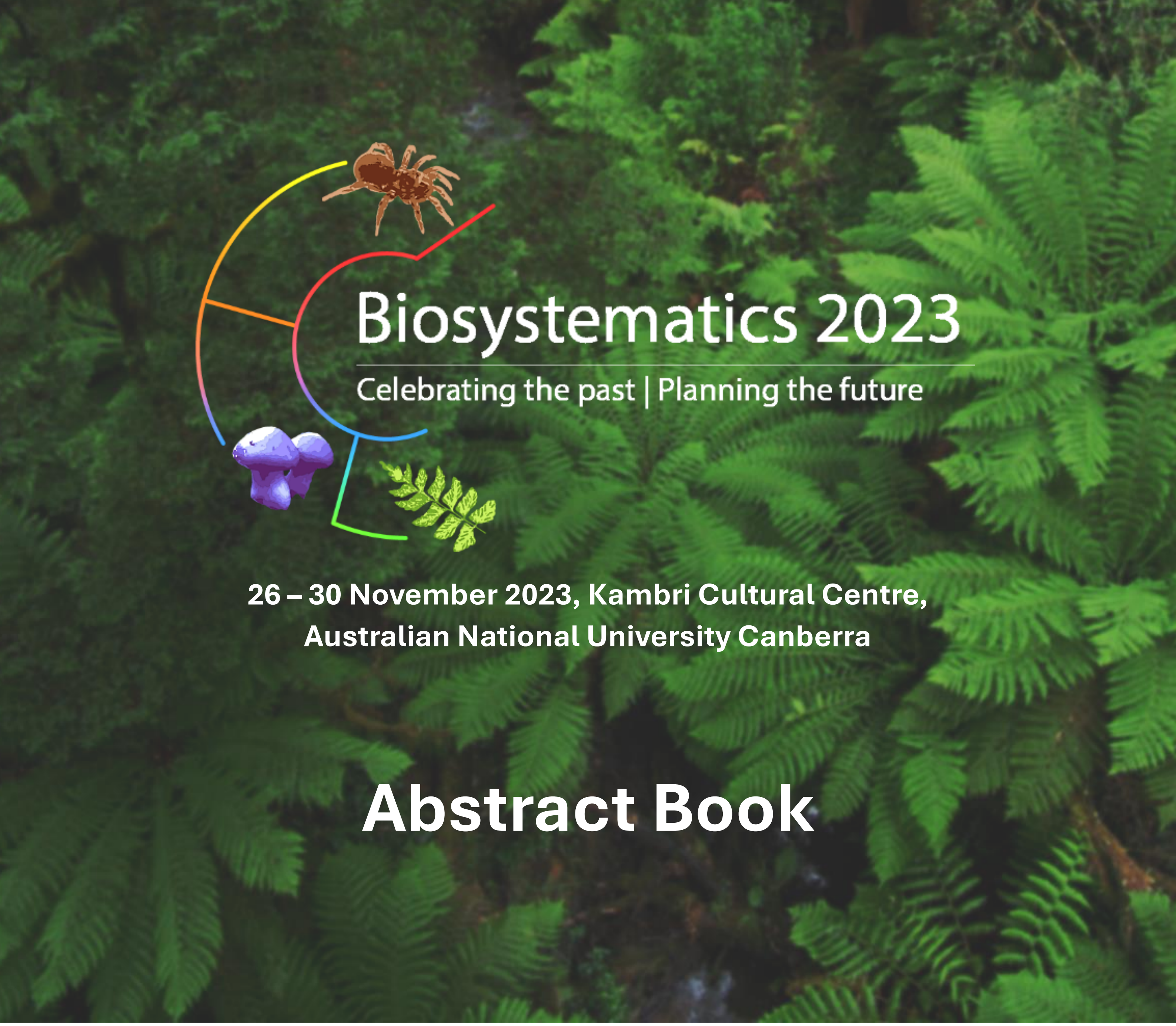

Biosystematics 2023

Celebrating the past | Planning the future

26 – 30 November 2023, Kambri Cultural Centre,
Australian National University Canberra

Abstract Book

Joint conference of the Australian Biological Resources Study, Society of Australian Systematic Biologists, Australasian Mycological Society and Australasian Systematic Botany Society

ASBS

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50 1973–2023
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Bioinformatic aspects of the GAP reference genome project.

Theo Allnutt (RBGV); Todd McLay (CSIRO); Gareth Holmes (RBGV); Ashley Jones (ANU); Mabel Lum (BPA); David Cantrill (RBGV).

The Genomics for Australian Plants (GAP) project is undertaking the large scale genome sequencing of key Australian plant species to provide reference genomes in taxonomic groups where no other genomes are available. As a final stage of this project, ~20 plant species have been selected for simultaneous DNA isolation, long-read sequencing, and assembly. In this presentation we will give an overview of the chosen bioinformatic pipelines for this work and their pros and cons.

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Is Angiosperms353 an effective tool for population genomics?

Benjamin M. Anderson (Western Australia Department of Biodiversity, Conservation and Attractions); Rachel M. Binks (Western Australia Department of Biodiversity, Conservation and Attractions); Margaret Byrne (Western Australia Department of Biodiversity, Conservation and Attractions).

Targeted sequence capture is a powerful tool for obtaining genomic datasets useful for inferring phylogenetic relationships. The Angiosperms353 (A353) bait kit targets 353 loci shared by most angiosperms and has been successfully used in the Genomics for Australian Plants (GAP) Phylogenomics initiative to reconstruct large-scale relationships among Australian plants. While A353 is a useful tool at the generic and family level, can it be used to tease apart population differentiation for species delimitation and conservation diversity studies? Some have suggested that sequence capture approaches hold promise for population studies while also producing data that can be combined with existing datasets, a feature not usually shared by typical population genomic tools like RADseq. To assess the effectiveness of A353 in comparison to RADseq, we undertook sequence capture for a set of samples previously sequenced with RADseq in the GAP Conservation Genomics initiative. The samples come from species complexes with conservation taxa and unclear taxonomic boundaries, and the original aim was to delimit taxa to inform conservation decisions. This talk will discuss analyses and results from the *Isopogon* dataset, highlight challenges to using the data, and provide a perspective on whether A353 is an effective tool for population-scale analyses.

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Combinatorial speciation and ongoing gene flow *Eucalyptus*.

Rose Andrew (University of New England); Jasmine Janes (Vancouver Island University); Kevin Murray (Australian National University); Scott Ferguson (Australian National University); Justin Borevitz (Australian National University).

Eucalypts are hard. It's part of why we love them, and a great stimulus for animated discussions or friendly disagreements. Some of us hope to find the secrets of eucalypts in their genomes, but it is a complex task. Like many speciose genera, incomplete lineage sorting and reticulate evolution are features of *Eucalyptus.* While eucalypts often have somewhat porous species boundaries and shared genetic variation, the evolutionary significance of ancient and ongoing gene flow is not well understood. I will describe our work disentangling the history of introgression in *Eucalyptus* section *Adnataria* at multiple scales using whole-genome short-read sequencing, in conjunction with new long-read-based reference genomes. We are able to identify signatures of ancient and recent introgression, and in some cases can tie them to chromosomal rearrangements. This work has implications for the management of threatened eucalypts, as well as our understanding of diversification and our approaches to classification in *Eucalyptus*.

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An enigmatic snapper parasite (Trematoda: Cryptogonimidae) found in an unexpected host.

Helen Armstrong (Murdoch University); Storm Martin (Murdoch University); Alan Lymbery (Harry Butler Institute, Murdoch University); Scott Cutmore (Queensland Museum).

The Cryptogonimidae are a group within the Trematoda that have a three host life-cycle: snail, fish, fish. The previously known final fish hosts of cryptogonimids have been larger reef associated fish such as snapper (Lutjanids), likely due to the intermediate stage relying on its host fish being eaten by a larger fish. During a field expedition to Ningaloo Reef, I discovered a cryptogonimid infection in the thick-lipped wrasses, *Hemigymnus fasciatus* and *H. melapterus*. Most wrasses (*Labridae*) do not prey substantially on fishes and so are atypical hosts for cryptogonimids and this worm is apparently absent in Queensland where these fishes have been well-examined. I have targeted multiple single marker regions, (ITS2, 28S and 18S and cox1 mtDNA) to identify the worm species and gut contents analysis to identify the host fish diet, I aim to provide taxonomic descriptions of these cryptogonimids. This study would be the first biogeographic comparison of cryptogonimids from Australia.

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***Coccygidium*? I hardly know 'em: A taxonomic revision of the genus *Coccygidium* throughout Australia.**

Tareva-Chine C. Atkin-Zaldivar (The University of Adelaide); Erinn P. Fagan-Jeffries (The University of Adelaide and South Australian Museum).

Coccygidium is a genus of parasitoid wasps in the family Braconidae, that despite being recorded as present in Australia in a 2010 publication no Australian species have been described. Overseas, the genus is most notably being trialled as a biocontrol agent against the invasive crop pest fall armyworm (*Spodoptera frugiperda* (Lepidoptera: Noctuidae)). As of 2020, fall armyworm has established in Australia, and species of *Coccygidium* have been reared from the pest. *Coccygidium* was also collected during the citizen science initiative Insect Investigators, where regional schools ran Malaise traps during March 2022. Using these specimens along with museum collections, and those from the rearing of fall armyworm, five species of *Coccygidium* were described using morphological data and CO1 DNA barcode molecular differentiation. Three of these species were collaboratively named by the schools that collected these specimens, and of these three species, two have also been reared for fall armyworm. These descriptions help add knowledge to hyper diverse Australian biota and show possible uses of targeted taxonomy for potential biological control agents.

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The role of short courses and workshops in systematics postgraduate and ECR training.

Andrew Austin (University of Adelaide).

There has been a reduction in systematics training at undergraduate level over the last 20+ years, particularly in content related to taxonomy. Because of this, the systematics group at Adelaide University, in conjunction with staff from the SA Museum and Herbarium organised the Postgraduate Training Workshop in Systematics. First run in 2009, it has been offered every two years since then. With financial support from ABRS, SASB, ASBS and Adelaide University's Environment Institute, it has been free for the 200+ students who have attended the workshops. The course is aimed at PhD students in the first half of their candidature, with the 5-day program comprising a range of specific and general topics. The Adelaide workshop is complemented by more focused short courses such as the 2-day phylogenetics workshop run annually at Sydney University and the specialist ad hoc workshops run by the Centre for Biodiversity Analysis at ANU which focus on advanced analytical and technical methods; including phylogenomics and biodiversity informatics. This talk will provide an overview of these and other workshops and discuss their importance for postgraduate and ECR training into the future.

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Soil-mediated effects of *Eucalyptus viminalis* dieback on plant performance and associations with mycorrhizal assemblages.

S.Ayyub (Division of Ecology and Evolution, Research School of Biology, Australian National University); C. Linde (Division of Ecology and Evolution, Research School of Biology, Australian National University); B. Gooden (CSIRO, Health & Biosecurity).

Various factors may be associated with Eucalyptus dieback in Australia. To investigate *Eucalyptus viminalis* woodlands' soil-mediated effects on plant performance, we conducted a greenhouse experiment comparing plants grown in soil from healthy and dieback stands. The soil was either live, sterilised or a mixture consisting of sterilised soil with a 7% live soil addition. After six months, various plant performance parameters were measured. Roots were harvested, stained and microscopically examined to determine the percentage of root length colonised by arbuscular mycorrhizae, ectomycorrhizae and dark septate endophytes. Plant performance grown in healthy soil was significantly ($P < 0.001$) better than those grown in dieback soil ($P<0.001$). Treatments (i.e live, sterilised and mixed) also showed a statistically significant ($P < 0.001$) effect with seedlings growing taller in healthy soil than in dieback soil. Root analyses showed that seedlings in healthy soil predominantly associated with ectomycorrhizae, while mostly arbuscular mycorrhizae were found in roots grown in dieback soil. Plants generally performed better in sterile soil than in live soil, suggesting negative biotic factors in live soil. This is confirmed by reduced growth in mixed soil compared to sterilised soil. Preliminary analyses suggest that mycorrhizal type has little influence on seedling performance contrary to expectations.

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A historical trend in the South Pacific Regional Herbarium (SUVA), Fiji, realised.

Marika Tuiwawa (The South Pacific Regional Herbarium, the Institute of Applied Sciences, the University of the South Pacific); Yumiko Baba (Auckland Museum Tāmaki Paenga Hira).

Examining an adequate reference set representing the regional flora at herbaria is fundamental to any collection-based biodiversity studies. This is because new species discovery, biodiversity inventory and conservation planning are reliant on these collections. The rich Pacific collections are better represented in major herbaria in developed countries, partly the result of colonial exploration in the 19th century. Conversely, there remains a negative legacy of these explorations in the South Pacific, namely, the historical collections being mostly housed in foreign herbaria, in many cases duplicates not being redistributed to the country of origin. In Fiji, the South Pacific Regional Herbarium (SUVA), the national herbarium, still lacks specimens for some of their endemic species. The resulting paucity of reference material has hindered the curatorial and collecting effort up to now. This fact was most noticeable during a recent project lead by the Global Biodiversity Information Facility (GBIF), when SUVA herbarium catalogues were assessed for uploading into GBIFs data aggregate. This problem is widespread across different taxonomic groups; Poaceae and Elaeocarpaceae to name few. However, there is a solution to this issue. With increasing global data sharing and digitisation of specimens, identifying herbaria that house specimens for under-represented taxa, has become much easier. Moving forwards, the next step is to retrieve high-resolution images from these foreign herbaria to store in the SUVA herbarium, so that local researchers can learn these taxa to build better reference collections more effectively, and to assist their efforts in updating a Flora of Fiji.

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Triodia hummock grass systematics, hybridization and polyploidy (Poaceae: Chloridoideae).

Matthew D. Barrett (Australian Tropical Herbarium); Ian D. Cowie (formerly Dept. of Environment, Northern Territory Government); Russell L. Barrett (National Herbarium of New South Wales); Benjamin M. Anderson (Western Australian Herbarium, Dept. of Biodiversity, Conservation and Attractions); Kevin R. Thiele (Australian Government, Dept. of Climate Change, Energy, the Environment and Water); Siegfried L. Krauss (Kings Park Science, Dept. of Biodiversity, Conservation and Attractions); Pauline F. Grierson (The University of Western Australia).

The Australian hummock grass genus *Triodia* R.Br. contains numerous morphological forms that have been discovered since the last revision of the genus in 2005. More than fifty novel species have been described or are in review since 2011. Here, we provide an overview of these new taxa, using the framework of a geographically comprehensive ribosomal phylogeny containing 533 terminals. Most of the new species occur on rocky substrates and have a range of between 1 and 200 km, often restricted to localised geological landforms. We consider evidence for hybridsation, particularly in relation to the status of *T. prona* Lazarides, and the role of polyploidy in diversification of the genus. With these new discoveries, *Triodia* will becomes the most species-rich grass genus in Australia, accounting for about 10% of Australian native grass species diversity. The new taxonomic and phylogenetic framework will provide resources for the conservation and utilisation of grassland diversity, enabling new insight into the evolution of seasonally arid biomes.

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More peas please? Progress towards completion of Fabaceae for the *Flora of Australia*.

Russell L. Barrett (Botanic Gardens of Sydney); James A.R. Clugston (Botanic Gardens of Sydney); Lyn G. Cook (University of Queensland); Mike D. Crisp (University of Queensland); Peter C. Jobson (Botanic Gardens of Sydney); Brendan J. Lepschi (Australian National Herbarium); Matthew A.M. Renner (Botanic Gardens of Sydney); Peter H. Weston (Botanic Gardens of Sydney).

The legume family Fabaceae is well-represented in Australia, with around 2,500 species. The former families Caesalpiniaceae and Mimosaceae were completed for the *Flora of Australia* more than 20 years ago, but the pea-flowered legumes have lagged behind. We here present ABRS-funded work from the last three years towards provision of a treatment for Fabaceae tribe Mirbelieae, which contains about half of Australia's pea flora. We will summarise progress, especially towards resolution of problematic generic boundaries, and outline what is still needed to 'complete' the legume treatments for the *Flora of Australia*. This presentation will particularly highlight ongoing work in *Pultenaea*, where many new species are coming to light.

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Systematics of tiny black acalyptrate flies as case studies for challenges in Australian biodiversity research.

Keith M. Bayless (CSIRO Australian National Insect Collection).

Flies (Diptera) are among the most poorly known Australian insects. These ecologically labile, fragile insects need specialised techniques to collect and preserve. While technological advances in sequencing and artificial intelligence will streamline aspects of biodiversity characterisation, shifts in researcher mindset and education policy are needed to circumscribe Australia's flies. 1. Tertiary education should renew emphasis on organismal biology to inspire and empower new researchers. 2. Standardised fieldwork methods should be developed to ethically maximise specimen volume and utility. 3. Laboratories should process and share samples more widely. A new Australian Biological Resources Study funded study on scale parasitoid *Cryptochetum* flies will be used as an example. To clarify higher-level groups, a phylogeny based on analyses of 160 taxa and 3000 markers yielded compelling hypotheses, clarifying the position of enigmatic Braulidae and Librella. *Cryptochetum* and Drosophilidae are sister groups and Librella and Braula are inside Drosophilidae subfamily Steganinae. This is supported by newly examined genitalic characters. Comprehensive sampling and character selection in hyperdiverse clades are critical. This project provides the impetus and foundation comprehensively revise Australian cryptochetids, a group in which biocontrol projects deployed species of unclear identities. Numerous new species will be described in concert with museomics illuminating parasitoid host records.

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Cave cricket capers: An extraordinary diversity and evolutionary history revealed by molecular phylogenetics (Orthoptera: Rhaphidophoridae).

Perry G Beasley-Hall (The University of Adelaide); Steven Trewick (Massey University, New Zealand); Liz Reed (South Australian Museum); Steven J B Cooper (South Australian Museum); Andrew D Austin (The University of Adelaide).

Cave crickets (Orthoptera: Rhaphidophoridae) are an understudied group of insects that act as keystone species in subterranean habitats. In the remnants of Gondwana–South America, South Africa, Australia, and New Zealand–the fauna is exclusively comprised of members of the ancient subfamily Macropathinae. While the New Zealand fauna have undergone something of a taxonomic renaissance in recent years, Australian cave crickets remain poorly known. Yet, several Australian species are at formal risk of decline, and local extinctions have been observed nationwide. Unfortunately, no taxonomic work has been undertaken on the Australian fauna for almost fifty years. There is clearly a need to revitalise research into this understudied, and often underappreciated, group of insects. Here, we detail how we are using molecular phylogenetics to illuminate new taxa, as well as an enigmatic evolutionary history, of this ancient orthopteran lineage. The entire Southern Hemisphere fauna have a Tasmanian origin, with at least three subsequent evolutionary origins for the remainder of the Australian Rhaphidophoridae. Phylogenetic evidence also suggests the existence of new species (and at least one genus) in Queensland, New South Wales, Victoria, and Tasmania, both in subterranean and above-ground habitats.

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Linking phylogenomics, genome evolution and ecology to globally distributed and biosecurity relevant bark and ambrosia beetles (Curculionidae: Scolytinae).

James Bickerstaff (CSIRO Australian National Insect Collection); (Tom Walsh, CSIRO Black Mountain Laboratories) Rahul Rhane (CSIRO Parkville & Applied BioSciences); Jiri Hulcr (University of Florida); Andrew Johnson (University of Florida); Anthony Cognato (University of Michigan); Sarah Smith (University of Michigan); Bjarte Jordal (University of Bergen); Hermes Escalona (CSIRO Australian National Insect Collection).

Scolytinae bark beetles are a globally distributed group of hyperdiverse weevils reliant on host plant tissues to complete their life histories. They engage in a rich array of ecological strategies, including polyphagous host tree preferences, sibling inbreeding and symbiotic associations (notably fungal farming). Multiple primary industries are impacted by bark beetles due to their life histories and they are one of the most frequently translocated insect pests globally. Despite this, few taxonomic and genomic resources exist for this group, and our understanding of the systematics of Scolytinae is plagued by a contentious taxonomic history and few specialists working on the group. Recent phylogenetic analyses have either used a handful of molecular markers to reconstruct a subfamily wide phylogeny or used genome wide markers focussing on specific taxon groups. Using whole genome sequencing data, we assembled draft genomes and reconstructed the phylogeny of Scolytinae, spanning 100 taxa with over 3000 single copy orthologue genes. Our findings suggest over a five-fold difference in genome assembly size variation across species, genera and tribes. This talk will explore genome evolution in the Scolytinae grounded in a phylogenomic framework, how this may be linked to ecological strategies and the implications this has for global biosecurity.

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How to train a systematist? A status check of plant and fungal systematics training at Australasian Universities.

Joanne L. Birch (School of BioSciences, University of Melbourne); Kristina Lemson (School of Science, Edith Cowan University)

The value of native biodiversity and ecosystems is broadly recognised. However, the capacity to engage and train students in plant and fungal biodiversity at Australasian tertiary institutions remains limited. Teaching of organismal diversity remains a component of first-year biology subjects; yet the breadth of that teaching is uneven. Plants, and to an even greater extent, algae and fungi, typically receive a much smaller allocation of teaching time than other lineages. Engaging students with biodiversity focused coursework is essential to ensure advanced systematics subjects are sought-after by students and maintained in Australasian tertiary education. The “Discovering Diversity” Decadal Plan prepared by Taxonomy Australia identifies the urgent need to increase the capacity of the taxonomy and systematics workforce. To do so, Australasian tertiary institutions must enable students to interact with the Australasian biota, provide field-, lab-, and herbarium-based training, and inform students of career pathways in taxonomy and systematics research. This presentation will provide an overview of the current experiences of staff at Australasian Universities, to assess the status of their biodiversity and systematics focused training at those institutions. Current initiatives towards optimising student engagement in these fields will be discussed.

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An investigation of Asteliaceae (Asparagales) systematics based on whole chloroplast genome sequencing.

Declan P. Blackburn (The University of Melbourne); Harvey K. Orel (The University of Melbourne); Rachael M. Fowler (The University of Melbourne); Kerry A. Ford (Allan Herbarium, Manaaki Whenua – Landcare Research); Joanne L. Birch (The University of Melbourne).

The Asteliaceae (Asparagales) are a relatively small but diverse family comprised of three genera and 36 species with an Austral-Pacific distribution. The largest genus, *Astelia* (30 species), is a perennial, rhizomatous herb, and contains species that are dominant in a diverse array of habitats, e.g. *Astelia alpina* in alpine herb fields in Australia and *Astelia menziesiana* in the understory of montane rainforest in Hawai'i. While subgeneric relationships are well understood, species relationships within three of the four subgenera are not well resolved. In addition, while *A. nervosa* (New Zealand) and *A. menziesiana* (Hawaii) are noted as widespread species complexes, their monophyly has not been tested and accurate circumscription of infraspecific taxa has not been possible based on morphological data or sequence data from a small number of chloroplast and nuclear markers. Field work was conducted throughout New Zealand to document the morphological and habitat diversity of *Astelia nervosa* across its geographic range. The Asteliaceae phylogeny, including 101 in-group taxa, is inferred based on Maximum Likelihood and Bayesian Inference analyses of whole chloroplast genome data. Preliminary results will be presented that are informative of species relationships and provide a framework for understanding the diversity within recognised *Astelia* species complexes.

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Population Genetics, Phylogeography and Taxonomy of Critically Endangered *Leptecophylla oxycedrus* and *L. juniperina.*

Molly Bloomfield (University of Melbourne); Dr Michael Bayly (University of Melbourne); Dr Daniel Murphy (Royal Botanic Gardens Victoria).

Leptecophylla oxycedrus (Ericaceae) is Critically Endangered in Victoria, where it is only found at Wilsons Promontory National Park and Phillip Island, but it is widespread in Tasmania. We undertook a population genetic study to inform conservation in Victoria, aligned with a recovery action plan prepared by Phillip Island Nature Parks, and to clarify taxonomic limits and phylogeographic history. In particular, it is unclear whether the closely related *L. juniperina*, endemic to New Zealand, is a distinct species from *L. oxycedrus*, as all previous treatments of this genus have been based on morphology only. 120 individuals including outgroups were sampled in Victoria, Tasmania and New Zealand. Sequencing by Diversity Arrays Technology (DArT) produced over 100,000 single nucleotide polymorphisms across the genome from the samples provided, which were filtered down to 7179 informative and unique SNPs. The analysis of the SNP data includes a STRUCTURE analysis, inbreeding and Fst, and isolation by distance which will be presented in this talk. The data show that the two Victorian populations are genetically distinct, with Wilsons Promontory populations genetically closest to those of eastern Bass Strait Islands, and that *L. oxycedrus* is also distinct from *L. juniperina*.

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Unearthing *Agaricus* down under: Exploring species boundaries in eastern Australasian *Agaricus* (Basidiomycota).

Amelia-Grace Boxshall (University of Melbourne, School of BioSciences); Joanne Birch (University of Melbourne, School of BioSciences); Jerry Cooper (Manaaki Whenua); Teresa Lebel (State Herbarium of South Australia).

Agaricus is a large basidiomycete genus estimated to contain >500 species globally. However, Australasian *Agaricus* remain underrepresented in taxonomic revisions of the genus and their diversity remains incompletely understood. Until recently, only twenty-eight species of *Agaricus* were described from Australasian type material. The majority of these were published between 1845 and 1974, and are unplaced in modern subgeneric classifications based on morphology or the phylogenetic inference of sequence data. Field observations indicate that current species do not accurately delimit the morphological and genetic diversity of Australasian *Agaricus*, and examination of herbarium and iNaturalist records indicate that several species names are applied too broadly. Over the last 2 years I have undertaken field work across four states, sampling 242 Australian *Agaricus* field and herbarium collections, and have received sequence data from 129 New Zealand *Agaricus* with a view to assessing species diversity, estimating the relationships of eastern Australasian *Agaricus* within a global framework, untangling species concepts, and investigating variation within the weedy *Agaricus xanthodermus* species complex. Here, I outline four novel *Agaricus* species described from the Northern Territory, revisit neglected morphological characters which remain significant for field identification, present preliminary phylogenetic results, and investigate the frequently misapplied name, *Agaricus austrovinaceus*.

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The taxonomic potential of integrating morphological and molecular approaches to enhance ant (Hymenoptera, Formicidae) identifications for biosecurity: bridging the gap between DNA sequences and reliable species-level confirmation.

James T. Buxton (Agriculture Victoria); Caitlin J. Selleck (Agriculture Victoria); Kate S. Sparks (Department of Agriculture, Fisheries and Forestry); Lea Rako (Agriculture Victoria); Francesco Martoni (Agriculture Victoria); Isabel Valenzuela (Agriculture Victoria); Mark Blacket (Agriculture Victoria).

In Australia, ants play a significant role as ubiquitous and ecologically influential components of terrestrial systems, boasting exceptionally high levels of endemic diversity. Despite this, there remains a great deal of uncertainty at the species level, with some of the most diverse, widely distributed, and ecologically dominant genera in urgent need of revision. Additionally, recent molecular studies strongly suggest the presence of overlooked cryptic diversity, even ‘megadiversity,’ in certain species groups, which is yet to be corroborated by traditional taxonomy. Introduced ant species can pose significant environmental and economic threats as destructive invasive species. These species are easily transported by human activities and possess traits that enable them to thrive in new environments, potentially outcompeting native species. The timely distinction between exotic species and their native counterparts is vital to reduce the risk of establishment in Australia. However, the lack of species-level knowledge within diverse genera can lead to substantial delays in detecting congeneric exotic species. Here, we present examples of the utility of biosecurity research and surveillance measures that combine molecular DNA barcoding (COI sequencing) and morphological identifications with high quality diagnostic images of specimens accessioned into collections to provide verifiable identifications, as well as taxonomic advances.

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Evolutionary history of Australian *Chenopodium* alliance.

Anze Zerdoner Calasan (Ludwig Maximilian University of Munich and Western Australian Herbarium); Karol Krak (Czech University of Life Sciences Prague and Czech Academy of Sciences); Bohumil Mandák (Czech University of Life Sciences Prague and Czech Academy of Sciences); Kelly A. Shepherd (Western Australian Herbarium); Gudrun Kadereit (Ludwig Maximilian University of Munich).

Covering approximately 70% of the continent, Australia's arid zone is among the largest and least investigated regions globally. One of the most ubiquitous and surprisingly diverse floral components of the Australian arid zone includes members of the *Chenopodium* alliance (*Chenopodium*, *Einadia* and *Rhagodia* of the family Amaranthaceae), which are known for their drought and salinity tolerance and thus suitability for land restoration. Despite a recent generic reclassification, the evolutionary history of this taxonomic group remains unclear. We aimed to test the littoral connection hypothesis, which postulates that contemporary desert floras arose via dispersal and diversification from coastal ancestors, as one mechanism to explain the diversity within this taxon. We conducted a phylogenetic analysis of all currently accepted species using a targeted sequencing approach with a custom-designed bait set. Our initial results indicate that the most recent common ancestor of this clade arrived in Australia by a long-distance dispersal event from continental Eurasia at the onset of the Pliocene. Subsequently, the alliance rapidly diversified inland without extensive polyploidisation, with the continuous aridification of the Australian interior during the Pleistocene and Holocene likely facilitating this process. Our findings also provide new insights into the recent nomenclatural revisions within this alliance.

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Phylogenetic diversity in conservation: why we should proceed with care.

Marcel Cardillo (Australian National University); Alex Skeels (Australian National University).

Phylogenetic diversity (PD) connects systematics with conservation, by using phylogenetic branch lengths to quantify an assemblage’s “evolutionary history”, which is widely regarded as worthy of protection. Although PD is still rarely used in practical conservation decision making, it is becoming more visible in the international policy arena, so it is important for policymakers to be aware of its limitations. Here we give an overview of the sensitivity of PD and downstream spatial analyses to methods and assumptions in phylogenetic inference, with some examples from our current work on phylogenomics of Grevilleoideae.

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Taxonomy and systematics of the ‘backobourkiine’ spiders, a putative new subfamily of orb-weavers (Araneae, Araneidae).

Pedro de S. Castanheira (Murdoch University); Volker W. Framenau (Murdoch University); Nikolaj Scharff (Natural History Museum of Denmark); Dimitar Dimitrov (University of Bergen); Abha Chopra (Murdoch University); Renner L. C. Baptista (Universidade Federal do Rio de Janeiro).

The spider family Araneidae includes medium-sized to large orb-weavers with generally vertical webs. A recent multi-gene molecular study supported a paraphyletic ‘Araneinae’, indicating the existence of new clades, including the Australasian/Pacific ‘backobourkiine’ spiders, with most of its species historically misplaced in *Araneus* and *Eriophora*. The backobourkiines are the most speciose and most abundant group of orb-weaving spiders in Australia and include species commonly referred to as Garden Orb-weavers. They can also be found in Asia, the Pacific and in New Zealand, and recent data suggests its presence in the Afrotropical region. The backobourkiines now consist of 70 species in 10 genera: *Novakiella* (two species), *Backobourkia* (four species), *Lariniophora* (one species), *Plebs* (22 species), *Hortophora* (13 species), *Socca* (12 species), *Salsa* (seven species), *Leviana* (five species), *Quokkaraneus* (one species) and *Kangaraneus* Castanheira & Framenau, 2023 (three species). As part of our current ABRS-funded revision of the backobourkiines, two more genera are currently being revised: *Acroaspis* (16 species) and *Carepalxis* L. Koch, 1872 (around 14). This presentation summarises our work on the dominant backobourkiines, including results of detailed phylogenetic analyses based on morphological and genomic data, that aims to clarify some relationships within the group that were poorly supported in previous studies.

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Drivers of Diversity of *Darwinia*'s Common Scents and Inflorescences with Style: Phylogenomics, Pollination Biology, and Floral Chemical Ecology of Western Australian *Darwinia* (Myrtaceae).

Patricia W. Chan (University of Wisconsin-Madison and Australian Tropical Herbarium); Thomas J. Givnish (University of Wisconsin-Madison); Matthew Barrett (Australian Tropical Herbarium and James Cook University).

This ongoing research strives to analyze the relative importance of different drivers of plant species diversification in the highly morphologically diverse and geographically limited genus *Darwinia* (Myrtaceae). This group is ideal to examine such factors due to many small species ranges, apparent sky-island biogeography of several taxa, and diversity of inflorescences and associated pollinators. The major aims of this research: **First**, to use phylogenomic data and a pending Myrtaceae bait set to construct a dated phylogeny to elucidate evolutionary relationships and species-level historical biogeography within *Darwinia*; **Second,** to investigate reproductive ecology and pollination syndromes of several species through studies of pollinator behavior, inflorescence morphometrics, floral volatiles, and nectar composition. Data resulting from these studies will funnel into an analysis of diversification rates to understand which factors drive diversification in *Darwinia*. This research is being conducted in conjunction with collaborators at the Western Australian Herbarium, Australian Tropical Herbarium, and King's Park Botanic Garden, and will aid in our understanding of plant speciation as well as contribute to our knowledge of the ecology and evolution of threatened elements of the Western Australian flora.

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In the Beginning – the Australian Plant Name Index.

Arthur D. Chapman (Australian Biodiversity Information Services)

In 1970, Professor William Stearn of the British Museum of Natural History gave a talk to the Australian Academy of Science. In that talk he lauded the need for a new Flora of Australia. After his address, a Fellow of the Academy approached and offered funds to begin the process. Following discussions by Australian biologists – led by Dr Hansjoerg Eichler, it was determined that the best way to use these funds would be to prepare an index to plant names as a precursor to a Flora. The process to develop the plant name index began in April 1973 under the direction of Dr Nancy Burbidge and with the appointment of Penelope Hack. They began working on Bentham's Flora Australiensis and Mueller's Framenta. I was appointed in late 1973 and began working on the project in January 1974. When the initial funds ran out in June 1976, the project was transferred to CSIRO and later to the Department of the Environment under the newly formed Bureau of Flora and Fauna – later to become the Australian Biological Resources Study. The Australian Plant Name Index was published in four volumes in 1991 and sometime later made available as an online searchable database.

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Assessing population structure and potential genetic declines in the cycad *Macrozamia moorei.*

Zjon T. Coleman (The University of Queensland), Lyn G. Cook (The University of Queensland), Alicia Toon (The University of Queensland).

Cycads, a group of plants that are globally and locally threatened with extinction, typically exist as isolated, patchy populations. In Australia, some populations have been reduced through deliberate clearing since European occupation because they are toxic to livestock. To date, we do not know what effect this has had on the genetic diversity and population structure of cycads. Here, we focus on *Macrozamia moorei*, a large trunk-forming cycad in central Queensland. It was directly targeted for destruction in some regions to prevent livestock loss and, in some areas abundance was severely reduced in the early 1900s. We use data derived from ddRADseq to assess the extent of recent gene flow within and among populations and test whether there has been a reduction in genetic diversity in those populations subjected to the greatest disturbance since European land clearing.

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Revealing the extent of phylogenomic discordance in the *Eucalyptus* rapid radiation using BUSCO genes.

Anne-Cecile Colin (Western Sydney University); Rose Andrew (University of New England); Collin Ahrens (Cesar Australia); Justin Borevitz (Australian National University); Paul Rymer (Western Sydney University).

The idea that discordance in phylogenomic datasets exists as actual biological signal is being increasingly accepted. Discordance is described as coming from a range of molecular processes such as introgression and incomplete lineage sorting (ILS). The evolutionary history of *Eucalyptus* is particularly rich in a fascinating array of these molecular processes: rapid radiations, hybridization events, ancient and recent introgression, ongoing speciation, ILS, a high recombination rate, and gene duplication events. Amidst this complex web of interconnected factors influencing phylogenetic relationships, we aimed to understand the extent of discordance and its origin by comparing two clades with very contrasting species diversity: the *Exsertaria* (~40 spp.) and *Adnataria* (~120 spp.) sections. We generated genomic sequences and curated a dataset of thousands of single-copy orthologous genes to perform phylogenomic analyses. Our results highlighted extreme levels of discordance due to ILS and introgression. These processes play a pivotal role in the evolutionary dynamics of Eucalyptus species. Understanding the origin and biological meaning of discordance is a necessary step forward in phylogenomics.

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Student training at CANBR.

Bronwyn Collins (Centre for Australian National Biodiversity Research).

Beginning with the first small group of students hosted by the then Australian National Botanic Gardens Herbarium in 1993 the Volunteer Botanical Training Program has trained and mentored over 300 students. For 3 decades participants have received training in collections curation and provided assistance to both curatorial and research staff at the Centre for Australian National Biodiversity Research. This presentation will look at the history of the program, outcomes for participants and some of the more recent challenges in running a successful program.

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Systematics education and training at the tertiary level: a case for an integrated approach

Lyn Cook (University of Queensland).

Systematics education and training in universities has often, but not always, been separated along taxonomic lines (plant systematics, insect systematics, etc). Consequently, low numbers of students enrolling in seemingly specialist courses has led to the demise of specialised systematics education in Australian universities. However, the fundamentals of systematics (phylogenetics, classification and taxonomy) are probably components of courses at most universities and are hidden to external scrutiny because course names do not specifically mention systematics—that is, "dark systematics". Here I will describe an integrated approach at UQ that has led to systematics training as part of the high school science curriculum, and systematics training at university that begins with modules in the compulsory first-year course, and follows up with systematics incorporated in second-year plant science, zoology and entomology, and five third-level courses (Biodiversity and Systematics, Marine Invertebrates, Plant Identification, Fungal Biology, and Insect Identification and Taxonomy) that each have enrolments of over 50 students.

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Your (Australian) National Species List.

Endymion Cooper (Centre for Australian National Biodiversity Research).

The Australian National Species List (AuNSL) is a unified, nationally accepted, taxonomy for the native and naturalised biota of Australia. It provides a reliable standard reference for recording, exchanging and connecting information about the living things that call Australia home. As the go-to resource for names and taxonomy for Australia's unique biodiversity, the AuNSL is an essential foundation for significant national biodiversity data infrastructures including the Atlas of Living Australia, the Terrestrial Ecosystem Research Network, the Biodiversity Data Repository, and the Species Profile and Threats Database. The AuNSL is built from a set of taxon-focussed resources including the Australian Plant Name Index and Australian Plant Census, the Australian Faunal Directory, and similar lists of fungi, lichens and bryophytes. These resources share a common infrastructure, contribute to the single national taxonomy (AuNSL), but retain their independent curation practices and online presentation. The AuNSL is published by the Australian Biological Resources Study (ABRS) in collaboration with, and on behalf of, the Australian taxonomic research community. Here we present a high-level overview of the infrastructure and tools for building and using this important national resource.

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The biogeographic and evolutionary history of an extraordinary species radiation across an extreme elevational gradient.

Adrián Villastrigo (SNSB-Zoologische Staatssammlung München); Steven J. B. Cooper (South Australian Museum and The University of Adelaide); Barbara Langille (The University of Adelaide and Huntsman Marine Science Centre, Canada); Erinn P. Fagan-Jeffries (The University of Adelaide), William F. Humphreys (Western Australian Museum and University of Western Australia); Lars Hendrich (SNSB-Zoologische Staatssammlung München); Michael Balke (SNSB-Zoologische Staatssammlung München and Ludwig Maximilians University).

One of the most biologically diverse and geologically complex areas of Earth is located in the Australopacific region. It comprises ancient landmasses that have undergone major climatic modifications, high altitude mountain ranges resulting from geotectonic landscape changes, and young tectonically active archipelagos. To explore how these climatic and landscape changes may have influenced species diversification, we reconstructed the biogeographic and evolutionary history of *Limbodessus* diving beetles (Dytiscidae). This genus is found across the Australopacific region, and shows multiple biome transitions, from underground aquifers in Australia to alpine meadows in New Guinea. Using low-coverage whole-genome sequence data, we estimated an almost complete time-calibrated phylogenetic tree, resolving *Limbodessus* as a mid-late Miocene genus that likely originated in the Sahul continent. We provide evidence for subterranean speciation within isolated underground aquifers, although multiple independent colonizations from surface/interstitial habitats were the most frequent scenario. Alpine biota formed a monophyletic clade, with evidence for one or two independent shifts to high altitudes. Overall, these analyses suggest parallel colonization processes occurred at opposing ends of an altitudinal gradient, led by extreme aridification in Australian lowlands and *in situ* diversification of alpine taxa by passive-uplifting of local biota in New Guinea.

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ABRS – 50 years of achievements for taxonomy.

Haylee Crawford-Weaver, Tina Gopalan, Jaever Santos (Australian Biological Resources Study).

The Australian Biological Resources Study was established in December 1973 to stimulate the study of taxonomy of Australia's "biological resources" and to provide research grant funding and support for taxonomy. ABRS has awarded over $89 million (unadjusted dollar value) for research on taxonomy and systematics of Australian biodiversity since its inception. It has also been a world-leader in development of collating and presenting biodiversity data and names information, via the Flora of Australia, Zoological Catalogue of Australia, and the Australian Faunal Directory. I will provide a short snapshot of the key achievements and highlights of ABRS's work over the last 50 years.

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What has the ABRS done for fish trematodes lately? (Plenty).

Thomas H. Cribb (The University of Queensland and Queensland Museum); Scott C. Cutmore (Queensland Museum); Storm B. Martin (Murdoch University); Terrence L. Miller (Queensland Museum); Nicholas Q.-X. Wee (Queensland Museum); Rodney A. Bray (Natural History Museum, London).

Australia's 5,750 fish species harbour many groups of parasites which, together, certainly far exceed the richness of their hosts. Arguably the best-known group is the Trematoda (Platyhelminthes). There are now just over 800 species known from nearly 600 Australian fishes. Species have been described from 1876, but study of the fauna became significant only from the 1960s and then accelerated from about 1990. The last 30 years has seen description of about 80% of the known species. This period correlates with and was enabled by sustained funding by the ABRS. How close have we come to a full description of this fauna? Given that the known fauna has been described from ~10% of the fish species, it is certain that there remain many hundreds of species to be found. The best-known component of the fauna is that of Great Barrier Reef fishes. Sampling there has focussed on large, common, conspicuous, shallow water species. We are now rarely surprised by what we find there. In contrast, the trematodes in southern regions and in small and deep-water fishes are poorly understood making estimates of total richness at best heroic. Total parasite richness for the fauna is even more mysterious.

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Two cryptic conifer species separated by a mid-Miocene aridity barrier in southern Australia.

Michael D. Crisp. (The University of Queensland); Meredith Cosgrove (CSIRO Plant Industry); Shota Sakaguchi (Kyoto University); Lyn G. Cook (The University of Queensland).

The conifer species *Callitris canescens* (Cupressaceae), as currently circumscribed, has a disjunct distribution in south-west Western Australia and south-east South Australia. The species is absent from the low, arid limestone plateau of the Nullarbor Plain, that separates the two populations. Here we segregate the South Australian population as a distinct species, *Callitris calcareana*, based on congruent differences between the populations in nuclear and chloroplast DNA. Moreover, the populations are reciprocally monophyletic, having multiple fixed differences in nuclear and chloroplast DNA. The two species also differ phenotypically: in stature, foliage colour and soil preferences.

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Morphological constraint obscures richness: a mitochondrial exploration of cryptic richness in *Transversotrema* (Trematoda: Transversotrematidae).

Scott C. Cutmore (Queensland Museum); Richard D. Corner (The University of Queensland); Thomas H. Cribb (The University of Queensland).

Species of *Transversotrema* Witenberg, 1944 (Transversotrematidae) occupy a unique ecological niche for the Trematoda, living externally under the scales of their teleost hosts. Previous studies of the genus have been impeded partly by limited variation in ribosomal DNA sequence data between closely-related species and partly by a lack of morphometrically informative characters. We assess richness of the genus in the tropical Indo-west Pacific through parallel molecular and morphometric analyses, generating cytochrome c oxidase subunit 1 mitochondrial data sequence and morphometric data for hologenophore specimens from Australia, French Polynesia, Japan and Palau. These analyses demonstrate that molecular data provide the only reliable basis for species identification; host distribution, and to a lesser extent morphology, are useful for identifying just a few *Transversotrema* species. We infer that a combination of morphological simplicity and infection site constraint has led to the group displaying exceptionally low morphological diversification. Phylogenetic analyses of the mitochondrial data broadly support previous systematic interpretations based on ribosomal data, but also demonstrate the presence of several morphologically and ecologically cryptic species. There are now 26 *Transversotrema* species known from Australian marine fishes, making it the richest trematode genus for the fauna.

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A species-level phylogeny of eastern Australian *Phebalium* Vent. sect. *Phebalium* Duretto & Heslewood (Rutaceae; Zanthoxyloideae).

Sangay Dema (Botany & N.C.W. Beadle Herbarium, University of New England); Rose L. Andrew (Botany & N.C.W. Beadle Herbarium, University of New England); Ian R.H. Telford (Botany & N.C.W. Beadle Herbarium, University of New England); Jeremy J. Bruhl (Botany & N.C.W. Beadle Herbarium, University of New England).

Phebalium Vent. sect. *Phebalium* Duretto & Heslewood is an Australian endemic monophyletic group of species. It has two geographic clades (Mole *et al.* 2004; Duretto *et al.* 2023), with 14 species distributed in south-western Australia and 21 in eastern Australia. We have hypothesised more than 35 taxonomic changes. SD's PhD project focussed on testing the species limits of the *P. squamulosum* complex has supported the recognition of at least 14 new species and raising seven subspecies to the rank of species. Duretto *et al.* (2023) subsumed *Microcybe* into *Phebalium* as two new sections in the genus. Most species-level relationships in *Phebalium* were unresolved, and the study did not include putative new taxa of the eastern Australian clade recognised at the N.C.W. Beadle Herbarium. Our SNP-based phylogenetic analysis of all eastern Australian *Phebalium* taxa, including newly delimited species, was carried out using maximum likelihood and maximum parsimony criteria in program IQ-TREE2 (Minh *et al.* 2020; Minh *et al.* 2022) and PAUP v.4.0a168 (Swofford 2003) respectively. We also inferred phylogenetic relationships under a coalescent model using SVDquartet (Chifman and Kubatko 2014) implemented in package PAUP*v.4.0a168. The phylogenetic relationships inferred under all models were concordant. Our results supported three major clades within eastern Australian *Phebalium* corresponding to three species complexes: namely, *P. squamulosum, P. glandulosum* and *P. nottii.* The monophyly and inter-specific relationships of most eastern Australian *Phebalium* were resolved and will be discussed.

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Testing species delimitation in *Acacia*: are gidgee (*A. cambagei*) and Georgina gidgee (*A. georginae*) two distinct species?

Barbara Azevedo de Oliveira (The University of Queensland); Rod Fensham (The University of Queensland, Queensland Herbarium); Lyn Cook (The University of Queensland).

Acacia cambagei R.T. Baker and *A. georginae* Bailey are dominant woody species found in the Australian arid zone, spanning from Queensland to the Northern Territory and into the north of South Australia. These species, commonly known as gidgee, gidyea or gidgea, have significant cultural value in indigenous communities. *Acacia georginae* is valued for its edible resin, while *A. cambagei* is renowned for its durable timber, fuelwood and soil stabilisation. Distinguishing between *A. georginae* and *A. cambagei* remains challenging because, although existing keys rely on differences in pod and seed shapes, there is actually a continuum in the field. Keys state that *A. cambagei* has thin, straight pods with small oval seeds, whereas *A. georginae* is listed as having curved pods with large circular seeds. *Acacia georginae* is toxic and can be lethal to livestock, although there is variation in toxicity among individuals. Applying the Biological Species Concept, we use Angiosperm 353 sequence data to assess gene flow between and among populations of both taxa in sympatry and allopatry. Initial morphological analysis of herbarium material has confirmed a continuum of pod and seed characteristics across their distributions. Clarifying the taxonomic status of *A. georginae* and *A. cambagei* will contribute to managing and conserving these valuable woody species.

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The systematist as a storyteller: reflections on the role of narrative in systematics.

André W. do Prado (Murdoch University, Australia).

Historical narratives play an important explanatory role in evolutionary biology. Systematics, as a scientific endeavour, has been criticized for a long time, often treated as an arbitrary classification, and for often avoided narrative explanations, as it was seen as highly speculative. This talk aims to provide reflections on how Systematics could take advantage of explanatory narratives as a contribution to both its theoretical framework and its public dissemination, since it is well-known how narratives are engaging humans. The discussion will address topics such as the similarities between the work of a systematist and of a historian, the concept of species as prospective narratives and the importance of nature appreciation, aiming to explore different ways of how narratives permeate the work of a taxonomist. The theoretical approach will be based on classical authors such as Ernst Mayr and Willi Hennig, as well as contemporary systematists as Robert O'Hara, Ronald Jenner, and Malte Ebach.

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Taxonomy and systematics of the artoriine wolf spiders (Araneae: Lycosidae): is *Artoria* monophyletic?

André W. do Prado (Murdoch University, Australia); Volker W. Framenau (Murdoch University, Australia), Cor J. Vink (Faculty of Agriculture and Life Sciences, New Zealand); Luis N. Piacentini (Museo Argentino de Ciencias Naturales "Bernardino Rivadavia", Argentina) & Renner L.C. Baptista (Universidade Federal do Rio de Janeiro, Brazil).

The genus *Artoria* currently represents the most speciose genus of wolf spiders in Australia represented by 42 described species and possibly another 120–150 undescribed species. Similar to most other genera in the subfamily Artoriinae, it includes comparatively small spiders of less than 10 mm body length which are generally found in leaf litter and near creeks and other water bodies, largely in the Bassian and Torresian Australian bioregions. The genus has also been reported from Asia, the Pacific, New Zealand and Africa. Morphological and molecular evidence suggests, however, that *Artoria* is paraphyletic although this assumption has never been tested with rigorous phylogenetic methods. This presentation will introduce our ABRS-funded taxonomic and systematic revision of the Australian and world-wide artoriine taxa with special reference to the genus *Artoria*. We will completely revise the Australian and New Zealand faunas of the genus and will test its monophyly with morphological and molecular methods, in particular with respect to other artorrine genera such as *Artoriopsis*, *Anoteropsis*, *Notocosa*, *Syroloma*, *Lycosella*, *Navira* and *Lobizon*.

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Lonely on Limestone: A conservation genomics study of *Gentianella calcis* (New Zealand) with taxonomic implications.

Robb W. Eastman-Densem (University of Canterbury); Hermann Frank (Timaru Museum); Jana R. Wold (University of Canterbury); David S. Glenny (Landcare Research); Peter B. Heenan (Landcare Research); Pieter B. Pelser (University of Canterbury).

Prioritisation of taxa for conservation often relies on taxonomy, and embracing the inherently interdisciplinary nature of the former is crucial to ensure the most positive outcomes given limited resources. In New Zealand this is especially true for *Gentianella calcis,* an obligate limestone taxon comprising four threatened (nationally critical) subspecies endemic to the eastern South Island. In addition to threats posed by the small (often with < 20 plants), isolated nature of many of its populations, questions surrounding the distinctiveness of its subspecies mean that it urgently needs a genomics-informed conservation plan. To do this, we used markers from Genotyping By Sequencing to inform conservation management by resolving the inter- and intra-specific taxonomic delimitation and investigate patterns of genetic diversity and connectivity, bridging the gaps between systematics, population genomics and conservation management.

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Declining rainforests and arid emergence: Ancient Kurrajongs (*Brachychiton*) of South Australia's Late Miocene-Pliocene (~7 – 2.3 Mya).

Tara A. Evans (University of Adelaide); Robert S. Hill (University of Adelaide).

Brachychiton is composed of 36 species, of which 34 are endemic to Australia. The genus is uniquely diverse, regarding distribution and morphology. Within the literature on the Australian fossil plant record, there are many unsubstantiated reports informally attributing various fossilised leaf specimens to *Brachychiton*. However, a distinct lack of a formal classification of these specimens and their relationship with living *Brachychiton* is apparent. However, there is no doubt that *Brachychiton* is a likely candidate for fossilization during the Cenozoic and many of the leaves attributed to *Brachychiton* are very similar in form to some living species of the genus. Stuart Creek in South Australia, a Late Miocene-Pliocene age fossil site, has been subject to reports informally attributing fossil specimens to *Brachychiton*. More than 500 individual silcrete rock specimens from the site, were examined for similarities with living Brachychiton. Comparisons between fossil specimens and extant *Brachychiton* (additionally, extant species with morphological similarity to *Brachychiton*), involved characters such as leaf shape, size, venation, and cuticle morphology. Results revealed two extant *Brachychiton* species fossilised at Stuart Creek. Furthermore, these species also inhabited the site at the same time, with several rock specimens found with both species fossilised together.

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Two perspectives on the Decadal Plan: public engagement, and the plight of parasitoid wasps.

Erinn P. Fagan-Jeffries (The University of Adelaide & South Australian Museum).

Meeting the challenges proposed by the Taxonomy Australia Decadal Plan will require a layered approach. We need to think bigger, and work more collaboratively with each other and with the public. In the field of hymenopteran taxonomy, where we deal with the issues associated with of a hyper-diverse insect order, there is considerable debate about the use of DNA barcodes as the main evidence for species documentation. This presentation will give an overview of the different approaches (both more traditional and perhaps quite radical) that are occurring within the hymenopteran (particularly the parasitoid wasp) community to accelerate biodiversity documentation, and discuss some of the issues and possibilities around rapid taxonomy using DNA data. I will also present a summary of the collaborative citizen science project Insect Investigators, that during 2022-23 partnered taxonomists with regional schools to name new species. Citizen science, and engaging people throughout Australia with the process of taxonomy, may not make the taxonomic process faster, but it has potential to make it more relevant, better supported, and with greater benefits to both society and to biodiversity conservation.

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Landscape genomics of the Eastern Red Gums (*Eucalyptus* sect. *Exsertaria* subser. *Erythroxylon*) in New South Wales: parapatric speciation or a legacy of population isolation?

Patrick S. Fahey (Research Centre for Ecosystem Resilience, Botanic Gardens of Sydney and The University of Queensland); Marlien M. van der Merwe (Research Centre for Ecosystem Resilience, Botanic Gardens of Sydney); Patricia M. Hogbin (Research Centre for Ecosystem Resilience, Botanic Gardens of Sydney); Maurizio Rossetto (Research Centre for Ecosystem Resilience, Botanic Gardens of Sydney and The University of Queensland).

As part of the Restore and Renew program, we have developed a large genomic dataset including all members of *Eucalyptus* sect. *Exsertaria* subser. *Erythroxylon* with the goal of developing genetically informed ecological restoration guidelines for the individual species. However, our approach of focussing on a phylogenetically constrained group has led to the discovery of complex, cross-species genetic patterns, where morphological species show limited genetic divergence and ongoing geneflow. Indeed, in some regions, we show there is no way to assign large and ecologically dominant populations to a single taxon, both morphologically and genetically. This is hypothesised to be due to historic distribution shifts in response to climatic changes, leading to divergence of lineages that have subsequently established secondary contact zones. These findings suggest that the conceptualisation of species as discrete, distinct and objective entities may be insufficient to allow for appropriate study, management, and restoration of natural populations, and may even be holding these practical outcomes back.

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Is there cryptic species diversity in *Apiomorpha strombylosa* (Tepper)?

Chen-hsin Fan (The University of Queensland); Lyn G. Cook (The University of Queensland).

Apiomorpha is the most species-rich genus of gall-inducing scale insect, and it is specific to *Eucalyptus*. It is also one of the most chromosomally diverse animal genera on the planet, with diploid karyotypes ranging from 2n=4 to about 192. Here, we test species boundaries in one morphospecies, *A. strombylosa*, reported to have considerable chromosomal variation. Gullan, in her 1984 revision of *Apiomorpha*, noted some morphological variation and referred to the variants as “eastern” and “western” forms. Subsequently, these forms have been found to have different karyotypes, with most specimens of the eastern form having about 2n = 32 and most of the western form having about 2n = 50. In this study we focus on the western form, in which a novel karyotypic form (2n = 14) has been found in Western Australia. We use DNA sequencing, morphometrics, karyotypes and host use to determine whether *A. strombylosa*, as currently defined, comprises a species complex.

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Carex kirkii s.l. Petrie *(Carex* section *Inversae* Kük., Cyperaceae). Two new rare species from the Eastern South Island of New Zealand*.*

Kerry A. Ford (Allan Herbarium, Landcare Research - Manaaki Whenua).

Carex section *Inversae* in New Zealand is composed of 11 species and is found in a variety of habitats, including, moraine outwash surfaces, grasslands, and alpine herbfield. While assessing herbarium specimens for a new flora of *Carex* subgenus *Vignea*, including the three varieties of *Carex kirkii*, it became apparent that many specimens did not match the types in the latter. Field survey was initiated to collect samples, specifically the two varieties described by George Kükenthal in 1909 which have rarely been collected, *C. kirkii* var. *elatior* and *C. kirkii* var. *membranacea.* A PCO analysis of morphology suggests the former is a hybrid between *C. kirkii* var. *membranacea* and *C. trachycarpa Cheeseman.* Secondly, comparison of specimens to types suggests that *Carex kirkii* var. *membranacea* is the correct name to apply to plants in montane areas of Western Nelson, Canterbury and Otago and should be raised to specific rank. Thirdly one new species is described, from moraine outwash surfaces of the eastern South Island, first collected by Thomas Cheeseman in 1893 in the Clarence Valley, Marlborough and overlooked for 130 years. This new species is assessed as critically rare in the New Zealand Threat Classification and *C. kirkii* var. *membranacea* is assessed as Nationally Vulnerable.

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To describe or to just document: making a case for the Fauna Portal using money spiders (Araneae: Linyphiidae).

Volker W. Framenau (Murdoch University); Heiko Metzner (psbrands).

The Fauna Portal Australia (www.faunaportal.org) is an innovative identification platform conceptualised for invertebrates, although it can be used for any faunal (and floral) group. It offers a unique filter for diagnostic images that allows to examine morphological characters in the same view side-by-side at the genus and family level. Geographic filters further allow restricting the choice of taxa for identification. A simple molecular module allows downloading species-specific sequence data. The Fauna Portal therefore provides a one-stop-shop for species identification, particularly in groups that have been taxonomically treated in scattered publications. Almost 1,000 Australian spider species are now online. Through the application of core taxonomic principles (designation of a reference specimen or 'type' and obligatory diagnosis) the Fauna Portal also facilitates the stable listing of undescribed species using a simple numerical parataxonomic code. This rapid documentation of biodiversity data has the potential to speed up taxonomy as a stopgap until species are formally described. The principles of the Fauna Portal will be presented using a poorly known spider family as exemplar, the sheet-web or money spiders (Linyphiidae). This is the second largest spider family world-wide and the current assumption that it is poorly represented in Australia is contested here.

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Newly discovered gall-inducing scale insects (Coccomorpha: *Apiomorpha*) on York gum (*Eucalyptus loxophleba*) in the Southwest Australian Floristic Region.

Karla M. Garcia (The University of Queensland); Lyn G. Cook (The University of Queensland).

The lack of information on invertebrate fauna, to the point that about 80% have yet to be named and described, prevents them from being listed in conservation schedules. Many of these "dark taxa" are probably at risk of extinction due to the loss of their host plants for agriculture expansion and urbanization. The York gum woodlands of the South West Australia Floristic Region, a global biodiversity hotspot, have undergone drastic loss since European colonization yet harbour unique biodiversity. Here, we report newly discovered species of the gall-inducing scale insect *Apiomorpha* that appear to be specific to York gum (*Eucalyptus loxophleba). We* use morphometrics and DNA of the mitochondrial gene cytochrome c oxidase subunit I (*COI*) and the nuclear genes small subunit ribosomal RNA (*18S*) and *Dynamin* to test species boundaries. Along with newly discovered species that are morphologically distinct, we also uncover cryptic species within previously described taxa.

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Heterodichogamy in *Ascarina lucida* (Chloranthaceae).

Phil Garnock-Jones (Victoria Uniiversity of Wellington).

Ascarina lucida (Chloranthaceae) is an endemic New Zealand wind-pollinated small tree. Its sexual system has been described variously, as dioecious, gynodioecious, or monoecious with strong protandry. Inflorescences are terminal thyrses of 2–3-flowered cymules. Flowers are unisexual and highly reduced: each male flower is a single anther with about 80,000 small pollen grains and each female flower is a single carpel with one ovule. I counted flowers weekly over three months on 30 plants at Ōkiwi Bay, Marlborough. The plants are dimorphic and flower in two pulses. In July, protogynous plants present stigmas and protandrous plants have dehiscent anthers. By September, protogynous plants have dehiscent anthers and protandrous plants present stigmas. In protandrous plants, the pulses were separated by 1–2 weeks when no flowers were open. In protogynous plants the few-flowered tails of the female and male phases overlapped by 2–3 weeks. Only one plant had a few dehiscing anthers and receptive stigmas simultaneously. These findings add *Ascarina* to the few plants known to exhibit heterodichogamy, a reciprocal dimorphism for dichogamy where about half the plants are protogynous and half are protandrous. This is the first record of heterodichogamy in Chloranthaceae and in the New Zealand flora.

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ANNiKEY: a taxonomic information system for Annelida.

Christopher J Glasby (Australian Museum & Museum & Art Gallery Northern Territory); Olga Biriukova (Museum & Art Gallery Northern Territory); Patrick Martin (Royal Belgian Institute of Natural Sciences); Robin Wilson (Museum Victoria).

Annelida are ubiquitous metazoans found in most terrestrial and aquatic (freshwater and marine) habitats on Earth. The phylum has recently undergone significant restructuring with the inclusion of formerly distinct marine phyla (Sipuncula and Echiura) together with the predominantly marine Polychaeta, which now includes Clitellata (oligochaetes and leeches). Annelida now comprise over 160 family-level taxa and almost 21 000 species. Comparative morphological studies of the expanded Annelida are arguably hamstrung by the current disparate system of morphological terminologies across each major group as a result of years of independent study. Further, there is no key to all families. With support from the Australian Biological Resources Study (ABRS), we developed ANNiKEY, a database of ~280 standardized morphological characters and biodiversity data coded for all annelid families using the open-source Delta program Intkey to enable effective data interrogation and interactive family identification. The database, fully illustrated for both characters and taxa and containing over 50 000 cells of data, will be linked to an online companion glossary of annelid terms to make it usable for both beginners and experts. We provide an overview of ANNiKEY prior to its public release online at Zenodo (https://zenodo.org).

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Plastid phylogenomics reveals evolutionary relationships in the mycoheterotrophic orchid genus *Dipodium* and provides insights into plastid gene degeneration.

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The orchid genus *Dipodium* R.Br. (Epidendroideae) comprises leafy autotrophic and leafless mycoheterotrophic species, the latter confined to sect. *Dipodium*. This study examined plastome degeneration in *Dipodium* in a phylogenomic and temporal context. Whole plastomes were reconstructed and annotated for 24 *Dipodium* samples representing over 80% of species diversity in sect. *Dipodium*. Phylogenomic analysis based on 68 plastid loci including a broad outgroup sampling across Orchidaceae found sect. *Leopardanthus* as sister lineage to sect. *Dipodium.* The leafy autotrophic species within sect. *Dipodium* (*D. ensifolium*) was found sister to all leafless, mycoheterotropic species, supporting a single evolutionary origin of mycoheterotrophy in the genus. Divergence time estimations found that *Dipodium* diversified ca. 11.3 Ma in the mid Miocene and the origin of mycoheterotrophy in the genus was estimated to have occurred in the late Miocene ca. 7.3 Ma, in sect. *Dipodium*. The comparative assessment of plastome structure in *Dipodium* revealed different degrees of plastid gene degradation of *ndh* genes within the genus, which ranged from moderately pseudogenised to physically lost, including leafy autotrophic species of both *Dipodium* sections. Our study showed that *Dipodium* exhibits an early stage of plastid genome degradation in which all species have retained a full set of functional photosynthesis-related genes and housekeeping genes.

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Towards an updated number of living species in Australia and the World.

Tina A.R. Gopalan; Matthew M. Lockett; Jaever M. Santos; Annabel Wheeler; Haylee Crawford-Weaver (Australian Biological Resources Study).

A national stocktake of our native species is vital to ensure we can protect and manage our unique biodiversity. Here, we catalogue an updated version of the 'Number of living species in Australia and the World'. The currently accepted number of Australian species was estimated at 11 million global species and 570,000 Australian species, published in 2009 by Arthur Chapman. With continuous taxonomic output over time, these numbers need updating. Last year alone, 626 new species were recorded in Australia. We update the number of living species by collating information from taxonomists, on-line databases, published literature and more. This comprehensive review places the number of living Australian species in a global context and where possible, calculates the percentage of flora and fauna endemic to Australia. We have found that since the last estimate in 2009, Australia has documented 17 additional mammal species and 20 less bird species. These differences could be attributed to synonymy, reclassification of taxa into sub taxa and species discovery. This important work provides an updated benchmark for future assessments of species numbers to better understand and preserve biodiversity.

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Biosystematics is foundational to achieving our goals for nature.

Olwen M. Grace (Royal Botanic Garden Edinburgh)

Biosystematics is foundational to achieving goals to halt the biodiversity crisis and implement nature-based solutions to the challenges facing humanity. Specialist taxonomic knowledge and comprehensive reference collections of the Earth’s biota—the core of our systematics community—are vital to identify, understand and conserve organisms that are hoped to hold such solutions, or to pose a management challenge. Valuable biodiversity information is being released at scale by the digitisation of natural history collections, and by innovations in their curation and use. Examples of how these data are useful includes the emerging species identification methods combining AI with computer vision, biochemical data including digital sequence information (DSI), and environmental monitoring. They are also integrated into identification tools available to anyone with an internet-connected device. Museomics, informatics tools to accelerate monographic work, and training for the next generation of taxonomists are other investment areas for systematists. To leverage these advances to maximum effect at this point in history, we must identify common goals and galvanize around delivering them: directing resources where the biodiversity challenge is greatest, focusing where extinction may outpace a description of the biota, and balancing pragmatism with high standards in our practice.

Cost-effective target sequence capture through drastically miniaturised DNA libraries and automatisation – a head-to-head test.

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Targeted enrichment of DNA libraries using target sequence capture is increasingly becoming an indispensable part of the molecular genetics toolkit, being used to recover genome-wide orthologous loci across highly divergent taxa and from difficult specimens. However, for many applications, this method remains prohibitively expensive, especially in a high-throughput context. One cost-effective solution may be to drastically scale down reactions, automate labour, and increase sample multiplexing, but tests are required to demonstrate no loss of data integrity. Here, we prepared libraries from 96 plant specimens spanning 15 families with both a newly-developed miniaturised workflow and a standard workflow, and compared target recovery post-enrichment with the myBaits Angiosperms353 kit. We found that while the amount of target data obtained from the miniaturised workflow was overall lower than the standard workflow, the phylogenetic tree generated was comparable in both topology and support to that generated from the standard workflow. This shows that adequate genome-wide genetic data suitable for phylogenetic analysis can be obtained from a wide variety of taxa and specimens using a miniaturised workflow, and at a fraction of the cost of alternative workflows. Thus, our high-throughput target sequence capture pipeline shows promise for future adoption by large-scale genomics initiatives.

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Fungi inhabiting the chambers of an epiphytic ant-plant are transported by resident ant workers.

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The ant-plant *Myrmecodia beccarii* grows chambers that serve different functions including ant-waste depositories, brood housing (nurseries), and airflow (ventilation). Fungal communities vary with chamber type, suggesting fungi play different roles, but how fungi become established in the chambers was unknown. We conducted an ant-exclusion experiment to test whether ant workers transport fungi between ant-plants. We placed mature ant-plants (with ant colonies) in cages with young ant-plantlets (grown ant-free). Plantlets were either accessible to or excluded from ant workers. At experiment end, we sequenced fungal DNA from the different chambers of the plants, and from exoskeletons, heads, and abdomens of ant workers. Abundances of fungal operational taxonomic units (OTUs) were 2.6 x higher in waste chambers and 1.9 times higher in nursery chambers of ant-accessible plantlets compared to ant-excluded plantlets. Mature ant-plants shared 60 OTUs with ant-accessible plantlets but only 6 OTUs with ant-excluded plantlets. Seven dominant OTUs in the waste chambers of ant-accessible plantlets and mature ant-plants were found on/in ant worker samples but were absent/occurred rarely in ant-excluded plantlets. To our knowledge, this is the first demonstration of ant worker dispersal of fungi in an ant-plant system, a vital step in better understanding how fungi are involved in this mutualism.

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The velvet parachute (*Marasmius elegans*): a surprisingly variable species across its range with an uncanny QLD doppelganger.

Frances E. Guard (University of Southern Queensland); John Dearnaley (University of Southern Queensland); Teresa Lebel (State Herbarium of South Australia).

1. First described in SA by John Cleland in 1933, *Marasmius elegans* has been recorded across southern Australia and in New Zealand. Specimens from southeast Queensland were generally less robust and considered a possible second species. The first QLD specimen sequenced supported this hypothesis, as did significant microscopic character differences of the stipe. However, a study of multiple collections from across the full putative range of *M. elegans,* showed the species does occur in Queensland, but a more complex picture has emerged. The material examined is highly variable across the geographic range, but molecularly shows less than 4bp difference in the ITS gene from SA to QLD & NZ. Western Australia is an outlier and more specimens need to be sequenced. But that QLD doppelganger?

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Biosystematics of Australia's native dung beetles (Coleoptera: Scarabaeidae: Scarabaeinae).

Nicole L. Gunter (The Cleveland Museum of Natural History and Queensland Museum).

Australia’s native dung beetles are unique and diverse, representing ~5% of the global dung beetle fauna. The comprehensive revisions of the Australian Scarabaeinae by Matthews (1972, 1974 & 1976) documented 284 native species and provided a framework for subsequent revisions. Since then, just over 100 additional species have been described but estimates suggest the total diversity may exceed 500 species. With support of the US National Science Foundation, Australian dung beetles have been developed as a model to examine how biogeographic history influences species distribution. The fauna is divided into two evolutionarily distinct lineages: one with Gondwanan origins referred to as the Australasian Endemic Clade, and the other comprised of native *Onthophagus* that colonized via Indo-Malaya in the Miocene. To date, over 1000 species-locality combinations have been barcoded to examine potential species complexes, while UCE have been generated for over 40% of Australian species to explore evolutionary relationships in a global context. These data will be used to guide future taxonomic research and unravel drivers of diversification across the Australian continent and beyond.

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Building a custom barcode reference library for subterranean groundwater.

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There are high stakes in regulatory biodiversity assessments especially for those associated with mineral exploration and resource developments. For such assessments there is a clear need for accurate, fast and consistent species identification with new molecular methods potentially offering a significant alternative to traditional morphological approaches. Use of environmental DNA (eDNA) metabarcoding as a tool for detecting subterranean species inhabiting groundwater ecosystems associated with mineral deposits is quickly gaining momentum in the area of environmental impact assessment. However, in subterranean ecosystems invertebrate dark taxa with ancient and genetically diverse evolutionary lineages dominate, making meaningful taxonomic assignment of eDNA metabarcoding Operational Taxonomic Units (OTU) extremely patchy. Therefore, a custom library of reference sequences is essential. Using one of the oldest hydrogeological environments on earth, Western Australia's Pilbara region, we have collaborated with taxonomic specialists and industry partners to generate extensive, verified taxonomic data to establish a custom reference library of sequences, which will be expanded over time to meet future needs. Here we present our current subterranean fauna reference library and demonstrate its effectiveness when we query it with eDNA metabarcoding OTU from Pilbara groundwater. We also identify the importance of taxonomic metadata in developing custom reference libraries.

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Insights into global brittle star diversity using a targeted exon capture approach.

Tim O'Hara (Museums Victoria); Maggie Haines (Museums Victoria); Andrew Hugall (Museums Victoria).

Ophiuroids, commonly known as brittle stars, are a class of marine invertebrates with over a quarter-billion-year-old evolutionary history. They are globally distributed, occurring from intertidal regions down to the abyssal sea floor. These attributes make them an ideal system to examine evolutionary processes and biogeographic patterns. Our initial phylogenomic work used transcriptomes to develop an exon capture system that targeted 1552 exons and captured approximately 90% of loci across all major lineages of Ophiuroidea. We have now expanded our dataset to include 2143 individuals, comprising 50% of described species. This vast amount of data has allowed us to refine the taxonomy of brittle stars and explore global patterns of diversification. Notable findings include contrasting rates of speciation at different depths and low genetic diversity within species that span from pole to pole.

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Delineating the Dilleniaceae: An update on the taxonomy and systematics of *Hibbertia* (Dilleniaceae).

Timothy A. Hammer (University of Adelaide and State Herbarium of South Australia); Ed Biffin (State Herbarium of South Australia); Kor-jent van Dijk (University of Adelaide); Kevin R. Thiele (Australian National University); Michelle Waycott (University of Adelaide and State Herbarium of South Australia).

Hibbertia (Dilleniaceae) is a genus with c. 310 species native to Australia, 24 species native to New Caledonia and one endemic to Madagascar. The number of species in Australia is likely to increase by more than a hundred with several forthcoming publications, especially those by retired botanist Hellmut Toelken (AD). These proposed species will make *Hibbertia* one of the largest plant genera in Australia. My postdoctoral project, funded by an ABRS National Taxonomy Research Grant Program (2020) and an ASBS Marlies Eichler Postdoctoral Fellowship (2021), has been to provide genus, species and infra-species profiles of Dilleniaceae for the *Flora of Australia* (i.e. including *Dillenia* and *Tetracera*), complete comprehensive identification keys for the Australian species, and to reconstruct a near-complete molecular phylogeny using hybrid capture methods of nuclear and plastid genomes, utilising Angiosperm353 and OzBaits kits and genome skimming. An initial 96 species were sequenced as part of the Genomics for Australian Plants initiative. In this presentation I will share the progress that has been made on this project, give an overview of the forthcoming taxonomic revisions in *Hibbertia*, and share preliminary insights into the evolution of this hyper-diverse genus.

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Over a decade of species discovery with Bush Blitz.

Jo Harding (Bush Blitz); Kate Gillespie (Bush Blitz).

Bush Blitz is Australia’s largest species discovery program. It is a unique multi-million dollar partnership between the Department of Climate Change, Energy, the Environment and Water, Parks Australia, BHP and Earthwatch Australia to document plants and animals across Australia. There are an estimated 580,000-680,000 species in Australia, with three-quarters of this biodiversity yet to be identified. Forty-five per cent of continental Australia and over 90 per cent of Australia’s marine waters have never been comprehensively surveyed. Since the Program began in 2010 Bush Blitz has undertaken 50 multidisciplinary expeditions supporting the discovery of almost 2,000 putative new species. Through this large body of work thousands of species records have also been added to public databases, increasing scientific knowledge to help protect Australia’s biodiversity for generations to come. Through Bush Blitz research funding the description of thousands of new species has also been supported. As we move into a further 5 years of funding Bush Blitz will expand to incorporate a continuing connection with first nations people to strength research collaborations and on-ground outcomes.

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Meeting the challenge of the Decadal Plan: the taxonomic documentation of the Australian arachnid fauna.

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The taxonomic documentation of Australia’s major arthropod lineages remains the biggest challenge posed by the Decadal Plan. The 13 extant orders of Arachnida present in Australia include the spiders (Araneae), scorpions (Scorpiones), pseudoscorpions (Pseudoscorpiones), harvestmen (Opiliones), tailless whip scorpions (Schizomida), whip spiders (Amblypygi), palpigrades (Palpigradi), and six acarine orders of mites (Trombidiformes, Sarcoptiformes, Holothyrida, Ixodida, Mesostigmata and Opilioacarida). These orders range from species-poor groups with less than 10 species (e.g. Palpigradi and Opilioacarida), to mega- or hyper-diverse lineages with likely > 10,000 Australian species (e.g. Araneae, Trombidiformes and Sarcoptiformes). Here, we summarise the scale of the task at hand required to document the Australian arachnid fauna, in the context of the number of undescribed species and the current available workforce. By dividing the arachnid challenge into three conceptual parts (the spiders, mites, and other ‘minor’ orders), and using worked examples, we identify key existing barriers to progress, as well as a vision for the step-change required to describe this iconic fauna within a generation.

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Environmental DNA metabarcoding tools for freshwater conservation: parallel characterisation of vertebrate and invertebrate communities.

Brock A. Hedges (The University of Adelaide); Perry G. Beasley-Hall (The University of Adelaide); Phil Weinstein (The University of Adelaide); Andy D. Austin (The University of Adelaide); Michelle T. Guzik (The University of Adelaide).

Surface freshwater is sporadic in its occurrence throughout much of semi-arid and arid Australia and where it does occur, it is often ephemeral. This is the case for freshwater granite rock-holes throughout remote southern Australia. These ecosystems act as a source of freshwater for a vertebrate community as well as habitat for aquatic invertebrates that display behavioural and physiological adaptations to the ephemerality of these systems. Climate change and the presence of invasive species are ongoing threats to this ecosystem, meaning it is likely to experience disruptions to historical hydrological patterns and potential declines. However, despite the ecological significance of the system and the likely threats, these rock holes are poorly understood. To establish baseline ecological information, we documented vertebrate and invertebrate species richness and variability at seven rock-holes in the Gawler bioregion of South Australia using environmental DNA (eDNA) metabarcoding methods. We recorded 19 vertebrate species and 22 orders of invertebrates, representing 45 families; finer taxonomic resolution was limited by a lack of robust molecular reference databases. Our findings demonstrate the importance of rock-holes as a water source for a wide range of endemic taxa and highlight the need for improved barcode reference libraries and associated metadata for accurate assignment of taxonomy to eDNA metabarcoding data in freshwater systems.

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Impact of fossils on reconstructing ancestral flowers in Ericales.

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Reconstructing ancestral states is an essential tool for understanding the evolution of traits and lineages, but the impact of including fossils in these reconstruction remains largely unexplored. The asterid order Ericales has both highly diverse flowers and a rich record of well-preserved fossil flowers, making them an ideal group to test the influence of including fossils on ancestral state reconstruction. We used a tip-dating approach with a total-evidence dataset in a Bayesian framework to reconstruct fossil positions in Ericales, taking into account both their morphology and age. We reconstructed ancestral floral characters including and excluding fossil species in a Bayesian framework, using a sample of posterior trees to account for uncertainty. While some fossils appear to be well constrained, most were characterised by high levels of uncertainty. The impact of fossils in the reconstruction varies among traits. We find three general scenarios: (1) no measured impact, (2) increased confidence for one state in otherwise uncertain reconstructions, (3) complete shift from one state to another in reconstruction at deep nodes. The demonstrable impact of fossils on ancestral state reconstructions, especially at deep nodes, shows that future trait evolution studies much to gain from including fossils.

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Phylogenetics and molecular dating in the genomic era.

Simon Ho (University of Sydney).

Genomic data present a rich source of information for improving and refining our knowledge of evolutionary relationships and timescales. These data sets present considerable challenges for analysis, given their size and the complexity of their evolutionary signals. In this talk, I will describe our recent phylogenetic and molecular dating analyses of genome-scale data sets from marsupials, birds, and flowering plants. I will also report on our ongoing studies of morphological and molecular evolutionary rates across the Tree of Life. I hope that our findings are useful to researchers working with phylogenomic data or analysing combined morphological and molecular data sets.

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Don’t trust a plastid for taxonomic advice: Strong incongruence between nuclear and plastid ddRAD derived phylogenies of the southern holly-leaf grevilleas.

Gareth D. Holmes (Royal Botanic Gardens Victoria, Melbourne); Elizabeth A. James (Royal Botanic Gardens Victoria, Melbourne).

The southern holly-leaf grevilleas (Proteaceae) are an informal grouping of shrubs from southeastern Australia, several of which are of conservation concern. The generation of a resolved nuclear DNA phylogeny for the group has been problematic due to low interspecific sequence variation. We utilised ddRAD markers to infer phylogenetic relationships within the group and compared this to a new plastid-derived phylogeny. Both the nuclear and plastid DNA phylogenies displayed two major clades: *Grevillea ilicifolia* and closely related taxa forming the first and the ‘core’ holly-leaf grevilleas including *G. aquifolium* in the second. Within the *G. ilicifolia* clade, groupings showed little correlation with current taxonomy. Within the core group, the current taxonomy was largely supported by the nDNA data. Some genetic structure was found within *G. aquifolium* but appears associated with geography rather than growth form or ecology. The plastid phylogeny was largely incongruous with the nuclear data within the two main clades. Evidence of extensive plastid sharing found among taxa in the core group is suggestive of incomplete lineage sorting or introgression which may have promoted variation. We suggest that the taxonomy of the *G. ilicifolia* clade requires reassessment, whilst minor revision of the core holly grevillea clade may be warranted.

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The current state of the field in using continuous shape data for phylogenetic reconstruction: A systematic review.

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Discrete morphological data are often important in traditional systematic methods for phylogenetic reconstruction and are crucial for merging fossils into the tree of life, calibrating molecular dating and enhancing accuracy in phylogenetic inference. However, a major limitation of discrete morphological data is subjectivity in character/character state definition. Quantitative data e.g., geometric morphometric (GMM; shape) data can allow for more objective integration of morphology into phylogenetic inference. This review describes the current state of the field in using continuous shape data for phylogenetic reconstruction using the PRISMA-EcoEvo v1.0. reporting guideline, and offers pathways for approaching this task with GMM data. A comprehensive search string yielded 12,062 phylogenetic studies published in English up to Aug 2023 in the Web of Science database. Title/abstract screening removed 11,907 articles and full-text screening was performed for 143 articles. Topologies reconstructed using GMM were compared to those using discrete morphological data. Most phylogenies did not show increased support and resolution with the inclusion of continuous data, as either continuous-only morphological datasets, or integrated into discrete morphological datasets. Despite the ongoing rarity of such studies, improved methods for the application of quantitative data to phylogenetic inference remain crucial to the advancement of morphological phylogenetics.

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Australian cereal cyst nematode (*Heterodera australis*): taxonomic woes and biosecurity implications.

Daniel C. Huston (Australian National Insect Collection, CSIRO); Manda Khudir (Australian National Insect Collection, CSIRO); John Lewis (South Australian Research and Development Institute, South Australia); Sarah Collins (Department of Primary Industries and Regional Development, Western Australia); Akshita Jain (Department of Energy, Environment and Climate Action, Victoria); Mike Hodda (Australian National Insect Collection, CSIRO).

A species of cyst nematode of the genus *Heterodera* has been known to parasitise cereals in Australia since the 1930s. It caused significant yield losses across Australia until resistance breeding brought it largely under control. Australian cereal cyst nematode has long been considered to represent *Heterodera avenae*. However, in 2002 the name *Heterodera australis* was proposed for this nematode, along with speculation that both *H. avenae* and *H. australis* might occur in Australia, and that *H. australis* might represent a native species. The name *H. australis* has generally not been accepted by Australian scientists, nor the notion that it is native. There remains some uncertainty as to the validity of *H. australis* and whether more than one species of cereal cyst nematode occur in Australia. Using a molecular approach, we examined cyst nematodes present in soil samples collected between 1989–2023 from Australian cereal growing regions. We find only one species of *Heterodera* parasitising cereals and, based on phylogenetic analyses, accept the validity of *H. australis* as the name best representative of this species. Most official biosecurity policy related to this nematode still used the name *H. avenae*, and the biosecurity implications of this are briefly discussed.

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Backlogs and botanical survey: streamlining data delivery in an under-collected region for taxonomy and systematics.

Shelley A. James (Department of Biodiversity, Conservation and Attractions, Biodiversity and Conservation Science, Western Australian Herbarium); Elycia Wallis (Atlas of Living Australia, CSIRO, Australia).

Western Australia (WA), being almost the quarter the size of Europe or the United States and often inaccessible, has a high collecting cost for botanical and faunal vouchers. According to specimen data available through the Australasian Virtual Herbarium (AVH), WA is the second least botanically collected Australian state. With an average of only 50.5 specimens per 100 km2 the state as a whole barely meets the minimum number of vouchers for adequate floristic inventory. Efficient processing of specimens and rapid accessibility of collection data through online data aggregators, such as Atlas of Living Australia (ALA) and AVH using community-accepted and developing information standards, is critical for understanding the status and trends of biodiversity, for evidence-based conservation, decision-making processes for the management of lands and waters, taxonomy and systematics, and other scientific products. Changes in collections workflows for accessioning specimens, including digital infrastructure improvements, help to reduce bottlenecks limiting the processing and availability of specimens and data. Automatic data quality checks assist with improving specimen data, but social limitations in receiving high quality data and the need for human processing of physical specimens, ensuring collections are not lost, mislabelled or mishandled, along with data enhancement post-field work, remain challenges worth exploring and minimising.

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Now we are 50: A comparison of the botanical activities of Australia from 1973 and now.

Peter Jobson (National Herbarium of NSW, Botanic Gardens of Sydney).

In 1973, over 85,000 specimens were made in Australia covering all aspects of the Australian flora from algae to angiosperms; of these, over 300 specimens became types. Using data from AVH, an examination of the collecting activities of botanists is examined: where did people go; what were they collecting; were they doing general collecting, surveys, or targeting specific research groups. This is compared with a compilation of recent activities to observe if and what changes there are in the collecting activities and behaviours of botanists.

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Rethinking the systematics, evolution and biogeographic history of the mahogany family (Meliaceae).

Elizabeth M. Joyce (Ludwig-Maximilians-Universität München).

Meliaceae is an economically valuable family of c. 740 species, with a high diversity of lifeforms and habitats throughout its predominantly pantropical distribution. Despite the economic and biological importance of the family, infra-familial relationships remain unclear. Further, recent fossil evidence brings the assumed African origin of the family into question. In an effort to resolve the phylogeny of Meliaceae and reconstruct its biogeographic history, we generated the first, genus-complete tree of the family using the Angiosperm353 loci. This tree improves the resolution of phylogenetic relationships for much of the tree, and indicates that many tribes and genera are not monophyletic and are in need of taxonomic revision. We also find evidence for a history of genome duplication and historic hybridisation within some clades of the family. We conducted a sequential divergence dating and ancestral area analysis on a species-level Meliaceae tree generated through the combination of our NGS data and Sanger data from GenBank, which sheds light on recent biogeographic history, but results in ambiguous ancestral areas for deeper nodes. We are now using a combined-evidence phylogenetic model under a Fossilized-Birth-Death process where tree topology, divergence ages and ancestral areas are simultaneously estimated, and informed by fossil age and locality.

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Making the Australian crustaceans known – the decadal plan and the generational challenge.

Rachael A. King (South Australian Museum, Adelaide); Shane T. Ahyong (Australian Museum and University of NSW).

Crustaceans, sometimes dubbed the insects of the sea, are the most abundant and speciose aquatic arthropods. Notwithstanding that hexapods are now known to be derived from within Crustacea (and are therefore also crustaceans), we focus here on the non-hexapod crustaceans. Of these, the dominant groups recorded from Australia are Copepoda, Ostracoda (seed shrimps), Decapoda (crabs, lobsters, prawns), Isopoda (slaters and allies), Amphipoda (sand hoppers and allies), Tanaidacea and Cirripedia (barnacles), but numerous smaller groups are also present. Most are marine, although there are also significant radiations in freshwater and on land. Here, we summarise what is known about the richness of the Australian crustacean fauna and explore the generational challenge of describing the remaining fauna in the context of high levels of undiscovered diversity and a shrinking taxonomic workforce.

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Meeting the challenge of the Decadal Plan- A bivalve's eye view.

Lisa A. Kirkendale (Western Australian Museum).

The goal of describing the Australian biota within a generation is daunting. This is doubly so for those of us working on invertebrates in a state as large and diverse as Western Australia! Focussing on molluscs, and bivalves in particular, I will review some of the familiar strategies being utilized to tackle dark taxa, such as nurturing international collaborations, developing industrial partnerships, integrating genomic and imaging methods and data and seeking fast publication options. I will also discuss how these strategies are not getting us far enough fast enough and analyze these and other key challenges. For example, reviewing how the current funding model for discovering species new to science could be extended. One aspect that it is important to consider in this conversation is how we tackle this problem, specifically, who are we bringing along and what legacy are we set to leave once we are done? I suggest circuit breakers that are challenging to implement but critical to embrace in order to greatly increase the pace of species descriptions.

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What do we know about Australian polychaete biodiversity and what we do not.

Elena Kupriyanova (Australian Museum); Pat Hutchings (Australian Museum); Christopher Glasby (Australian Museum and Museum and Art Gallery of the Northern Territory), Anna Murray (Australian Museum); Robin Wilson (Museums Victoria).

Our knowledge of polychaete (marine Annelida) diversity in Australia has been improving over the years as a result of new region exploration, taxonomic revisions, and cryptic diversity revealed by molecular studies. In 2003, the records of Australian polychaetes (as per Australian Faunal Directory) comprised 1216 species in 56 families, mostly from shallow coastal southeastern waters. Twenty years on, we re-analysed AFD to update these estimates: currently 1606 valid species from 61 families are reported. Thus, taxonomic efforts in the past two decades have increased known species richness by about 24%, mainly from western Australia and from depths below 1000 m. While significant regions in Australia remain un-sampled or poorly sampled, newly collected specimens deposited in museums constitute an important reservoir of undescribed species. Application of molecular data to morphospecies typically leads to cryptic species being discovered, thus species richness data based on morphology is an underestimate. Furthermore, records of Australian species from shelf depths and shallower are dubious where those species have type localities in remote regions. Revisions typically reveal these records represent new species – another source of undescribed diversity. It is important to continue taxonomic work on existing collections and to promote their availability to researchers undertaking world-wide revisions.

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Confirming the identity of a toxic exotic *Lepiota*.

Teresa Lebel (Botanic Gardens & State Herbarium of South Australia); Pamela Catcheside (Hon. Assoc., Botanic Gardens & State Herbarium of South Australia).

Identifying toxic mushrooms can be problematic as the remnants left after ingestion are often fragmentary and in poor condition. While microscopic examination can help narrow down possible genera, it is often difficult to determine species. Another issue is that many cases of ingestion occur in urbanised areas, which means the mycologist must consider the possibility of exotic as well as native fungi. DNA was extracted and the nuclear ITS and LSU sequenced from 9 symptomatic poisons case samples, ranging from 1961 to 2022. Five of the cases involved humans, and 4 dogs. One sample was confirmed as a species of *Cortinarius*, one a *Psathyrella*, and the remaining seven as the exotic toxic species, *Lepiota brunneoincarnata*. A fresh sample of tissue was tested with an AMATOXtest, designed to detect amatoxins, resulting in a positive reaction.

Teresa Lebel: teresa.lebel@sa.gov.au

Museum genomics resolves cryptic species in the Australasian arbovirus vector mosquito *Culex annulirostris* Skuse, 1889 (Diptera: Culicidae).

Bryan D. Lessard (Australian Biological Resources Study, CSIRO Australian National Insect Collection), Juanita Rodriguez (CSIRO Australian National Insect Collection), Nigel Beebe (University of Queensland), Cameron Webb (Westmead Hospital), Nina Kurucz (NT Health, Public Health), David Yeates (CSIRO Australian National Insect Collection), Andreas Zwick (CSIRO Australian National Insect Collection) & Chris Hardy (CSIRO Land and Water).

The common banded mosquito *Culex (Culex) annulirostris* Skuse, 1889 is the primary vector of Japanese encephalitis virus (JEV) in Australia, among other arboviruses. Although sanger-based molecular studies reported putative cryptic species, taxonomic resolution has been hampered due a lack of employed mosquito taxonomists, destructive sampling techniques and a lack of authoritatively identified reference specimens. By using genome skimming from only one or two legs, we successfully sequenced the complete mitochondrial genome of specimens to identify mosquito species held in Australian museums or reference collections dating back to 1951. We used mitogenome data and morphology to diagnose four cryptic species: *Cx. annulirostris* sensu stricto, *Culex (Culex) somerseti* Taylor, 1912 stat. rev., an undescribed species from Papua New Guinea and north Queensland, and another from the Solomon Islands. Ancestral state reconstruction revealed the recent migration of two independent *Cx. annulirostris* populations from Australia to Papua New Guinea and Timor-Leste, respectively. Adoption of museum genomics will enable improved biosecurity diagnostics, origin tracing of historical incursions using historical collections, and description of the remarkable 170 unnamed mosquito species documented in Australia. Epidemiologists can now complete vector competence testing on each revised species to identify specific roles in disease transmission, including the recent JEV outbreak.

Bryan Lessard: bryan.lessard@dcceew.gov.au

A guide to strategically communicating taxonomy: from public to parliament.

Bryan D. Lessard (Australian Biological Resources Study, Department of Climate Change, Energy, the Environment and Water).

Taxonomy underpins our understanding of biodiversity and its effective management. Despite its significance as a foundational science, wider interest in the science of taxonomy, systematics and collections-based research is in decline. Science communication has the power to reach and inform a large audience through a combination of media platforms, including print, radio, television and social media. Each of these platforms have unique benefits to both institutions conducting taxonomic research and their taxonomists, and reach different target audiences including fellow researchers, granting bodies, politicians, journalists, industry leaders and the public. Tips are provided on how to craft a successful multiplatform media campaign to promote taxonomists and their vital research using case studies from the ABRS. This includes how to write a media release, deliver engaging radio and television interviews, and sustain momentum during the campaign using social media. By embracing science communication, taxonomists and research institutions can positively influence a wide audience in a meaningful way, attract future funding and inspire the next generation of taxonomist.

Bryan Lessard: bryan.lessard@dcceew.gov.au

From phylogenomics to macroevolution: evolution across the adaptive landscape in a hyperdiverse beetle radiation.

Yun 'Living' Li (Australian National Insect Collection & Australian National University); Craig Moritz (Australian National University); Ian Brennan (Australian National University); Andreas Zwick (Australian National Insect Collection); James Nicholls (Australian National Insect Collection); Alicia Grealy (Australian National Herbarium); Adam Slipinski (Australian National Insect Collection).

The extraordinary diversification of beetles on earth is a textbook example of adaptive evolution. Yet the tempo and driver of this super-radiation remain largely untested. Here, we explore this issue by investigating the macroevolutionary dynamics in darkling beetles (Coleoptera: Tenebrionidae), one of the most eco-morphologically diverse beetle family. Using genomic datasets and multiple approaches, we resolve the century-long inconsistency over deep relationships in the family. On a global scale, we show the dynamic evolutionary history of darkling beetles is marked by ancient rapid radiations, frequent ecological transitions, and rapid bursts of morphological diversification. On a regional scale, two major Australasian radiations, Adeliini and the Heleine clade, exhibited contrasting patterns of eco-morphological diversification, representing a prime case of phylogenetic niche conservatism versus adaptive radiation. These findings highlight a significant role of ecological opportunity in driving the immense eco-morphological diversity in a global mega-radiation. More broadly, this study underscores the value of synthesizing large-scale phylogenetic and trait data to enrich our understanding on the accumulation of biodiversity.

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Characterising the invasive *Lantana camara* complex using a population genomic approach.

Patricia Lu-Irving (Botanic Gardens of Sydney); Francisco Encinas-Viso (CSIRO); Eilish McMaster (Botanic Gardens of Sydney); Jason Callander (Department of Agriculture and Fisheries); Michael Day (Department of Agriculture and Fisheries); Johannes Le Roux (Macquarie University)

The *Lantana camara* species complex is one of the world’s worst weeds, with serious economic and environmental impacts globally. The management of invasive lantana is hindered by its complicated taxonomy and wide range of morphological variation. Biological control efforts spanning over a century have yielded limited success in Australia, in part due to the diverse nature of the complex, with several agents failing to establish on some or all lantana varieties present. There is a clear need to characterise the variation within invasive lantana and to unravel the genetic and biogeographic patterns which underlie it. Using geographically extensive sampling and trait data combined with genome-wide marker sequencing, this study reveals unprecedented insight into the genetic composition and ancestry of invasive lantana. Several highly divergent lineages are present across Australia, New Zealand, South Africa, and Hawaii, consistent with the notion that the complex comprises multiple species and their hybrids. The results from this study can inform a worldwide taxonomic treatment of *Lantana camara sensu lato*, with accurate identification of invasive populations expected to enable better management.

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Searching for a leaf in a forest: A taxonomic and phylogenetic revision of leaf mining moths *Phyllocnistis* (Lepidoptera: Gracillariidae) in Australia.

Ying Luo (Australian National Insect Collection, CSIRO & Australian National University); Scott Keogh (Australian National University); Andreas Zwick (Australian National Insect Collection, CSIRO).

Phyllocnistis is a genus of of leaf mining moths in the family Gracillariidae. Globally there are over 110 described species of *Phyllocnistis*. Previously, only 15 species of this genus were known from Australia. In this project, over 480 specimens of *Phyllocnistis* from various entomological collections around Australia were examined to determine the diversity of this group. A majority of these specimens were located at the Australian National Insect Collection (ANIC). Many of the specimens at ANIC have unpublished associated host plant information, which allows us to better understand the host plant specificity of this group. Whole genome shotgun sequencing was used to extract 13 protein-coding mitochondrial genes from the degraded DNA of museum specimens, and this data was combined with morphological and life history information to delineate new species and to understand their relationships.

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The first 1,000 images of Australian leaf mines: How an iNaturalist project has discovered new species and records.

Ying Luo (Australian National Insect Collection, CSIRO and Australian National University)

In this talk, I'll discuss how utilising the free Projects feature on iNaturalist has allowed users to collate over 1000 records of Australian leaf miners. Leaf miners are insects whose larvae feed inside leaves. They leave distinctive trails on leaves, which means that they can be easily photographed in the field. However, not much is known about their distribution or occurrence, so it would be inefficient for someone to go out and sample across Australia. This is where iNaturalist comes in. For the group of leaf mining moths I study (*Phyllocnistis* from the family Gracillariidae), we have records of what their host plants are, but only herbarium records of what the leaf mines look like. Through this project, I was able to get fresh images of leaf mines and even determine that the distribution of some leaf miners is larger than first expected.

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Insect gall development on *Eucalyptus*.

Misha Mangila (The University of Queensland); Lyn Cook (The University of Queensland); Peter Crisp (The University of Queensland).

The ability to induce the growth of novel plant organs (galls) has evolved repeatedly among arthropods, with about 20,000 species of insects able to induce galls today. Gall-inducing insects tend to be more host-specific than their non-galling relatives, which may be due to the intimate association between insect and its host plant: the insect needs to overcome plant defences and to influence plant development pathways. However, to date, how insects influence plant development is not understood. Here, we investigate gene expression in leaf galls induced on *Eucalyptus* by males of *Apiomorpha*, Australia's most species-rich genus of gall-inducing insect. Compared with ungalled tissue, we find repression of photosynthesis and plant defences in gall tissue but an increase in genes associated with floral development and nutrient transport. We also find differences in gene expression of plant defence-related genes and nutrient transport genes between the apex of the gall and the base where the insect feeds. Our next step will be to investigate how *Apiomorpha* initiates galls.

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The genus *Carex* (Cyperaceae) in New Zealand: a southern hemisphere diversity hotspot in a boreotemperate genus.

Santiago Martín-Bravo (Universidad Pablo de Olavide, Spain), James McCarthy (Landcare Research, New Zealand), José Ignacio Márquez-Corro (Royal Botanic Gardens Kew, England), María Sanz-Arnal (Universidad Pablo de Olavide, Spain), Ana Morales-Alonso (Universidad Rey Juan Carlos, Spain), Pablo García-Moro (Universidad Pablo de Olavide, Spain), Kerry A. Ford (Landcare Research, New Zealand).

Carex is a megadiverse genus with about 2000 species of cosmopolitan distribution, which is especially diversified in temperate and cold regions of the Northern Hemisphere. In New Zealand, however, it is remarkably the second largest angiosperm genus with 115 native species (c. 85% endemic), but has received comparatively little attention. We provide a general revision of the natural history of *Carex* in New Zealand, including systematic, biogeographic, ecological, morphological and evolutionary aspects. In the context of the latest dated phylogeny of *Carex*, New Zealand has been recurrently colonized by multiple lineages via long distance dispersal. Two lineages (sects. *Echinochlaenae* and *Uncinia*) which concentrate most species diversity (>70%) could have undergone evolutionary radiation processes. A wide array of disjunction patterns are revealed by the distribution of non-endemic taxa. On the other hand, restricted endemics shed light on putatively important areas for *Carex* speciation. Some morphological features are remarkable, including the unique presence of red-leaved species in four different lineages, a feature that could have evolved as a possible adaptation to escape herbivory by the extinct moas. Our revision remarks the extraordinary multidisciplinary interest of the study of New Zealand *Carex*, and paves the road for future specific research on this group.

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Calibrating biogeographical expectations for richness of trematode flatworms parasitic in coral reef fishes.

Storm B. Martin (Murdoch University); Scott C. Cutmore (Queensland Museum); Thomas H. Cribb (The University of Queensland).

The Trematoda are obligate endoparasitic flatworms at their richest and most diverse in marine teleost fishes. Biogeographic understanding for fish trematodes remains rudimentary and is perhaps the greatest impediment to furthering evolutionary insight and estimating the true richness of the group. Substantial progress has been made to characterise the fauna in Queensland waters, including with genetic sequence data, but from nowhere else, worldwide, is the state of genetic coverage sufficient to enable meaningful comparisons of diversity and richness across the breadth of the fauna. We have been working towards the first genetics based, broad-scale biogeographic comparison for fish-trematodes, by intensively surveying fishes at Ningaloo Reef, Western Australia, and sequencing every trematode species encountered to compare against the decades of accumulated data from Queensland. By comparing the trematode faunas relative to the similarity of the fish faunas, we are beginning to calibrate expectations of biogeographic distributions across the breadth of trematode taxa. I will present the overarching trends detected so far, and discuss the implications for estimations of regional and global richness and the future of trematode taxonomy.

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Four decades among fungi – perspectives of an accidental mycologist

Tom W. May (Royal Botanic Gardens Victoria).

I have been fortunate to work in a fungarium (reference collection of fungi) for much of the last four decades. I trace how my interest in population genetics morphed into a career in mycology, inspired by the simple question "what fungus is that?". I explore the step changes in mycology that I have participated in around nomenclature, bioinformatics, DNA barcoding, conservation and ecology. I emphasise the importance of the re-conceptuliasation of fungi from "lower plants" to kingdom Fungi and why fungi-specific language (such as fungarium and sporing body) matters. I highlight the critical role of citizen science in advancing mycology in Australia. I stress the importance of collections and name infrastructure for taxonomic and systematic research on fungi. I have participated in the founding of organisations including the Australasian Mycological Society, Fungimap and Taxonomy Australia and I discuss the challenges around effectively connecting in an under-resourced sector. I take inspiration from the myriad interconnections between fungi and other organisms to underline the importance of mentoring and networking in tackling the task to describe all Australian fungi. I conclude by discussing opportunities for scientists to communicate their research and engage in discussions on pressing issues around habitat protection and the climate emergency.

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Comparative phylogeography of east Australian carnivorous plants and kleptoparasitic bugs.

Zoe McCarthy (University of New South Wales) Gerry Cassis (University of New South Wales) Dan Murphy (Royal Botanic Gardens Victoria) Dieter Hochuli (University of Sydney).

The sundews (*Drosera sp.)* are a diverse family of carnivorous plants with about 160 species occurring in Australia. Their leaves are covered with sticky hairs that act as fly paper-style traps that catch invertebrates to be digested as supplemental nutrition. However not all invertebrates are prey to the sundew; the sundew bug (*Setocoris sp*., Hemiptera) is a kleptoparasite that lives obligately on the plant and feeds by stealing the plant's prey. The aim of my PhD project is to study the comparative phylogeography of five sundew species in eastern Australia, and the several species of associated *Setocoris* bugs. I am testing the theory that these plants and insects are cospeciated by analysing single nucleotide polymorphism (SNP) data generated by Diversity Arrays Technology. In this talk I will present my preliminary analysis of SNP data from populations of *S. binataphilus* bugs and their *Drosera peltata* complex host plants from New South Wales, Victoria and Tasmania. There is strong geographically-structured variation within species and similar patterns of variation are seen in bugs and their plant hosts, suggesting they may be cospeciated.

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Resolving the taxonomy of the *Caladenia patersonii* and *C. reticulata* Orchidaceae) species complexes in South Australia.

Andrew E. McDougall (The University of Adelaide); Ed Biffin (State Herbarium of South Australia); Tim Hammer (The University of Adelaide and State Herbarium of South Australia); Michelle Waycott (The University of Adelaide and State Herbarium of South Australia).

Intense taxonomic activity over the past thirty years within the *Caladenia patersonii* and *C. reticulata* species complexes in South Australia (~31 spp.) has not resulted in a functional taxonomic framework. Species within these groups, including those listed as endangered, have been difficult to identify, impeding conservation efforts and wasting valuable resources. My PhD project aims to resolve this confusion from a systematic approach. The initial part of my project has involved examining the species that can be recognized and documenting incongruencies among the diagnoses, descriptions, and types. This has been followed by sample collection of these *Caladenia* spp. throughout South Australia for morphological and molecular analyses. The molecular dataset was constructed using DNA sequences derived from hybrid capture utilizing the Angiosperm353 and OzBaits kits (including nuclear and chloroplast loci) and a genome skim. The collection material shows that there is more morphological variation in contemporary populations than is recorded in descriptions or types. Initial phylogenetic analyses of these data show paraphyletic taxa. Hybridization with *C. dilatata* species complex appears common. Some clades conflict with our current understanding of this genus in South Australia. The next step will be to analyze population level structure in these taxa through SNP array data.

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Genetic differentiation between sympatric sister species of eucalypts.

Rachael M. Fowler (School of Biosciences, The University of Melbourne) Harvey K. Orel (School of Biosciences, The University of Melbourne) David Cantrill (Royal Botanic Gardens Victoria) Daniel J. Murphy (Royal Botanic Gardens Victoria) Patrick Fahey (Research Centre for Ecosystem Resilience, The Royal Botanic Garden Sydney) Mike J. Bayly (School of Biosciences, The University of Melbourne) Todd G.B. McLay (School of Biosciences, The University of Melbourne; Botanic Gardens Victoria; National Biodiversity DNA Library, CSIRO).

Extensive hybridisation among related species is well-documented in the eucalypts, which raises questions about how speciation occurs and high species diversity is maintained. We explored genetic diversity and differentiation between two sister species of eudesmid eucalypts, *Eucalyptus tetrodonta* and *Eucalyptus megasepala*. The two species have overlapping distributions in northern Queensland, where *E. megasepala* is restricted to the Cape Yorke Peninsula, including areas where both species can occur within metres of one another; *E. tetrodonta* is widespread from northern Western Australia, through the Northern Territory and into Queensland. Despite their overlapping geographic ranges and apparently limited physical and environmental barriers to gene flow, significant genetic differentiation and population structure were observed with limited evidence of gene flow between the two species. Outlier loci associated with divergent selection were identified, suggesting genetic adaptations underpinning ecological differences. Additionally, flowering time analysis revealed temporal isolation, potentially contributing to reproductive barriers. Over its entire range, *E. tetrodonta* genetic diversity follows an isolation by distance pattern with a modestly supported genetic split occurring near the Gulf of Carpentaria. These findings provide valuable insights into the intricate mechanisms driving speciation in *Eucalyptus* species and have broader implications for understanding biodiversity in temperate tree genera.

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Unravelling *Ochrogaster lunifer*, a cryptic species complex.

Nicole McMullen (The University of Queensland).

Ochrogaster lunifer Herrich-Schäffer 1855, commonly known as the bag shelter moth, is a relatively ubiquitous and abundant Australian native moth species. The caterpillars' behaviour of processioning in single file has meant that many Australians are familiar with them. Their nest, a silken 'bag', is used as a retreat during the day and the caterpillars generally feed at night. The nests can be located within the canopy of their host tree or shrub, on branches, on the trunk or at the base of the host plant species. There are also differences in caterpillar behaviours and the species of plant they feed on, positioning of the egg mass by adult females, the colour of abdominal setae of female moths and differences in wing patterns in adult males. DNA sequence data have revealed that there are at least two species currently under the concept of *O. lunifer*, but there are likely more. Here, we will use morphological and DNA sequence data to further unravel the *O. lunifer* species complex.

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Can we use DArT sequencing to identify our herbarium collections?

Hannah McPherson (Botanic Gardens of Sydney); Guy Lowe (Botanic Gardens of Sydney); Lisa Woods (Botanic Gardens of Sydney); Melissa Wong (Botanic Gardens of Sydney); Claire Brandenburger (Botanic Gardens of Sydney); Andre Badiou (Botanic Gardens of Sydney); Patrick Fahey (Botanic Gardens of Sydney); Maurizio Rossetto (Botanic Gardens of Sydney); Trevor Wilson (Botanic Gardens of Sydney).

The opportunities to extract better value out of herbarium collections are increasing with the improved DNA extraction success and genomic approaches increasing in affordability and efficiency. We present a collections-based workflow that outlines a comprehensive instructional toolkit for sampling herbarium specimens following an earlier protocol developed in the early sampling strategy stage by Genomics for Australia Plants (GAP). Our methodology provides a versatile module of solutions for effective controls over sampling, annotating and tracking data of herbarium specimens that are used for genomic study. Its design ensures a priority of care while at the same time improves access to the incredible biological research resource that herbarium collections provide for answering fundamental questions associated with identification, systematics and taxonomy, and evolutionary change through time. As a proof of concept we describe our pilot study using SNP-based genomic scans of 94 *Indigofera australis* Willd. herbarium collections.

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Using high-throughput species discovery with robots and Nanopore sequencing to overcome taxon biases in biodiversity science.

Rudolf Meier (Museum für Naturkunde, Berlin).

Biodiversity science tends to neglect hyperdiverse arthropod clades although they are species-rich and provide many ecosystem services. In this seminar, I first document that more than half of the flying insect diversity in many samples is concentrated in 20 family-level clades regardless of where the samples were collected. I then demonstrate how little is known about most of these clades by comparing the species richness in samples with the number of described species. This leads to the conclusion that we need new approaches to species discovery and taxonomy of “dark taxa”. At the Center for Integrative Biodiversity Discovery at the Natural History Museum Berlin, we are currently optimizing a robot ("DiversityScanner") that detects, images, and measures individual specimens before they are placed into microplates for DNA barcoding with rapid and cost-effective techniques involving Nanopore sequencers. After presorting the specimens based on DNA barcodes, we use morphological data for selected specimens to validate/fix "barcode clusters" to become species ready to be identified or described. I will show that this approach allows for quickly converting a "dark taxon" from largely unknown to sufficiently well known for biomonitoring. I will also show how the images for common species can be used to train Convolutional neural networks (CNNs) for future specimen identification with images alone. Overall, I will argue that dark taxa can be tackled by applying high throughput methods to one local sample at a time.

Phylogenetics of Australian archaeococccoid scale insects to assist in decision making for classical biological control.

Penelope J. Mills (The University of Queensland); Umar K. Lubanga (Department of Energy, Environment and Climate Action, Agriculture Victoria); Greg K. Lefoe (Department of Energy, Environment and Climate Action, Agriculture Victoria).

A recently detected pest in Australia is the gymnosperm-feeding giant pine scale *Marchalina hellenica* (Hemiptera: Marchalinidae). This archaeococcoid scale insect originates from the eastern Mediterranean and in its native range it is one of the most important species used in the apiculture industry for pine honey production. However, high numbers of *M. hellenica* on its gymnosperm host plants can negatively impact the health of trees including a reduction in wood production and even tree death. A biocontrol program to control *M. hellenica* in Australia is currently underway, however a rigorous risk assessment process must be conducted before any new biocontrol agent can be considered for introduction. Risk assessment includes prey-specificity testing of selected non-target species such as native scales, and one of the most important criteria for selecting which non-target species to test is relatedness to the target pest. We are constructing a phylogeny of Australian scale insects to resolve uncertain relationships amongst archaeococcoid taxa. Reducing uncertainty of the phylogenetic relationships between Australian native scale insects will make a significant contribution to the selection of test species, biological control risk assessment, and biological control agent introduction decisions.

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Acacia phylogenomics: an initial assessment using the Angiosperms353 target capture bait set.

Daniel J. Murphy (Royal Botanic Gardens Victoria); Bruce Maslin (Western Australian Herbarium); Theodore Allnutt (Royal Botanic Gardens Victoria); Todd McLay (National Biodiversity DNA Library, CSIRO).

This study marks the initiation of a Genomics for Australian Plants (GAP)-supported, phylogenomic analysis of the genus *Acacia* – Australia's largest genus of flowering plants - using the Angiosperms353 target capture bait set. While Sanger amplicon sequencing datasets have previously been compiled for approximately 50% of *Acacia* species, those datasets comprised fewer than 10 markers and lacked phylogenetic resolution in certain parts of the tree, demonstrating the need for a deeper phylogenomic-based sampling of the *Acacia* genome in order to resolve the phylogeny. In this talk, results are presented of an initial phylogenomic analysis of around 10% of *Acacia* species, sequenced for the Angiosperms353 target capture baits and representing all major evolutionary lineages of *Acacia* that had previously been discovered in molecular phylogenies and morphological classifications. Initial phylogenetic analyses, including appropriate outgroups and using several analytical approaches, have revealed clades that are generally congruent when compared to the topologies found in previous molecular phylogenetic studies, and several previously recognised taxa are shown to be monophyletic, although some novel clades and relationships are resolved in our analyses. Topological differences may be due to increased phylogenetic resolution of the markers or differences in the sampling for clades. Due to the level of support for relationships, in combination with the very high success rates for sequencing of silica-dried and older herbarium samples, the Angiosperms353 bait set shows great potential to use as the basis for a larger-scale study of *Acacia* species, with the ultimate aim of generating a new formal classification of the genus.

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The unknown highly diverse and endemic invertebrate communities of forest floors in south-eastern Australia threatened by the new fire regime.

Nick Murphy (Department of Environment and Genetics, La Trobe University);
Nick Porch (Deakin University), Heloise Gibb (La Trobe University).

Terrestrial decomposer communities play a crucial role in forest biodiversity. However, many invertebrate groups within these communities, such as millipedes, arachnids, and crustaceans, remain poorly described. To better understand the impact of the 2019/2020 megafires on this vulnerable community, we conducted a survey of litter-dwelling invertebrates in fire-affected rainforest and wet forest sites in South Eastern Australia. We employed a pooled-DNA barcoding approach from a subset of the invertebrates collected and discovered significant evolutionary diversity among crustaceans, arachnids, and myriapods, along with substantial evidence of short-range endemism. We also found very high levels of regional evolutionary diversity and substantial community turnover between regions. It's noteworthy that none of the groups we studied were listed as priorities to determine the impact of the Black Summer fires, however our studies indicate that more than 60 billion litter invertebrates were consumed by the fires. Given that short-range endemics are clearly at risk from landscape-level fires, our results underscore the urgent need for comprehensive systematic studies of these vulnerable invertebrate fauna. Whilst this is clearly a substantial task, our research suggests that conducting landscape-level studies on endemism at the community level may could offer a solution to the taxonomic challenges associated with these groups.

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Patterns of diversification and trait evolution in Australian orchids.

Consolata Nanjala (James Cook University); Lalita Simpson (James Cook University); Mark Clements ((Centre for Australian National Biodiversity Research (Joint Venture between CSIRO and Parks Australia)); Heidi Zimmer ((Centre for Australian National Biodiversity Research (Joint Venture between CSIRO and Parks Australia)); Darren Crayn (James Cook University); Katharina Nargar (James Cook University & CSIRO).

Orchidaceae are one of ten largest vascular plant families of the Australian flora, constituting a rich and highly endemic orchid flora with more than 1600 species and displaying a high degree of endemism with over 90%. Many Australian orchid lineages have diversified significantly during the Cenozoic era amidst dramatic environmental shifts. Their diverse morphological, physiological, and ecological traits offer valuable insights into macroevolution, yet unresolved evolutionary relationships pose challenges to understanding the forces driving their unique diversity. Overcoming these challenges requires addressing issues such as minimal genetic differentiation among closely related taxa and the prevalence of hybridization and whole-genome duplication events in Australian orchids. The advent of high-throughput DNA sequencing methods presents an opportunity to untangle these intricate evolutionary relationships. This study aims to construct robust, extensively sampled phylogenies for selected Australian orchids lineages using high-throughput DNA sequencing data to explore the evolution of key morphological, physiological, and ecological traits. Through the application of macroevolutionary models, this study aims to identify traits associated with increased speciation or extinction rates, trace the evolutionary trajectory of these traits, and shed light on the processes that have shaped the present-day diversity of orchids in Australia.

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Biogeography of the only irises disjunct across the Pacific Ocean.

Sophie S. Newmarch (Massey University); Richard C. Winkworth (Massey University); Dan J. Blanchon (Auckland War Memorial Museum); Joanne L. Birch (University of Melbourne); Nicolás García (Universidad de Chile); Jennifer A. Tate (Massey University).

Taxa with disjunct distributions have long fascinated biologists and have provided important insights into biological evolution in the southern hemisphere. *Libertia* and *Orthrosanthus* are two understudied genera, and the only representatives of Iridaceae (~70 genera), that are disjunct across the Pacific Ocean. Both groups naturally occur in South and Central America, and in Australia; *Libertia* is also found in New Zealand and New Guinea. Previous studies have suggested that *Libertia* and *Orthrosanthus* are sister within the tribe Sisyrinchieae, which likely arose in South America ~21.6 million years ago. Since previous studies have included only one species from each genus, their biogeographic origins and distribution remains uncertain. Here we present a dated phylogeny based on a large plastome data set, assembled from a combination of genome-skimming and Angiosperms353 by-catch, that includes representatives of all species of *Libertia* and *Orthrosanthus*. The results provide novel insights into the biogeography of these two genera and provide a foundation for further studies into polyploidy and floral evolution.

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Reconciling incongruence and implications for taxonomy/systematics in the phylogenomic era.

Francis J. Nge (Institut de Recherche pour le Développement and National Herbarium of New South Wales, Botanic Gardens of Sydney).

Incongruence could arise through different datasets (e.g. molecular vs. morphological or nuclear vs organellar), analytical methods (e.g., concatenated vs. coalescent), and even across different genes in the phylogenomic era. Conflicting results from any of these would complicate not only taxonomic and systematic outcomes, but also downstream analyses and interpretations that rely on these results. Incongruence across datasets will increase as we get greater access to molecular sequence data across an increasingly large number of organismal groups. Thus, ensuring that these incongruences be taken into account is ever more crucial, e.g. in order to meet the challenge of the Decadal Plan. Here, I present several case study examples based on different plant groups across a broad range of scenarios and how incongruent results have affected taxonomic, systematic, and conservation outcomes. Increasing awareness, current solutions, and future directions will also be discussed.

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Tetramolopium ornans **Ngugi (Asteraceae), a new species from the Wet Tropics of Queensland, Australia*.***

Lorna B. Ngugi (Queensland Herbarium and Biodiversity Science).

Tetramolopium ornans Ngugi (Asteraceae), a new species from the Wet Tropics of Queensland, Australia. Tetramolopium ornans is described as a new species from the Wet Tropics of north Queensland. It is distinguished from the related *T. vagans* Pedley by the presence of sparse hairs on cypselae and longer leaves with an acuminate apex. Notes will be presented on distinctive features, habitat, phenology and conservation status, along with detailed illustrations, images, and a distribution map. The ongoing molecular phylogeny study of this species will also be introduced.

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Serendipita fungi from Australian orchids as possible barley root endophytes.

H.A. C. Nisha (Australian National University); J.D.W. Dearnaley (University of Southern Queensland); C.C. Linde (Australian National University).

Serendipita (syn *Piriformospora*) *indica* has been shown to be an effective root endophyte, plant growth promotor, and inducer of disease resistance in a number of plant systems. Australia is rich in *Serendipita* species which have a mycorrhizal association with orchids. The aim of this study is to determine whether *Serendipita* orchid mycorrhizal fungi are able to colonize barley roots as endophytes. We tested the ability of 14 *Serendipita* isolates representing eight species or operational taxonomic units, from five orchid species to colonize barley root cells. Surface sterilized seed of barley variety Skiff was added to tissue culture jars containing colonies of each fungus on Murashige and Skoog medium. Root colonization by *Serendipita* was microscopically assessed after 60 days. The formation of microsclerotia, monilioid cells, chlamydospores, and mycelium within barley roots was observed for all *Serendipita* species, indicating successful colonization. Preliminary analyses suggest variation among *Serendipita* species at forming endophytic associations with barley. Future studies will include testing these fungi for their ability to promote barley growth, induce phosphorus uptake, and promote disease resistance. This research sheds light on the potential of utilizing orchid mycorrhizal *Serendipita* species as beneficial endophytes in barley cultivation, with potential applications in sustainable agriculture.

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First assessment of cryptic species in the gall-inducing scale insect *Apiomorpha calycina* (Coccomorpha: Eriococcidae).

Torin R. O'Connell (The University of Queensland); Lyn G. Cook (The University of Queensland).

Apiomorpha calycina is a member of the most species-rich, gall-inducing scale insect genus. Females induce vase-shaped galls on eucalypts in *Eucalyptus* sections *Bisectae*, *Latoangulatae* and *Dumaria*. The species was first described by Tepper in 1893 from specimens collected on *Eucalyptus dumosa* in South Australia, but its distribution is now known to range from NSW, Victoria and South Australia to Western Australia. Genetic studies of other species of *Apiomorpha* that occur across multiple eucalypt sections and across such a broad geographic distribution have typically found the presence of cryptic species. Here, we use DNA sequencing and morphology to assess whether there are cryptic species also present in *A. calycina*. In particular, we focus on specimens from Western Australia that have atypical gall morphologies.

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Rise up, *Rhizoctonia*: moving to one fungus, one name in the Cejpomycetaceae (Agaricomycetes; Cantharellales).

Ryan P. O'Donnell (Australian National University); Tom W. May (Royal Botanic Gardens, Victoria); Celeste C. Linde (Australian National University).

Cejpomycetaceae is a family of cryptic basidiomycetous fungi, most notable for the plant pathogens known under generic names such as *Rhizoctonia*, *Ceratobasidium*, *Thanatephorus* and *Ceratorhiza*. While responsible for billions of dollars in crop losses annually, members of these genera also serve important ecological functions as orchid mycorrhizal symbionts and saprotrophs. While teleomorph-typified (*Thanatephorus* and *Ceratobasidium*) and anamorph-typified (*Rhizoctonia* and *Ceratorhiza*) names have been utilised, molecular studies have repeatedly demonstrated these genera to be paraphyletic. In addition, the type of *Ceratobasidium* is not con-generic with the many other species introduced in the genus. Despite previous attempts to synonymise various names under a broadly-defined *Rhizoctonia*, authors have continued to describe new species using outdated generic names. Using publicly-available ex-type sequences, we recovered a phylogeny of the Cejpomycetaceae that reiterates the paraphyly of various genera within a well-supported clade to which we apply the name *Rhizotonia*. We review the validity of a number of epithets in *Ceratobasidium*, *Thanatephorus*, and *Ceratorhiza*, and formalise their transfer to *Rhizoctonia*. Using *Rhizoctonia* as a case study, we argue that continued use of dual nomenclature is out of step with contemporary fungal taxonomic practice and precludes a holistic understanding of the classification and biology of this group.

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Conservation genetics of Critically Endangered *Zieria* (Rutaceae): confirming existing species boundaries and identification of a species new to science.

Harvey K. Orel (The University of Melbourne); Todd G. B. McLay (The University of Melbourne, Royal Botanic Gardens Victoria and CSIRO); Lydia K. Guja (Australian National Botanic Gardens and CSIRO); Marco F. Duretto (Botanic Gardens of Sydney); Michael J. Bayly (The University of Melbourne).

Zieria is a genus of 63 described species of shrubs or small trees in the family Rutaceae that are almost all endemic to eastern Australia. Many species are rare and threatened, and these are usually restricted to small geographic ranges, often growing on or around rocky outcrops and mountain peaks along Australia's Great Dividing Range. *Zieria buxijugum*, *Z. formosa* and *Z. parrisiae* are three closely related, Critically Endangered species of questionable taxonomic validity that occur within six kilometres of each other on the south coast of New South Wales (NSW). Using ddRADseq data and sampling comprehensively from wild plants and *ex situ* living collections, we investigated genetic relationships and diversity of these species, along with two taxonomically stable congeners, *Z. granulata* and *Z. tuberculata*, and a possible undescribed taxon, *Z. aff. tuberculata*. Our results support the current taxonomic status of *Z. buxijugum*, *Z. formosa*, and *Z. parrisiae*. Genetic data and morphology support and inform the description of *Z. aff. tuberculata* as a distinct species, which is known from a single mountain in south-east NSW. This research highlights the value of genetic data for species delimitation and identification, and for understanding wild vs. *ex situ* genetic diversity.

Taxonomists in training: the feasibility of learning from the literature, or lack of it.

Ben A. Parslow (South Australian Museum and University of Adelaide);
Rebecca J. Hill (South Australian Museum).

A compelling need exists for expanding the taxonomic workforce, particularly in our pursuit of comprehensive biodiversity documentation. The current state of this workforce presents substantial risks to its long-term sustainability with the loss of knowledge and capacity building. Traditional taxonomic training heavily relies on direct mentorship from experts with substantial experience. However, challenges arise when access to such experts is restricted or when dealing with taxonomic groups lacking contemporary resources and treatments. This study explores the feasibility of training novice students in taxonomy, leveraging published literature, and offering minimal mentor guidance to address these challenges. To assess the feasibility of this approach, we developed a structured workflow with the objective of characterising the small wasp genus *Aulacus* (Aulacidae: Hymenoptera) to assist in describing new species by an inexperienced taxonomist. Our results shed light on the myriad of challenges faced by a new taxonomist and paves the way for open dialogue regarding the future of training the next generation of taxonomists in environments where expert guidance may be scarce.

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Abiotic correlates with diversity and distinctiveness in Sunshine Coast heathlands: moisture, old landscapes, and ancient mounds.

Hilary R. Pearl (University of the Sunshine Coast); Tim Ryan (Queensland Herbarium); Marion Howard (University of the Sunshine Coast); Yoko Shimizu (University of the Sunshine Coast); Alison Shapcott (University of the Sunshine Coast).

Abiotic factors associated with diversity and phylogenetic dispersion within communities, as well as distinctiveness between communities, may potentially be impacted by climate change or changes in hydrology due to urbanisation. Understanding these factors can inform on how we can manage the ongoing integrity of protected communities. This study used a range of metrics, along with abiotic factors, to examine correlates with diversity patterns in the Sunshine Coast heathlands, ecosystems under pressure from urban development. Metrics for 80 heathland sites over a variety of substrates, moisture levels, and topographic factors were compared using univariate and multivariate statistics. Moisture was found in this study to be a key abiotic factor correlated with the diversity and distinctiveness of heath, and also with the higher phylogenetic dispersion of moist and wet sites, and the location of potential refugia. Observed vegetation composition patterns highlighted the distinctiveness of heaths on ancient rocky volcanic substrates. The presence of ancient natural landscapes of "mounds" and "trenches" was associated with phylogenetic evenness, and a "refugial environment". This study suggests that both the management of hydrological changes, and protection of potential refugial areas are likely to be critical in maintaining the integrity and diversity of the Sunshine Coast heathlands.

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Mycorrhizal associations: biotic correlates of phylogenetic dispersion patterns in the Sunshine Coast Heathlands, Queensland, Australia?

Hilary R. Pearl (University of the Sunshine Coast); Alison Shapcott (University of the Sunshine Coast).

This study provides the first overview of mycorrhizal functional groups in Queensland Sunshine Coast heathlands, a community of low phylogenetic diversity. Broad proportions of mycorrhizal functional groups in the heathlands were compared with patterns in the surrounding rainforest flora, and across the heath strata. This study found patterns of mycorrhizal associations in the Sunshine Coast flora to be strikingly different between the rainforest and heath communities. Similar to other low-fertility environments, a greater diversity of mycorrhizal strategies and an increased number of plant genera with non-mycorrhizal association were found in the Sunshine Coast heathlands. Mycorrhizal patterns across the heath strata suggest competitive interactions and facilitation are contributing to plant assembly patterns. This may be enabling the coexistence of plant species in the heath and resulting in greater phylogenetic dispersion of the heath community than would otherwise be the case.

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Biosystematics 2023
Celebrating the past | Planning the future

Molecular ecology and systematics of New England Tablelands Bioregion endemic outcrop shrub populations.

Peter J Pemberton (University of New England); Manu E Saunders (University of New England); John T Hunter (University of New England); Elizabeth M Wandrag (University of York); Rose L Andrew (University of New England).

Old Climatically Buffered Infertile Landscapes (OCBILs) theory explains why certain areas have a high incidence of endemic and rare species, and instances of granite rock outcrops in the New England Tableland Bioregion qualify as OCBILs. These granite outcrops often exist as terrestrial islands, that are isolated in a larger landscape matrix. Flora species confined to OCBILs have a high incidence of endemicity and rarity. Many OCBIL shrub species have gravity-dispersed seeds and are only pollinated by localised insects. These characteristics will limit gene flow, and relatively small distances may be sufficient for allopatry if pollen or seeds are not transferred between disjunct outcrops. The genetic isolation may drive diversification and create OCBIL speciation cradles. To understand how OCBIL shrubs diversify and persist, I will be conducting systematics, molecular ecology and pollinator research on several granite outcrop shrub species in the New England Tablelands Bioregion. Using multi-species coalescent analysis, I will investigate aspects of the systematics of *Cyanothamnus inflexus* subspecies that has not been previously tested. In addition, I will examine patterns of divergence in a broader set of OCBIL and non-OCBIL taxa, to understand the evolutionary history and adaptations terrestrial island flora in a relatively understudied OCBIL region.

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Extraordinary diversity and patterns of distribution in tiny subterranean crustaceans: Parabathynellidae (Bathynellacea) of Western Australian arid zone.

Giulia Perina (Western Australian Museum and Curtin University and Biologic Environmental Survey); Ana I. Camacho (Museo Nacional de Ciencias Naturales); Nicole White (Curtin University); Joel Huey (Biologic Environmental Survey); Shae Callan (Biologic Environmental Survey); Michelle Guzik (The University of Adelaide).

Parabathynellidae are small interstitial/subterranean crustaceans that have been restricted to groundwater habitats for a long time, as suggested by the absence of extant surface species, potentially millions of years longer than contemporaneous taxa within the same assemblages. Their present-day ranges are influenced by a combination of restricted habitats, complex lifestyles, and biogeographical patterns reflecting ancient hydrology. Providing ecosystem services such as water purification and nutrient cycling, species in this important stygobitic (organisms inhabiting only groundwater) group are still poorly described. To date, only 52 species are formally recognised in Australia. However, an abundance of material, routinely collected and sequenced for environmental impact assessment surveys related to mining developments, has uncovered an extraordinary diversity, especially in the northern Western Australia, with intriguing distribution patterns. Australian Parabathynellidae include nine mostly endemic genera, and two genera that have ‘cosmopolitan’ and ‘Gondwanan’ distributions: respectively, *Hexabathynella* (25 described species to date), and *Atopobathynella* (17 described species to date). Recent morphological and molecular studies conducted have revealed an abundance of species within these two genera, with complex distribution patterns. Understanding Parabathynellidae diversity and species boundaries is crucial for the conservation of stygobitic taxa and their important groundwater habitats in a landscape increasingly impacted by human activities.

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Resolving species complexes among taramea, speargrasses, *Aciphylla* (Apiaceae) using ddRADseq.

Leon Perrie (Museum of New Zealand Te Papa Tongarewa); Lara Shepherd (Museum of New Zealand Te Papa Tongarewa).

The 40 species of *Aciphylla* endemic to New Zealand make it one of the country's biggest indigenous genera. In the Apiaceae, the colloquial name of speargrasses reflects that the leaflets of most species have sharp, stiff, skin-piercing apices with the potential to draw blood from trampers incautious through tussocklands. The bigger species are known as taramea in Te Reo Māori. Despite being icons of New Zealand's uplands, *Aciphylla* includes many species-level taxonomic uncertainties. In some instances, morphological variation is correlated with geography, and it has been unclear whether two species are present or a single clinal species. Additionally, there are some ten tag-names of uncertain status. Initial analyses indicate that the genomic sequencing method of ddRADseq has promise for resolving many of these taxonomic uncertainties. Examples will be discussed ranging from the giant *Aciphylla scott-thomsonii* to the petite *A. polita* and the abundant *A. aurea*.

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Assembling the genome of rātā Moehau and applications for other NZ *Metrosideros*.

Jessie M. Prebble (Manaaki Whenua - Landcare Research).

The 12 *Metrosideros* native to Aotearoa New Zealand (AoNZ) are facing a growing number of threats, particularly since the arrival of myrtle rust (*Austropuccinia psidii*) in 2017. Despite their iconic status (e.g. Pohutukawa *M. excelsa* known as the AoNZ Christmas tree) we have surprisingly little genetic data to help us understand how diversity is partitioned across the landscape for most species. One of the most threatened species is rātā Moehau (*M. bartlettii*), a critically endangered rātā tree found only in the far north of AoNZ. At the last count only 14 trees were found in the wild. In conjunction with the iwi (tribe) Ngāti Kuri we have assembled a genome of rātā Moehau. This will allow us to resequence samples representing (almost) the entire wild population, plus representatives of additional closely related species. At the same time, we are using the assembled genome to develop new markers and are gathering a dataset of as many AoNZ *Metrosideros* species as we can to sequence using amplicon sequencing. The end goal is an understanding of how the genetic diversity of each AoNZ *Metrosideros* species is distributed in space, with a particular focus on modelled refugia in the face of climate change and projected myrtle rust spread to help prioritise conservation effort.

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Expanding the Epacrid Tree of Life.

Caroline Puente-Lelievre (University of Auckland); Cinthy Jimenez Silva (University of Auckland); Lars Nauheimer (Australian Tropical Herbarium); Francis Jason Nge (Institut de Recherche pour le Développement and National Herbarium of New South Wales, Botanic Gardens of Sydney); Katharina Nargar (Australian Tropical Herbarium); Nicholas J. Matzke (University of Auckland); Darren Crayn (Australian Tropical Herbarium).

Ericaceae subfam. Epacridoideae comprises about 580 taxa. It is an important component of the Australian native flora, particularly in the southern Australian heaths. Generic circumscription based on morphological characters has been problematic and unstable since the group was first described by Robert Brown in 1810. Molecular phylogenetic studies over the past 20 years have provided the basis for a phylogenetic reclassification of several genera eg. *Androstoma, Cyathopsis, Lissanthe, Monotoca*, and *Styphelia*. The resolution of generic boundaries is now well settled, but the relationships within and between genera remain poorly supported, particularly in the largest tribe Styphelieae, which contains 336 accepted species and about 116 phrase-named species, many of which are of conservation concern. Here, we analyse 250 loci generated through the Genomics for Australian Plants (GAP) and the Plant and Fungal Trees of Life (PAFTOL) consortia. The result is a well-supported and resolved phylogeny of the Epacridoideae with just over 100 species across 11 genera. Moreover, we use StarBeast3 to estimate divergence times and BioGeoBEARS to reconstruct ancestral distributions for each genus.

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A new species of endophytic *Coprinopsis* from subtropical rainforest in south-east Queensland.

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Endophytic fungi are microbes that occur in plant tissues without enacting disease symptoms. Fungal endophytes are not well studied in Australia, and little is known of their diversity, ecology, and physiological roles in native plants. As part of a PhD project focusing on the fungal endophytes of subtropical rainforests in south-east Queensland, 180 endophytic fungi have been grown out from the leaves of 15 native plant species. Isolates were identified via morphology and sequencing of ITS-DNA. The majority of isolated endophytes were identified as ascomycetes, but a single endophyte was shown to be a basidiomycetous *Coprinopsis* sp. Phylogenetic analysis of the ITS-DNA of this isolate confirms it to be a new species that is related to *C. alnivora* and *C. gonophylla*. Given that the fungus was collected as an endophyte in its mycelial form, rather than from fruiting bodies, the novel species needs to be cultivated *in vitro* to provide morphological descriptions. Three protocols to induce fruiting of the fungus have been tested with varying results. To our knowledge, this is the first report of an endophytic *Coprinopsis* sp. in Australia and highlights the wealth of knowledge yet to be learned about this little explored ecological niche.

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Phylogenetic analyses of the liverwort family Lepidoziaceae reveals the position of Micropterygioideae.

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Lepidoziaceae are the third-largest family of liverworts, with about 860 species found on all continents. With many taxa occupying a diverse range of habitats, these plants perform a variety of ecological roles. The evolutionary history of this family has not been satisfactorily resolved, with taxa such as the subfamily Micropterygioideae yet to be included in phylogenetic analyses. We inferred the position of the subfamily within Lepidoziaceae using a data set consisting of 13 genetic markers, sampled from 198 species. It was revealed that Micropterygioideae and Lembidioideae are sister lineages. Based on our phylogenetic estimate, we used statistical dispersal-vicariance analysis to reconstruct the biogeographic history of the family. Our study reveals the influence of past geological events and climatic conditions on the evolution and distribution of a widespread and diverse family of liverworts.

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Taxonomy, biogeography and the evolution of twig-lining behaviour in the trapdoor spider genus *Idiosoma* (Mygalomorphae: Idiopidae): the challenge of documenting one of Australia's most diverse spider genera.

Michael G. Rix (Queensland Museum and Western Australian Museum); Jeremy D. Wilson (University of Western Australia, Queensland Museum and Western Australian Museum); Andrew D. Austin (University of Adelaide); Steven J. B. Cooper (South Australian Museum and University of Adelaide); Mark S. Harvey (Western Australian Museum and University of Western Australia).

The assembly of the biota of the Australian arid zone has long fascinated biogeographers, and trapdoor spiders of the infraorder Mygalomorphae are a conspicuous and diverse guild of arthropod predators in arid zone ecosystems. The last decade has revealed a hitherto unrecognised diversity of mygalomorph species throughout arid Australia, with the genera *Idiosoma* (family Idiopidae) and *Aname* (family Anamidae) likely to be two of the country's most speciose spider genera, and possibly two of the most diverse mygalomorph genera in the world. Here, we explore the dual challenges of understanding the evolution and biogeography of the iconic spiny trapdoor spiders of the genus *Idiosoma*, and using this phylogenetic foundation to taxonomically document – in a reasonable timeframe – a remarkable fauna of conservation significance. The phylogeny of *Idiosoma* is inferred using a continent-wide taxon sample assembled over the last decade, with 252 terminals incorporating 120 putative species. Arid zone incursions have occurred in multiple lineages out of temperate southern Australia, with behavioural adaptive shifts and the convergent evolution of twig-lining burrow ornamentations a conspicuous feature of the fauna. Complementary taxonomic monography is ongoing, and we discuss the acute challenge of developing an integrative taxonomy for such a highly diverse lineage.

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The role of museums in training the next generation of systematists – challenges and opportunities.

Michael G. Rix (Queensland Museum).

The national distributed faunal collections housed in Australia's major public museums have long played a significant, if understated, role in systematics training. Access to authoritative collections of specimens, and to the expertise of those staff employed at museums, are both central elements of a modern postgraduate training programme in faunal taxonomy or systematics. However, the specific ways in which individual institutions and museum staff facilitate this training are many and varied, with numerous opportunities but also significant challenges. There is an underlying 'tension' that has always existed between publicly-funded (usually State or Territory) museums and those universities charged with directly administering training programmes for students, resulting in a sometimes difficult balance of competing priorities. In this short presentation, I will explore the central role of museums in training the next generation of Australian systematists, highlight the major challenges and opportunities, and discuss some of the ways in which museum institutions can successfully balance the demands of staff and resources to deliver optimal outcomes for students.

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Comparative Analysis of Whole Genome Sequencing and Target Capture of Ultra Conserved Elements for Phylogenetic Studies in Hymenoptera.

Juanita Rodriguez (CSIRO, Australian National Insect Collection); Olivia Evangelista (CSIRO, Australian National Insect Collection); Alicia Grealy (CSIRO, National Collections and Marine Infrastructure).

In this study, we present a comparative analysis of Whole Genome Sequencing (WGS) and Target Capture of Ultra Conserved Elements (UCE), within the context of phylogenetic research. We utilized a set of aculeate Hymenoptera (Pompilidae, Mutillidae, Colletidae, and Apidae) as our study subjects. We extracted DNA from 205 fresh and museum specimens and prepared libraries in miniaturized reactions with an initial quantity of 5 ng of DNA. The libraries underwent two processing methods: 1) target capture in pools of 16 using the UCE Hymenoptera 2.5Kv2A bait set, followed by sequencing, and 2) whole genome sequencing at a target 10x coverage, assuming genome sizes of 300Mb-600Mb depending on the taxon. UCE loci, were extracted with Phyluce from assemblies derived from both approaches. Our findings indicate that whole-genome sequencing surpasses target capture when applied to fresh specimens, in terms of ultra-conserved elements (UCEs) recovered and contig length at coverage levels exceeding 10x. However, under conditions of DNA degradation, target capture can potentially outperform whole-genome sequencing. This study not only elucidates the relative advantages and limitations of these methodologies but also underscores their adaptability to specific taxonomic groups.

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Clarifying the *Lepidosperma laterale* assemblage (Cyperaceae) in north-eastern New South Wales.

Shelley Rowntree (University of New England); Jeremy Bruhl (University of New England); Karen L. Wilson (Royal Botanic Gardens and Domain Trust); Russell Barrett (Royal Botanic Gardens and Domain Trust); Rose Andrew (University of New England).

Lepidosperma Labill., or ‘sword’ sedge, is a genus of 81 described species found primarily in Australia. The genus contains far more morphological variation than is explained by current taxonomy. The assemblage of *L. laterale* (variable sword sedge) and its close relatives has been challenging to resolve because of morphological variability within and between putative species. Previous studies of the assemblage identified both congruence and incongruence between morphology and molecular data. Current taxonomy within the *L. laterale* assemblage is based almost entirely on morphological characters. In my Honours project, I applied reduced representation sequencing to increase the power of molecular analysis in an integrative taxonomic assessment of the *Lepidosperma laterale* assemblage in north-eastern New South Wales. Multiple lines of evidence provided strong support for three new species from the New England Tableland and North Coast of New South Wales and the narrowing of the concept of *L. laterale sens. strict.* This approach provides a framework to resolve the remaining taxonomic issues within the assemblage.

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Phylogenomic analysis of the generic limits of *Chrysocephalum*.

Shelley Rowntree (University of New England); Alexander Schmidt-Lebuhn (CSIRO, Centre for Australian National Biodiversity Research); Jeremy Bruhl (University of New England); Ian Telford (University of New England); Rose Andrew (University of New England).

Chrysocephalum Walp. is a medium-sized genus in the Waitzia clade of the Australian Gnaphalieae (Asteraceae), comprising nine currently recognised species and two phrase-named species. Detailed relationships within the clades of the Gnaphalieae remain largely unresolved, and generic concepts are often based on a small number of morphological characters traditionally considered important. In a recent revision of the *C. apiculatum* and C. *semipapposum* complexes (Wilson 2016), 34 subspecies were named based on morphological characters, with a high level of complexity making distinction difficult among them. Towards my Ph.D. project, I have inferred a molecular phylogeny of selected Australian native Gnaphalieae (Asteraceae) using target capture sequences to test the monophyly of the *Chrysocephalum*. A group of three species formed the "core" *Chrysocephalum* clade, *C. apiculatum* (type species), *C. semipapposum* and *C. vitellinum*. Arid zone species formed separate clades. Further studies are underway to identify morphological and anatomical synapomorphies for clades and to resolve species limits and species-level relationships with molecular and morphological analyses.

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Speciation across biomes: rapid diversification with reproductive isolation in the Australian delicate mice.

Emily Roycroft (Australian National University); Fred Ford (NSW Department of Planning and Environment); William G. Breed (University of Adelaide); Till Ramm (Museum für Naturkunde Berlin); Rhiannon Schembri (Australian National University); Phoebe A. Burns (Zoos Victoria); Kevin C. Rowe (Museums Victoria); Craig Moritz (Australian National University).

Phylogeographic studies of continentally distributed clades provide powerful insight into how environment drives speciation across climatic contexts. Australia, a continent of disparate modern biomes and dynamic climate change, is a model system for reconstructing the impact of past and present environments on diversification. Here we use genomic-scale data to investigate Pleistocene diversification, cryptic diversity, and secondary contact in the Australian delicate mice (Hydromyini: *Pseudomys*), a recent radiation spanning almost all Australian environments. Across northern Australia, we find no evidence for introgression between cryptic lineages within *Pseudomys delicatulus* sensu lato, with palaeoclimate models supporting contraction and expansion of suitable habitat since the last glacial maximum. Despite multiple contact zones, we also find little evidence of introgression at a continental scale, with the exception of a potential hybrid zone in the mesic biome. In the arid zone, combined insights from genetic data and palaeomodels support a recent expansion in the arid specialist *P. hermannsburgensis*, and contraction in the semi-arid *P. bolami*. Based on genomic and morphological data, we revise the taxonomy of the delicate mice. In the face of repeated secondary contact, sperm morphological differences and chromosomal rearrangements are potential mechanisms that maintain species boundaries in these recently diverged species.

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Volcaniclastic silcrete floras in eastern Australia provide new fossil evidence of the fern genus *Pteridium* (bracken).

Andrew C. Rozefelds (Queensland Museum Network).

Pteridium is a cosmopolitan genus occurring in all continents, except Antarctica, and is among the most widespread vascular plant species known; and yet the fossil record world-wide is poor. This is because the fronds disintegrate while they are still on the plant, and the potential for fossilization is therefore limited. At four fossil sites in eastern Australia, however, fern foliage referable to *Pteridium* is identified. Characters traits useful in identification of *Pteridium* include vein arrangement, shallowly grooved stipe and costa, recurved margins of the pinnules, free laminal lobes on rachis, large frond size (several times pinnate), and a polycyclic siphonostele rhizome. All sites occur with Oligocene-Miocene volcanism and the ferns are preserved *in situ* in volcaniclastic sediments (palaeosols) - time capsules of the vegetation growing at each site. *Pteridium* today is associated with dry *Eucalyptus* forest, disturbed pastures and occurs along forest edges. Disturbance due to regional volcanism in Australia would have allowed *Pteridium* and other ferns to colonize these new volcanic terrains and they are therefore interpreted as early successional floras. The character traits in fossil *Pteridium* indicates closer links to *P. esculentum* than to *P. aquilinum,* which suggests that species divergence had occurred earlier than previously suggested.

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OZBONEPROT: New protein sequences for Australian marsupials with applications to zooarchaeological and palaeontological samples.

Sofia C. Samper Carro (ANU and ARC Centre of Excellence for Australian Biodiversity and Heritage); Vera Weisbecker (Flinders University); Sue O'Connor (ANU and ARC Centre of Excellence for Australian Biodiversity and Heritage).

New biomolecular approaches are rapidly increasing the zoological information that can be retrieved from archaeological and palaeontological sites. Palaeoproteomics, the study of ancient proteins has received much attention and is rapidly becoming a standalone discipline. Nevertheless, advances in the field have been mainly limited to research on European sites and collections. As such, the application of proteomics to old mammal assemblages in Australia requires building curated and validated protein sequences from modern specimens. This presentation will examine the work carried out in Australia as part of the *Ozboneprot* project, the first project aimed at implementing palaeoproteomics in Australian archaeological and palaeontological sites. Using shotgun proteomics and genomics, this project is developing open-access protein sequences (including collagen and other non-collagenous proteins) for modern marsupials, as well as designing screening methods to test collagen preservation; a significant challenge in tropical and sub-tropical environments. This presentation will present the results thus far, analytical pipelines, and projected outcomes of our project, as well as providing space for discussion on future steps and challenges in the study of human-animal interactions with mammals more generally.

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Impacts of the ABRS National Taxonomy Research Grant Program on Australia's threatened species.

Jaever M. Santos; Tina A. R. Gopalan; Bryan D. Lessard (Australian Biological Resources Study).

The Australian Biological Resources Study (ABRS) has supported biodiversity research since its establishment in 1973. Throughout its 50 years as Australia's focal point for taxonomy and systematics, the ABRS has provided this support to the taxonomic community through the National Taxonomy Research Grant Program (NTRGP), the only national grant scheme for taxonomic research. To date, the ABRS has funded more than 84 million Australian dollars unadjusted (156 million adjusted for inflation to 2022) across 2,400 taxonomic research projects. While our knowledge and understanding of native Australian biodiversity continues to grow each year, so do the emerging threats caused by climate change, habitat loss and invasive species. Here, we highlight several NTRGP-funded projects that have had significant impacts for threatened species. The NTRGP has enabled the discovery, naming and description of many new species that are now recognised as at-risk species and made accessible for conservation-based decision making via the Species Profile and Threats Database (SPRAT) under the Environment Protection and Biodiversity Conservation Act 1999. Relational databases such as the Australian National Species List will allow us to more rapidly capture new species data in the hopes of expediting the assessment of the conservation status of new species.

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The Auckland University of Technology Lab for Cephalopod Ecology and Systematics (ALCES): an introduction to the lab with a highlight on two new bottletail squids (Sepiadariidae: Sepioloidea) from New Zealand.

Jaever M. Santos (Australian Biological Resources Study; Auckland University of Technology).

The Auckland University of Technology Lab for Cephalopod Ecology and Systematics (ALCES) is a university lab group based in Auckland, New Zealand. As the name suggests, we research cephalopod ecology and systematics focusing on the diversity of squid in the waters surrounding New Zealand. In addition to research outputs, our lab is committed to developing collaborative partnerships with other research institutions, training early-career cephalopod researchers from around the world, and boosting the public's curiosity of cephalopods through science communication. We highlight one of our recent papers from 2022 in which we described two new bottletail squid species (Cephalopoda: Sepiadariidae). Over 600 specimens were examined for morphological characters and genetic samples (n=61) were analysed from viable material. As a result, two new species, *Sepioloidea virgilioi* and *Sepioloidea jaelae* were described. Diagnostic morphological characters include the tentacular club sucker arrangement and hectocotylus structure. Molecular data supported the recognition of these two new taxa, with sampled populations of each of the three available Sepioloidea falling within three monophyletic clades following analysis of COI (cytochrome c oxidase subunit I) sequence data.

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AusTraits: Australia's plant trait database.

Hervé Sauquet (Botanic Gardens of Sydney and University of New South Wales); Elizabeth Wenk (University of New South Wales); Rachael Gallagher (Western Sydney University); David Coleman (Western Sydney University); Lily Dun (Western Sydney University); Fonti Kar (University of New South Wales); Sophie Yang (University of New South Wales); Daniel Falster (University of New South Wales).

AusTraits is an open-source, harmonised database of Australian plant trait data. First released in 2021, AusTraits is establishing itself as the key resource for trait data on Australian plants, with data distributed through multiple portals including Zenodo, the Atlas of Living Australia, and the austraits R package. AusTraits includes some data for nearly all of Australia's 26,000+ plant species and ~500 traits, with near-complete datasets for plant growth form, life history, and woodiness. At its core, AusTraits is committed to the FAIR Data Principles (Findable, Accessible, Interoperable, and Reusable), to ensure data and the trait database workflow are readily discoverable and available for reuse. All traits included in AusTraits are documented in the AusTraits Plant Dictionary (APD), a comprehensive vocabulary that includes trait descriptions, keywords, references, and links to other trait databases, allowing straightforward, consistent interpretation of trait data within AusTraits and the reuse of trait definitions by other researchers. Here we present an overview of these resources and recent developments, including an effort to increase coverage of floral traits for a sample of species matching the Australian Angiosperm Tree of Life and a new workflow to extract trait data from taxonomic descriptions.

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Inferring the Australian Angiosperm Tree of Life: paralogy, phylogenetics, and technical hiccups along the way.

Alexander Schmidt-Lebuhn (CSIRO); Ziad Al Bkhetan (Australian BioCommons); Theodore Allnutt (Royal Botanic Gardens Victoria); Matt Barrett (James Cook University); Jason Bragg (Royal Botanic Garden Sydney); Gareth Holmes (Royal Botanic Gardens Victoria); Chris Jackson (Royal Botanic Gardens Victoria); Mabel Lum (Bioplatforms Australia); Steven Manos (Australian BioCommons); Todd McLay (CSIRO); Daniel Murphy (Royal Botanic Gardens Victoria); Katharina Nargar (CSIRO); Lars Nauheimer (James Cook University); Harvey Orel (University of Melbourne); Hervé Sauquet (Royal Botanic Garden Sydney); Kelly Shepherd (Department of Biodiversity, Conservation and Attractions); Lalita Simpson (James Cook University); Michelle Waycott (The University of Adelaide); Trevor Wilson (Royal Botanic Garden Sydney); Darren Crayn (James Cook University).

The Phylogenomics activity area of the Genomics for Australian Plants consortium aims to assemble the Australian Angiosperm Tree of Life (AAToL). In its stage 1, Australian native flowering plants were sampled at one specimen per genus by a collaboration of six teams, each centred on a major herbarium, and additional sequences were obtained from mutual data exchange with the Plant and Fungal Tree of Life consortium. After several iterative rounds of analysis, our 'big tree' comprising 2,006 terminals has now been inferred, and we are preparing its publication. In this talk, we will present the methodology used in this project with a focus on the resolution of paralogy, phylogenetics, and aspects of quality control. We will also discuss technical problems encountered during analysis and how we explored solutions that may be relevant to other large phylogenomic datasets.

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Angiosperm flowers reached their highest morphological diversity early in their evolutionary history.

Andrea M. López-Martínez (Universidad Nacional Autónoma de México); Susana Magallón (Universidad Nacional Autónoma de México); Maria von Balthazar (University of Vienna); Jürg Schönenberger (University of Vienna); Hervé Sauquet (National Herbarium of New South Wales and University of New South Wales); Marion Chartier (University of Vienna).

Flowers are the complex and highly diverse reproductive structures of angiosperms. Because of their role in sexual reproduction, the evolution of flowers is tightly linked to angiosperm speciation and diversification. Accordingly, the quantification of floral morphological diversity (disparity) among angiosperm subgroups and through time may give important insights into the evolutionary history of angiosperms as a whole. Based on a comprehensive dataset focusing on 30 characters describing floral structure across angiosperms, we used 1201 extant and 121 fossil flowers, as well as 15 reconstructed ancestral nodes to measure floral disparity and explore patterns of floral evolution through time and across lineages. We found that angiosperms reached their highest floral disparity in the Early Cretaceous. However, decreasing disparity towards the present did not preclude the innovation of other complex traits at other morphological levels, which likely played a key role in the outstanding angiosperm species richness. Angiosperms occupy specific regions of the theoretical morphospace, indicating that only a portion of the possible floral trait combinations is observed in nature. The ANA grade, the magnoliids, and the early-eudicot grade occupy large areas of the morphospace (higher disparity), whereas nested groups occupy narrower regions (lower disparity).

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Persoonia angustiflora? I hardly knew her! Reinstatement of a Western Australian taxon.

Lindsay R. J. Shelton (Western Botanical Consultancy and The Western Australian Herbarium); Nicole Dakin (Western Botanical Consultancy) and Geoff Cockerton (Western Botanical Consultancy).

Preliminary data supports the reinstatement of an Eastern variety of *Persoonia angustiflora* endemic to the Parkers Range area in the Western Australian Goldfields. *P. angustiflora* var. *burracoppinensis* is morphologically readily separable from the Western form of *P. angustiflora* and should be reinstated either at the subspecies or species level.

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Can the relationships of speargrasses/taramea (*Aciphylla*; Apiaceae) be resolved with ddRADseq?

Lara Shepherd (Museum of New Zealand Te Papa Tongarewa); Leon Perrie (Museum of New Zealand Te Papa Tongarewa).

Aciphylla is a genus of plants in the carrot family with a huge diversity of forms, ranging from tiny, soft-leaved herbs, to large spiky mounds a few metres across with huge, pointed clusters of flowers. *Aciphylla* comprises ~42 species, two of which are endemic to Australia with the remainder confined to New Zealand. A further ~10 tag-name entities have also been identified in New Zealand, some of which are of conservation concern. *Aciphylla* was last revised completely in the 1950s, with a later revision of some species published in the 1970s and further unpublished morphological work undertaken in the early 2000s. ITS sequences published in 2001 showed low variation and poor resolution, indicating a recent radiation. Here we trial ddRADseq to examine its usefulness for examining the relationships and species boundaries within *Aciphylla*. The ddRADseq data supports some of the relationships between species suggested based on morphology but also indicates some unexpected relationships. The parental species of several putative hybrids included in the analysis were able to be confirmed. The relationships of *Aciphylla* to the other New Zealand Apioideae (*Anisotome*, *Gingidia*, *Lignocarpa* and *Scandia*) remains to be resolved, as published genetic data (Sanger sequencing) indicates some generic boundaries may need revision.

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Discoveries in the *Cassia tomentella* and *Samadera bidwillii* species complexes provide information for conservation.

Laura Simmons (Royal Botanic Gardens Victoria); Jason Halford (Queensland Herbarium); Gordon Guymer (Queensland Herbarium); Todd McLay (National Biodiversity DNA Library, CSIRO).

The Queensland Herbarium in collaboration with the Royal Botanic Gardens Victoria embarked on three Genomics for Australian Plants (GAP) Conservation Genomics projects in 2020 focusing on *Gompholobium*, *Cassia* and *Samadera*. Each project investigated the morphological and genetic distinctiveness of narrow range phrase name taxa or morphological entities compared to widespread described congeners. The combination of morphological and ddRADseq data has successfully been used to provide clarity on taxonomic boundaries and resolve cryptic taxa. This talk will focus on the analyses and results from the *Cassia tomentella* and *Samadera bidwillii* species complexes and will discuss the challenges involved in working on these groups, the exciting discoveries and how the results have informed conservation decisions.

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Phylogenomics of a megadiverse Australian plant radiation (subtribe Hakeinae, family Proteaceae) reveals entangled gene trees and widespread discordance.

Alexander Skeels (ANU); Jessica Fenker (Museums Victoria); Zoe Reynolds (ANU); Peter Weston (Royal Botanical Gardens Domain); Peter Olde (Royal Botanical Gardens Domain); Alan Lemmon (Florida State University); Austin Mast (Florida State University); Hervé Sauquet (Royal Botanical Gardens Domain); Marcel Cardillo (ANU).

Resolving phylogenetic relationships in the presence of conflicting signal across genes is one of the major challenges of the phylogenomic era. Conflicting signal can emerge from biological processes, such as incomplete lineage sorting, or have technical origins, such as from misaligned sequences. As such, decisions made in the process of estimating species trees may result in alternative tree topologies and large variation in branch support values with important systematic consequences. Here we compare alternative alignment cleaning and filtering strategies, and phylogenetic estimation methods (coalescent versus concatenated) in 553 taxa in the plant family Proteaceae, to explore how these methodological choices affect the estimation of relationships in the subtribe Hakeinae. We found that, using concatenated approaches, branch support values were high and the two largest Hakeinae genera, *Hakea* and *Grevillea*, were reciprocally monophyletic. However, using coalescent approaches, we regularly found that *Hakea* was nested within *Grevillea,* branch support values were low, and gene discordance was rampant, regardless of alignment processing decisions. Our results suggest that widespread gene discordance may be the result of rapid radiation and incomplete lineage sorting which demonstrates the importance of assessing the drivers of discordance to understand phylogenetic relationships.

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Miracine parasitoid wasps (Braconidae, Miracinae): First Australian record and new species described as part of the *Insect Investigators* citizen science project.

Mollie-Rosae Slater-Baker (The University of Adelaide); Andrew D Austin (The University of Adelaide and South Australian Museum); James B Whitfield (Department of Entomology, University of Illinois); Erinn P Fagan-Jeffries (The University of Adelaide and South Australian Museum).

Miracinae is a poorly known and rarely collected subfamily of parasitoid wasps belonging to the megadiverse family Braconidae. As parasitoids of leaf-mining caterpillars, they play important roles in regulating natural populations of their hosts, and have applications in the biological control of agricultural pests. Here, we present the first record of Miracinae in Australia, and the subsequent documentation of seven new Australian species. DNA barcodes (*COI*) for Australian specimens were compared to all available miracine barcodes on the Barcode of Life Database using phylogenetics and molecular species delimitation. The results suggest that Australia may be home to a diverse fauna of endemic miracine wasps, and provided a guiding framework for morphological description of four new species. More recently, three additional new miracines are being described in collaboration with Australian regional schools as part of the Insect Investigators citizen science project. While much of the diversity of this subfamily likely remains unexplored, this work lays a foundation which will aid in more rapid documentation of Australian Miracinae, and increases awareness of the presence of these wasps in Australia.

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Dealing with allopolyploidy in the genomic age: a pragmatic approach using amplicon sequencing of COS markers in Australasian *Lepidium.*

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New Zealand is home to 16 endemic species of *Lepidium* (Brassicaceae) including two species considered to have become extinct since European colonisation, and one species shared with Australia (with c. 26 endemic species). Previous meiotic chromosome counts suggest at least some are high polyploids. A hybrid origin has been proposed for some of them, with African and American species implicated as parents. We generated amplicon sequence data for 15 Conserved Orthologous Sequence derived markers from a selection of New Zealand endemic species and species of African and American and Australian origin naturalised in New Zealand. These were analysed along with publicly available genomic data from other *Lepidium* species. Our results are consistent with earlier work in supporting two main groups of endemic New Zealand *Lepidium* corresponding with different dominant nrDNA sequences. Our data suggest these two groups differ in ploidy (octoploid or decaploid). The octoploid species combine four distinguishable subgenomes and the decaploid species are the products of allopolyploidisation between octoploid species and a diploid species closely related to, if not, *L. africanum*. Previously proposed links to American *Lepidium* are also supported with at least two New Zealand *Lepidium* subgenomes related to subgenomes present in American polyploid species.

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Illuminating the mesophotic: taxonomy on the hidden half of coral reefs

Yi-Kai Tea (Australian Museum Research Institute and University of Sydney).

Mesophotic coral ecosystems are rich and unique realms within tropical and subtropical reefs, characterized by deep coral communities typically found at depths of 30 to 150 m. At this depth, light is very attenuated, though present in sufficient quantity to support some primary production via photosynthesis. As a result of this difference in depth and photic properties, the faunal composition of mesophotic reefs are unique and brimming with species new to science, many of which display high levels of localised endemism and depth specificity. While these communities provide an exciting new frontier for coral reef taxonomists, research on mesophotic ecosystems is not homogenous at the global level. Australia in particular has received comparatively little attention in the mesophotic scene, yet the few studies conducted all show support for Australian reefs rich in new species and new distribution records. Here I summarise the research conducted on mesophotic fish communities across the Indo-Pacific, with special attention to Australasian coral reef fish fauna.

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Systematics and Taxonomy of Australian Mesostoinae on Kangaroo Island using next generation sequencing (Braconidae: Mesostoinae).

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The subfamily Mesostoinae (Hymenoptera: Braconidae) has historically been poorly understood, with challenging morphology and many poorly resolved phylogenies. There are six endemic Australian genera currently known, however most only contain a few described species. In order to broaden the understanding of the biodiversity of Mesostoinae in Australia, new species and genera need to be formally described, supported by robust phylogenies of the subfamily. The first Kangaroo Island (KI) endemic species of Mesostoinae was recently described, *Ovaustra aurantia*, and displays a unique biology and host relationship to the critically endangered enigma moth, *Aenigmatinea glatzella*. This discovery was the catalyst to a broader study of Kangaroo Island's mesostoines. We revisited existing KI collections and conducted field work to find additional specimens through coarse morphological identifications. Specimens were shotgun sequenced and mitochondrial genes were extracted to be added to an existing mitogenomic dataset of the subfamily. The resulting phylogeny identified nine potentially new species of Mesostoinae from KI, which are currently undergoing diagnostic descriptions. This small study, restricted to just a single region of South Australia, implies that there are potentially many more undescribed species of Mesostoinae throughout Australia.

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World spatial phylogenetics of the angiosperms.

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Spatial phylogenetic analyses combine phylogenies and spatial data at any taxonomic and geographic level. All studies to date have concentrated on either a particular taxonomic group, for example Australian *Acacia*, or the flora of a particular geographic region, for example the analyses on the flora of Australia, California and Chile. The PAFTOL angiosperm phylogeny created the opportunity to make a spatial phylogenetic world analysis at the genus level. We cleaned institutional plant records stored in the Global Biodiversity Information Facility (GBIF) so that they reflected the worldwide native range of each species (over 200000 species). The final spatial dataset contained over 23 million records and projected using World Mollweide at 50 ×50 km grid cells. The PAFTOL tree and spatial data were combined using Biodiverse to make diversity analyses and randomisations for the CANAPE, Relative Phylogenetic Diversity and Phylogenetic Diversity Randomisation tests. The results of two spatial phylogenetic analyses will be presented, one using a raw branched PAFTOL phylogram and one using a PAFTOL chronogram. We will also present comparisons of results against climatic variables and the biodiversity hotspots of the world.

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Towards a Taxonomic Revision of *Trachymela* (Coleoptera: Chrysomelinae).

Lyn G. Cook (the University of Queensland); Peisong Tian (the University of Queensland).

Eucalyptus, the most dominant native tree group in Australia, is host to many genera of insects. In contrast with the eucalypts themselves, most of the diversity of insects feeding on them has not yet been described or, when it has, there is no way of actually identifying specimens to species. Leaf beetles of the genus *Trachymela* are an example of this. There are 127 named species and about135 synonyms, but the genus has not been revised for more than 100 years, and only four species have been described in the past century. Here, we report the first attempt to provide a taxonomic framework for *Trachymela* using *COI* DNA barcodes for 80 specimens. We then assess species diversity among specimens that match the description of *T. alticola* using DNA sequences from the mitochondrion (*COI*) and nuclear loci (*28S*, *EF1a* and ITS2), and morphometrics.

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A big burst of blindsnakes: Phylogenomics and historical biogeography of Australia's most species-rich snake genus.

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Blindsnakes are cylindrical-bodied snakes with reduced vision and have scales that completely cover their eyes. Out of over 450 described species of blindsnakes globally, the Australo-Papuan blindsnake radiation is among the most species rich comprising ~50 described in the genus *Anilios*. We extend the phylogenetic understanding of *Anilios* using a phylogenomic approach with over 4500 Squamate Conserved Loci markers. Using phylogenomic data from 130 specimens, including previously unsampled species and divergent lineages, we reconstructed a near-complete phylogeny of the Australo-Papuan blindsnake genus *Anilios* and closely related kin. We then used this phylogeny along with information about their distribution and estimates of paleo temperature and aridity during the Neogene to explore how changes in the environment influenced diversification of Australian blindsnakes.

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Phylogenomics of South West Pacific nocturnal foraging bees.

Simon M. Tierney (Western Sydney University).

The hyperactivity of foraging bees is typically associated with spring blossoms on bright sunny days, however, a diverse range of distantly related bee lineages are unusual in their habit of exclusively foraging in dim-light conditions between dusk and dawn. The successful colonisation of a novel photo-temporal niche, and subsequent speciation within it, is the hallmark of adaptive evolution. Halictidae (Apoidea: Anthophila) contains the most prevalent radiations of obligate dim-light foraging among all bees. Two independently evolved lineages have arisen in parallel within different subfamilies in different geographic hemispheres that display a suite of convergent morphologies. The biology of the eastern hemispheric lineage is effectively unknown - evolutionary origins and systematic relationships to their closest day-flying relatives are unresolved and very little is known of their basic natural history and pollination ecology. This project will provide the first integrative assessment of nocturnal bee diversity in the South West Pacific region by assimilating diverse data sets (phylogenomic systematics, morphology, behaviour, plant visitation) to provide a comparative assessment of the factors driving adaptive evolution in novel dim-light sensory environments.

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The complex history of the *Macrozamia plurinervia* complex helps explain the challenges of delimiting species in this group.

Alicia Toon (The University of Queensland); Paul Forster (Queensland Herbarium); Lyn Cook (The University of Queensland).

The *Macrozamia plurinervia* complex is a group of cycads comprising seven described species that are distributed inland in southern Queensland and northern NSW. They occur in small populations, with many isolated by disturbed or cleared habitat. Four members of the complex are listed as either vulnerable or endangered under the EPBC Act. Previous work on morphology and microsatellite variation in the *M.plurinervia* complex has been unable to resolve species boundaries and phylogeography within this group. The recent construction of wind turbines on the Southern Downs (Queensland) has resulted in the translocation of a population of one species, *M. conferta*, highlighting the need to clarify gene flow between and within putative taxa. Here, we use analyses of Single Nucleotide Polymorphisms (SNPs) to test ideas about the history and population structure of the *M. plurinervia* complex. Our increased breadth of genetic data suggests a complex history among populations and reveals discrepancies between gene flow and the current taxonomic classification, underscoring the difficulty of defining species within this group.

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Enlightening the Australian “dark” Fungi: Linking DNA barcodes to fungal names.

Camille Truong (Royal Botanic Gardens Victoria); Luke Vaughan (Royal Botanic Gardens Victoria); Gareth Holmes (Royal Botanic Gardens Victoria); Miranda Boyle (Royal Botanic Gardens Victoria); Tom W. May (Royal Botanic Gardens Victoria).

eDNA metabarcoding of Fungi has revolutionized our views of biodiversity and enables monitoring of ecosystem functions and soil health across all groups of Fungi. Currently, the lack of knowledge about Australian Fungi hinders accurate species identifications that rely on reference DNA barcode sequences. Therefore, most eDNA studies end up with more than half of the molecular operational taxonomic units (mOTUs) not assigned at species level or even to a functional guild. While many fungal species await formal description, a good proportion of these unidentified mOTUs are simply lacking corresponding reference sequences. To assess this information gap, we review the state of knowledge about Australian fungal barcodes by combining the checklist of fungal names from the National Species List, with GBIF data on observations and specimens, along with data on ITS barcodes from the UNITE reference database. We further explore the potential and effectiveness of ITS barcoding of fungarium specimens for 1) filling this gap and 2) the rapid identification of specimens by non-specialists. We conclude that fungarium collections contain an untapped wealth of taxonomic, ecological and biodiversity information that is currently undervalued.

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Defining the diversity of Australia’s micro marsupials (Dasyuridae: *Planigale*).

Linette S. Umbrello (Queensland University of Technology and Western Australian Museum); Andrew M. Baker (Queensland University of Technology and Queensland Museum); Kenny J. Travouillon (Western Australian Museum); Michael Westerman (La Trobe University).

Defining diversity is critical for conservation planning and the taxonomy of most Australian mammals is thought to be well resolved. Enter planigales—Australia’s smallest mammals. Previously, only four species were recognised in Australia with multiple molecular studies suggesting additional undescribed forms. We recently resolved part of this by describing two morphologically and genetically unique species from the Pilbara, Western Australia, as part of a generic revision of *Planigale*. We take an integrative taxonomic approach by combining molecular and morphological data from all planigale species throughout Australia. Thus far, with our expanded genetic sampling we have corroborated the findings of previous studies, which have identified multiple lineages within *Planigale*, but can now better define the geographic boundaries of the genetic clades. We will match morphotypes to various genetic clades and propose new species hypotheses for the genus. This work will result in drastically increasing the known species of Australia’s smallest mammals with implications for how these species are managed during a time when mammal species continue to decline.

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Undescribed fungal diversity: documenting Australia’s little brown mushrooms.

Luke J. Vaughan (Royal Botanic Gardens Victoria and University of Melbourne); Samuel Craig (Royal Botanic Gardens Victoria and Monash University); Gareth D. Holmes (Royal Botanic Gardens Victoria); Camille Truong (Royal Botanic Gardens Victoria); Jo Birch (University of Melbourne); Tom W. May (Royal Botanic Gardens Victoria).

Documenting species is critical for understanding biological diversity and facilitating research on the biology and ecology of organisms. Recent estimates of fungal diversity are in the millions, but so far only around 150,000 species are described and named. Many commonly encountered, colourful or charismatic species of macrofungi in Australia are well documented, but many more of the more hidden, less commonly encountered, dull or small species remain undocumented, and some of these are lumped together as LBMs or ‘little brown mushrooms’. While they are undescribed, questions about the biology, ecology, interactions and ecosystem services provided by species remain unanswered. This talk will report on the progress of documenting and describing novel species of fungi from herbarium collections with macro- and micromorphological studies and phylogenetic analyses of DNA sequences. The role of citizen science and observation data will be discussed as an important tool for identifying hotspots of diversity for taxa of interest, including *Auriscalpium*, *Hodophilus*, *Pseudobaeospora* and Pezizaceae.

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The value of targeted biological surveys: an assessment of Australia's Bush Blitz program.

Chris Ware (CSIRO); Kristen J. Williams (CSIRO), Simon Ferrier (CSIRO), Daniel P. Faith (The Australian Museum); Glenn Manion (Cryzan); Brian Hawkins (NSW Department of Planning and Environment); Tom Harwood (CSIRO and Oxford University); Art Langston (CSIRO); Jacqui Meyers (CSIRO); Justin Perry (CSIRO); Jo Harding (Australian Government Department of Agriculture, Water and the Environment); Sue Fyfe (Australian Government Department of Agriculture, Water and the Environment).

Biodiversity assessment and decisions rely on knowledge of the spatial distribution of species, yet most global biodiversity is inadequately represented by occurrence records. In this work, we evaluated nearly eight years of biodiversity record collection by Bush Blitz (www.bushblitz.org.au), Australia's largest species discovery program, to test how efficiently the program improved our knowledge of the distribution of biodiversity. Our assessment is based on Bush Blitz data for six taxa, benchmarked against data accumulated over the same period in the Atlas of Living Australia (ALA, http://www.ala.org.au/) – Australia's largest aggregation of biodiversity records – as a comparison of effectiveness to the Bush Blitz program. We found that environments surveyed through the Bush Blitz program are highly complementary to environments from which 'background' observations were made over the same period and aggregated in the ALA. This sampling of complementary environmental diversity translated into large numbers of records of new, or previously unrecorded, species. Bush Blitz additions were made highly efficiently with respect to survey effort, relative to background survey effort represented in the ALA. Our results demonstrate the ability of the Bush Blitz program to contribute valuable data to conservation assessment and planning, and the value of assessing environmental diversity in planning new surveys.

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Twisted flowers and tales to match: phylogenetic inference of Australian *Caesia* (Asphodelaceae, Hemerocallidoideae).

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Caesia R.Br. (Asphodelaceae, Hemerocallidoideae) is a predominantly Australian, tepaloid monocot genus with high species diversity in the east and south-west. It contains 14 species and at least eight additional entities recognised by phrase names. Identification and morphological analysis of *Caesia* from herbarium material is challenging, due to a paucity of distinguishing features retained on specimens (e.g. flower colour, roots). The phylogeny of Australian *Caesia* was inferred, based on five chloroplast regions generated using targeted amplicon sequencing. *Caesia* is polyphyletic, as Western Australian ‘rigid-leaved’ species are more closely related to *Corynotheca* F.Muell. ex Benth. *Caesia* species relationships are elucidated. *Caesia parviflora* is polyphyletic, with *C. parviflora* var. *vittata* more closely related to *C. calliantha* and *C. chlorantha*. *Caesia walalbai*, a south-east Queensland endemic, is newly described, segregated from the *C. parviflora* complex. *Caesia calliantha* is also polyphyletic. Northern species, *Caesia chlorantha* and *C. setifera,* represent species complexes; each is monophyletic and includes lineages with distinct morphological features or geographic distributions. *Caesia* sp. Mt Zeil (NT), *C.* sp. Foster Cliff (NT) and *C.* sp. Wheatbelt (WA) are each monophyletic and their relationships are inferred. Further work and additional collections are required to clarify species complexes in Australian *Caesia*.

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Evolution of Australian sundews (*Drosera* spp.).

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Since the first sundews (*Drosera* L. spp.) were described in 1753, the taxonomy of *Drosera* has been in a state of flux, with additional species described regularly. *Drosera* is most diverse in Australia; however, the evolutionary relationships between taxa within the major groups remain poorly understood. Previous phylogenetic studies show conflict between phylogenetic tree topologies and the traditional higher classifications for some taxonomic groups; however, these studies included comparatively few Australian taxa and were limited mainly to *rbc*L and *ITS* sequence data. In order to assess the monophyly of each group, we partnered with the Genomics for Australian Plants Initiative (GAP) to sequence representatives from all Australian *Drosera* subgenera and sections. Using the Angiosperms353 and OzBaits bait sets, we recovered genomic data from hundreds of nuclear regions for 96 *Drosera* samples from field collections and herbarium accessions across Australia, including the type species for each subgenus and section where possible. Here, we present our preliminary analyses of this large genomic library. These results provide a backbone phylogeny for the genus in Australia and show that the current infrageneric classification requires updating, especially for the tuberous sundews (section *Ergaleium* Planch.).

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The wishbone spiders of Eastern Australia (Mygalomorphae: Anamidae: *Aname*): A workflow for the description of 40+ new species in one year.

Jeremy D. Wilson (University of Western Australia and Western Australian Museum); Leigh W. Simmons (University of Western Australia); Mark S. Harvey (Western Australian Museum and University of Western Australia); Michael G. Rix (Queensland Museum).

The wishbone spiders of the genus *Aname* (Anamidae) have radiated across the Australian tropical and arid zones, and, along with another Australian arid-zone specialist group *Idiosoma* (Idiopidae), represent some of the most diverse genera of mygalomorph spiders (trapdoor spiders and relatives) in the world. Estimates based on collections and molecular datasets suggest 250+ species of *Aname* across the continent, of which 48 were described at the commencement of our revisionary project in late 2022. Revising such diverse genera inevitably comes with challenges including a legacy taxonomy, pronounced sexual dimorphism, and the workload of producing images and descriptions. In year one of the project we focused on tropical/sub-tropical eastern Australia, documenting and describing 40+ new *Aname* species from this region. During this time, we developed a workflow for expediting large revisionary works on mygalomorph spiders without compromising quality, and this will be refined over the coming years as it is applied to the centre of *Aname* diversity, in Western Australia. In this talk I will highlight the strategies we have employed to increase our rate of species description during the revision of the eastern *Aname* in year one of our project, and the plan going forward to revise the remaining fauna.

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The National Biodiversity DNA Library: an authoritative DNA reference library for Australia's species.

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Molecular identifications are becoming more widely utilised, and in some cases are the only useful method available (e.g. for specimens that are damaged, modified or represent life stages without diagnostic morphology). This is also intensified by the steep uptake of eDNA applications. While these techniques are potentially powerful, the interpretation of these data is limited by the reference databases that DNA sequences are compared to. CSIRO is developing partnerships with the collections community to create comprehensive and reliable genetic data to enable high-integrity DNA species identifications for all named Australian plants, animals and macroalgae. Working with partners, the National Biodiversity DNA Library (NBDL) will generate data from expertly-identified specimens held in natural history collections to underpin robust molecular identifications. By using specimens archived in collections, identifications can be re-checked and updated into the future. CSIRO has developed a cost effective, highly miniaturised, genome-skimming technology ideally suited to collection specimens. Starting with marine taxa, the NBDL is working in targeted campaigns to generate authoritative sequence data and make these publicly available through a dedicated portal. To achieve this ambitious goal, we are working with collections, philanthropic and research organisations, and the Australian Government, with guidance from taxon-experts and the end-user community.

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Celebrating the past | Planning the future

A first perspective on evolution and diversification of Australasian *Teucrium* (Lamiaceae) and improved insight to selecting contemporary genomic techniques.

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Teucrium L. (Lamiaceae) is a cosmopolitan genus with a Mediterranean centre of diversity. We tested recently-made generic synonymies and species concepts using phylogenomic analysis of nuclear genes sequenced via targeted enrichment (Angiosperms-353 baits) for replicates of all (27) Australasian species and phrase names. We show that the diversity of *Teucrium* across Australasia constitutes two distantly related clades. The most speciose clade is a component of the 'core Teucrium clade' and has diversified across Australia and into New Zealand whereas the second consists of three eastern Australian species belonging to the 'Polium clade'. The former clade consists of basally-derived branches of western Australian species, hinting at a southwestern origin. It also exhibits two independent radiations into the Australian arid inland, one coinciding with a distinctive shift in pollination strategy and seed dispersal. Overall, analysis of target-bait capture data produced a tree with high support for most species clades and was able to unequivocally place most 'unknowns'. We identify advantages and limitations of using the technique for better-equiping future systematic studies through examining its ability to resolve *Teucrium* species complexes (e.g. *T. corymbosum*) and through comparative assessment with SNP-based genomic scans.

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Systematic revision of *Pedicularis* L. (Orobanchaceae) for the Flora of Bhutan.

Rinchen Yangzom (University of New England)

Pedicularis, a charismatic genus of hemiparasitic plants in Orobanchaceae, predominantly thrives in the alpine and artic regions of the Northern Hemisphere. Bhutan is home to 69 taxa of *Pedicularis*, of about 800 species worldwide. Despite several taxonomic efforts a considerable number of *Pedicularis* taxa remain taxonomically unresolved and a significant portion of species from Bhutan are known from a limited location. Further, there is no taxonomic consensus, spatial records are sparse, and a global phylogeny is lacking. I will address these knowledge gaps in my PhD. Using existing collections, I will conduct a revision of the endemic taxa within Bhutan. I will then integrate these taxa into a comprehensive phylogeny of *Pedicularis* being developed by collaborators. I will also investigate a particularly difficult group, the *P. gracilis* complex. I will test the hypothesis that the effects of altitude on germination timing plays a crucial role in determining the distinct habits of *P. gracilis* vs. *P. pennelliana.* through morphological, ecological, biogeographic and molecular approaches. Finally, this study will assess the conservation status using IUCN red list categories and criteria to inform and prioritize conservation initiatives essential for protecting these enigmatic and ecologically significant species.

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Global variation in the relationship between avian phylogenetic diversity and functional distance.

Keaghan J Yaxley (ANU); Alexander Skeels (ANU); Robert A Foley (University of Cambridge).

If evolutionary distance is akin to evolutionary chance, then it follows that species assemblages that are distantly related will also be more disparate in terms of their traits, features and the niches they occupy. Yet, studies have found that the total phylogenetic distance of an assemblages, known as phylogenetic diversity, is an unreliable surrogate for functional diversity. We investigate global variation in the relationship between Faith's Phylogenetic Diversity (PD) and Mean Pairwise Functional Distance (MPFD) across latitude and the influence of migratory species on both these aspects of diversity. We measure PD and MPFD for over 9,000 species of bird across more than 17,000 globally distributed assemblages. We obtain standardised effect sizes for both indices by simulating assemblage composition under an ecologically informed null model. We employ path analysis to characterise variation in the relationship between PD's and MPFD across latitude, elevation and with proportion of migratory species. Globally, assemblages that were phylogenetically diverse tended to be less functionally dispersed than expected; however this relationship showed considerable variation across latitude decreasing with distance from the equator. The proportion of migratory species in an assemblage was found to be an important predictor of functional diversity, with migrant rich assemblages generally showing less functional diversity than expected. We identify the Andes and Hengduan Mountains as regions of exceptional bird functional diversity. The relationship between phylogenetic diversity and function diversity is context specific, varying across environmental gradients such as latitude, and influenced by ecological phenomena such a migration. Thus, care should be taken using phylogenetic diversity as a proxy for functional diversity, particularly in clades with sparse functional data. Instead we recommend that studies consider how phylogenetic diversity's surrogacy for functional diversity may be impacted by environmental context and evaluate empirical observations against biogeographically constrained and ecological informed null models.

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The first study to discover population-level genomic structural variants (SVs) in wild populations of *Eucalyptus viminalis*.

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Rapid advancements in long-read sequencing technologies have enabled us to discover large structural variations in eukaryotic genomes. Algorithms for discovering structural variants (SVs) via read mapping have proliferated in recent years with the increase in computing power and accessible long-read sequencing. Here we present the first discovery and characterisation of structural variants in wild populations of Eucalyptus viminalis, an ecologically important species. Eucalyptus species are highly heterogeneous, which result in noisy alignments, making reliable discovery of SVs challenging. Using a combination of recently developed bioinformatics tools, we have discovered ~ 300,000 structural variants (multi-nucleotide polymorphisms) among 45 E. viminalis individuals. After transcriptome discovery using direct RNA sequencing, we have observed that most instances of the terpene synthase (TPS) gene family (important for oil production and tree defence) are avoided by SVs, but some TEs were observed to be inserted into the introngenic regions of certain TPS genes. Together, this study establishes our foundational understanding of SVs in wild populations of E. viminalis and provides insights into pangenomic studies of Eucalyptus in the future.

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Using numerous contact zones to delimit species and calibrate a reference-based taxonomy in a challenging lizard group (*Heteronotia*).

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What happens where divergent populations come into secondary contact? Is there evidence of reproductive isolation and restricted gene flow, or do they gradually intergrade into each other? Assessing where populations sit along this continuum is useful for species delimitation in sexually reproducing organisms, as nearly all species concepts agree that populations that remain distinct in sympatry represent species. Furthermore, by sampling many contact zones one can understand how divergence across genomes and phenotypic traits correlate with contemporary gene flow. This information can then be used to calibrate thresholds of divergence that inform a reference-based taxonomy when working with allopatric or poorly sampled populations. Here we aim to resolve species boundaries in *Heteronotia* geckos using RAD sequencing and dense geographic sampling to assess contemporary gene flow across ~20 contact zones. We then assess how gene flow between populations correlates with genomic divergence, thus calibrating divergence thresholds to inform taxonomic decisions for populations that lack contact zone sampling. This species delimitation approach combines direct assessment of evolutionary independence among candidate species while also calibrating a reference-based taxonomy to apply more broadly. Among other lessons, we highlight how accurate species delimitation of taxonomically difficult animal groups might often require data from contact zones.

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