes from this workshop.

This presentation will then discuss the many motivations for undertaking this type of digital outreach work and how this can benefit botanical researchers, botanical collections and botany-related institutions as well as the wider world’s access to and ability to reuse botanical knowledge. We will highlight examples such as the improved access to and increased impact of research undertaken by botanists, the reuse of Wikipedia articles and Wikidata items in databases such as the Atlas of Living Australia and iNaturalist, and how links to Wikipedia and Wikidata can enrich botanical institutions’ collection management systems.

In conclusion, we assert that Wiki platforms are relevant to botanists and their institutions, and we will encourage attendees of the ASBS 2025 Conference to play a role in improving botanical knowledge in the Wikiverse. We will argue these digital outreach undertakings should be recognised and valued as work by our institutions. We will also outline ways you can get involved in your local, regional or international Wiki community.

Brendan J. Lepschi[1,3] & Kelly A. Shepherd[2]

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Camouflaged by the obvious: a revision of *Goodenia connata* and allies

Following on from the 2020 re-circumscription by Shepherd, Lepschi and colleagues, of the genus *Goodenia* to include *Velleia*, *Verreauxia*, *Selliera* and *Pentaptilon*, based on well-resolved phylogenies combining chloroplast and nuclear data, a ‘simple curation exercise’ was undertaken to apply the new taxonomic concepts in the author’s respective institutions (PERTH and CANB). Independently we found a disturbing degree of morphological variation across the collections of the distinctive and obvious connate bracteole group of *Goodenia* (formerly *Velleia*) and began to suspect several undescribed taxa may be present. Working together we soon confirmed several discrete species, which had been previously included in pre-existing concepts, even from well-surveyed and well-studied areas such as the Pilbara region of Western Australia. We speculate that the very conspicuousness of these taxa may have contributed to them being overlooked by previous workers and collectors.

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Phylogenetic and population level analyses of South Australian *Caladenia patersonii* and *C. reticulata* spp. complexes

Intense taxonomic activity over the past thirty-five years within the *Caladenia patersonii* and *C. reticulata* species complexes in South Australia (~30 species) has resulted in an inconsistent and dysfunctional taxonomic framework. Sixteen of these taxa currently hold IUCN-based conservation ratings, yet their identification is complicated by limited diagnostic characters and poorly defined species boundaries.

This study addresses these challenges through a systematic revision of the group. An initial assessment highlighted inconsistencies among diagnoses, descriptions, and type material. Leaf and floral specimens were subsequently collected across South Australia for morphological and molecular analysis. DNA was extracted and sequenced using hybrid capture (Angiosperm353, OzBaits, and genome skim), supplemented by SNP array data for population-level analyses.

Phylogenetic analyses (*BEAST, weighted-ASTRAL) provided low support for the currently recognised species, revealing instead paraphyletic taxa, evidence of frequent hybridisation with the *C. dilatata* complex, and clades inconsistent with current taxonomic concepts. Notably, no South Australian *C. patersonii* or *C. reticulata* related species had phylogenetic support. Morphological variation within extant populations was found to exceed that documented in descriptions or type material, and similar variation was detected in historical collections predating the recent surge of taxonomic activity. However, population genetic structure analyses identified some groupings within the region. Collectively, these results demonstrate that current species concepts fail to reflect biological and geographical realities The findings will have important implications for taxonomic revision and for the development of effective conservation strategies.

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Pretty in pink, purple and orange: fungal fans in *Crepidotus*

Crepidotus (Crepidotaceae) are a large genus of macrofungi that form brown-spored sporebodies that range from often smaller, fan-shaped to larger stipitate and mushroom-like.

They are saprotrophic on wood and other organic matter. Here we provide details of several colourful pink, purple and orange species. Two already have names, the hot pink *Crepidotus boninensis* (1982), that has an Oceania distribution, and the appropriately named Cleland (1918) species, the salmon-coloured *C. salmonicolor*. A recently described species, that has hints of purple, *Crepidotus innuopurpureus* (2021), has a surprising distribution of rainforest remnants from the western Kimberley to southeast Queensland. Last for this brief glimpse into this colourful group within the genus, is a new and relatively large orange taxa, known from FNQ through SEQ and into NSW. We hope that by barcoding these taxa we can start getting these less common taxa onto conservation lists, sooner rather than later. As modern scientists our goals are not only to update the taxonomy, phylogeny and nomenclature but educate the growing interest in fungi so that verifiable records are collected on bioinformatic systems from community driven iNaturalist to Global Biodiversity Information Facility (GBIF). By finally having these species barcoded will enable environmental and ecological studies.

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Forget-me-not phylogenomics: improving the resolution and taxonomy of a rapid island and mountain radiation in Aotearoa New Zealand (*Myosotis*; Boraginaceae)

Island and mountain systems represent natural laboratories for studies of species radiations, but they often present several challenges for phylogenetic inference and species delimitation. The southern hemisphere forget-me-nots (*Myosotis*, Boraginaceae) comprise a geologically recent radiation centred in Aotearoa New Zealand, a mountainous archipelago, with about 50 species that are morphologically and ecologically divergent but lack genetic variation sufficient to resolve phylogenetic relationships and species boundaries using standard DNA Sanger sequencing markers, AFLPs, or microsatellites. Many of these *Myosotis* species are geographically restricted in alpine areas, uncommon or threatened, have polyploid and dysploid genomes, and are of high taxonomic and conservation priority. Here we present phylogenomic analyses using target-capture of Angiosperms353 baits, and genome skimming of whole plastomes and nrDNA, to improve resolution of the radiation, explore biogeographic and morphological patterns within it, and address specific taxonomic questions for each species. Our comprehensive sampling includes over 300 individuals representing nearly all species from New Zealand and Australia, which is ~ 2–3 × more taxon sampling and ~ 80–120 × more molecular data than previously published for *Myosotis*. Exploration of different data filtering, curation and analyses (coalescent vs. concatenation) improved the resolution of the Angiosperms353 tree, which despite short backbone branches with low support values, showed taxonomic and geographic patterns, including multiple switches between ebracteate and bracteate inflorescences and multiple expansions within New Zealand from Te Waipounamu South Island to Te Ika-a-Māui North Island, Rakiura Stewart Island, subantarctic islands, and Australia. Some of these patterns were also seen in the genome skimming datasets, and comparison of the three datasets was useful for improving our understanding of the taxonomy and resolution of this radiation. Although this phylogenomic study does not fully overcome all of the challenges regarding species delimitation of this rapid island and mountain species radiation, it nevertheless makes an important contribution to an integrative taxonomic revision of the southern hemisphere species of *Myosotis*.

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New developments in spatial phylogenetics, a global discipline with Australian roots

The developing field of spatial phylogenetics adds a phylogenetic dimension to biodiversity assessment and thus gives evolutionary depth to spatial inferences about diversity, endemism, and their causes. In addition to its uses in academic science, the field also contributes significantly to applied conservation assessments. Spatial phylogenetics is premised on the idea that species are not the only units of biodiversity but rather are just one level on a hierarchical evolutionary continuum that contains rich biological information valuable for quantifying spatial biodiversity patterns.

The fundamental metric phylogenetic diversity (PD) sums the branch lengths connecting the terminals that occur in a location to the base of an encompassing phylogeny. Importantly, for every distinct phylogenetic topology (defined by the connections among branches) there are a large number of facets, which represent different ways of scaling the branch lengths. PD can be measured on any of these, with each facet yielding different information that is useful for addressing different questions. My goal here is to review three recent areas of methodological progress, each briefly illustrated with some empirical applications.

(1) Phylogenetic endemism (PE) is a range-weighted variant of PD. In the common case where equal-area spatial units are considered individually, PE can be viewed as a facet, i.e., a range-weighted phylogenetic tree with each branch down-weighted proportionally to the size of its range (thus emphasizing the contribution of range restricted branches). A new method called Range Weighted Branch Length Difference (RWiBaLD), is based on the difference between the length of a branch on a range-weighted observed tree and its length on the corresponding range-weighted comparison tree (i.e., a tree with the same topology as the observed tree but with branches adjusted to be of equal length before range-weighting). The goal of this method is to detect the branches of the phylogeny that contribute most to PE, and to distinguish among neo-endemism, paleo-endemism, and a novel category: meso-endemism.

(2) Another new method called trait diversity (TD) uses a different facet, a phylogram where the branch lengths represent reconstructed evolutionary change in functional traits. Contrasting TD with an older approach called functional diversity (FD), which by contrast is measured in Euclidean distance among taxa in ecological space, allows one to distinguish among different ecological and evolutionary processes that may have been operating in a location: habitat filtering, competitive exclusion, trait convergence, or trait divergence.

(3) Most spatial phylogenetic methods to date discard valuable information about spatial patterns by converting continuous variables into binary categories. This includes representing geographic ranges using binary presence-absence data, classifying statistical significance into categories, and quantifying biogeographic gradients into discrete regions. Recent advances

have shown that a full suite of spatial phylogenetic analyses, including analyses of alpha and beta diversity, neo- and paleo-endemism, biogeographic hypothesis testing, and spatial conservation prioritization, can be implemented with "smooth" methods that never remove information content by categorizing continuous data. E.g., SNAPE (Smooth Neo- And Paleo-Endemism analysis), a modification of the previously published CANAPE (Categorical Analysis of Neo- And Paleo-Endemism) method that contains no thresholding.

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Next Generation systematic botany in Australasia: looking back, looking forward

For any scientific field it is beneficial to occasionally look back on past predictions of where the field was heading, and compare that to what actually unfolded. Sometimes it feels we are so busy with various research projects and applying current methods that we rarely pause to reflect on broader trends. Given the theme of this year's ASBS meeting is "Next Generation Botany", I am taking this chance to reflect on the past and look to the future, particularly the 16 years since the last ASBS conference was held in Armidale when I then spoke about some technical limitations for DNA barcoding – which has prompted this talk. Some earlier predictions have indeed materialised, albeit in somewhat different forms perhaps than we anticipated, e.g. whole genomes have been, and are now routinely, sequenced, and artificial intelligence has advanced greatly in its power and application (for better and worse?). Whereas in other areas, the predictions have perhaps proven more elusive. For instance, what is the status of a hand-held botanical "tricorder" for identification and DNA barcoding for plants? I will illustrate some aspects of how systematics has evolved, drawing, where possible, on examples from research on Australasian plants such as *Acacia* and eucalypts. In terms of the future, I will raise my own "wish list" for systematics and taxonomy, with the hope this may generate some discussion and reflection on where our discipline might be heading next.

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Phylogenomics provides insights into the diversification and range evolution of the mega genus *Bulbophyllum* (Orchidaceae)

The hyperdiverse orchid genus *Bulbophyllum* constitutes the second largest genus of flowering plants with close to 2,200 known species. It exhibits exceptional morphological and ecological diversity. *Bulbophyllum* is a pantropical genus, with the highest species diversity in tropical Asia (>1,560 species), particularly in the floristic regions of Malesia and Papuasia. The great majority of the species are epiphytes. The high species richness and complex patterns of morphological diversity within this genus present major impediments to constructing a stable and informative infrageneric classification, and to understanding patterns of evolutionary relationships and trait evolution, including ancestral range reconstruction. Poor resolution of phylogenetic trees in previous molecular studies based on few DNA loci has so far limited our understanding of the diversification of its lineages in time and space.

Here, we present a broad-scale plastid phylogenomic analysis of 374 samples representing 322 species and 65 of 97 sections, with a taxonomic focus on the largest lineage within the genus, the Asian clade. Maximum-likelihood analyses of 63 plastid markers yielded well-resolved, strongly supported phylogenetic reconstructions that clarified infrageneric relationships. Several currently recognized sections (e.g., *Stachysanthes*, *Hyalosema*, *Hoplandra*) were supported as monophyletic, whereas others (e.g., *Brachyantha*, *Cirrhopetalum*, *Cirrhopetaloides*, *Brachypus*, *Polymeres*) were found to be non-monophyletic. Divergence-time analyses in BEAST, using secondary calibrations within a broad Orchidaceae outgroup, placed the origin of the genus in the late Oligocene and the onset of crown diversification in the middle Miocene. Ancestral ranges were inferred in BioGeoBEARS under six alternative biogeographic models and the Most Recent Common Ancestor of the genus *Bulbophyllum* was inferred to be widespread across Malesia, the Indo-China/Indian subcontinent, and Australia. The findings of this study provide important insights into the phylogenomic relationships and spatiotemporal dynamics of this vast genus, addressing long-standing questions surrounding its evolutionary history and contributing towards an improved infrageneric classification.

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Update from Taxonomy Australia on Discovering Biodiversity: A Decadal Plan for Taxonomy and Biosystematics in Australia and New Zealand 2018–2027

The Australasian Systematic Botany Society (ASBS) was a key initiator of and central participant in the development of the *Decadal Plan for Taxonomy and Biosystematics in Australia and New Zealand 2018–2027*. This high-profile strategic advocacy document for our sector was published under the auspices of the Australian Academy of Science and New

Zealand's Royal Society Te Apārangi in 2018. Following on, Taxonomy Australia was established as a professional network in Australia to support the ambitions of our sector as laid out in the *Decadal Plan* through coordinated science advocacy.

Since the launch of the *Decadal Plan*, significant progress has been made in some of the key priorities it enunciated, in particular through increased investment in large-scale programs to enhance our research infrastructure. These include the Australian Reference Genome Atlas (ARGA), the National Biodiversity DNA Library (NDBL), the CSIRO national collections building, and the work of the Atlas of Living Australia (ALA) in mobilising biodiversity data, as well as several collaborative large-scale 'omic initiatives such as the Genomics for Australasian Plants Initiative supported through Bioplatforms Australia and partnering institutions. Discussion is ongoing about implementation of a nationally distributed collections infrastructure as part of the National Collaborative Research Infrastructure Strategy (NCRIS) National Research Infrastructure (NRI) Roadmap.

In alignment with the key strategic goals of the *Decadal Plan*, Taxonomy Australia set out to provide advocacy for a targeted mission to document all Australian biota within a generation. A '*Cost benefit analysis of a mission to discover and document Australia's species'* by Deloitte Access Economics demonstrated considerable benefits from increased investment in the taxonomy and biosystematics sector, thus providing support for the mission. Taxonomy Australia identified increased funding for Australia's major funding scheme for taxonomic research– the National Taxonomy Research Grant Program administered through the Australian Biological Resources Study – as a key priority for its current advocacy to support such a mission. As an important contribution to accelerate discovery, Taxonomy Australia has successfully established an innovative platform for the publication of new species of Australian biota, the *Australian Journal of Taxonomy*. To date, more than 100 issues have been published, covering more than 300 species. A current priority for Taxonomy Australia is formal incorporation to provide a sound governance and financial underpinning for its activities, along with fostering a discussion in the sector about the need for and the capacity to prepare a new *Decadal Plan* beyond 2027.

This talk will reflect on the advancements made since the development of the first *Decadal Plan for Taxonomy and Biosystematics in Australia and New Zealand*, the opportunities that it has created as well as the various challenges that have been encountered in its implementation. The learnings from the first *Decadal Plan* will be critical for the development of a fit-for-purpose strategic plan for the next decade.

Francis Nge (Keynote II)

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Flora-wide trends in macroevolution: Australia and beyond

Australia harbours a highly diverse and endemic flora. Substantial progress has been made on its biogeography and evolution, accelerated in recent years by phylogenomic studies. In this keynote, I present several examples of flora-wide biodiversity and macroevolutionary trends: (1) common biogeographic patterns seen across multiple plant groups in Australia, the Pacific, and Asia; (2) the evolutionary assembly of hyperdiverse regional floras, including the southeast Asian and Sydney Basin floras; and (3) region-specific diversification dynamics in southwest

Australia and other global biodiversity hotspots. These insights rely on well-sampled, dated phylogenies, which are essential in uncovering flora-wide signals. I will also discuss the current state and approaches of Australasian systematics, and advocate for revising current approaches through a more holistic multi-purpose taxonomic sampling framework.

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Long-read whole genome sequencing reveals novel lineages and genomic divergence thresholds in *Rhizoctonia* (Ceratobasidiaceae; Cantharellales)

Rhizoctonia (Ceratobasidiaceae; Cantharellales), inclusive of genera such as *Ceratobasidium*, *Ceratorhiza* and *Thanatephorus*, is a genus of cryptic basidiomycetes of major ecological and economic significance. Alongside several devastating plant pathogens which are responsible for billions of dollars of crop losses annually, members of the genus also function as one of the dominant groups of symbiotic orchid mycorrhizal fungi. As *Rhizoctonia* harbours both plant pathogens and symbionts, it presents an ideal system to study plant-fungal interactions at the genomic level. While several whole genomes of pathogenic *Rhizoctonia* lineages are published, there are relatively few genomes available of orchid mycorrhizal lineages. To remedy this gap, we used long read sequencing to produce 38 new, high-quality whole genome assemblies of *Rhizoctonia* lineages predominantly associated with Australian *Pterostylis* orchids. Using these assemblies in combination with published *Rhizoctonia* genomes, we calibrate genome-wide divergence thresholds using Mash dissimilarity indices and average nucleotide identity (ANI), and for the first time perform species delimitation analyses within the genus. We show that genome divergence thresholds within *Rhizoctonia* based on Mash dissimilarity and ANI are consistent with divergence thresholds across the kingdom Fungi, and the Tree of Life more broadly. We use whole genome data to support the recognition of at least six new species of *Rhizoctona* and identify several lineages that are entirely new to science. Moreover, we demonstrate that ITS barcode divergence thresholds currently in use drastically underestimate the number of extant *Rhizoctonia* species and show that the genus is far more diverse than previously recognised.

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Population genomics provides molecular support for morphological species hypotheses and hybridisation among sexually deceptive greenhood orchids (*Pterostylis*; Pterostylidinae)

Pterostylis (Pterostylidinae; Cranichideae) is a large, predominantly Australian genus of terrestrial orchids where pollination by the sexual deception of fungus gnats is widespread across several clades. Other sexually deceptive orchid systems are characterised by strong chemically mediated reproductive isolation, despite often limited genomic and morphological variation. Therefore, while the majority of *Pterostylis* species have been described solely based on morphology, it is likely that cryptic species may be uncovered with molecular evidence. Using a group of closely related species within the sexually deceptive clade *P*. sect. *Squamatae* as a case study, we 1) used contemporary genotyping-by-sequencing technologies to quantify the extent of genomic variation between putative species of *Pterostylis*; and 2) determined whether there is molecular support for existing species hypotheses based on morphology. Population genomic analyses revealed discrete and genetically divergent clusters that correspond with existing taxonomies. Unexpectedly, we also identified the presence of both F1 and backcrossed hybrid individuals in one population where two divergent lineages occur sympatrically. While hybridisation has been previously documented in *Pterostylis*, this finding represents the first molecular evidence of hybridisation between sexually deceptive species.

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On the effect of chimeric assemblies in target capture studies: investigating the evolution of *Flindersia* (Rutaceae) using a novel method for chimera detection

Flindersia is a genus of 17 species that predominantly occur in rainforests throughout eastern Australia, New Guinea, New Caledonia, and the Maluku Islands. The morphological, ecological and geographical features of the genus make it a useful study system for investigating questions relating to speciation and historical biogeography in Australasia. In addition, its palaeopolyploid karyotype, along with more recently derived polyploid species, make it an ideal group for investigating potential pitfalls in target capture phylogenomics related to polyploidy. One such pitfall is presented by “chimeric sequences”, consensus sequences which include regions from paralogous genes that are mistakenly stitched together during the assembly process. Using target capture data generated with the Angiosperms353 bait kit and a recent draft genome for *Flindersia*, we developed a new method for identifying chimeric sequences produced during the assembly of target capture data. In this talk I will show that chimeric sequences can represent a considerable proportion of sequences produced using standard bioinformatic pipelines. I will also discuss the effect of chimeric sequences on the topology, support and concordance for branches in the *Flindersia* phylogeny, and if time permits talk about species relationships and results from molecular divergence dating and ancestral range estimations.

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Phylogenomics and evolutionary reconstruction of *Lepidosperma* (Cyperaceae): An Integrative Approach

Lepidosperma Labill. (sword sedges) is a diverse genus of sedges comprising about 83 accepted species and more than 200 putative taxa, distributed mainly in Australia, with a few species extending to New Zealand, New Caledonia, and south-east Asia. Sword sedges occupy a diverse range of habitats, including grasslands, swampy areas, and rocky outcrops. Despite its diversity, *Lepidosperma* remains one of the most understudied genera in the Australian flora. Previous molecular studies have largely focused on broader relationships within the tribe Schoeneae and the family Cyperaceae, with little attention paid to the phylogeny of *Lepidosperma*, which remains unresolved. Species delimitation is particularly problematic in areas of high diversity, due to limited morphological variation among taxa. This taxonomically complex genus is therefore in urgent need of revision.

The present study aims to: (1) conduct a comprehensive phylogenetic analysis of *Lepidosperma* with extensive sampling across species complexes; (2) prepare a taxonomic revision of the genus; and (3) investigate its evolutionary history to identify events underlying the current distribution of its species. By integrating molecular and morphological data, this project will provide critical insights into the systematics, evolution, and biogeography of *Lepidosperma*, providing insights for the conservation and ecological understanding of this significant lineage within Cyperaceae.

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Anglesea amber from Australia as new archive for Eocene liverwort and moss species

Five bryophyte fossils recovered in amber at Anglesea, Victoria (Australia) are presented, dating from the late middle Eocene (42Ma), reinforcing the significance of ancient tree resin deposits. Exceptional detail preserved in two of these specimens provide adequate basis for their description as new species, *Radula panduriformis sp. nov.*, and the new genus *Hyponychium pentadactylum gen. et sp. nov.* The deeply dissected five-lobed underleaves of *Hyponychium* differ from extant and extinct taxa, and in the absence of sporophytic characters, the affinity of this fossil is uncertain. Other fossils described herein retain significant detail, but the absence of sporophytic characteristics limits their classification to the genus level or higher, highlighting the difficulty of precisely identifying fossil bryophyte relationships. All fossils presented are the earliest recorded examples of their families from the Southern Hemisphere and supports established knowledge of the presence of warm and humid forests in middle Eocene Victoria.

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Hiding in plain sight: a proposed new species of *Homoranthus* (Myrtaceae: Chamelaucieae)

The genus *Homoranthus* Cunn. ex Schauer has 32 endemic species in Eastern and Southern Australia. Surrounding the NSW and QLD borders on the Great Dividing Range, at the northern section of the New England Tableland (NET) bioregion, there are eight rare described species of *Homoranthus* endemic to granite outcrops. In a 500,000-hectare area, all these species have niche habitats and small disjunct distributions, except for *H. lunatus*, with populations 70 km apart and spanning across other species' ranges. Preliminary genetic analyses of these eight *Homoranthus* species revealed an unexpected genetic structure suggestive of an undescribed taxon, prompting a targeted morphological assessment of *H. lunatus* of its Torrington State Conservation Area, Boonoo Boonoo National Park and Basket Swamp National Park populations.

Though the morphological assessment found 44 of the 48 characters assessed between the populations were not meaningfully different, four characteristic differences, including a subtle difference in the mature leaf shape and distinctly modified flowering branchlets, supported the genomic analysis of a new undescribed *Homoranthus* species, *H. wissmannii ined*. Further, the genomic analysis identified that *H. lunatus* and *H. wissmannii* were not sister taxon despite their similar appearances.

In addition to the NET outcrop endemics, we included several further *Homoranthus* species from surrounding areas in the genetic study. Our genomic analysis identified restricted gene flow amongst populations over small distances, but intraspecific species diversity was being maintained. The *Homoranthus* species had strong genetic distinctiveness between them, despite some species having ranges that are less than 10 to 15 km apart. We suggest that ecological isolation, life history traits and limited gene dispersal may contribute to speciation in *Homoranthus* taxa through a combination of genetic drift and natural selection.

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Genetic characterisation and conservation of New Zealand *Pimelea*

Species radiations often present challenges for species delimitation, and the genus *Pimelea* (Thymelaeaceae) in New Zealand is a good example of this. A recent taxonomic revision identified *c.* 54 taxa in the region, yet many remain hard to distinguish in the field based solely on morphological traits. More than 60 % of the species are considered threatened or at risk of extinction. Additional un-named entities have been identified, which if they prove to be species would also be of conservation concern.

Previous molecular phylogenetic work using ITS and plastid markers has shown that the New Zealand species, along with several Australian endemics, form a clade nested within the broader Australian *Pimelea* phylogeny. However, these commonly used markers often lack sufficient resolution for species-level delimitation in recent radiations.

To address this, we have developed a suite of low-copy nuclear markers to better resolve species boundaries and test the morphological hypotheses proposed in the recent taxonomic revision. We assess how well these markers work for this purpose, including challenges involving polyploidy, and present two case studies of applying the markers to taxonomic questions with conservation implications:

The first example, *P. villosa*, is a coastal species that has undergone a significant decline, and may be made up of two subspecies. Numerous community conservation groups across New Zealand are actively engaged in its restoration. We assess the genetic diversity of remnant wild populations and compare these to individuals propagated *ex situ* for conservation purposes, evaluating the genetic representativeness of cultivated stock.

The second example is that of the critically endangered *P. ignota* – Is this a threatened species on the brink, or a hybrid? What are the conservation implications?

In addition to their botanical interest, New Zealand *Pimelea* species are ecologically important as host plants for several endemic *Notoreas* moths, many of which are themselves threatened. Understanding the evolutionary relationships and genetic distinctiveness of *Pimelea* species is therefore critical not only for their own conservation, but also for the persistence of associated invertebrate biodiversity.

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Species at the edge of evolution: a population-level assessment of species delimitation in *Pterostylis* section *Parviflorae* (Orchidaceae)

Orchidaceae is one of the largest families in the world, containing many species recently diverged or in active states of divergence, Species concepts within recently evolved lineages present many challenges for taxonomic classification and identification. Here, we test species limits in 15 described Tiny Greenhood species in *Pterostylis* section *Parviflorae* (the *Speculantha* group) using population-level genomic sampling of 15,263 single nucleotide polymorphisms (SNPs). We recovered ten genetic clusters, in five broader groups. *Pterostylis parviflora*, *P. bicornis* and *P. uliginosa* are genetically distinct from each other, and comprise three of the groups. The first of the remaining two comprises *P. antennifera*, *P. borealis* and a complex including *P. rubescens* and similar species. The second includes *P. nigricans*, *P. furva* and similar species. Not all species currently recognised based on morphological characters can be distinguished in our population genetic data set, including four range-restricted species from north-east New South Wales and south-east Queensland. Individuals of *Pterostylis ventricosa* nest among those of *P. rubescens*. Individuals of *Pterostylis exsquista*, *P. recta* and *P. rubiginosa* all nest among individuals of *P. amabilis*. Individuals of the range-restricted *P. crebra*, from the Blue Mountains, nest among individuals of *P. furva*. Two threatened species listed under both the Commonwealth EPBC Act and the NSW BCA Act, *P. bicornis* and *P. vernalis* are supported as distinct species. *Pterostylis antennifera* forms two genetic clusters, with individuals from Kroombit Tops distinct from the remainder. An individual from Wentworth Falls, Blue Mountains, is genetically distinct from other members of the *furva-nigricans* subgroup and warrants further investigation.

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Born of Fire – The sub-basaltic silcrete floras of eastern Australia and the role for volcanism in shaping the modern Australian flora

Australia was subjected to extensive intraplate volcanism throughout the Cenozoic and subsequent erosion has resulted in the distinctive topography and landscapes of eastern Australia. Lava fields and central volcanoes attest to our volcanic past and burial by volcaniclastics has also resulted in the preservation of fossil floras. These fossil floras in Australia include autochthonous elements, e.g. carbonised wood and roots in basalt flows, trees buried by ash falls and entire floras buried by volcanic activity. Transported leaves and branches occur in high energy ash flows (lahars) and pyroclastics and dispersed leaves and fruits accumulate in lacustrine sediments in lakes or other depositional environments. Weathering of volcaniclastics is responsible for the release of silica and this mobilization of this silica has also resulted in the development of eastern Australian diatomites and silcretes. These sub-basaltic silcretes, that are the focus of my research, are restricted to eastern Australia and the fossil plants represent autochthonous assemblages derived from the local flora which are often palaeosols consisting of leaf litter, soil horizons and roots. Weathering of overlying volcanics, as noted above, is the likely source of silica and the acidic (humic) conditions of the fossil plant material provide ideal geochemical conditions for the deposition of silica and subsequent permineralisation of plant remains. The plants in sub-basaltic silcretes are typically silicified and the internal anatomy and cellular structures are preserved. Terrestrial (ground-dwelling) ferns have been preserved in-situ and are often conspicuous elements in these sub-basaltic silcretes. The exceptional preservation has resulted in soft tissue preservation including of the exocarps of fruits, actively growing vegetative shoots (fern croziers), bark of trees, roots and root nodules which collectively indicate that burial by volcaniclastic sediments and/or basalt flows was rapid. In this talk we investigate the unique opportunities provided by these floras which has resulted in the discovery of new taxa. The remarkable preservation provides the opportunity for high resolution studies of plant anatomy including fruit and seed morphology that allows detailed comparisons with extant genera. The autochthonous floras that occur in these sub-basaltic silcretes in eastern Australia are discrete ‘time capsules’ of the local vegetation growing at that site at that time. These floras clearly indicate that distinct plant communities were represented in northeastern Australia by the early Oligocene. These remarkable plants represent a completely new set of data to understand the history and evolution of Australia’s flora but remain little studied. While there are many opportunities for new research there also remain many challenges in working on these new floras and I will use our current work on the Melastomataceae to highlight some of these challenges in studying and interpreting these floras, and that would also need to be addressed by the next generation of researchers who study this material.

Hervé Sauquet[1,2] (Keynote I)

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Angiosperm macroevolution: embracing the unknown (and the unknowable)

The origin and extraordinary diversification of angiosperms over the past 150 million years is well known as one of the most transformative events in the history of Earth, with a profound impact on all terrestrial environments and numerous other life forms. Phenomenal progress has been made over the past 30 years on reconstructing and understanding many aspects of this revolution, drawing from all disciplines of biology, including palaeontology, morphology, phylogenetics, physiology, ecology, evolutionary developmental genetics, and genomics. Yet, numerous key questions remain. In this talk, I will illustrate some of these questions, drawing from my research on angiosperm macroevolution, including floral evolution and divergence time estimation. I will show how diving deeply into some of these questions, using ever larger datasets and diverse methods, has often led to far more uncertainty than previous paradigms. Though vexing at first sight, I will argue why finding and accepting these unknowns, while improving our capacity to measure and embrace uncertainty, can be a formidable driving force for research and new ideas, complementary to essential continued confirmation or refutal of established facts. I will then share a few reflections on my own trajectory as a scientist over the past 20 years. In particular, I will focus on learnings from diverse rejections, periods of high uncertainty and instability, and unexpected life and career turns to demonstrate why I strongly believe that embracing the unknown (and the unknowable) may be a helpful metaphor as we navigate the ever-evolving landscape of research opportunities and technological revolutions.

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What species of fleabanes (*Erigeron*, Asteraceae) have been introduced to Australia?

An accurate understanding of the taxonomy of invasive weeds is critical for their management and containment. As of writing, the Australian Plant Census recognises one species of the genus *Erigeron* as native (*E. conyzoides*), and six as introduced. In recent years, we have conducted field work and taxonomic research to support study design and risk assessments in weed biocontrol efforts conducted by CSIRO Health & Biosecurity for *Erigeron bonariensis* (flaxleaf fleabane), a globally invasive weed that is common and widespread across Australia. We located a population of the rare and threatened species *E. conyzoides*, sourced the first seed accessions for experimental research, and found that it is morphologically and genetically indistinguishable from the northern hemisphere *E. acris* complex. Most recently, we generated a comprehensively sampled target capture dataset for several species of *Erigeron* formerly treated as part of the segregate genus *Conyza*. Our data suggest that the following nine species should be recognised as introduced to Australia: *Erigeron acris, E. bellioides*, *E. bonariensis*, *E. canadensis*, *E. floribundus* (syn. *E. bilbaoanus*), *E. karvinskianus*, *E. primulifolius*, *E. pusillus*, and E. sumatrensis. We will discuss key spotting characters for these difficult-to-identify weeds and implications of our results for invasion history and weed management.

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Morphological insights into species delimitation within the *Phebalium glandulosum* complex (Rutaceae)

The *Phebalium glandulosum* complex is a morphologically variable group of shrubs distributed across eastern Australia. Despite its wide range, the group has received little dedicated study, leaving species boundaries poorly defined. A central part of my integrative taxonomic study has involved extensive morphological and anatomical study of herbarium specimens and field collections to identify diagnostic traits and patterns of variation within the complex. By assessing more than 130 characters, including novel features such as endocarp form, leaf gland form, and branchlet indumentum, the study provides new insights into species delimitation. These morphological data clarify taxonomic relationships and shed light on how morphological variation reflects evolutionary processes within the group. The outcomes will enhance systematic understanding of *Phebalium*, contribute to accurate identification, and provide a foundation for further studies on adaptation and diversification in Australian Rutaceae.

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Exploring target sequence capture for multi-scale conservation genomics of Australian orchid species complexes

Orchids remain at the forefront of Australia's conservation challenge, representing approximately 17% of the nation's threatened flora, with the Diurideae subtribe dominating terrestrial diversity and comprising many threatened taxa. High-throughput DNA sequencing techniques have significantly improved conservation genomic assessments of genetic diversity and species delimitation for threatened species. However, standard approaches such as restriction site associated techniques, including RADseq and DArT, perform poorly on low-quality or historical DNA and produce datasets that can be challenging to combine or expand upon. These limitations are acute for threatened taxa where only limited or preserved material is available, and where further sampling may risk population viability.

Target sequence capture or hybrid enrichment sequencing offers a transformative alternative, enabling high-throughput recovery of large genomic datasets even from degraded or archival samples. Customisable bait kits permit the targeting of specific genes to achieve the desired level of phylogenetic resolution and facilitate the integration of datasets across studies or over time. Target sequence capture approaches have traditionally been used to resolve deep evolutionary relationships. However, recent research demonstrates their potential for resolving relationships at shallower evolutionary scales, which is required for assessing species boundaries and within-species genomic diversity.

To evaluate the utility of target sequence capture for conservation genomics, a collaborative team of plant systematists, bioinformaticians, ecologists, and biodiversity managers are applying the method to clarify genetic diversity and species boundaries in rare and threatened Australian orchid species complexes. The data from this project will directly inform conservation management of critically endangered species, with robust species delimitation enabling more effective and efficient use of conservation resources. More broadly, the project aims to provide a critical proof-of-concept for implementing target sequence capture approaches in Australian orchid conservation, with the potential to deliver improved phylogenetic and population-level resolution, evidence-based taxonomic clarity, and robust cross-project data integration nationally.

In this talk we will outline the development of a customised bait kit optimised for Diurideae orchids, combining lineage-specific and universal flowering plant markers, and share early results on sequence recovery and phylogenetic resolution across four Australian orchid species complexes: *Corybas aconitiflorus* complex, *Thelymitra variegata* complex, *Thelymitra fuscolutea* complex and the genus *Rhizanthella*. We also discuss ongoing challenges, including bait design for phylogenetically underrepresented groups or lineages that have undergone rapid or recent radiations, as well as the need for effective translation of genomic data into conservation management resources and practice.

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The Austral Antarctic Forest during the Early Eocene Climatic Optimum – biogeography, diversity and the fate of polar lineages

The biogeographic patterns evident in the floras of the Southern Hemisphere have long fascinated naturalists. To explain these patterns, hypotheses have been proposed that invoke either vicariance through Gondwana's break-up or long-distance dispersal.
The fossil plant assemblage of the Macquarie Harbour Formation (MHF) in Tasmania, southeastern Australia, offers a unique window into this complex puzzle. Situated at near the south polar circle (~65°S), and dating back approximately 53–50 million years to the Early Eocene Climatic Optimum (EECO), it represents one of the oldest post-Cretaceous plant assemblages in Australia. Importantly, it predates the final continental break-up of Australia from Antarctica, with Tasmania forming the last land connection between the two continents. We present new data from a near-polar forest, including systematics, diversity and ecophysiological adaptations to the high latitudes. Furthermore, we reveal taxon- and ecosystem-scale biogeographic patterns across the Southern Hemisphere.
We identified at least 10 conifer species (e.g., Araucariaceae, Podocarpaceae), two cycads (*Bowenia*, *Pterostoma*), one fern (*Lygodium*), abundant remains of the relict umkomasialean 'seed fern' (*Komlopteris*) and several angiosperms (e.g., *Nypa*, *Ripogonum*, and eucalypt-like fossils).

Intriguingly, many of these taxa are extant relicts with small populations in Australasia (mostly tropical Oceania) and South America (mostly the neotropics), often confined to high-altitude and/or humid habitats. The presence of these lineages in the early Eocene assemblages of South America and Australia, as well as the Palaeocene of Antarctica, demonstrates a continuous extent of the Austral Antarctic Forest, thus favouring the vicariance hypothesis for many taxa that are today shared between these continents.

Furthermore, the assemblage contains extinct lineages, Mesozoic relicts, such as *Araucarioides* and *Komlopteris*, that appear to have had a Gondwana-wide distribution. We associate their extinction with the northward continental migration of Australia, and the rise of the Andes in South America, which led to significant aridification, changes in insolation and increased angiosperm competition.

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The Witness Tree Project: Long-Term Plant Monitoring for a Changing Climate and Urban Pollution

The Witness Tree Project is a long-term research initiative launched in 2022 by the Plant Atmosphere Interaction Lab at Trinity College Dublin. The project monitors how trees respond to environmental stressors such as climate change and assesses their effectiveness in filtering air pollution. It focuses on 21 tree species, chosen for their botanical, ecological, and cultural significance. Continuous monitoring has been implemented at two botanical gardens in Dublin, and two additional European gardens will join from next year. The project aims to establish an expanding international network of monitoring sites, with the long-term goal of fostering collaboration and sparking interest in regions.

Researchers collect annual data on key physiological traits, such as stomatal conductance and water-use efficiency, as well as particulate matter accumulation on leaf surfaces. These metrics help evaluate each tree's health and its potential to mitigate urban air pollution. Designed to span at least 30 years, the project will generate a valuable long-term dataset that can track both climate trends and the impacts of environmental policy changes.

All data, protocols, and data management plans are open access, inviting global collaboration. The project is gaining international interest, with other botanic gardens exploring participation. This presentation will outline the project's methodological framework, share early insights into the results, and the project’s potential impact on research, outreach and policy making.

Rodrigo Neregato[1], Rosemarie Rohn[2], **Anne-Marie Tosolini**[3, 4] & Vera Korasidis[3]

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Eocene-Oligocene Floras from Fildes Peninsula, King George Island, Antarctic Peninsula

Fossil plants and pollen from Palaeogene strata on King George Island, Antarctica, are being investigated to determine past vegetation and climate in southern high latitudes. The fossil assemblages represent vegetation which once grew on the terrestrial volcanic arc that now forms the Antarctic Peninsula. Fossil leaves from four different localities on King George Island, Antarctic Peninsula, were collected during the Brazilian Antarctic Program (PROANTAR) expedition in the summer of 1986/7. Fossil Hill and Suffield Point sites are laterally equivalent, contemporaneous deposits in the Fossil Hill Formation.

The age of the Fossil Hill Formation leaf sites is late Eocene to early Oligocene. The Winkle Point site age is unknown, but possibly Cretaceous to Palaeocene. The fourth site, Price Point, has a previously published age of latest Cretaceous to Palaeogene, but palynological analysis in this study has constrained the age to Campanian.

Analyses of Eocene – Oligocene leaf floras from the Fossil Hill Formation have identified a pteridophyte (*Coniopteris*), three conifers (*Papuacedrus*, *Podocarpus* and *Phyllocladus*) and 19 different angiosperm leaf morphotypes. The angiosperm assemblage is dominated by leaves with affinities to extant families typical of cool-warm temperate (e.g. Nothofagaceae, Proteaceae) to sub-tropical (e.g. Lauraceae, etc.) climates. Six new leaf morphotypes are described for the first time in this region. The remaining specimens are similar to previously reported morphotypes from this locality, in which the most abundant taxa are *Nothofagus* spp., *Podocarpus* sp., *Phyllocladus aspleniifolium*, *Fildesia pulchra*, *Dicotilophyllum latitrilobatum*, *Laurophyllum* spp. and *Rhoophyllum* sp.

In the Fossil Hill floras on King George Island, Nothofagus diversity is unusually low. These floras had higher rainfall and greater disturbance, caused by volcanic eruptions, and forest ecosystems similar to modern Valdivian rainforests. Comparisons with contemporaneous Seymour Island floras indicate divergent responses to climate change. Seymour Island records declining diversity and increased dominance by *Nothofagus* under cooling, seasonal climates preceding Antarctic glaciation. The presence of temperate vegetation indicates that the climate was warm enough to sustain large forests with relatively high diversity at high-latitudes and Antarctica experienced much warmer climates during the early Cenozoic.

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What would Nancy think?

Dr Nancy Burbidge's illustrious career ended nearly fifty years ago. Coincidentally, that was when my career began, so this seems a good opportunity to reflect on changes to systematic botany over that period. Nancy was a leading figure in Australian botany, both in her own areas of research and as an advocate for change. She was among those whose advocacy led to creation of bodies that we take for granted now, notably the Australian (now Australasian) Systematic Botany Society, the Australian Biological Resources Study, and the Committee (now Council) of Heads of Australian (now Australasian) Herbaria. Her efforts also resulted in the *Flora of Australia* and the Australian Plant Name Index. There are some aspects of the current systematic botany scene that Nancy's history suggests she might have found disappointing if she were alive today, but she would have welcomed the revolution wrought by advances in molecular and information and communications technologies.

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Comparative rhizotaxy of fossil and living isoetalean rhizomorphs reveals development through rootlet intercalation within a triangular lattice

- Background and Aims: The Isoetales are a clade of lycopsids that evolved colossal arborescent forms during their Palaeozoic prime but today are represented solely by the small herbaceous monogeneric *Isoetes*. Despite the differences in scale of taxa in the clade the rooting system of all members consists of two-parts, a rhizomorph from which rootlets develop in a regular pattern termed rhizotaxy. Rhizomorphs are highly diverse in different members leading to different terminology being used to describe rhizotaxy in different lineages. Here we set out to investigate how conserved rhizotaxy was between taxa and to provide a standard geometric definition, and developmental interpretation of rhizotaxy applicable to all members.
- Methods: We developed a pipeline to quantitatively describe rhizotaxy. This pipeline allowed rootlet arrangement to be captured in 3D, before being visualised on a 2D lattice where Deluany Triangulation could be applied. This method offers a standard method to investigate

rhizotaxy across disparate rhizomorphs. Next, to investigate the evolution and development of rhizotaxy we applied our pipeline to a 3D model we generated of the rooting system of the extinct Carboniferous lycopsids *Oxroadia*. Finally, we made direct observations of rootlet development in *Isoetes* using time course imaging.

• Key Results: We demonstrate that rhizotaxy can be described as an equallateral triangular lattice for all members of the Isoetales including *Oxroadia*. By combining evidence from direct observation of rootlet development in *Isoetes* with inferences of rootlet development and the early stages of sporophyte ontogeny of *Oxroadia* we conclude that the conserved rhizotaxy developed by the process of rootlet intercalation.

• Conclusions: We provide a single geometric definition, and predicted developmental mechanism for rhizotaxy that applies to all Isoetales. Our findings call into question the literal interpretation that the rhizomorph is a modified shoot.

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The taxonomic status of the Oceanian species of *Carex* section *Indicae* (Cyperaceae)

Carex section Indicae is an exclusively tropical or subtropical group with bizarre morphology. Its species have racemiform or paniculiform (highly branching) inflorescences with each branch subtended by a utriculiform cladoprophyll. Earlier taxonomic treatments of the section are scarce and cover only a small subset of its species. This study is a part of my comprehensive revision of the group with the aims of clarifying species limits and providing a more accurate picture of *Carex* diversity in the tropics. A morphological study covering the entire section involved the examination of 2,699 herbarium (A, E, GENT, K, MO, NY, P, US, Z + ZT) and ca. 300 digitized (JSTOR, LINN, PE, SBT) specimens. Section Indicae species were found to occur in Northeastern Australia, Fiji, Mariana islands, New Caledonia, Papua New Guinea, and Vanuatu. The species can be found mostly in moist environments such as creek banks, river floodplains, moist grassy cliffs, streambeds, and open swamps, but also in other habitats such as roadsides, limestone cliffs, and montane forests at 25 – 3,393 m.a.s.l. The status of *Carex dietrichiae*, *C. fissilis*, *C. fleckeri*, *C. horsfieldii*, *C. melanophora*, *C.neo-guineensis*, *C. papuana*, *C. sclerioides*, *C. tyttholepis*, and *C. xestogyne* as synonyms of other taxa is rejected and are recognized as distinct species based on leaf, inflorescence, pistillate glume, and utricle details. Specimen issues were also observed such as types with inconsistent morphologies and widespread misidentification.

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Pedicularis bhutanica ined. (Orbanchaceae), a new species from Bhutan and taxonomic clarification of *P. heydei* Prain and *P. pheulpinii* Bonati

Pedicularis L. (Orobanchaceae) is highly diverse in the Himalayan–Hengduan region, yet its taxonomy remains unstable due to high intraspecific variation, reliance on morphology, and limited historical sampling. Using an integrative approach that combines detailed morphological comparisons, nuclear ribosomal ITS sequence data, and herbarium assessments, we clarify relationships within Bhutanese *Pedicularis*. We will describe *Pedicularis bhutanica ined*. from the Dagala region, Bhutan, distinguishable from its closest allies, *P. heydei* Prain and *P. pheulpinii* Bonati, by the absence of basal leaves, stem indumentum, and unique floral and fruit characters. Phylogenetic analyses recover *P. bhutanica* as a well-supported monophyletic lineage, confirming its recognition as a species new to science. In contrast, *P. heydei* and *P. pheulpinii* show substantial morphological overlap and no phylogenetic separation, leading us to synonymise *P. pheulpinii* under *P. heydei*. These findings highlight the importance of integrative taxonomy in resolving species oversplitting and strengthening the framework for biodiversity and conservation studies in *Pedicularis*.

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