

Systematics 2017—Integrating Systematics for Conservation and Ecology

Proceedings of the Australasian Systematic Botany Society & Society of
Australian Systematic Biologists Conference and the Invertebrate
Biodiversity and Conservation Biennial Meeting

27–29 November, 2017—Adelaide, Australia

Swainsona Supplement 5

systematics.ourplants.org

Swainsona Supplement 5 (2017)
Editor: Ainsley Calladine & Jürgen Kellermann
ISBN 978-1-922027-52-8

Swainsona (formerly Journal of the Adelaide Botanic Gardens)
The journal is published by the State Herbarium of South Australia on behalf of the Board of the Botanic Gardens and State Herbarium (Adelaide, South Australia).

Editor: Jürgen Kellermann
flora.sa.gov.au/swainsona

State Herbarium of South Australia
GPO Box 1047
Adelaide SA 5001
environment.sa.gov.au/stateherbarium

Australasian Systematic Botany Society
Secretary: Jennifer Tate, secretary.asbs@gmail.com
asbs.org.au

Society of Australian Systematic Biologists
Secretary: Michael Rix, michael.rix@qm.qld.gov.au
sasb.org.au

Cover image: Clare Valley, South Australia, by Michelle Waycott (CC BY 4.0)

Foreword

On behalf of the Organising Committee, we are delighted to welcome you all to *Systematics 2017—Integrating Systematics for Conservation and Ecology*. This is a joint meeting of the Society of Australian Systematic Biologists, the Australasian Systematic Botany Society, and incorporating the Invertebrate Biodiversity and Conservation Biennial Meeting.

The theme for the conference seeks to provide a link between research in taxonomy and phylogenetics of the Australian and New Zealand biota with ecological studies and conservation issues. Several of the special symposia (listed below with the organisers) will inform this theme during the three days of our proceedings. The overall program is a reflection of the diversity and depth of systematics in Australia and New Zealand today.

- eTools for taxonomy (Anthony Whalen)
- Systematics in the sea (Rachael King)
- The role of systematics and ecology in monitoring of groundwater ecosystem biodiversity (Michelle Guzik)
- Asian–Australian biotic exchange (Darren Crayn, Paul Oliver and Sarah Mathews)
- Advances in Australasian arachnology (Michael Rix and Mark Harvey)
- Palaeobotany and long term ecological change (Kathryn Hill and John Conran)

We have the wonderful Professor Gonzalo Giribet from Harvard University as our plenary speaker. Gonzalo has an international reputation for leading large phylogenetic studies on major groups of invertebrates using next generation technologies.

Our five keynote speakers will be covering a diverse array of topics and they will highlight several of the major challenges our discipline faces at this time. We also have an excellent poster session where conference goers can mingle and talk to poster presenters.

The conference is hosting a number of important events, these include the national launch of a reinvigorated Flora of Australia in electronic form; a presentation and discussion of the Australasian Biosystematics and Taxonomy Decadal Plan; also presentations by the winners of the inaugural SASB Distinguished Research Award and the ASBS Nancy T. Burbidge Medal where we celebrate excellence on commitment in our field.

The campus of the University of Adelaide is a wonderful venue for hosting this conference given the facilities for meeting and presenting, its central location adjacent to city, accommodation and restaurants, and also being close to the Museum and Herbarium.

Our two major social events, the welcome mixer on Sunday and the conference dinner on the Tuesday will be held at the National Wine Centre of Australia, a fitting venue for a scientific conference! We wish you an enjoyable and productive time during the conference, and look forward to meeting as many of you as possible.

Andy Austin and *Michelle Waycott* co-convenors (on behalf of the Organising Committee)

November, 2017

Acknowledgements

Systematics 2017 was substantively supported by

State Herbarium of South Australia—Department of Environment, Water and Natural Resources (Government of South Australian) and the Board of the Botanic Gardens and State Herbarium

The University of Adelaide

Society of Australian Systematic Biologists

Australasian Systematic Botany Society

South Australian Museum

The Environment Institute, University of Adelaide

ourplants.org

Sponsorship through funding was provided by

Ian Potter Foundation



CSIRO Publishing



ABRS (eTools Symposium)



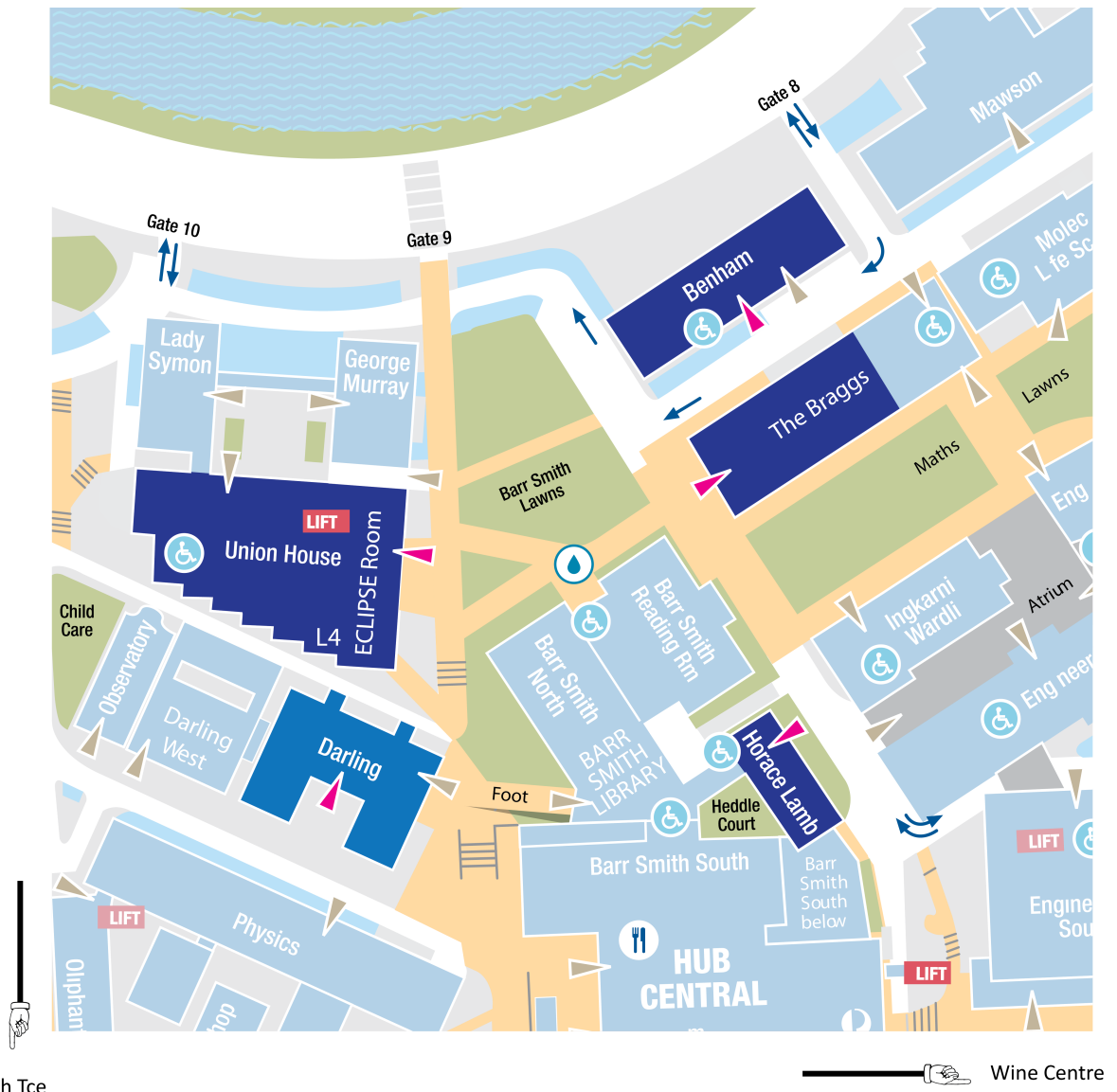
Environment Institute, The University of Adelaide



Australian Centre for Evolutionary Biology and Biodiversity,
The University of Adelaide



Venues

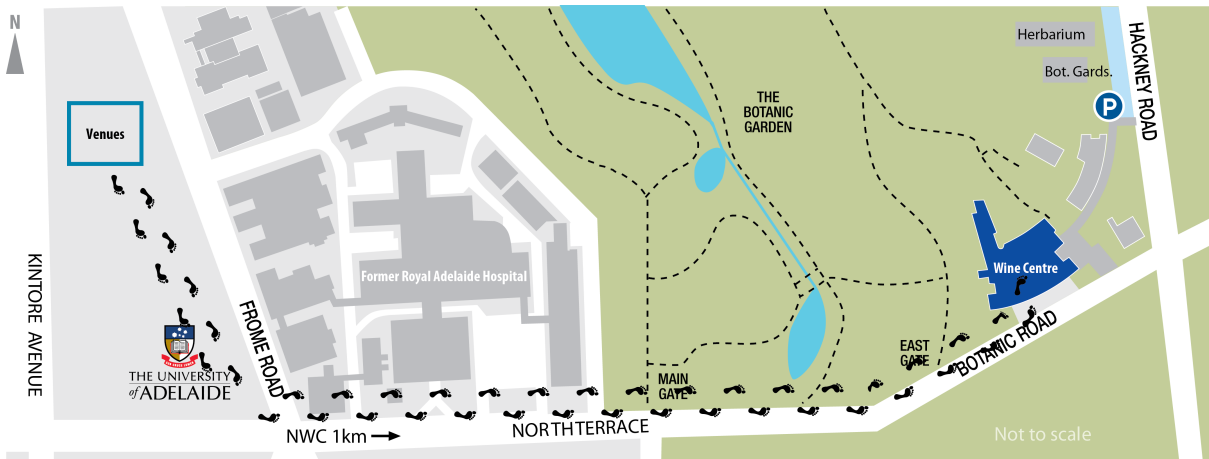


The main conference venues are centred around the northern, lower part of the North Terrace campus of the University of Adelaide.

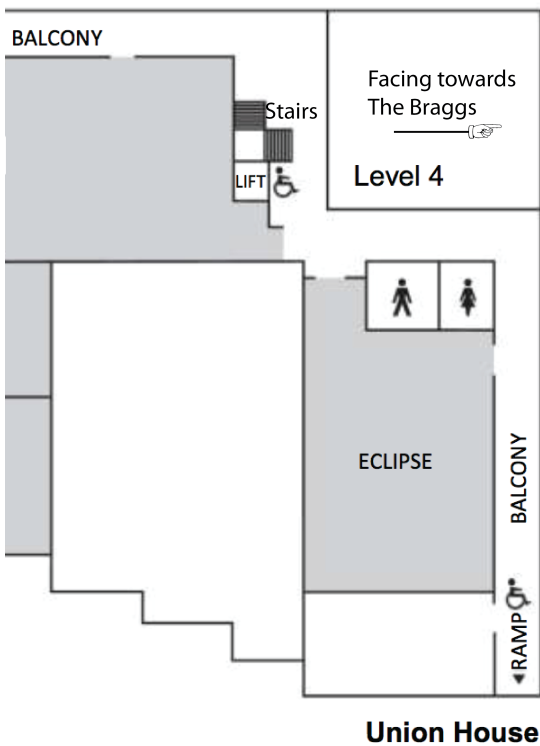
Day 1—our presentations are in The Braggs and Horace Lamb lecture theatres, catering will be in the foyer area of The Braggs.

Days 2 & 3—we are in the Horace Lamb and Benham lecture theatres, catering and the afternoon poster session will be in the Eclipse Room, Union House, which is on Level 4—only a short set of stairs or lift trip to the room.

Posters are to be put up on Tuesday morning, although our registration desk will hold them for you on Monday if you wish.



To get to the National Wine Centre, walk up to North Terrace, and follow the footpath to the Wine Centre, past the building works of the Old Royal Adelaide Hospital, and the main gate of the Botanic Gardens, then enter the Wine Centre off Botanic Road (the continuation of North Terrace). Our function will be sign-posted. Pay parking is available off Hackney Rd, the very first entry after the lights. If you miss the turn, there is more parking further down off Plane Tree Drive.



The catering on Tuesday and Wednesday will be in the Eclipse Room, level 4 of Union House. This is a short walk across from Benham and Horace Lamb and up a flight of stairs or in the lift that can be found at street level.

The poster session will be in the Eclipse Room, and several workstations to look at the eFlora platform.

Monday overview

Welcome	09:00–09:30
Plenary Talk—The Braggs	09:30–10:30
Morning Break	10:30–11:00
eTools for Taxonomy / FoA—Concurrent (I), The Braggs	11:00–12:30
Parasites, crustaceans and vertebrates—Concurrent (II), Horace Lamb	11:00–12:30
Lunch	12:30–13:15
Decadal Plan discussion—Plenary, The Braggs	13:15–14:10
Biosecurity—Plenary, The Braggs	14:10–14:25
move into concurrent sessions	14:30–
Systematics in the sea—Concurrent (I), The Braggs	14:30–15:15
Stygofauna and groundwater—Concurrent (II), Horace Lamb	14:30–15:15
Afternoon Break	15:15–15:45
Challenges and conservation—Concurrent (I), The Braggs	15:45–17:00
SASB AGM and business meeting—Concurrent (I), The Braggs	17:00–17:30
Systematic botany—Concurrent (II), Horace Lamb	15:45–17:30
SASB Distinguished Research Award—Plenary, The Braggs	17:30–18:00

Monday venues

Plenary and Concurrent sessions (I)—The Braggs Lecture Theatre

Concurrent sessions (II)—Horace Lamb Lecture Theatre

Monday breakout area (morning and afternoon breaks, lunch)—The Braggs foyer

Tuesday overview

Housekeeping	08:30–08:45
Keynote Talk—Plenary, Horace Lamb	08:45–09:25
move into concurrent sessions	09:30–
Asian–Australian biotic exchange—Concurrent (I), Horace Lamb	09:30–10:30
Insects—Concurrent (II), Benham	09:30–10:30
Morning Break	10:30–11:00
Asian–Australian biotic exchange (cont.)—Concurrent (I), Horace Lamb	11:00–12:30
Insects (cont.)—Concurrent (II), Benham	11:00–12:30
Lunch	12:30–13:15
Keynote Talk—Plenary, Horace Lamb	13:15–13:55
move into concurrent sessions	14:00–
Plant systematics—Concurrent (I), Horace Lamb	14:00–14:45
Advances in Australasian arachnology—Concurrent (II), Benham	14:00–14:45
Posters and Afternoon Break	14:45–15:30
ASBS AGM and business meeting—Horace Lamb	15:30–16:30
Advances in Australasian arachnology (cont.)—Concurrent (II), Benham	15:30–16:30
Nancy T. Burbidge Medal Presentation and Address—Plenary, Horace Lamb	16:30–17:30
Conference Dinner—National Wine Centre	18:30–

Tuesday venues

Plenary and Concurrent sessions (I)—Horace Lamb Lecture Theatre

Concurrent sessions (II)—Benham Lecture Theatre

Tuesday breakout area (morning and afternoon breaks, poster session and lunch)—Eclipse Room, Adelaide University Club, Level 4, Union House

Conference Dinner—National Wine Centre of Australia, Corner of Hackney and Botanic roads (accessible via North Terrace)

Wednesday overview

Housekeeping	08:30–08:45
Keynote Talk—Plenary, Horace Lamb	08:45–09:25
move into concurrent sessions	09:30–
Stygofauna and groundwater—Concurrent (I), Horace Lamb	09:30–10:30
Palaeobotany and systematic botany—Concurrent (II), Benham	09:30–10:30
Morning Break	10:30–11:00
Stygofauna and groundwater (cont.)—Concurrent (I), Horace Lamb	11:00–12:30
Palaeobotany and systematic botany (cont.)—Concurrent (II), Benham	11:00–12:30
Lunch	12:30–13:15
Keynote Talk—Plenary, Horace Lamb	13:15–13:55
move into concurrent sessions	14:00–
Systematic botany and methods—Concurrent (I), Horace Lamb	14:00–15:15
Pollination and conservation botany—Concurrent (II), Benham	14:00–15:15
Afternoon Break	15:15–15:45
Wrap up and prizes—Horace Lamb	15:45–16:15

Wednesday venues

Plenary and Concurrent sessions (I)—Horace Lamb Lecture Theatre

Concurrent sessions (II)—Benham Lecture Theatre

Wednesday breakout area (morning and afternoon breaks, and lunch)—Eclipse Room, Adelaide University Club, Level 4, Union House

Programme – Monday

09:00–9:30 Welcome

09:30–10:30 Plenary Talk: Biogeography meets genomics – new trends in data analysis of biogeographic data, by **Gonzalo Giribet** M–P–1

10:30–11:00 Morning Break

11:00	<i>eTools for Taxonomy – Concurrent (I), The Braggs</i>	p17	<i>Parasites, crustaceans and vertebrates – Concurrent (II), Horace Lamb</i>	p21
-------	---	-----	--	-----

11:00–11:15 **Barbara Waterhouse**, Bringing it all together – role of eTools in frontline biosecurity surveillance M–1–2 **Olivia Davies**, Are parasites as problematic for biologists as they are for their hosts? student M–2–2

11:15–11:30 **Mark McGrouther**, Australasian Fishes – a new citizen science resource M–1–3 **Dan Huston**, Integrated taxonomic investigation of the Ehunteridae, a curious lineage of parasitic flatworms, reveals undiscovered diversity and provides new ecological insights student M–2–3

11:30–11:45 **Zoe Knapp**, The Flora of Australia – we've taken the covers off M–1–4 **Kara Layton**, Exploring an undocumented diversification of parasitic gastropods in Antarctica student M–2–4

11:45–12:00 **Judy West (Chair)**, Flora of Australia eFlora – National Launch M–1–5 **Amelia Lewis**, Uncovering the diversity of deep-sea crustaceans (Isopoda and Amphipoda) from the Great Australian Bight student M–2–5

12:00–12:15 cont. **Carlos Pavón-Vázquez**, Of volcanoes and lizards – phylogenomics and biogeography in a group of Mexican skinks student M–2–6

12:15–12:30 cont. **Linette Umbrello**, Small marsupials, big data – population genomics reveals structure in desert-dwelling Dasyuridae student M–2–7

12:30–13:15 Lunch

13:15–14:10 **Kevin Thiele**, The Biosystematics and Taxonomy Plan discussion – Plenary, The Braggs M–P–8

14:10–14:25 **Gillian Brown**, ALERT lessons from a biosecurity disaster move into concurrent sessions M–P–9

14:30	<i>Systematics in the sea – Concurrent (I) The Braggs</i>	p29	<i>Stygofauna and groundwater – Concurrent (II) Horace Lamb</i>	p32
-------	---	-----	---	-----

14:30–14:45 **Nicole Foster**, Taxonomic challenges to an independent evidence base for assessing coastal environmental change through time student M–1–10 **Giulia Perina**, Remarkable biodiversity of subterranean Bathynellidae (Bathynellacea, Crustacea) in the north of Western Australia and the status of the *Bathynella* genus student M–2–10

14:45–15:00	Charlotte Nitschke , Biodiversity and conservation of sea snakes (Hydrophiinae) in Western Australia	M–1–11	Josephine Hyde , Phylogenetic revision of subterranean Dytiscidae from Western Australia—sister species validate sympatric or parapatric speciation underground	M–2–11
15:00–15:15	Kor-jent van Dijk , Finding solutions to ‘complex’ seagrass relationships	M–1–12	Patrick Fahey , The systematics of <i>Chloris</i> in Australia—colonisation events and a newly discovered Artesian spring endemic	M–2–12
15:15–15:45	Afternoon Break			
15:45	<i>Challenges and conservation — Concurrent (I), The Braggs</i>		<i>Systematic botany — Concurrent (II), Horace Lamb</i>	
		p35		p40
15:45–16:00	Haylee Weaver , The state of taxonomy and systematics in Australia — results of the 2016 Survey of Taxonomic Capacity	M–1–13	Tim Collins , Integrative taxonomic revision of <i>Xerochrysum</i> and <i>Coronidium</i> (Asteraceae: Gnaphalieae)	M–2–13
16:00–16:15	Russell Barrett , Order out of chaos — have we reached a turning point in botanical taxonomy?	M–1–14	Tim Hammer , The noble and the exalted — resolving the relationships within <i>Ptilotus nobilis</i> (Amaranthaceae)	M–2–14
16:15–16:30	Barry Richardson , Subspecies definitions and conservation legislation	M–1–15	Mike Crisp , <i>Callitris</i> — a molecular phylogenetic chronicle of extinction, survival and rediversification	M–2–15
16:30–16:45	Alexander Schmidt-Lebuhn , The use of phylograms and chronograms in the identification of biodiversity hotspots	M–1–16	Rismita Sari , The Phylogeny of Australian <i>Garcinia</i> (Clusiaceae)	M–2–16
16:45–17:00	Michael Braby , Threatened species conservation—the need for national Action Plans of insects and other invertebrates	M–1–17	Kerry Gibbons , The <i>Hedyotis-Oldenlandia</i> complex (Spermacoceae, Rubiaceae) in Australia—polyphyly, multiple dispersals and new genera in an Asian-Australian-Pacific lineage	M–2–17
17:00–17:15	SASB AGM and business meeting		Francis Nge , Biogeographic history and evolution of the two Australian temperate floras	M–2–18
17:15–17:30	cont.		Allison Mertin , Phylogenomic insights into the evolution of Greenhood orchids (subtribe Pterostylidinae) in time and space	M–2–19
17:30–18:00	SASB Distinguished Research Award, The rise and rise of systematics by Mark Harvey —Plenary, The Braggs			M–P–20

Programme — Tuesday

08:30–8:45 Housekeeping

08:45–09:25 Keynote Talk. Can systematics evolve beyond its years? by **Judy West** — Plenary, Horace Lamb
 move into concurrent sessions T-P-1

09:30	<i>Asian–Australian biotic exchange — Concurrent (I), Horace Lamb</i>	p49	<i>Insects — Concurrent (II), Benham</i>	p59
-------	---	-----	--	-----

09:30–9:45 **Paul Oliver**, Crossing lines — a saurian perspective T-1-2
Ben Parslow, The systematics and host associations of the Australian parasitic wasp genus *Gasteruption* (Hymenoptera: Gasteruptionidae) student T-2-2

09:45–10 **Emily Roycroft**, Murid rodents as a model for decoding the genomic basis of adaptive radiations across Indo-Australia student T-1-3
Erinn Fagan-Jeffries, Using high-throughput amplicon sequencing to explore the biodiversity of Australian microgastrine parasitoid wasps student T-2-3

10:00–10:15 **Damien Esquerré**, Phylogenomics and biogeography of the pythons — a Trans-Wallacean clade of giant snakes student T-1-4
Rung-Juen Lin, The immature stages and biology of *Rotunda rotundapex* (Miyata & Kishida) (Lepidoptera: Bombycidae) student T-2-4

10:15–10:30 **Scott Groom**, Origins of the Australian bee fauna T-1-5
James Dorey, Drivers of speciation in Fijian *Homalictus* — past climate cycles and geographic isolation student T-2-5

10:30–11:00 Morning Break

11:00–11:15 **Katharina Nargar**, Australasian orchid diversification in time and space — a phylogenomic study T-1-6
Yuchi Lin, Multiple losses of defence hairs in cup moths (Lepidoptera: Limacodidae) student T-2-6

11:15–11:30 **Elizabeth Joyce**, Origins of the northern Australian flora — role of the Sunda-Sahul floristic exchange student T-1-7
Mark Stevens, Revision of 'giant' Collembola within Neanuridae reveals convergent evolution of character traits and lack of support for Uchidanurinae T-2-7

11:30–11:45 **Sarah Mathews**, The biogeography of Indonesian forests T-1-8
Craig Edwards, Species delimitation and description of scale insects (Ericoccidae) that induce galls on *Melaleuca* (Myrtaceae) student T-2-8

11:45–12:00 **Lalita Simpson**, Asian–Australasian biotic exchange — phylogenomic insights from the mega diverse genus *Bulbophyllum* (Orchidaceae) student T-1-9
Liz Milla, Exploring the possible co-evolution of *Boronia* (Rutaceae) and their pollinator moths (Heliozelidae, Lepidoptera) student T-2-9

12:00–12:15	Andrew Huggall , Crossing lines—steps towards synthesis	T–1–10	Alicia Toon , Population structure of <i>Macrozamia</i> cycads and their <i>Cycadothrips</i> pollinators—congruence in a plant-pollinator obligate mutualism	T–2–10
12:15–12:30	Charles Foster , Plastome-scale sequencing and a methodological arsenal begin to unravel the evolutionary history of <i>Pimelea</i> (Thymelaeaceae)	T–1–11	Juanita Rodriguez , The evolution of Müllerian mimicry in Australian velvet ants	T–2–11
12:30–13:15	Lunch			
13:15–13:55	Keynote Talk. Systematics and other collections-based sciences in the Anthropocene, by Kristofer Helgen —Plenary, Horace Lamb move into concurrent sessions			T–P–12
14:00	<i>Plant systematics—Concurrent (I), Horace Lamb</i>	p 70	<i>Advances in Australasian arachnology—Concurrent (II) Benham</i>	p 73
14:00–14:15	Todd McLay , Fine scale genetic variation and introgression in ash eucalypts in the highlands of Victoria	T–1–13	Kym Abrams , Surprising schizomids (Arachnida)—a <i>Draculoidea</i> in disguise and other oddities	T–2–13
14:15–14:30	Gillian Brown , Taxonomic clarification of the critically endangered <i>Noteleae ipsiviciensis</i>	T–1–14	Barbara Baehr , Australian Arachnology advanced through European heritage—the origin of spider research in Australia and the importance of the Godeffroy Collection for current spider taxonomy and diversity assessments	T–2–14
14:30–14:45	Patricia Lu-Irving , Untangling the systematics and invasion history of <i>Lantana camara</i>	T–1–15	Mark Harvey , Phylogenetic relationships of the Australian open-holed trapdoor spiders (Nemesiidae: Anamimae)—a multi-locus molecular analysis resolves generic classification	T–2–15
14:45–15:30	Posters and Afternoon Break			p 113
15:30–15:45	ASBS AGM and business meeting—Concurrent (I), Horace Lamb		Michael Rix , Systematics, biogeography and conservation of Australia's spiny trapdoor spiders (Idiopidae)—progress and prospects	T–2–16
15:45–16:00	cont.		Cor Vink , The spider tree of life—what does it mean for the New Zealand fauna?	T–2–17
16:00–16:15	cont.		Jeremy Wilson , Spiny trapdoor spiders (<i>Euoplos</i>) of eastern Australia—broadly sympatric clades are coupled with burrow architecture and male morphology	T–2–18 student
16:15–16:30	cont.		Renan Santana , Phylogeny of the Eastern Australian tarantula	T–2–19 student
16:30–17:30	Nancy T. Burbidge Medal Presentation and Address			T–P–20

Programme – Wednesday

08:30–8:45 Housekeeping

08:45–09:25 Keynote Talk. Out of sight, out of mind—marine invertebrate systematics and conservation, by **Nerida Wilson**—Plenary, Horace Lamb W-P-1
move into concurrent sessions

11:00	<i>Stygofauna and groundwater</i> — <i>Concurrent (I)</i> , Horace Lamb	p82	<i>Palaeobotany and systematic botany</i> — <i>Concurrent (II)</i> , Benham	p92
-------	---	-----	---	-----

09:30–9:45 **William Humphreys**, Towards subterranean fauna conservation in arid Australia—realisation, establishment and consolidation W-1-2 **Greg Jordan**, Palaeoendemics W-2-2

09:45–10:00 **Michelle Guzik**, Biodiversity assessment of a groundwater community in the Pilbara, Western Australia W-1-3 **Vera Korasidis**, A Cenozoic southern hemisphere peatland rainforest record of climate, floral evolution and fire W-2-3

10:00–10:15 **Steve Cooper**, Systematics, evolution and conservation management of troglofauna from the Yilgarn calcretes W-1-4 **Anne-Marie Tosolini**, Eocene ecosystems determined from fossil plant–insect interactions from Anglesea, Victoria, Australia W-2-4

10:15–10:30 **Grant Hose**, Preliminary analysis of metabarcoding for the assessment of stygofauna assemblages W-1-5 **Andrew Rozefelds**, What role can palaeobotany play in integrating systematics for conservation and ecology? W-2-5

10:30–11:00 Morning Break

11:00–11:15 **Emma Matthews**, Identifying short range endemic Parabathynellidae (Crustacea: Bathynellacea) and stygofauna in the Pilbara and Browns Range, Western Australia student W-1-6 **John Conran**, Cretaceous to Recent araucarian forests in New Zealand—evidence from pollen, wood, leaves, amber and biotic inclusions W-2-6

11:15–11:30 **Danielle Stringer**, Taxonomy and sequence capture of *Haloniscus* isopods from threatened arid zone groundwater habitats W-1-7 **Bob Hill**, Can plant fossil data inform future environmental options? W-2-7

11:30–11:45 **Rachael King**, Where to draw the line? Defining sygobitic amphipod species for conservation and management W-1-8 **Myall Tarran**, The fossil record of *Syzygium* and *Metrosideros* (Myrtaceae) in the Cenozoic of South Eastern Australia student W-2-8

11:45–12:00 **Barbara Langille**, Molecular evolution of ‘eye genes’ in blind beetles—evidence for neutral evolution of phototransduction genes student W-1-9 **Keelin Smith**, Species delimitation and morphometric analysis of *Anthotium humile* (Goodeniaceae) student W-2-9

12:00–12:15	Kurt Petersen , The ecological advantage of heterosporous in <i>Selaginella</i> and <i>Isoetes</i> student	W-1-10	Bill Barker , The diversification of Australian <i>Lindernia</i> (Linderniaceae)	W-2-10
12:15–12:30	Nik Tatamic , Sexual conflict and coevolution of sexually antagonistic armature in the ripple bug genus <i>Nesidovella</i> (Veliidae)	W-1-11	Peter Wilson , Resolution of taxonomic limits in <i>Haloragis serra</i> and the <i>Haloragis exalata</i> species complex	W-2-11
12:30–13:15 Lunch				
13:15–13:55 Shelley James , Herbarium data—global biodiversity and societal botanical needs for novel research—Plenary, Horace Lamb move into concurrent sessions				
14:00	Systematic botany and methods—Concurrent (I), Horace Lamb p103		Pollination and conservation botany—Concurrent (II), Benham p108	
14:00–14:15	Matt Renner , Phylogenetic niche conservatism and release in <i>Acacia</i>	W-1-13	Hervé Sauquet , The ancestral flower of angiosperms and its early diversification	W-2-13
14:15–14:30	Matt Buys , Phylogenomics and island radiation—applying Anchored Hybrid Enrichment to <i>Leptospermum scoparium</i> (Myrtaceae)	W-1-14	Jennifer Tate , Host specificity in the New Zealand mistletoe <i>Korthisella salicornioides</i> (Viscaceae)	W-2-14
14:30–14:45	Nathalie Nagalingum , Can NGS data resolve relationships in a recently-radiated genus? An example using the cycad genus <i>Cycas</i>	W-1-15	Juliet Wege , Saving our 'Attractions'—vascular plant taxonomy informing conservation efforts in Western Australia	W-2-15
14:45–15:00	Lars Nauheimer , Plastome structure and phylogenomics in Nymphaeales	W-1-16	Bronwen Keighery , Systematics and the conservation of Perth's vascular native flora	W-2-16
15:00–15:15	Ed Biffin , Probing the State's flora—a hybrid enrichment approach for vascular plants	W-1-17	Greg Keighery , Rainbows end—orchid systematics and conservation in south-west Western Australia	W-2-17
15:15–15:45 Afternoon break				
15:45–16:15 Wrap up and prizes—Horace Lamb				
16:15–16:45 SASB incoming council meeting				

Abstracts (in presentation order)

Monday

Plenary Talk

The Braggs

Biogeography meets genomics – new trends in data analysis of biogeographic data

M–P–1

Gonzalo Giribet

Museum of Comparative Zoology, Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA

Since the advent of Next Generation Sequencing (NGS) phylogenetic and thus biogeographic analyses have shifted from using a handful of genes to very large amounts of loci. This paradigm shift has suddenly allowed to test for evolutionary processes that could not be addressed with single-gene or small genetic data sets. This change is evident in how phylogenetic analyses can now address gene conflict and the inherent biogeographic relationships of, for example, secondary contacts, but also has repercussion over dating phylogenies. In the case of closely related species or populations, NGS data can detect the genetic contribution of and gene flow between populations. We thus have applied different NGS approaches, including ddRAD-seq and phylotranscriptomics to address questions in biogeography; from the recent diversification of living fossils (e.g., *Nautilus* and Onychophora) to the ancestral cladogenesis of Gondwanan relicts (e.g., Opiliones and Ricinulei). In this talk I will address some of the progress and challenges in analysing such data sets in the context of biogeography.

Morning Break

Monday, 10:30–11:00

Bringing it all together—role of eTools in frontline biosecurity surveillance

M–1–2

Barbara M. Waterhouse

Department of Agriculture and Water Resources, Cairns International Airport, Qld

Northern Australia Quarantine Strategy (NAQS) plant health scientists complete surveys across northern Australia and in neighbouring countries to provide a snapshot of the biosecurity status of these regions and to facilitate early detection of new pest, disease and weed incursions. Some regions such as the Torres Strait Islands are visited regularly, while others such as the Indian Ocean Territories, have been visited only once previously. In all cases our surveys are of short duration.

With rapid advances in ‘smart technology’, increasingly there is an expectation that field data will be collected directly onto ‘smart’ devices. Notwithstanding limitations of the broadband network; the ever-expanding availability of on-line keys and other identification aids such as image libraries, and of collections databases, means that these same devices can be used to assist preliminary on-the-spot identifications and determine whether there are existing records from the locality and thus whether a specimen should be collected. The overall outcome is enhanced capacity for early identification and reporting of new incursions, and more strategically targeted collecting activities.

NAQS botanists have a dual role within the plant health team, providing timely identifications of host plants and weeds. We also provide plant identifications for stakeholders including land protection staff and rangers. When working in the field our ‘eToolbox’ already includes regular use of online tools such as Australian Tropical Rainforest Plants, KeyBase, AusGrass2, Flora of China, The Australasian Virtual Herbarium and the PNGplants Database, alongside geographical tools such as Google Earth.

Existing and future treatments in the Flora of Australia Online represent an important addition to this toolbox. The launch is timely. A NAQS plant team is expecting to visit the Indian Ocean Territories in early 2018, the first time since 1999. Online access to the previously published volume Oceanic Islands excluding Norfolk and Lord Howe Islands will help focus and streamline botanical components of the survey during the brief time spent on Christmas Island and the Cocos (Keeling) Islands.

Mark McGrouther and Paul Flemons

Australian Museum, Sydney, NSW

Australia is home to nearly 5000 species of fishes. In a changing world it is vitally important to learn as much as we can about biodiversity of the region. Diving and angling are huge sports in Australia and New Zealand. The Australasian Fishes Project taps the enthusiasm of fish-spotters and fish scientists who upload, identify and comment on observations of fishes from within Australian and New Zealand waters. The project has been online for less than 18 months, but has had over 17000 uploads from user groups. Using these data we have made over 100 ‘discoveries’ that include information on distributional changes, parasitism, new colour morphs, hybrids, beach strandings, habitat information, fish biology, tagged fishes, new records for many regions/islands and potentially new species.

Zoe Knapp and Anthony Whalen

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

Following an almost 40 year history as a hard copy book series, the Flora of Australia (FoA) is now being delivered on an interactive eFlora platform. A collaborative project between the Australian Biological Resources Study, Council of Heads of Australasian Herbaria and the Atlas of Living Australia, the “electronic” FoA provides an opportunity to build momentum towards completing a comprehensive coverage of the nation’s flora.

This eFlora project builds on (and is enabled by) existing projects such as the National Species List and integrated resources such as the Australasian Virtual Herbarium. “Taking the covers off” the FoA and moving to an interactive eFlora will require the careful transfer, review and update of existing floral treatments. It will also require consideration of governance, workflows and cultural changes associated with building and managing an eFlora.

This presentation will provide an overview of the FoA on the new eFlora platform and include background, display of content, platform functionality and the challenges experienced and overcome so far. Priorities for future contributions to the FoA will also be discussed. The mix of science, technology and ability for people to work together are all important factors in successfully creating an eflora.

Chair: Judy West

Brief introduction to ABRS, Flora of Australia and the partnership project to deliver the Flora of Australia through an electronic Flora delivery platform (eFlora).

Presentations from major partners in the development of the platform including the Council of Heads of Australasian Herbaria by Michelle Waycott, current Chair, The Atlas of Living Australia Director, John La Salle and Director of ABRS, Anthony Whalen.

Formal launch by Professor Bob Hill, The University of Adelaide, Environment Institute.

Opportunities to view the platform will be available to conference participants following the launch.

Lunch

Monday, 12:30–13:15

Are parasites as problematic for biologists as they are for their hosts?

M–2–2

Olivia K. Davies¹, Mark I. Stevens², Michael G. Gardner¹ and Michael P. Schwarz¹

¹College of Science and Engineering, Flinders University, Adelaide, SA; ²South Australian Museum, Adelaide, SA

Wolbachia is an intracellular parasite that is highly prevalent in insects. It is known to hijack host reproduction, to increase its transmission rate via mother to daughter inheritance. With a complex and largely unknown life history, the interactions that take place between the host, host cells and *Wolbachia* remain a mystery. Hylaeinae are an incredibly species rich group of bees, native to Australia. The only known social hylaeine, *Amphylaeus morosus* is known to harbour two strains of *Wolbachia*, but is also afflicted with another condition—mitochondria heteroplasmy. Generally considered rare, heteroplasmy is the existence of two or more mitochondrial haplotypes per individual or cell. In *A. morosus*, this condition exists at an unrepresented rate, and we propose that *Wolbachia* enables this. We are exploring the relationship between these two phenomena in other hylaeine species, to identify the mechanisms that facilitate the maintenance of deviant molecular systems, as well as highlight the systematic issues associated with these systems.

Student Presenter

Integrated taxonomic investigation of the Enenteridae, a curious lineage of parasitic flatworms, reveals undiscovered diversity and provides new ecological insights

M-2-3

Daniel C. Huston, Scott C. Cutmore and Thomas H. Cribb

School of Biological Sciences, The University of Queensland, St Lucia, Qld

Although the Lepocreadioidea family Enenteridae is morphologically intriguing, exploration of the biodiversity, ecology and evolutionary relationships of this group remains largely incomplete. The Enenteridae has diversified almost entirely in one host group, herbivorous marine fishes of the family Kyphosidae, and until recently, the Enenteridae was thought to contain few species with relatively broad geographic ranges and host specificities. However, our recent molecular explorations have begun to reveal patterns of unrecognised species richness and high host-specificity. Molecular exploration of this group is facilitating new species descriptions and taxonomic revisions within the family. Our increased understanding of the evolutionary relationships and convergent morphologies of the digenean parasites of kyphosids has also begun to provide clues into the ecology of the Enenteridae. While endoparasites have little use for pigmentation, as is seen in nearly all known trematodes, enenterids are brightly orange-coloured in life, suggesting the presence of carotenoids, which cannot be manufactured by animals *de novo*. Furthermore, species of nearly all digenean families have incomplete digestive systems with blind caecae. In contrast, enenterids have complete digestive systems with a functional anus. These characteristics suggest that this lineage might have adapted to feed on the food of the host, rather than the host itself.

Student Presenter

Exploring an undocumented diversification of parasitic gastropods in Antarctica

M-2-4

Kara K.S. Layton and Nerida G. Wilson

Aquatic Zoology and Molecular Systematics Unit, Western Australian Museum, Welshpool, WA; School of Biological Sciences, The University of Western Australia, Crawley, WA

Asterophila is a genus of endoparasitic gastropod found inside asteroid sea stars and exhibiting a highly simplified body plan with few diagnostic morphological characters. There are currently four known members in this genus, one of which has been described from the Antarctica Peninsula and forms part of a putative radiation of species in this region. In order to further explore this radiation, 61 *Asterophila* specimens were collected from a variety of asteroid hosts in Antarctica. Four genes (COI, 16S, H3, 28S) were used for phylogenetic reconstruction and species delimitation and a test of host–parasite co-evolution was conducted by constructing tanglegrams and employing event-based reconciliation and global congruence analysis. This work also employs scanning electron microscopy for analysing morphological characters in larval shells. The resulting *Asterophila* phylogeny is partially unresolved, but shows high support for nine species-level entities, suggesting undocumented diversity in this group. These nine putative species show varying degrees of host specificity and species with more extensive sampling show higher host diversity. Significant global congruence between host and parasite phylogenies was detected, suggesting that these lineages are not evolving independently, but only a few cases of strict co-speciation were recovered with the majority of links explained by duplication and host switching. Lastly, the umbilicus and shape of larval shells appear to vary between species in this region, but future work should look to incorporate more individuals to assess the validity of these characters. Investigating co-phylogenetic patterns provides insight into whether host and parasite lineages are evolving in synchrony, which may have important implications for biodiversity conservation. In all, these results advance our understanding of diversity and the processes driving this diversity in Antarctica.

Student Presenter

Uncovering the diversity of deep-sea crustaceans (Isopoda and Amphipoda) from the Great Australian Bight

M-2-5

Amelia Lewis¹, Andrew D. Austin¹, Michelle Guzik¹, Rachael King², Jason Tanner^{3,4} and Alan Williams⁴

¹School of Biological Sciences, The University of Adelaide, SA; ²South Australian Museum, Adelaide SA; ³SARDI Aquatic Sciences, Henley Beach, SA; ⁴CSIRO, Battery Point, Tas

The deep-sea is a largely unexplored, complex environment where benthic invertebrate diversity is poorly known and mostly undescribed. Australian deep-sea benthic faunal surveys have previously concentrated on the western and eastern mainland coasts and northern Tasmania, leaving the deep-sea benthos of the Great Australian Bight (GAB) virtually unstudied. Recent collections made through the Great Australian Bight Research Program (GABRP) have provided fresh material for analyses, indicating high levels of diversity present in the GAB including large numbers of Isopoda and Amphipoda (Crustacea). These two groups are well known as dominant members of benthic deep-sea habits world-wide, yet the Australian deep-sea assemblages of these groups lack a modern phylogenetic and taxonomic framework. This project aims to provide a comprehensive taxonomic checklist to deep-sea species of amphipods and isopods in the GAB and robust multigene phylogenies for both groups, with targeted taxonomic evaluation of the Serolidae. This isopod family is cosmopolitan with both shallow and deep-sea representatives. Australian deep-sea serolids have been documented previously but only employing traditional morphology-based approaches. Two genera (*Brucerolis* and *Acutiserolis*) are recorded from areas around Tasmania, New Zealand, south-eastern Australia and now, based on recent surveys, the GAB. The present study is employing CO1 sequence data to explore relationships for these two genera including additional Southern Ocean and Antarctic material from the National Institute of Water and Atmosphere. This will enable us to place the GAB taxa within a broader Southern Ocean serolid phylogeny. New species will be documented based on molecular and morphological criteria. Preliminary results indicate the possibility of morphologically cryptic species within existing morphospecies (e.g. *Brucerolis victoriensis*). This project is part of the GABRP: a collaboration between BP, CSIRO, the South Australian Research and Development Institute (SARDI), the University of Adelaide, and Flinders University. The Program aims to provide a whole-of-system understanding of the environmental, economic and social values of the region; providing an information source for all to use.

Student Presenter

Of volcanoes and lizards—phylogenomics and biogeography in a group of Mexican skinks

M-2-6

Robert W. Bryson Jr.¹, Charles W. Linkem², *Carlos J. Pavón-Vázquez^{3,4}, Adrián Nieto-Montes de Oca⁴, John Klicka¹ and John E. McCormack⁵

*Presenting; ¹Department of Biology and Burke Museum of Natural History and Culture, University of Washington, WA, USA; ²Department of Biology, University of Washington, WA, USA; ³Division of Ecology and Evolution, Research School of Biology, Australian National University, ACT; ⁴Departamento de Biología Evolutiva, Facultad de Ciencias, Universidad Nacional Autónoma de México, Mexico; ⁵Moore Laboratory of Zoology, Occidental College, CA, USA

We investigated the biogeographic history of the skinks in the *Plestiodon brevirostris* group, whose members are distributed across the major mountainous regions of Mexico. The group is almost endemic to Mexico, with only one of the thirteen described species found outside the country. We obtained data for 3282 loci employing target enrichment of ultraconserved elements. We then generated time-calibrated phylogenetic trees using concatenation and coalescent methods. Based on these trees, we reconstructed ancestral geographic distributions using likelihood-based models of range evolution. The two methods of phylogenetic reconstruction led to different results, but some of the nodes supported by both analyses contradict previous trees based on mtDNA sequences. The formation of the Transmexican Volcanic Belt appears to have played a major role in the diversification of the *P. brevirostris* group, promoting both dispersal and *in situ* speciation. Additionally, our work with the group has revealed the existence of unrecognised and likely endangered specific diversity. Some of these undescribed species have small geographic ranges and are threatened by human activities such as open-pit mining and deforestation.

Student Presenter

Small marsupials, big data—population genomics reveals structure in desert-dwelling Dasyuridae

M-2-7

Linette S. Umbrello^{1,2}, Jose I. Carvajal², Raphael K. Didham^{1,3}, Ric A. How^{1,2} and Joel A. Huey²

¹Western Australian Museum, Welshpool, WA; ²School of Biological Sciences, The University of Western Australia, WA; ³CSIRO Ecosystem Sciences, Floreat, WA

The rise in high-throughput sequencing has allowed us to explore the population genetics and phylogeography of non-model species at a deeper level. Population genomic studies using double-digest restriction site-associated DNA (ddRAD) sequencing as an alternative to traditional microsatellite and Sanger sequencing methods has the advantage of producing powerful datasets with fewer individual samples. The genetic structure of most Australian desert mammals is poorly understood, and ddRADseq is a suitable method for addressing questions about population structure where samples are sparsely distributed in remote regions. In this comparative study we sampled tissues from 190 individuals of four dasyurid species (*Sminthopsis* and *Planigale*) held in museum tissue collections. This included two Pilbara endemic species and two species distributed more broadly across the arid zone. Tissues were chosen to give uniform sampling across the large distributions of each species. The ddRADseq data were generated using ipyRAD and Python scripts, and the results compared with a previous mtDNA study of each species. Different types of population structure were detected for each of the four species, showing that species biology and landscape features drive population differentiation. Examples of isolation by distance, landscape driven population differentiation, and the role of Pleistocene refuges will be discussed. The results show that ddRADseq is a useful method for investigating the population structure of desert and rare mammals where high-quality DNA samples are available.

Student Presenter

Lunch

Monday, 12:30–13:15

Decadal Plan discussion

Plenary – The Braggs

13:15–14:10

The Biosystematics and Taxonomy Plan discussion

M–P–8

Kevin Thiele

Biosystematics and Taxonomy Plan, Australian Academy of Science, Canberra, ACT

The taxonomy and systematics community in Australia and New Zealand, under the auspices of the Australian Academy of Science, the Royal Society Te Apārangi and with funding from the Ian Potter Foundation and key stakeholder and sector bodies including ASBS and SASB, is developing a decadal strategic plan for the sector. As with other decadal plans for other sectors of science, this will be a forward-looking document that establishes the value and importance of our science and of the services we provide, documents the current state of the sector and its trends, opportunities and challenges, and develops a series of strategic goals and actions to guide both funding decisions and activities over the next decade. If successful, the decadal plan may play a role in reversing the trends that concern us all and that have been documented in many jurisdictions around the world. After extensive discussions and workshops with many people from the sector and with key stakeholders and end-users of taxonomy, a draft of the plan requires careful consideration by the community to ensure that it meets both community and stakeholder needs and expectations, and is politically achievable. This forum will be an opportunity for constructive comment on the plan, and to help ready it for release.

ALERT lessons from a biosecurity disaster

M–P–9

Gillian Brown^{1,5}, Brendan Lepschi^{2,5}, Pina Milne^{3,5}, Jo Palmer^{2,5} and Frank Zich^{4,5}

¹Queensland Herbarium, DSITI, Brisbane Botanic Gardens, Toowong, Qld; ²Australian National Herbarium, Centre for Australian National Biodiversity Research, Canberra, ACT; ³National Herbarium of Victoria, Royal Botanic Gardens of Victoria, South Yarra, Vic; ⁴Australian Tropical Herbarium, James Cook University Cairns Campus, Cairns, Qld; ⁵Managers of Australasian Herbarium Working Group

The Managers of Australasian Herbarium Collections (MAHC) have been working with the Plant Import Operations Branch of the Commonwealth Department of Agriculture and Water Resources (DAWR) to align our processes to significantly reduce the risk of herbarium specimens being destroyed when being imported into Australia. The two groups worked together productively to bring about change and to enable the resumption of the international movement of herbarium specimens. These changes include amendments to the BICON import conditions and onshore outcomes for herbarium specimens, changes to procedures at the border (gateway facilities) where biosecurity documentation is assessed and parcels released, and updates to existing herbarium parcel labels, guidelines and supplier declaration templates. We will discuss lessons learned, as well as what this means to you as researchers who may need to bring material into the country.

Taxonomic challenges to an independent evidence base for assessing coastal environmental change through time M-1-10

Nicole Foster¹, Michelle Waycott^{1,2}, Ed Biffin² and Kor-jent van Dijk¹

¹School of Biological Sciences, University of Adelaide, SA; ²State Herbarium of South Australia, Adelaide, SA

Coastal ecosystems, both natural and disturbed, contain biological communities that have undergone profound changes in response to increasing human influence. The ability to define anthropogenic impacts on these environments and to then be able to forecast responses to future climate change is highly sought after. Evaluating coastal environmental change through time will enable us to determine how environments have changed in association with human occupancy of our coastal environments. Traditional methods used to look back in time have so far been limited to direct observations of plant fragments in sediment cores, along with historical reconstruction based on observations from satellite and aerial photography and fossil/subfossil and fossilised pollen evidence. New methods to evaluate changes in species presence in communities are available as a result of advancements in DNA technology. We are developing a toolkit for utilising historical plant samples from coastal and nearshore marine sediments to improve our ability to document change. Coastal and nearshore marine plants have also been poorly characterised in the fossil record due to the paucity of fossil evidence globally and for seagrasses a lack of a pollen fossil record due to their inability to be preserved. A comprehensive reference library with a multigene region approach is being adopted. This will also serve to build a high resolution reference library for all studies using NGS tools to determine species identity in coastal and marine plants in temperate Australian ecosystems. The taxonomy of some of these groups is poorly resolved and we need a high quality, well vouchered and curated reference collection to form the foundation of ongoing analyses.

Student Presenter

Biodiversity and conservation of sea snakes (Hydrophiinae) in Western Australia

M-1-11

Charlotte Nitschke¹, Vinay Udyawer², Mathew Hourston³, Arne Rasmussen⁴ and Kate Sanders¹

¹School of Biological Sciences, The University of Adelaide, Adelaide, SA; ²Australian Institute of Marine Science, Darwin, NT; ³Department of Primary Industries and Regional Development, Perth, WA; ⁴The Royal Danish Academy of Fine Arts, Schools of Architecture, Design and Conservation, Copenhagen, Denmark

Sea snakes are the most speciose group of marine reptiles—and the only extant group that spend their entire lives in the sea. Western Australia (WA) is a recognised biodiversity hotspot for sea snakes, with many regional endemics, and yet there are major gaps in both sampling effort and knowledge of species biology. Recent enigmatic declines in WA have led to increased research focus on the threats facing sea snakes, such as trawling, coastal development and climate change. Here we present the mitochondrial phylogeography of 11 species of sea snakes, in combination with species distribution models (SDMs) based on their extant distributions and climate models for the mid Holocene and last glacial maximum (LGM). Molecular analyses indicate highly varied phylogeographic histories among the sampled species, with much stronger geographic genetic structure among *Aipysurus* compared to *Hydrophis* populations. The highest mtDNA divergences were generally found between the WA coastal versus Timor Sea and Queensland populations. For most species, these splits were dated to the late Pleistocene, but two specialist egg-eating *Aipysurus* species showed deeper divergences suggestive of cryptic species. Our genetic inferences of population persistence across multiple glacial cycles are consistent with the SDMs, which indicate suitable climatic conditions along the WA paleo-coastline during the LGM. These results demonstrate the value of combining analytical approaches and have important implications for sea snake conservation.

Student Presenter

Kor-jent van Dijk¹, Ed Biffin² and Michelle Waycott^{1,2}

¹School of Biological Sciences, University of Adelaide, SA; ²State Herbarium of South Australia, Adelaide, SA

Seagrasses are a small functional group of marine flowering plants within the Alismatales. Molecular and fossil record indicate that these angiosperms became adapted to marine life around 100 million years ago. Currently c. 70 species are recognised and are distributed over four separate lineages, each of these probably having adapted to marine life independently. Defining species in some of the seagrass genera is difficult and has led to debate and disagreement. Morphological characters are few and mostly based on overlapping size or quantity ranges, flowering is rarely observed and is thus not a practical taxonomical recourse.

In this presentation, I will show three examples of seagrass species ‘complexes’ where morphology and/or molecular genetic data do not agree, and where species taxonomy has not been resolved in an unambiguous way.

The first group is the *Halophila ovalis* ‘complex’, a group of small oval-shaped seagrasses of the Hydrocharitaceae that are extremely plastic in their shape and size. Traditional phylogenetic sequence data indicate that several lineages exist, and confirm that the commonly used morphological characters do not delimit the members of the complex. The second is part of the Posidoniaceae, the ‘ostenfeldii’ complex, consisting of five species. This group of seagrasses is hyper-variable, particularly in size, but this is not reflected in the molecular data where all traditionally used loci are almost identical. The third potential complex lies within the genus *Halodule*. Only two species are described in the Indo-Pacific, primarily based on leaf tip morphology. Genome wide screening of single nucleotide polymorphisms (SNPs) suggest that at least 3 lineages exist, potentially indicating the existence of cryptic species.

Our research group has worked on resolving these uncertainties in the past 15 years and we have made significant progress, but the resolution of genetic markers has not been sufficient. With high throughput sequencing methods becoming more affordable we have developed a new RNA-baits Hybrid Capture approach that has great potential. Soon we will be able to sequence dozens to hundreds of loci for hundreds of samples in one experiment. The HybCap methods have the potential of becoming the next generation “to go” method for phylogenetics and species barcoding.

Remarkable biodiversity of subterranean Bathynellidae (Bathynellacea, Crustacea) in the north of Western Australia and the status of the *Bathynella* genus

M–2–10

Giulia Perina^{1,2}, Joel Huey², Ana I. Camacho³, Pierre Horwitz¹ and Annette Koenders¹

¹School of Science, Edith Cowan University, Joondalup, WA; ²Western Australian Museum, Welshpool, WA; ³Museo Nacional de Ciencias Naturales (CSIC), Dpto. Biodiversidad y Biología Evolutiva, Madrid, Spain

In the past decades the number of subterranean taxa discovered in Australia has increased consistently thanks to environmental and biological studies, often associated with mining surveys. The north of Western Australia, and especially the Pilbara region, has been declared a hot spot for underground fauna. Different studies on troglo-stygofauna are also revealing interesting biogeographic that reflect the climate and hydro-geological history of the craton.

Bathynellidae occur in most Australian aquifers, but their study and identification are very difficult due to their small and fragile bodies, and their conservative morphology.

Additionally, the poor and incomplete description of the type genus and species of this family (*Bathynella natans* collected in Prague in 1882) have led to the assignment of many species occurring around the world, including Australia, to this genus. The taxonomic framework is therefore not well defined, and the aid of molecular techniques is needed to support and define species-genera boundaries and their phylogenetic relationships.

I will present results on Bathynellidae from the northern Western Australia.

Morphological and molecular data reveal new genera and species with fascinating relationships. Also, the collection of some fresh material from type localities belonging to *Bathynella* clarifies the position of this “cosmopolitan” genus. A better understanding of the biodiversity and distribution of Bathynellidae will improve the knowledge of the delicate subterranean ecosystem, and contribute to the management and monitoring of the underground resources.

Student Presenter

Phylogenetic revision of subterranean Dytiscidae from Western Australia—sister species validate sympatric or parapatric speciation underground

M-2-11

Josephine Hyde¹, Barbara Langille¹, Steven J.B. Cooper², William F. Humphreys^{3,4} and Andrew D Austin¹

¹Australian Centre for Evolutionary Biology and Biodiversity, School of Biological Sciences, University of Adelaide, Adelaide, SA; ²Evolutionary Biology Unit, South Australian Museum, Adelaide, SA; ³Western Australian Museum, Welshpool DC, WA; ⁴School of Animal Biology, The University of Western Australia, Crawley, WA

The Yilgarn Region of Western Australia contains a rich diversity of subterranean invertebrates and comprises hundreds of physically isolated calcrete aquifers which resemble a subterranean archipelago. Each calcrete has a unique combination of aquatic species (known as stygofauna) including diving beetles (Dytiscidae). Two different genera of diving beetle are found in the aquifers: *Paroster* and *Limbodessus* within which 100 species have now been described. Recent phylogenetic analyses of mitochondrial DNA (mtDNA) data suggest that most (c. 85%) species have independently evolved from surface ancestors, but also provide evidence for the existence of 11 sister species pairs and two sister species triplets living in sympatry within the same calcrete. This latter finding raises the possibility that speciation occurred within the calcrete from a common stygobitic ancestor (i.e. obligate subterranean species). However, as previous phylogenetic studies were solely based on mtDNA, there is a possibility that hybridisation among species led to introgression of mtDNA leading to the apparent sister species relationships. Therefore, we further tested the sister species status of these taxa using multiple independent nuclear gene markers and, in addition, generated a multi-gene phylogeny for *Paroster* and *Limbodessus*. Two mitochondrial (COI, 16S) and three nuclear (WG, TOPO, ARK) genes were sequenced for 55 species of *Limbodessus*, and 31 species of *Paroster*. Phylogenetic analyses of the nuclear gene data provide further support for the presence of sympatric sister species, suggesting that they diversified underground through a process of sympatric or parapatric speciation. Our phylogeny also provides a basis for future studies of the regressive and adaptive evolution of the diving beetle fauna.

Student Presenter

The systematics of *Chloris* in Australia – colonisation events and a newly discovered Artesian spring endemic

M-2-12

Patrick Fahey¹, Rod Fensham^{1,2} and Lyn Cook¹

¹School of Biological Sciences, The University of Queensland, Brisbane, Qld; ²Queensland Herbarium, Brisbane, Qld

Chloris (Poaceae: Chloridoideae) is a specious genus that occurs across the tropical, subtropical and warm temperate parts of the globe. The taxonomy of the genus in Australia was last investigated in 1972, prior to molecular studies in the Chloridoideae subfamily which provided insights into the systematics of the wider genus. These studies lacked sampling of species native to Australia, a gap we sought to fill using morphological and molecular data. As the genus originated outside the continent, a key question posed is whether the Australian species formed a monophyletic clade, and related to this, how many historical colonisation events have occurred.

Additionally, populations of *Chloris* have been identified at two Artesian springs complexes in central Queensland which could not be assigned to any described species. These populations grow in the scalds surrounding the spring wetlands, a unique habitat that is particularly harsh, making them of interest from an ecological and physiological perspective.

Student Presenter

Afternoon Break

Monday, 15:15–15:45

Challenges and conservation

Concurrent (I)—The Braggs

15:45–17:00

The state of taxonomy and systematics in Australia—results of the 2016 Survey of Taxonomic Capacity

M-1-13

Haylee Weaver

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

The field of taxonomy is often represented as having an ‘impediment’, where the gap on our knowledge of species and a dwindling pool of experts to study those species combines to produce a perception that there is not enough research being done.

However, Australian researchers are often described generally as ‘punching above their weight’ in terms of their academic outputs relative to their global representation in a particular field. Are these two things true for Australian researchers in the field of taxonomy and systematics? Since 1975, the Australian Biological Resources Study has conducted periodic surveys of the taxonomic research workforce, the most recent in 2016. Using the results of this longitudinal data set, I will take you on a white-knuckle ride exploring the current trends for taxonomy and systematics in Australia over the past 40 years. I will discuss the changes to ratios for gender representation and age of Australian taxonomists, shifts in taxon bias studied over time, and the changes to the structure of the workforce. Further, I will explore the concerns scientists have for their field of research, and compare how these have changed over time.

Order out of chaos—have we reached a turning point in botanical taxonomy?

M-1-14

Russell Barrett

National Herbarium of New South Wales, Royal Botanic Gardens, Sydney, NSW

Taxonomists are regularly criticised for ‘changing names for the sake of it’ and ‘always changing their minds’. Some perceive taxonomy as ‘a never-ending process’, so expect names to keep on changing. This presentation will analyse real trends in name changes in Australian botanical taxonomy to determine whether there is any truth to these assertions. Contrary to these perceptions, I argue that botanical taxonomy as a discipline is rather on the verge of stability, as the available data now outweigh uncertainty regarding relationships, particularly above species level. The last two decades have indeed seen a flurry of name changes due to molecular data revealing new relationships, but overall, we are really stabilising names at a very rapid rate. This means that the number of name changes should rapidly decrease in the relatively near future (much to the relief of the general public, ecologists and conservation practitioners). The notion that there is no end to name changes at a broad level is patently untrue, but is persistent, and greatly weakens the scientific validity of taxonomy as a discipline. I believe we need to shift our thinking on the future of taxonomic changes, and pitch our research and public communication accordingly.

Barry J. Richardson

Australian National Insect Collection, CSIRO, ACT

As a consequence of genetic studies of population structuring, the usefulness of the subspecies category has been questioned, with opinions divided. The situation is further confused by the use of varying concepts of a subspecies. The phylogenetic species concept has led to very large increases in the apparent number of taxa in some groups, though strong objections have been raised by conservation biologists to this approach. An alternative, the ecological species concept, has been opposed by phylogeneticists. These two approaches are compared for subspecies using the morphological and genetic structure of wallaroo (*Osphranter robustus*) populations as an example. How the use of the different subspecies definitions would affect legislative decisions is explored.

Meg J. Elliott^{1,2}, Nunzio J. Knerr¹ and *Alexander N. Schmidt-Lebuhn¹

*Presenting; ¹CSIRO, Centre for Australian National Biodiversity Research, Canberra ACT; ²Current address: Walter and Eliza Hall Institute, Parkville, Vic

Phylo-diversity metrics such as phylogenetic diversity (PD) and phylogenetic endemism (PE) combine branch length information from phylogenetic trees with spatial distribution data to produce maps of biodiversity scores. These scores can be used to identify biodiversity hotspots and to rank candidate areas for conservation. Phylogenetic trees underlying these phylo-diversity metrics, however, come in two main forms, phylograms and chronograms. Branch lengths on phylograms indicate the number or probability of character changes, whereas branch lengths on chronograms indicate divergence times between sister lineages. We surveyed the use of these two types of phylogenies in previously published spatial studies to examine how often either was used and how the authors interpreted their results. We then reanalysed several published datasets and one new dataset to test to what degree the use of phylogram or chronogram would influence the resultant diversity hotspot localities given the same tree topology and spatial data. Both types of trees are frequently used in spatial studies, and there does not appear to be an explicit agreement on or discussion of this issue. Our analyses showed that anywhere between 11% and 91% of the locations of diversity hotspots can differ between phylogram and chronogram, suggesting that tree choice can have a major impact on the results.

Threatened species conservation—the need for national Action Plans of insects and other invertebrates

M-1-17

Michael F. Braby

Research School of Biology, The Australian National University, ACT; Australian National Insect Collection, ACT

Invertebrates make up about 80% of all species, yet they rarely attract conservation attention compared to the more ‘charismatic’ vertebrates such as birds and mammals. Threatened species conservation, a field of conservation biology in which individual species are targeted for protection and conservation management, complements the landscape approach to biodiversity conservation and could be used more effectively to promote the plight of threatened or imperilled invertebrates given the current global biodiversity crisis and estimated rates of anthropogenic species extinction. Steps in the species-oriented conservation process are outlined, including evaluation of conservation status, listing under legislation, preparation of Action and Recovery Plans, recovery actions, recovery teams and monitoring, in order to prevent extinction or minimise risk of extinction. The process is not without its challenges, but it does provide valuable information that is not always obtainable with the protection and management of threatened habitats and ecological communities. However, for it to be most effective a more strategic approach to listing species is required. It is argued that more national Action Plans, either of higher taxon groups, suites of species indicative of threatened ecological communities, habitats and/or key threatening processes, or species with co-dependent threatened host species, are needed. These plans would provide a national overview of threatened and imperilled invertebrates in conservation need that is far more comprehensive than presently available. A detailed list of threatened invertebrate species could then be promoted (and nominated for listing under the *EPBC Act*) for greater advocacy of conservation need.

SASB AGM and business meeting

Concurrent (I)—The Braggs

17:00–17:30

Integrative taxonomic revision of *Xerochrysum* and *Coronidium* (Asteraceae: Gnaphalieae)

M–2–13

Timothy L. Collins¹, Alexander N. Schmidt-Lebuhn², Rose L. Andrew¹, Ian R.H. Telford¹ and Jeremy J. Bruhl¹

¹School of Environmental and Rural Science, University of New England, NSW; ²Australian National Herbarium CSIRO, ACT

The everlasting daisy genus *Xerochrysum* is recorded in every Australian state and territory as well as the highlands of Papua New Guinea. The genus is best known for cultivars of *X. bracteatum*, which has widely distributed, disjunct natural populations and has long considered part of a polymorphic species complex. The morphologically similar genus *Coronidium* is endemic to eastern and southern Australia, including Tasmania.

Initial work at the N.C.W. Beadle Herbarium and a subsequent student Honours project indicated that there were putative new, undescribed species in the *Xerochrysum bracteatum* complex. A preliminary study of evolutionary relationships between selected Australian *Gnaphalieae* found *Coronidium* polyphyletic, with *Xerochrysum* and two species previously assigned to *Helichrysum* nested within a clade containing the type of *Coronidium*. A more recent morphological study of *Xerochrysum* constituted a partial revision of the genus, and segregated four new species from the *X. bracteatum* complex.

This ABRS-funded project and associated PhD study aims to resolve generic boundaries in *Xerochrysum* and *Coronidium* and delimit and describe species in *Xerochrysum* s. lat. by integrating morphological, cytological and molecular analyses; infer the phylogeny of *Xerochrysum* s. lat. using extensive sampling of populations and a broader range of data than are presently available; and document chromosome number variation and genome size in *Xerochrysum* s. lat. to understand evolution of ploidy in the group. An overview of the project will be presented.

Student Presenter

The noble and the exalted—resolving the relationships within *Ptilotus nobilis* (Amaranthaceae)

M-2-14

Timothy Hammer¹, Paul Macintyre¹, Francis Nge², Robert Davis³, Ladislav Mucina¹ and Kevin Thiele¹

¹School of Biological Sciences, The University of Western Australia, WA; ²School of Biological Sciences, University of Adelaide, SA; ³Western Australian Herbarium, Department of Biodiversity, Conservation and Attractions, WA

A previous molecular study of *Ptilotus nobilis* Nees and *P. exaltatus* (Lindl.) F.Muell. has led to the conclusion that these taxa are conspecific, and subsequently to the synonymisation of the latter under the former. We tested previous species concepts of all taxa in the *P. nobilis* – *P. exaltatus* species group by examining (1) the morphology of specimens in the herbarium and field, and (2) ecological and geographic partitioning of taxa using Maxent and CART models. We provide strong evidence supporting the reinstatement of *P. exaltatus* as distinct from *P. nobilis*, on the basis of multiple morphological characters and strong ecological and geographic partitioning, the latter showing how large-scale ecological data can be used to help resolve taxonomic issues. In addition, we propose to raise *P. nobilis* subsp. *angustifolius* (Benl) Lally & W.Barker and *P. exaltatus* subsp. *semilanatus* (Lindl.) A.R.Bean to the rank of species as *P. angustifolius* (Benl) T.Hammer and *P. semilanatus* (Lindl.) F.Muell. ex J.M.Black.

Student Presenter

Callitris — a molecular phylogenetic chronicle of extinction, survival and rediversification

M-2-15

Mike Crisp¹, David Bowman², Lyn Cook³, Meredith Cosgrove¹, Yuji Isagi⁴ and Shota Sakaguchi⁵

¹Research School of Biology, The Australian National University, Canberra, ACT; ²School of Plant Science, University of Tasmania, Hobart, Tas; ³School of Biological Sciences, University of Queensland, Brisbane, Qld; ⁴Division of Forest and Biomaterials Science, Kyoto University, Japan; ⁵Graduate School of Human and Environmental Studies, Kyoto University, Japan

Callitris belongs to one of the three most diverse extant conifer families and currently is the most species-rich conifer genus in Australia. And a 30-Myr-old fossil trove in north-west Tasmania has more conifer species (living or fossil) than found at any other site on Earth. Yet, between then and now, conifers have undergone massive extinction and rediversification. This presentation will relate our ongoing research on the molecular phylogeny, evolutionary history and biogeography of this fascinating group of trees.

Rismita Sari^{1,2}, Sandra Abell^{1,2}, Darren Crayn², Paul Gadek¹ and Natalie Dillon³

¹College of Science and Engineering, James Cook University, Qld; ²Australian Tropical Herbarium, Qld;

³Department of Agriculture and Fisheries, Queensland Government

The 12 species of Australian *Garcinia* have been taken into a molecular and pollen study to analyse the relationship with *Garcinia* from other regions. A total of 75 taxa including Australian *Garcinia* were analysed using internal transcribed spacer (ITS) of nuclear DNA. The molecular data indicated that Australian *Garcinia* are divided into five groups of infrageneric groups according to Jones (1980), Section I. *Garcinia* (*G. mangostana* L.), Section IV. *Rheedia* (*G. livingstonei* Anderson, *G. xanthochymus* Hook.f. ex T.Anderson), Section V. *Macrostigma* (*Garcinia brassii* C.T.White, *G. gibbsiae* S.Moore, *G. russelii* W.E.Cooper, *G. warrenii* F.Muell.), Section VIII. *Brindonia* (*G. leggeae* W.E.Cooper, *G. mestonii* F.M.Bailey) and Section XIII. *Discostigma* (*G. jensenii* W.E.Cooper, *G. zichii* W.E.Cooper). Only eight species out of 12 have mature pollen that could be taken into the investigation. The pollen types of Australian *Garcinia* are dominated by echinate (*G. brassii*, *G. jensenii*, *G. russelii*, *G. warrenii*), followed by gemmate (*G. gibbsiae*, *G. leggeae* and *G. zichii*) and reticulate (*G. mestonii*). The pollen types are similar with other species in the infrageneric groups.

Student Presenter

The *Hedyotis*-*Oldenlandia* complex (Spermacoceae, Rubiaceae) in Australia—polyphyly, multiple dispersals and new genera in an Asian-Australian-Pacific lineage

M-2-17

Kerry Gibbons and Marco Duretto

National Herbarium of NSW, Royal Botanic Gardens and Domain Trust, Sydney, NSW

The *Hedyotis*-*Oldenlandia* complex is a morphologically recognisable group of genera within Spermacoceae (Rubiaceae), characterised by multiovulate locules, 4-merous flowers, and \pm fimbriate stipules. Generic classification within this group has long been controversial, with past authors ranging from recognising a very broadly circumscribed *Hedyotis* L. to splitting the group into numerous smaller genera. Recent molecular studies have demonstrated that *Hedyotis* and *Oldenlandia* L. as generally circumscribed were polyphyletic and a core *Hedyotis* and a core *Oldenlandia* have been resolved. Australian representatives of this pantropical and subtropical assemblage are currently placed in *Hedyotis*, *Oldenlandia* or the endemic *Synaptantha* Hook. f., but little Australian material has been included in international studies.

We conducted Bayesian and maximum likelihood analyses of nuclear ribosomal (ETS, ITS) and chloroplast (petD, rps16) nucleotide sequence data to assess the generic placement of Australian species and to explore their biogeographic history. Two of the four Australian species currently recognised in *Hedyotis* were placed in *Hedyotis* s. str. (a predominantly Asian genus) but were not closely related. Only the naturalised *Oldenlandia corymbosa* was placed in *Oldenlandia* s. str. The remaining Australian representatives of the group were all placed within a well-supported Asian-Australian-Pacific clade, but were polyphyletic within this clade. This clade includes several recently reinstated genera, including *Exallage* Bremek., *Leptopetalum* Hook. & Arn. and *Scleromitron* (Wight & Arn.) Meisn. The remaining Australian *Hedyotis* were placed in *Exallage*. Although many Australian species currently included in *Oldenlandia* were placed in *Scleromitron*, and *O. biflora* has recently been transferred to *Leptopetalum*, two new endemic genera are required to accommodate the remaining Australian species. Morphological characters distinguishing genera will be discussed. Australian representatives of the *Hedyotis*-*Oldenlandia* complex, and their relatives, appear to have a complex biogeographic history, with multiple dispersals between Asia, Australia and the Pacific required to explain their current geographic distribution.

Biogeographic history and evolution of the two Australian temperate floras

M-2-18

Francis Nge¹, Michelle Waycott^{1,2}, Ed Biffin² and Kevin Thiele³

¹School of Biological Sciences, University of Adelaide, SA; ²State Herbarium of South Australia, Adelaide, SA; ³Eubio Consulting, Perth, WA

Understanding how and why disparities in diversity across regions and taxonomic groups arise is one of the primary goals of biology. Current interest focuses on comparative studies on hotspot regions and their counterparts across the globe, with debates on whether differences in clade age or diversification rates are the primary drivers in the differences in taxonomic richness across regions. Here, I will focus on the two Australian temperate floras, distinguished by the southwest hotspot region for species richness and non-hotspot region in the southeast. Many floristic elements across both regions arose prior to their separation, where lineages were widespread across the Australian continent and subsequently retreated to the southern mesic fringes due to progressive aridification of the continent since the Miocene. Available palaeorecords and phylogenies across the two regions support the clade-age hypothesis, where evidence indicate an earlier differentiation of current dominant flora elements in the southwest than compared with the southeast. However, studies on differences in diversification rates across the regions are currently lacking and so far have not been explicitly tested. I will first review theories that serve to explain these differences in richness, then current studies on this topic, and finally propose an evolutionary framework to guide further research on this area.

Student Presenter

Phylogenomic insights into the evolution of Greenhood orchids (subtribe Pterostylidinae) in time and space

M-2-19

Allison A. Mertin^{1,2}, Mark A. Clements³, Lars Nauheimer² and Katharina Nargar²

¹University of Wollongong, Wollongong, NSW; ²Australian Tropical Herbarium, Cairns, Qld; ³Centre for Australian National Biodiversity Research, CSIRO, Canberra, ACT

Pterostylidinae (Orchidoideae) are a terrestrial orchid subtribe with over 200 species of terrestrial herbs. The subtribe has its centre of diversity in Australia and extends to neighbouring regions in Australasia and Malesia. In its traditional circumscription, Pterostylidinae comprises one genus, *Pterostylis*, however different taxonomic concepts have been proposed to accommodate for the morphological diversity of the group. Previous molecular systematic studies in Pterostylidinae were based on one to two molecular markers and provided only limited insights into phylogenetic relationships within the subtribe. So far, the spatio-temporal evolution of the subtribe has not been investigated in a phylogenetic framework.

We generated plastome data for 121 species, comprising 100 Pterostylidinae samples and 21 samples representing outgroup taxa from the Cranichideae and Diurideae. Phylogenetic analyses of the concatenated data set were carried out using RAxML. Divergence age estimations were conducted based on secondary calibrations from a previous family-wide divergence dating study using BEAST. To infer the historical biogeography of the subtribe, 15 538 distribution records were downloaded from the Australian Virtual Herbarium and distributions coded based on major disjunctions. Ancestral area analyses were carried out in the R package BioGeoBEARS comparing four different biogeographic models.

The phylogenomic analysis provided a well-resolved and highly supported phylogeny of Pterostylidinae. The monophyly of the subtribe was supported, and three main lineages were retrieved that were highly supported. Molecular divergence estimations provided the first insights into the temporal evolution of Pterostylidinae and placed the origin of the subtribe into the Eocene. Ancestral range reconstruction and character mapping of key floral characters provided insight into biogeographical and character evolution within Pterostylidinae. Further, the phylogenomic reconstruction allowed for a re-assessment of divergent taxonomic concepts within the subtribe.

Student Presenter

SASB Distinguished Research Award

Plenary – The Braggs

17:30–18:00

The rise and rise of systematics

Mark S. Harvey

Department of Terrestrial Zoology, Western Australian Museum and School of Animal Biology, The University of Western Australia

End of Monday

Tuesday

Keynote Talk

Plenary – Horace Lamb

8:45–9:25

Can systematics evolve beyond its years?

T–P–1

Judy G West

Australian National Botanic Gardens, Canberra, ACT

Australia's unique biodiversity has stimulated and challenged our taxonomists and systematists in documenting the flora and fauna and in attempting to understand and unravel relationships and evolutionary histories. We have explored various ways of changing the business model, especially addressing impediments to the rate of progress and identifying tools and technologies to apply to the discipline. Biological systematics and the study of the diversification of living forms, is a field with a long history that in recent years has experienced a notable resurgence, particularly incorporating extensive use of molecular biology, the genome revolution and digital information systems. Can our biological community and infrastructure keep pace with the rapid technological changes that will help advance systematics? Impacts of the outcomes from systematics research and taxonomic decisions on other scientific fields such as conservation, functional biology and ecology will be discussed, together with the relationships between systematics and policy.

move into concurrent sessions

9:30–

Asian–Australian biotic exchange

Concurrent (I)—Horace Lamb

9:30–12:30

Crossing lines — a saurian perspective

T–1–2

Paul Oliver¹, Rebecca Laver¹, Nick Matzke¹, Craig Moritz¹ and Andrew Hugall²

¹Australian National University, Canberra, ACT; ²Museums Victoria, Melbourne, Vic

Since Alfred Russell Wallace, biogeographers have often focused on the differing character of the Asian (Sunda) and Australian (Sahul) biotas. However, many lineages have clearly dispersed between these regions. Here, for the most diverse component of the Australian endemic vertebrate fauna (lizards and snakes), we synthesise current data on the direction, timing, path and evolutionary consequences of these dispersal events. These data emphasise that the extant Sahul lizard fauna is dominated by lineages with Asian origins. Conversely, the very small number of lineages that may have recolonised Sunda tend to be species poor and ecologically marginalised. Dispersal events began in the late Oligocene to early Miocene. Island arcs between Australia and Asia may also have played an important role in dispersal and diversification since as long ago as the Oligocene. A majority of lineages show evidence of radiation and ecological diversification following colonisation of Australia. The numerous independent shifts between Asia and Australia provide an outstanding opportunity to compare and understand the processes shaping, and consequences of, dispersal between major biotic realms.

Murid rodents as a model for decoding the genomic basis of adaptive radiations across Indo-Australia

T-1-3

Emily J. Roycroft^{1,2}, Adnan Moussalli¹ and Kevin C. Rowe¹

¹Sciences Department, Museums Victoria, Melbourne, Vic; ²School of BioSciences, The University of Melbourne, Vic

Murid rodents (old world rats, mice and gerbils) are the most species rich mammalian family, and are renowned for their exceptional propensity for over-water colonisation. Rodents of the Indo-Australian Archipelago have transitioned from the Sunda region across Wallace's Line on at least ten independent occasions to reach Sulawesi (7 colonisations), the Philippines (3 colonisations, 2 from Sulawesi) and Sahul (2 colonisations from Sulawesi or the Philippines). These transitions into novel environments were followed by rapid adaptive evolution to fill a range of ecomorphological niches (e.g. arboreal, amphibious, saltatorial, vermivorous, folivorous). Extensive trait convergence, divergence and parallelism across these independent radiations enable us to examine drivers and constraints of ecological opportunity and adaptive evolution.

Using genomic data, we can begin to understand the genetic basis of adaptive evolution, including insights into a putative molecular basis for convergent evolution. Using phylogenomic data, we characterise the rapid radiation of rodents since their colonisation of Sahul c. 7 million years ago, and in the context of broad scale patterns across the Indo-Australian Archipelago.

Student Presenter

Phylogenomics and biogeography of the pythons— a Trans-Wallacean clade of giant snakes

T-1-4

Damien Esquerré¹, Stephen Donnellan², Alan Lemmon³, Emily Lemmon³, Ian Brennan¹, Hussam Zaher⁴, Felipe Grazziotin⁴ and Scott Keogh¹

¹The Australian National University, ACT; ²The University of Adelaide, SA; ³Florida State University, FL, USA; ⁴University of São Paulo, Brazil

The last years have seen great advances in genomic data production for use in phylogenetic inference. Among these methods, anchored hybrid enrichment phylogenomics is one that can produce hundreds of independent nuclear loci that vary in informativeness from deep to shallow evolutionary time-scales. We used this method to obtain 376 loci and used coalescent and coalescent-based species tree methods to reconstruct the phylogenetic history of pythons, one of the most morphologically and size diverse families of reptiles. There are 44 species that are found across the Old World tropics and subtropics. However, by far their greatest phenotypic and taxonomic richness is found in the Australo-Papuan region. Using fossil calibrations, our results show that pythons more likely did not originate in Africa but in Asia, and from there migrated through Wallacea into Australasia giving rise to their most diverse clade.

Student Presenter

Scott V.C. Groom

School of Agriculture, Food and Wine, University of Adelaide, SA

The Australian bee fauna is considered one of the most unique in the world. Over two-thirds of species represent one family, Colletidae, with its exclusively-Australian sister clade, Stenotritidae, the only known endemic bee family in the world. Yet, otherwise globally-distributed families are absent. Several recent papers have provided insight into the timing of divergence and subsequent radiations, highlighting the importance of continental connections to the assembly of our bee fauna. Early components comprised a common ancestor of Colletidae and Stenotritidae that traversed cool Antarctic forests, a typical constraint for bees potentially eased by floral associations maintained in extant lineages. But the subsequent exchange with Asia facilitated an influx of multiple major bee groups, many resulting in very broad radiations across and out of Australia. Given the role of bees as pollinators, these two distinct periods have implications for the evolution of the Australian biota and how it has influenced neighbouring regions.

Katharina Nargar^{1,2}, Natascha Wagner³, A. Kamolphet Atsawawaranunt⁴, Lars Nauheimer¹ and Mark Clements⁵

¹Australian Tropical Herbarium, Cairns, Qld; ²CSIRO National Collections and Marine Infrastructure, ACT; ³University of Göttingen, Göttingen, Germany; ⁴Imperial College London, London, UK; ⁵Centre for Australian National Biodiversity Research, ACT

Australia harbours a rich and highly endemic orchid flora, with 90% of species occurring nowhere else, and many threatened species. A recent phylogenomic study identified Australia as the second most important source area in the evolution of Orchidaceae. However, the spatio-temporal evolution of Australasian orchid lineages, their origin and their biogeographic relationships with neighbouring regions across Wallace's Line is still poorly understood.

Here we present a phylogenomic study of two contrasting, large orchid lineages of the Australian flora: the mainly temperate, terrestrial orchid tribe Diurideae with centre of diversity in Australia and the mainly tropical, epiphytic orchid subtribe Dendrobiinae with centres of diversity in Asia and New Guinea. Maximum likelihood analyses and Bayesian tree inference were carried out with RAxML and MrBayes based on concatenated alignments of c. 46,000 bp length representing 64 plastid genes. Divergence time estimation was conducted based on fossil and secondary calibration points in BEAST. Distributions were coded based on major disjunctions, and ancestral areas were reconstructed based on the BEAST chronogram using model based inference methods using BioGeoBears.

The phylogenetic analyses for these two highly diverse groups yielded well resolved and supported tree topologies. This greatly improves our understanding of phylogenetic relationships within Diurideae and Dendrobiinae, e.g. the relationships between the nine Diurideae subtribes are now fully resolved and well supported. The ancestral area analyses revealed contrasting biogeographic histories for Diurideae and Dendrobiinae and provided further insights into the floristic interchange between Sunda and Sahul and the assembly of the Australian orchid flora.

Origins of the northern Australian flora – role of the Sunda-Sahul floristic exchange

T-1-7

Elizabeth M. Joyce^{1,2}, Lars Nauheimer¹, Katharina Nargar^{1,3}, Joseph A.M. Holtum^{4,5}, Kevin R Thiele⁶ and Darren M Crayn^{1,3}

¹Australian Tropical Herbarium, James Cook University, Cairns, Qld; ²College of Science and Engineering, James Cook University, Cairns, Qld; ³Centre for Tropical Biodiversity and Climate Change, James Cook University, Cairns, Qld; ⁴Centre for Tropical Biodiversity and Climate Change, James Cook University, Townsville, Qld; ⁵Smithsonian Tropical Research Institute, Balboa, Ancón, Republic of Panama; ⁶School of Biological Sciences, The University of Western Australia, WA

The origins, evolution and exchange of the Sundanian, Wallacean and Sahulian floras remains poorly understood. Most studies exploring floristic exchange in this region have been founded on evidence from the fossil record, assumptions of origin based on areas of species diversity and endemism, or have examined biogeographic patterns of single lineages. This study aims to achieve a more complete and rigorous characterisation of the spatio-temporal patterns of the Sunda-Sahul floristic exchange by comparing multiple dated molecular phylogenies of lineages distributed across Sunda, Wallacea and Sahul. Dated phylogenies will be generated from published, unpublished and *de novo* sequence data using consistent methodologies to enable meaningful comparisons of timing and directionality of exchange. This research will be focussed on identifying the origins of the northern Australian flora, exploring the role of biome conservatism in the exchange and identifying dispersal tracks between Sunda and Sahul. A major outcome for this research will be the compilation of a database of phylogenies for regional lineages to encourage further empirical research into the origins and biogeography of flora as new information emerges in this complex and understudied region.

Student Presenter

Sarah Mathews¹, Campbell O. Webb² and Teguh Triono³

¹Australian National Herbarium, CSIRO, Canberra ACT; ²University of Alaska Fairbanks, Fairbanks AK, USA; ³The Indonesian Biodiversity Foundation, Jakarta, Indonesia

To better understand the biogeography of Indonesian forests and to link data on regional diversification and local community assembly, we collected DNA barcodes from five pairs of forest plots on five islands, Borneo, Flores, Seram, Sulawesi, and Waigeo. We are analysing the barcoding data along with data from focal genera to understand where ancestral taxa originated and how they spread across the archipelago, diversified within islands, and assembled into communities. Working with Indonesian botanists, students, members of local villages and their governments, herbarium specimens, tissue samples, and high-resolution photographs were collected for each individual. All data and images were uploaded to malesia.info and field-based taxon determinations were checked by a team at the Bogor Herbarium. Taxon-specialists also participated in determinations by accessing the uploaded images. Preliminary analyses of phylogenetic floristic structure suggest that the presence and absence of major clades such as palms and lowland conifers drives the deep phylogenetic structure of Indonesian islands. These analyses also provide some evidence that Seram has an overabundance of locally diversified clades, but provide little evidence of within-community phylogenetic structure. Preliminary biogeographic analysis of *Syzygium*, one of the more species-rich genera that was sampled, suggest that from Sulawesi, *Syzygium* spread to Borneo and Papua, three times to each island. This talk will discuss results from expanded biogeographic analyses of several of the more species-rich genera, including *Aglaiia*, *Artocarpus*, *Diospyros*, and *Syzygium*, and include a greater sample of species from outside of Indonesia.

Asian–Australasian biotic exchange – phylogenomic insights from the mega diverse genus *Bulbophyllum* (Orchidaceae) T–1–9

Lalita Simpson^{1,2}, Mark Clements³, Darren Crayn^{1,2} and Katharina Nargar^{1,2}

¹Australian Tropical Herbarium, James Cook University, Cairns Qld; ²Centre for Tropical Biodiversity and Climate Change, James Cook University, Townsville, Qld; ³Centre for Australian National Biodiversity Research, CSIRO Plant Industry, Canberra, ACT

The mainly epiphytic orchid genus *Bulbophyllum* (Dendrobieae, Bulbophyllinae) is the second largest genus of flowering plants with c. 2200 species in 97 sections. The genus has a pantropical distribution with main centres of diversity in Australasia (New Guinea) and Asia, which harbour 67 sections and c. 1700 species. So far, phylogenetic relationships and the spatio-temporal evolution of *Bulbophyllum*, in particular of the Asian and Australasian lineages, have been little investigated.

Broad-level phylogenetic relationships were inferred based on a plastid data set of 70 genes and 53 samples representing all major lineages within the genus and over 60% of Asian and Australasian sections. Within the Australasian section *Adelopetalum*, interspecific relationships were reconstructed based on a supermatrix of 71 plastid and nuclear markers. Species distributions were downloaded from the Atlas of Living Australia and GBIF and distributions coded based on major disjunctions. Molecular divergence dating was carried out in BEAST based on one fossil and three secondary calibration points and ancestral area analyses were conducted comparing four different biogeographical models in BioGeoBEARS. Population genomic analyses based on restriction site associated DNA sequences (ddRAD) of two endemic species of the Australian Wet Tropics region were undertaken, and phylogeographic patterns examined.

The three phylogenomic studies provide new insights into evolutionary relationships within *Bulbophyllum* at different taxonomic scales and elucidate the spatio-temporal evolution of the genus in the Asian-Australasian region.

Student Presenter

Andrew Hugall

Sciences Department, Museums Victoria, Melbourne, Vic

Since Joseph Banks there has been a long-standing debate on why the Australian continent has such a distinctive biota, with Hooker (1859) the first to recognise the deep historical origins as a mix of “Antarctic and tropical elements”—the Gondwanan endemic overlain by a more recent immigrant component. After the major compilations of Keast (1959–81), and in the absence of a precise fossil record, molecular phylogenetic research over the last twenty years is now providing information on the origins and age of major components of this biota. The issues now are how to best synthesise this information and represent what patterns it reveals. I will present some approaches—and pitfalls—to these matters, drawn from my back-catalogue of snails, lizards, birds and brittlestars; keeping in mind that often the key issues are not so much methodological as inferential.

Plastome-scale sequencing and a methodological arsenal begin to unravel the evolutionary history of *Pimelea* (Thymelaeaceae)

T-1-11

Charles S.P. Foster, Murray J. Henwood and Simon Y.W. Ho

School of Life and Environmental Sciences, University of Sydney, Sydney, NSW

Data sets comprising small numbers of genetic markers are not always able to resolve phylogenetic relationships. This has frequently been the case in molecular systematic studies of plants, with many analyses being based on sequence data from only two or three chloroplast genes. An example of this comes from *Pimelea* Banks & Sol. ex Gaertn. (Thymelaeaceae), a large genus of flowering plants predominantly distributed in Australia. Despite the considerable morphological variation in the genus, low sequence divergence in chloroplast markers has led to the phylogeny of *Pimelea* remaining largely uncertain. In this study, we resolve the backbone of the phylogeny of *Pimelea* in comprehensive Bayesian and maximum-likelihood analyses of a plastome-scale data set from 41 taxa. However, some relationships received only moderate to poor support, and the *Pimelea* clade contained extremely short internal branches. By using topology-clustering analyses, we demonstrate that conflicting phylogenetic signals can be found across the gene trees estimated from chloroplast protein-coding genes. A relaxed-clock dating analysis reveals that *Pimelea* arose in the mid-Miocene, with most divergences occurring during a rapid radiation. Our new phylogenetic estimate offers better resolution and is more strongly supported than previous estimates, providing a platform for necessary future taxonomic revisions of both *Pimelea* and the broader subfamily. Our study has demonstrated the substantial improvements in phylogenetic resolution that can be achieved using plastome-scale data sets in plant molecular systematics.

Student Presenter

Lunch

Tuesday, 12:30–13:15

The systematics and host associations of the Australian parasitic wasp genus *Gasteruption* (Hymenoptera: Gasteruptionidae) T-2-2

Ben A. Parslow¹, Michael P. Schwarz¹, Michael G. Gardner¹ and Mark I. Stevens²

¹College of Science and Engineering, Flinders University, Adelaide, SA; ²South Australian Museum, Adelaide, SA

Wasps in the genus *Gasteruption* (Hymenoptera: Gasteruptionidae) are an ancient and highly diverse group whose larvae are predator-inquilines of cavity nesting bees and wasps. The current taxonomy is in a state of neglect in Australia, with an abundance of material in collections but limited information on their systematic relationships, biodiversity and the evolutionary relationships with their hosts. This project aims to review the genus in Australia by using an integrative taxonomy approach to assist in prioritising taxa for description. *Gasteruption* material stored in ethanol across Australian collections has been coarse-sorted using morphological characters before sequencing the CO1 mitochondrial gene to determine species delimitations. Priority taxa are selected based on the gene tree with additional nuclear DNA genes collected to produce a robust phylogeny of the genus. The preliminary phylogeny reveals high species diversity but low support for basal relationships. This study identifies numerous new species with host information while further sequencing will effectively better resolve the evolutionary relationships within the group.

Student Presenter

Using high-throughput amplicon sequencing to explore the biodiversity of Australian microgastrine parasitoid wasps T-2-3

Erinn Fagan-Jeffries¹, Steve Cooper^{1,2} and Andy Austin¹

¹Australian Centre for Evolutionary Biology and Biodiversity and Department of Genetics and Evolution, School of Biological Sciences, University of Adelaide, SA; ²Evolutionary Biology Unit, South Australian Museum, SA

The Microgastrinae are a large and diverse subfamily of endoparasitoid wasps of lepidopteran caterpillars. Approximately 97 species have been described from or have been introduced into Australia, but the real species diversity for the region is clearly much larger than this. Whilst thorough morphological taxonomic work is important for species descriptions, gaining a first impression of the species-richness of an under-studied group requires faster tools—namely molecular data. In this study, several museum ethanol collections were mined for hundreds of specimens of microgastrine wasps, which were then barcoded for the COI region using a pooled sequencing approach on an Illumina MiSeq System. Over 1000 specimens were acquired, 700 were extracted, and over 500 full COI barcodes were obtained. This study highlights DNA sequencing from older material employing high-throughput methods, and the importance of bulk ethanol museum collections (such as unsorted malaise traps) for biodiversity assessment and large scale phylogenetic work.

Student Presenter

The immature stages and biology of *Rotunda rotundapex* (Miyata & Kishida) (Lepidoptera: Bombycidae)

T-2-4

Rung-Juen Lin

Department of Life Science, National Taiwan Normal University, Taipei, Taiwan

The life history and general biology of *Rotunda rotundapex* are described and illustrated. We present an overview of the morphology, larval host plants and immature stages of this species. Eggs are laid in clusters and are covered by scales during female oviposition. Larvae feed on young leaves of *Morus* (Moraceae), and are yellow or white with black dots. The species is univoltine, and the life cycle from egg to adult is completed in about three weeks. Our morphological data provides basic information that compliments phylogenetic studies based on molecular data currently in progress. These studies aim to further our understanding of the evolutionary history and general biology of bombycid moths.

Student Presenter

Drivers of speciation in Fijian *Homalictus* – past climate cycles and geographic isolation

T-2-5

James Dorey¹, Mark Stevens^{2,3}, Alejandro Velasco Castrillon² and Michael Schwarz¹

¹College of Science and Engineering, Flinders University, Adelaide, SA; ²South Australian Museum, Adelaide, SA; ³School of Pharmacy and Medical Sciences, University of South Australia, Adelaide, SA

The theory of island biogeography remains an active area of research that is used to explain many ecological and biodiversity patterns on islands and island-like systems. A key parameter in island biogeography is topographic complexity, which is thought to increase available ecological niches that can be exploited through adaptive radiation. Recent studies have indicated that tropical ectotherms are often thermal specialists with low tolerance for changing climates. Using a combination of mtDNA barcoding and morphology we show a remarkable species diversity in an endemic monophyletic Fijian halictine bee clade, most of which are restricted to highlands. Our phylogenetic analyses provide little evidence for gradual extensions of elevational niches, such as predicted by the ‘taxon cycle’ hypothesis, and instead suggest that elevational niches are conserved across most speciation events. Mitochondrial variation within multiple species suggest recent genetic sweeps, possibly due to *Wolbachia*-like infections. Our results suggest that cool-adapted tropical ectotherms may have retreated into highland refugia during interglacial warming periods, promoting allopatric speciation. In turn, this would suggest a role for adaptive inertia, rather than adaptive radiation, for speciation in tropical islands.

Student Presenter

Multiple losses of defence hairs in cup moths (Lepidoptera: Limacodidae)

T-2-6

Yu-Chi Lin, Rung-Juen Lin and Yu-Feng Hsu

School of Life Science, National Taiwan Normal University, Taipei, Taiwan

Convergent evolution, the independent evolution of similar features in different evolutionary lineages, is an important and common phenomenon. It may reveal that natural selection produces optimal solutions to repeated problems posed by similar environments, or that constraints are caused by shared biases in the production of variation. The moth family Limacodidae has undergone an interesting morphological evolution. The Limacodidae are a broadly distributed monophyletic family containing three interesting and diverse larval types: (1) larvae with urticating (defensive) hairs, (2) larvae with detachable hairs, and (3) larvae without hairs. However, it remains unknown whether these morphological forms are synapomorphic traits or the result of convergent evolution in which the traits have evolved more than once. We collected limacodids from Australia and Asia to test these hypotheses of character evolution of larval morphology. The ancestral state reconstruction on a robust molecular phylogeny indicates that character transitions from defensive hairs to without defensive hairs has occurred independently in different lineages on different continents. While it has been demonstrated that larvae with defensive hairs are better adapted to avoid generalist predators, our result implies that larvae without defensive hairs may be suited to different ecological niches.

Student Presenter

Revision of ‘giant’ Collembola within Neanuridae reveals convergent evolution of character traits and lack of support for Uchidanurinae

T-2-7

Mark I. Stevens^{1,2} and Cyrille A. D’Haese³

¹South Australian Museum, Adelaide, SA; ²School of Pharmacy and Medical Sciences, University of South Australia, Adelaide, SA; ³MECADEV, UMR 7179 CNRS–MNHN, Dpt Systematics and Evolution, Muséum National d’Histoire Naturelle, CP50 Entomology, Paris, France

Collembola are often regarded as inconspicuous fauna inhabiting, but not restricted to, soils, leaf litter, and rotting wood. Within the latter, there are numerous species that play an important role as saproxylic decomposers in forest ecosystems in their contribution to nutrient cycling and some are amongst the largest Collembola known. Here, we compared specimens across relevant subfamilies within Neanuridae and outgroup representatives with a focus on the ‘giant’ Collembola from the subfamily Uchidanurinae within a phylogeny using four genes (mtDNA COI, 16S, 18S rDNA, D1-D5 of 28S rDNA). Interspecific variability in gross morphological characters was high. The genera and species relationships within the molecular phylogeny reveal that the subfamily Uchidanurinae do not form a natural group, and we discuss the placement of all genera involved based on morphological and molecular characters.

Species delimitation and description of scale insects (Eriococcidae) that induce galls on *Melaleuca* (Myrtaceae) T-2-8

Craig Edwards, Alicia Toon and Lyn Cook

School of Biological Sciences, The University of Queensland, Brisbane, Qld

Only four species of eriococcid (felt scale insects) have been described that induce galls on *Melaleuca*, all in the late 19th century. Over the past decade or so, specimens from over 400 populations of eriococcids that induce galls on *Melaleuca* have been collected from across Australia. We have sequenced specimens from most of these populations for the mitochondrial barcode gene, *COI*, as well as for three nuclear genes (*dynammin*, *enolase* and *18S*). Using congruence across gene trees as evidence for lack of recent gene flow, we think that there are at least thirty species yet to be described. We are also incorporating host use and morphology of galls and adult females in determining species boundaries. Galls are considered extended phenotypes of the inducers, but one problem we have encountered is that more than one gall form is sometimes present on the one plant. Using DNA barcoding, we are assessing whether the different galls represent a developmental series (ontogeny) or represent distinct species.

Student Presenter

Exploring the possible co-evolution of *Boronia* (Rutaceae) and their pollinator moths (Heliozelidae, Lepidoptera) T-2-9

Liz Milla¹, David Andre Young², Thérésa Melanie Jones¹, Axel Kallies¹ and Douglas James Hilton¹

¹The University of Melbourne, Melbourne, Vic; ²D'Estrees Entomology and Science Services, Kingscote, SA

Heliozelidae are a family of evolutionarily primitive, day-flying moths, often overlooked due to their tiny size. Rich undescribed diversity is found worldwide, particularly in Australia, where a subgroup of species have formed close associations with their native *Boronia* (Rutaceae) plant hosts. At least one of these associations appears to be an obligate mutualism, involving a rare case of active pollination. I will describe morphological and behavioural adaptations exhibited by several Heliozelidae species and morphological traits in their plant hosts that have potentially co-evolved. I will also examine signs of co-evolution in the molecular phylogenies of both moths and their hosts.

Student Presenter

Population structure of *Macrozamia* cycads and their *Cycadothrips* pollinators—congruence in a plant-pollinator obligate mutualism

T-2-10

Alicia Toon, Andrew Mather and Lyn Cook

School of Biological Sciences, The University of Queensland, Brisbane, Qld

Obligate pollination mutualisms are intimate relationships between plants and pollinators that because of their specificity are thought to track each other and coevolve. Several well studied angiosperm–pollinator systems exemplify these intricate interactions, yet little work has been done on similar systems in gymnosperms. Several species of *Macrozamia* cycads are pollinated exclusively by *Cycadothrips*, with which they have obligate relationships. Understanding the basis of this dependent interaction is essential for the management and conservation of threatened species of *Macrozamia*. We estimate population structure and recent phylogeographic history in closely related species of *Macrozamia* and compare them with patterns in *Cycadothrips*. We show that while patterns of structure are similar, *Macrozamia* and their thrips pollinators have vastly different tempos of evolution. We discuss the implications for conservation and management of obligate pollination mutualisms.

The evolution of Müllerian mimicry in Australian velvet ants T-2-11

Juanita Rodriguez¹, Kevin Williams², Claudia Schipp³, Thekla Pleines¹ and Joseph Wilson⁴

¹Australian National Insect Collection, CSIRO, Canberra, ACT; ²California Department of Food and Agriculture, Sacramento, California, USA; ³The University of Queensland, Brisbane, Qld; ⁴Utah State University, Tooele, Utah, USA;

Müllerian mimicry, in which two or more harmful species share a similar appearance for mutual benefit, is observed in vertebrate and invertebrate species worldwide, but most of the commonly studied systems only occur in the American tropics. This project aims to study Müllerian mimicry rings in Australian velvet ants with the use of morphological characters. Colouration patterns will be analysed using NMDS and human perception tests. For the first time, an Australian mimicry complex will be described. This will be the first step in our understanding the evolution of this mutualistic interaction for this continent. Future steps include molecular analysis and mimicry mapping to understand the evolution of this mimicry complex.

Lunch

Tuesday, 12:30–13:15

Keynote Talk

Plenary — Horace Lamb

13:15–13:55

Systematics and other collections-based sciences in the Anthropocene

T-P-12

Kristofer M. Helgen

Biological Sciences, The University of Adelaide, Adelaide, SA

Studies characterising biological variation, diversity, relationships, and distributions are enormously valuable to science and society and have been the main use for natural history museum collections for centuries. Even with rapidly changing technologies, such as genomic, biochemical, and imaging techniques, systematics and biogeography remain the principal collections-based disciplinary emphases for biological research programs. Studies relevant to modern environmental change, and health and disease, among other subjects, also represent important uses for archived biological collections, though these receive less attention within natural history institutions, collections, or curator-led research programs. Very large economic and other impacts of rapidly changing environments, climates, and disease landscapes in the Anthropocene highlight a need for organised efforts to expand natural history research programs and training efforts to incorporate additional uses of collections to complement studies of systematic biology. Indeed, critical documentation of Anthropocene impacts, and the future of natural history museums, including public impressions of their relevance, may depend on it.

move into concurrent sessions

14:00–

Fine scale genetic variation and introgression in ash eucalypts in the highlands of Victoria

T-1-13

Alice Crowe¹, *Todd McLay², Frank Udovicic³ and Mike Bayly¹

*Presenting; ¹School of Biosciences, University of Melbourne, Melbourne, Vic; ²Centre for Australian National Biodiversity Research, CSIRO, Canberra, ACT; ³Royal Botanic Gardens Victoria, Melbourne, Vic;

Chloroplast genome introgression through hybridisation events is known to occur between many species of *Eucalyptus*, but the extent of nuclear genome introgression is less well known. We collected samples from four co-occurring species from four different locations in the Victorian highlands: *E. obliqua* and *E. regnans* (both green ashes); *E. pauciflora* and *E. delegatensis* (both blue ashes). Genome skimming was used to obtain the complete chloroplast genome for 128 samples. Five well-supported chloroplast clades were identified (54 total haplotypes); these clades showed little support for monophyletic species but a strong association with geographic locality. ddRAD-seq was used to obtain SNPs from the nuclear genome for 75 samples representing the four different species and the four locations. The nuclear data showed clear differentiation between species and a lower signal of introgression. Both the chloroplast and nuclear genome data was then analysed to identify loci that were under selection at the species level and between geographic locations; selection for genes at the landscape level may indicate the importance of hybridisation for obtaining locally adapted loci. Our results provide the most detailed investigation proving the extent of chloroplast genome sharing between species of *Eucalyptus* compared to a relatively low level of nuclear genome introgression.

Taxonomic clarification of the critically endangered *Notelaea ipsviciensis*

T-1-14

Gillian Brown¹, Laura Simmons¹ and Todd McLay²

¹Queensland Herbarium, DSITI, Brisbane Botanic Gardens, Toowong Qld; ²School of BioSciences, University of Melbourne, Melbourne, Vic

Notelaea ipsviciensis (Oleaceae) is a critically endangered species restricted to the Ipswich area or South East Queensland and has a very low total number of mature individuals recorded in the wild. It is considered to have close affinities to *N. ovata*, differing in leaf shape and venation pattern but there are several other species of *Notelaea* located close by, including *N. lloydii* and *N. macrocarpa*. There have been several suggestions that *N. ipsviciensis* may be a hybrid but no genetic studies have investigated this. The Queensland Department of Transport and Main Roads commissioned this study to determine whether *N. ipsviciensis* plants in the wild comprise a hybrid or distinct species. To do this we also aimed to build a phylogeny of *Notelaea* to determine the placement of *N. ipsviciensis* in the genus.

Field collections were supplemented with herbarium specimens to sample 144 individuals from 11 species of *Notelaea*. Samples of *N. ipsviciensis* and putative parents were collected in the field but due to smaller than anticipated population sizes, particularly in *N. microcarpa* and *N. ovata*, these were supplemented with herbarium specimens from the Queensland Herbarium (BRI). A new method, RAPDseq, was used to generate SNP data for phylogenetic and population genetic analyses. The results of these will be presented, the taxonomic nature of *N. ipsviciensis* will be clarified and conservation implications discussed.

Untangling the systematics and invasion history of *Lantana camara*

T-1-15

Patricia Lu-Irving¹, Richard G. Olmstead² and Katrina M. Dlugosch¹

¹University of Arizona, Tucson, Arizona, USA; ²University of Washington, Seattle, Washington, USA

The *Lantana camara* species complex includes some of the world's most highly invasive plants, but their classification and identification is made difficult by complicated patterns of morphological variation and introgression. The taxonomic challenges posed by the complex hinder weed control efforts, and obscure the number and origins of invasive taxa. It has recently been proposed that successful invaders represent three separate species, implying three independent origins of invasiveness. We evaluated genomic support for this hypothesis using restriction site-associated DNA tag sequencing (RADseq) to generate single-nucleotide polymorphism (SNP) data for a sample of populations representing both the native and invaded range of the *Lantana camara* complex. The implications of our findings will be discussed in the broader contexts of systematics and conservation.

Posters and Afternoon Break

Tuesday, 14:45–15:30

ASBS AGM and business meeting

(Horace Lamb) 15:30–16:30

Surprising schizomids (Arachnida)—a *Draculoides* in disguise and other oddities

T-2-13

Kym Abrams^{1,2}, Joel Huey^{1,2}, Mia Hillyer², Mark Harvey^{1,2} and Raphael Didham^{1,3}

¹School of Biological Sciences, The University of Western Australia, Perth, WA; ²Terrestrial Zoology, Western Australian Museum, Perth, WA; ³CSIRO Land and Water, Perth, WA

Schizomids are a small group of arachnids, comprising about 304 species worldwide. Their typical habitat is leaf litter, soil or cave environments and because of this, they are rarely seen and less widely known than their distant relatives, the spiders and scorpions. Australia currently has the most diverse schizomid fauna, with 53 described species. Our current project has been investigating a large collection of specimens (more than 2000) held at the Western Australian Museum, using molecular and morphological methods. Recent research has revealed a large subterranean radiation of schizomids in the Pilbara with approximately 70 putative new species awaiting description. Until now, all of those species belonged to two closely related genera, *Draculoides* and *Paradraculoides*. Here we report on a new genus in the Pilbara, which has unusual biogeographic affinities to surrounding bioregions including Cape Range and islands of the Buccaneer and Bonaparte archipelagos of the Kimberley. While faunal surveys have been run for many years in the Pilbara, new taxa are still consistently being discovered. Most schizomids have narrow ranges that overlap with mining activities, rendering them vulnerable to extinction. Consequently, ten species are listed as either ‘endangered’ or ‘vulnerable’ under the WA *Wildlife Conservation Act 1950*. Effective conservation and management of schizomids is currently hindered by a lack of knowledge of the diversity and distributions of this group, which our project aims to overcome.

Australian Arachnology advanced through European heritage— the origin of spider research in Australia and the importance of the Godeffroy Collection for current spider taxonomy and diversity assessments

T-2-14

Barbara Baehr

Biodiversity and Geosciences, Queensland Museum, Brisbane, Qld

The historical Godeffroy Collection of spiders at the Centre for Natural History (CeNak) in Hamburg comprises several hundred type specimens from Australia which are an essential source for Australian spider taxonomists. Taxonomists working with this collection are faced with the usual problems of old collections, the necessity to re-interpret locality data, unclear type status of the specimens and the original type specimens have long been difficult to access.

Sometimes, this may hamper taxonomic progress and one prime example is that of the Lynx Spiders (family Oxyopidae) in Australia where no taxonomic revision so far exists. The published record of Australian Oxyopidae lists 14 *Oxyopes* species of which the types of 13 species are at CeNak.

Most specimens were collected by C.F. Eduard Dämel for the Godeffroy Museum and described in 1878 by pioneering arachnologist Ludwig Carl Christian Koch as part of the first monograph on Australian spiders: *Die Arachniden Australiens*. Twelve species were redescribed and properly illustrated during the documentation of the Australian types in June 2017: *Oxyopes amoenus* L. Koch, 1878, *Oxyopes attenuatus* L. Koch, 1878, *Oxyopes elegans* L. Koch, 1878, *Oxyopes gratus* L. Koch, 1878, *Oxyopes gracilipes* (White, 1849), *Oxyopes macilentus* L. Koch, 1878, *Oxyopes molarius* L. Koch, 1878, *Oxyopes mundulus* L. Koch, 1878, *Oxyopes punctatus* L. Koch, 1878, *Oxyopes quadrifasciatus* L. Koch, 1878, *Oxyopes rubicundus* L. Koch, 1878, and *Oxyopes variabilis* L. Koch, 1878. *Oxyopes lautus* L. Koch, 1878 is treated as a *nomen dubium* because both palps are lost.

Six syntypes of *Oxyopes elegans* L. Koch, 1878 actually include three females of *Oxyopes elegans*, one male of *Oxyopes gracilipes* and two females of the new species, *Oxyopes godeffroyi* Baehr et al., 2017.

As *Oxyopes* species are often used in biodiversity assessments it is vital to get the identification right!

Phylogenetic relationships of the Australian open-holed trapdoor spiders (Nemesiidae: Anaminae)—a multi-locus molecular analysis resolves generic classification

T-2-15

Mark S. Harvey^{1,2}, Mia J. Hillyer¹, Barbara Y. Main², Timothy A. Moulds¹, Robert J. Raven³, Michael G. Rix^{1,3,4}, Cor J. Vink⁵ and Joel A. Huey^{1,2}

¹Department of Terrestrial Zoology, Western Australian Museum, WA; ²School of Animal Biology, The University of Western Australia, WA; ³Biodiversity and Geosciences, Queensland Museum, Qld;

⁴Australian Centre for Evolutionary Biology and Biodiversity, School of Biological Sciences, The University of Adelaide, SA; ⁵Canterbury Museum, Christchurch, New Zealand

The spiders of the mygalomorph family Nemesiidae occur in many different parts of the world. Past morphological and molecular studies suggest the family is not monophyletic and that the subfamily classification is unstable. The most diverse nemesiid group in the Australasian region, the subfamily Anaminae, is currently represented by 12 valid genera, but the status of some, such as *Chenistonia*, has vacillated in different taxonomic treatments. Using a wide selection of specimens from Australia and New Zealand, we evaluate the relationships of the Australasian members of Anaminae using two different analyses. The first added several new 18S and 28S ribosomal RNA and Elongation Factor 1 gamma (EF-1 γ) sequences to a previously published dataset; the resulting tree showed that most Australasian Anaminae formed a monophyletic group, but that the genus *Stanwellia* failed to group with this clade. The second analysis recovered three major clades using mitochondrial (12S and 16S ribosomal RNA, CO1) and nuclear (18S and 28S ribosomal RNA, Histone 3) sequence data. The results of the study are used to stabilise the generic classification. Molecular divergence dating revealed that the major Australian radiation occurred during the Miocene, with multiple independent incursions from temperate habitats into the arid zone. The New Zealand exemplars of *Stanwellia* analysed for this study were nested deeply within a clade including otherwise Australian taxa, with a highest posterior density divergence estimate for the entire genus of between 8 and 38 Mya, strongly suggesting that their presence in New Zealand is the result of transoceanic dispersal, rather than continental vicariance.

Systematics, biogeography and conservation of Australia's spiny trapdoor spiders (Idiopidae) – progress and prospects T-2-16

Michael Rix^{1,2,3}, Andy Austin², Steve Cooper⁴, Mark Harvey³, Robert Raven¹ and Jeremy Wilson¹

¹Biodiversity and Geosciences Program, Queensland Museum, Brisbane, Qld; ²School of Biological Sciences, University of Adelaide, Adelaide, SA; ³Department of Terrestrial Zoology, Western Australian Museum, Perth, WA; ⁴South Australian Museum, Adelaide, SA

The arbanitine spiny trapdoor spiders (Idiopidae) are an iconic and highly diverse component of the Australasian ground-dwelling spider fauna, renowned for their longevity, cryptic fossorial life history, biogeography and conservation significance. The Australian fauna is remarkably diverse and highly endemic, with southern-temperate ‘on-the-continent’ biogeographic origins, and four lineages that have independently radiated in the arid zone since the Eocene. Using integrative molecular methods and comprehensive monography, we have now started to understand the phylogeny, biogeography and species-level taxonomy of these spiders across mainland Australia. These insights have revealed a complex fauna of unexpectedly high diversity, especially in the transitional and arid zones of Western Australia, where topography, substrate heterogeneity and rainfall appear to be important drivers of speciation. The biodiversity hotspot of south-western Australia is especially diverse, although severe population declines in some species are evidence of an increasingly threatened fauna. We outline how molecular phylogenetic research, complementary taxonomic revisions and detailed natural history studies have helped to shine a light on the Idiopidae of Australia, and how a ‘conservation systematics’ approach may help to conserve these spiders in the future.

Cor J. Vink

Canterbury Museum, Christchurch, New Zealand

A massive phylogenetic analysis of spiders, which has been over ten years in the making, has recently been published by Wheeler et al. 2016. The phylogenetic analysis was performed on a dataset of 932 spider species, representing 115 families, 700 known genera and additional representatives of 26 unidentified or undescribed genera. The dataset includes DNA sequences from three mitochondrial genes (12S, 16S, COI) and three nuclear genes (histone H3, 18S, 28S). These were analysed by multiple methods, including constrained analyses using a highly supported backbone tree from transcriptomic data. Most of the higher-level structure of the spider tree was well supported. New Zealand spiders make up 9% of the species in the phylogeny, which is pretty good considering its fauna is 1–2% of the world fauna. This indicates the importance of the New Zealand spider fauna when trying to understand spider systematics.

Of particular relevance to the New Zealand fauna is the support for a large group termed the marronoid clade, which includes the families Amaurobiidae, Desidae, Dictynidae, Hahniidae, Stiphidiidae, Agelenidae and Toxopidae. These families have been redefined and New Zealand genera have been moved around between them. Numerous New Zealand species in the marronoid clade can be a source of misery when trying to identify them to family but now many can be cast into Desidae, which has been redefined to include five subfamilies, four of which are found in New Zealand: Amphinectinae, Ischaleinae, Porteriinae and Desinae.

Spiny trapdoor spiders (*Euoplos*) of eastern Australia—broadly sympatric clades are coupled with burrow architecture and male morphology

T-2-18

Jeremy D. Wilson¹, Jane M. Hughes¹, Robert J. Raven¹, Michael G. Rix² and Daniel J. Schmidt¹

¹Australian Rivers Institute, Griffith University, Nathan, Qld; ²Biodiversity and Geosciences Program, Queensland Museum, Brisbane, Qld

Spiders of the infraorder Mygalomorphae are becoming model organisms for the study of biogeography and speciation. However, these spiders can be difficult to study in the absence of fundamental life history information. In particular, their cryptic nature hinders comprehensive sampling, and linking males with conspecific females can be challenging. Recently discovered differences in burrow entrance architecture and male morphology indicated that these challenges may have impeded our understanding of the trapdoor spider genus *Euoplos* Rainbow, 1914 in Australia's eastern mesic zone. We investigated the evolutionary significance of these discoveries using a multi-locus phylogenetic approach. Our results revealed the existence of a second, previously undocumented, lineage of *Euoplos* in the eastern mesic zone. This new lineage occurs in sympatry with a lineage previously known from the region, and the two are consistently divergent in their burrow entrance architecture and male morphology, revealing the suitability of these characters for use in phylogenetic studies. Divergent burrow door architecture and observed differences in microhabitat preferences are suggested to facilitate sympatry and syntopy between the lineages. Finally, by investigating male morphology and mapping it onto the phylogeny, we revealed that the majority of *Euoplos* species remain undescribed, and that males of an unnamed species from the newly discovered lineage had historically been linked, erroneously, to a described species from the opposite lineage. This paper clarifies the evolutionary relationships underlying life history diversity in the *Euoplos* of eastern Australia, and provides a foundation for urgently needed taxonomic revision of this genus.

Student Presenter

Renan Castro Santana^{1,2}, Bryan G. Fry¹, Robert J. Raven² and Lyn Cook¹

¹School of Biological Science, University of Queensland, Brisbane, Qld; ²Department of Terrestrial Environment, Queensland Museum, Brisbane, Qld

With the increase in the use of molecular data in taxonomic revisions of Australian mygalomorph spiders, new genera and many cryptic species are being revealed. To date, the systematic studies of Australian tarantulas have not incorporated such data. Indeed, apart from *Coremiocnemis tropix*, no tarantulas have been described for Australia for over a century.

The Eastern Australian tarantula is the biggest spider species in Australia and has an extensive distribution, from the tropical lowland forests near Rockhampton to the tropical rainforests and savannahs of Cape York. Here, we re-evaluate the species status of the Eastern Australian tarantula using DNA sequence data from multiple mitochondrial and nuclear loci. The phylogeography of the species will also be discussed.

Student Presenter

Nancy T. Burbidge Medal Presentation and Address

Plenary – Horace Lamb

16:30–17:30

Conference Dinner

National Wine Centre

18:30–

Wednesday

Keynote Talk

Plenary – Horace Lamb

8:45–9:25

Out of sight, out of mind – marine invertebrate systematics and conservation

W-P-1

Nerida G. Wilson

Western Australian Museum, Perth, WA

Marine invertebrates are considerably neglected with regard to conservation actions. There are a number of reasons for this, and here I review some of the similarities and differences with terrestrial systems. There are few fundamental differences, but some of the obvious ones have serious ramifications. As with most biodiversity conservation efforts, the ‘taxonomic impediment’ continues to hamper efforts worldwide. I will present case studies for the Rhodopemorpha, an interstitial worm-like gastropod, and for the Xenoturbellida, a deep-sea invertebrate. I will discuss known marine invertebrate extinctions and contemporary conservation actions in Australian systems. Here I advocate for a ‘slow food movement’ analogue in science that can promote and sustain research on rare or difficult to access species. This is the only way that we can gather the information necessary to properly assess the conservation needs of taxa, which are currently slipping through cracks in the legislative process.

move into concurrent sessions

9:30–

Towards subterranean fauna conservation in arid Australia— realisation, establishment and consolidation

W-1-2

William F. Humphreys

Western Australian Museum, WA; School of Biological Sciences, The University of Western Australia, WA; School of Earth and Environmental Sciences, The University of Adelaide, SA; Western Australian School of Mines, Faculty of Science and Engineering, Curtin University, WA

Expeditions in the late 1980s to Cape Range in north-western Australia uncovered a diverse relictual rainforest fauna inhabiting caves. The presence of arid zone subterranean faunas has now been extended to cover the Western Shield of Australia—notably lacking caves and so accessed down boreholes—and in inland Northern Territory and South Australia. Together, researchers from more than 30 countries have uncovered an estimated several thousand subterranean species some having Tethyan or Gondwanan connections.

Grant funded research through the Yilgarn recorded subterranean fauna distinct from the Pilbara with over 70 priority conservation areas recognised for subterranean fauna.

There was early recognition of the significance of these faunas and their frequent association with resources (water, petroleum, soft and hard rock mines). This led to the Western Australian Environmental Protection Authority to require, uniquely, the inclusion of subterranean fauna in the environmental approval process and to develop standards for subterranean fauna sampling.

The EPA requirements led to massive and intensive collecting of subterranean fauna in the mineraliferous Pilbara region suitable for DNA. An enormous diversity of subterranean taxa was and continues to be discovered, mostly by consultants and largely comprising very short range endemic species.

The extensive and intensive collections from the contiguous regions have and are being used as a foundation from which to construct regional scale molecular phylogenies alongside taxonomic studies of various orders, especially crustaceans which dominate the stygofauna and arachnids prominent in the troglofauna.

The profusion of biogeographic and systematic studies in the Pilbara has not, generally, been coupled with any great understanding of the natural history and ecology at the population or community levels, nor of ecosystem functioning. This absence has been recognised and broad based ecological studies are currently being developed through the conservation agency to inform conservation management in an area of intense mining activity overlaying the most diverse subterranean faunas globally.

Michelle T. Guzik¹, Steve J.B. Cooper^{1,2}, Andy D. Austin¹, Bill Humphreys³, Mia J. Hillyer⁴, Andrew M. Hosie³, Lisa Kirkendale⁵ and Joel A. Huey⁶

¹Australian Centre for Evolutionary Biology and Biodiversity, The University of Adelaide, SA; ²South Australian Museum, SA; ³Western Australian Museum, WA; ⁴Marine Zoology and Molecular Systematics Unit, Western Australian Museum, WA; ⁵Department of Aquatic Zoology, Western Australian Museum, WA; ⁶Terrestrial Zoology and Molecular Systematics Unit, Western Australian Museum, WA

Many groundwater aquifers are under significant anthropological pressure, as water sources for agriculture and mining operations. Also of concern is the impact that global climatic change may have on these groundwater ecosystems. Groundwater fauna have survived millions of years, including major climatic shifts during the Pleistocene and the spread of aridity on the Australian continent. However, future climatic conditions may lead to high evaporation with increasing global temperatures and reduced rainfall, resulting in a rapid reduction of groundwater recharge, potential increased salinization of groundwater and potential extinction of key macro-invertebrate taxa. If these groundwater ecosystems are to be preserved, it is important to develop robust methods that can be used to monitor fauna and predict the likely impact of environmental change. We aimed to develop novel molecular tools for biodiversity assessment in subterranean ecosystems. Such methods are currently not available for groundwater fauna, with environmental surveys generally relying on morphological assessment, requiring considerable taxonomic expertise to determine the presence or absence of subterranean species. With samples from one representative alluvial aquifer in the Pilbara, Western Australia, we have created a DNA barcode library to use for future environmental DNA (eDNA) metabarcoding methods. Preliminary results from this library reveal new and significant biodiversity, especially for the crustacean fauna. We will also outline how these results will be applied to implementing eDNA and next generation sequencing technology.

Systematics, evolution and conservation management of troglofauna from the Yilgarn calcretes

W-1-4

Steven J.B. Cooper^{1,2}, Mohammad Javidkar^{1,5}, Rachael A. King^{1,2}, Michelle T. Guzik¹, Mark I. Stevens^{2,4}, William F. Humphreys^{1,3} and Andrew D. Austin¹

¹Australian Centre for Evolutionary Biology and Biodiversity and School of Biological Sciences, The University of Adelaide, SA; ²South Australian Museum, Adelaide, SA; ³Western Australian Museum, Perth, WA; ⁴School of Pharmacy and Medical Sciences, University of South Australia, SA; ⁵Department of Biodiversity and Ecosystem Management, Environmental Sciences Research Institute, Shahid Beheshti University, Tehran, Iran

Groundwater calcretes of the Yilgarn region of central Western Australia contain a diverse aquatic subterranean (stygobitic) fauna, with species generally being endemic to individual isolated calcrete bodies (i.e. ‘subterranean islands’). Calcrete and groundwater are widely used as a resource in the mining industry and there is a potential for stygofaunal species to go extinct if these resources are not managed appropriately: maintaining groundwater levels within calcretes and providing adequate habitat for species to survive.

Surveys have also uncovered a diverse troglofauna (terrestrial subterranean fauna living above the water table), including species of a recently described isopod family/genus, Paraplatyarthridae: *Paraplatyarthrus*, and the collembolan genus *Pseudosinella*. Here, we present analyses of the diversification history of these genera in Western Australia, assessing the ‘subterranean island’ hypothesis using multi-gene phylogenetic and clock analyses, and further discuss the conservation management implications of these findings.

Our analyses suggest that the aridity of the Australian continent after the late Miocene (ca. 10 million years ago) was a major driver of the evolution of distinct isopod species, in line with the climate relict hypothesis of cave animal evolution. Troglobites (eyeless and pigmentless species) appear to have been restricted to individual calcretes over millions of years, and most likely evolved from troglophile (partial-eyed troglofauna) ancestral species. Several troglophile species were found in more than one calcrete body, reflecting an ongoing history of calcrete colonisation and diversification. A similar pattern of restricted and widespread ‘species’ or lineages was also found for Collembola, suggesting that species may be passively moved around the landscape during major flood events. Overall, our findings suggest that troglobites require similar conservation management strategies to stygofauna, but troglophiles may be less impacted by localised mining operations.

Preliminary analysis of metabarcoding for the assessment of stygofauna assemblages

W-1-5

Grant Hose, Kathryn Korbelt and Anthony Chariton

Department of Biological Sciences, Macquarie University, NSW

The cryptic nature of many stygofauna species and their heterogeneous distribution over space and time means that eDNA has great potential to improve bioassessments of groundwater ecosystems. The aim of this study was to compare assessments of groundwater bores using metabarcoding of 18S rDNA with traditional assessments of stygofauna identified from sediments and groundwater collected using from pumping and net hauls. Sampling was undertaken in shallow alluvial aquifers across the Murray-Darling Basin in western NSW and southern Queensland.

As expected, 18S rDNA amplicon sequencing identified a large number of micro eukaryote taxa not found in the pump/net collected samples. Importantly however, large crustaceans including amphipods that were recovered in the traditional samples were not identified in the amplicon sequencing. The lack of some stygofauna in the amplicon sequencing highlights the need for using multiple primers in eDNA studies of groundwater and reflect common difficulties in barcoding with crustaceans. We discuss further the limitations of using eDNA in groundwater and potential solutions to the challenges faced.

Identifying short range endemic Parabathynellidae (Crustacea: Bathynellacea) and stygofauna in the Pilbara and Browns Range, Western Australia

W-1-6

Emma Matthews¹, Michelle Guzik¹, Andrew Austin¹, Joel Huey², Kym Abrams², Mia J. Hillyer³ and Bill Humphreys²

¹The Australian Centre for Evolutionary Biology and Biodiversity, The University of Adelaide, Adelaide, SA; ²Terrestrial Zoology and Molecular Systematics Unit, Western Australian Museum, WA; ³Marine Zoology and Molecular Systematics Unit, Western Australian Museum, WA

Western Australia's groundwater systems have a highly diverse and unique subterranean stygofauna. Threatened by human activities such as mining, and comparatively poorly described, stygofauna in the Pilbara are a conservation priority. Parabathynellids are an ancient family of tiny microcrustaceans, which are diverse in Western Australia, and are considered strong bioindicators, both signifying and maintaining healthy subterranean ecosystems.

This study places Pilbara and Browns Range Parabathynellidae in the existing evolutionary framework to present a revised phylogeny using DNA barcoding and multigene phylogenetic analysis. Conservatively, 24 new putative parabathynellid lineages from Western Australia were identified, with most constricted to a single borehole, or several very closely positioned sites. Exceptional genetic diversity among parabathynellids was observed, with typical genetic differences between taxa as high as 20–30%, highlighting the susceptibility of these ancient, and highly isolated organisms to threats such as mining developments. This study contributes to the development of environmental DNA meta-barcoding tools by improving the DNA sequence database for Australian bathynellacean stygofauna. The continued documentation of stygofaunal groups will allow for the development of more effective biomonitoring tools for monitoring aquifer health, highlighting species and areas of conservation priority, and informing management of these unique systems.

Student Presenter

Taxonomy and sequence capture of *Haloniscus* isopods from threatened arid zone groundwater habitats

W-1-7

Danielle N. Stringer¹, Terry Bertozzi², Michelle T. Guzik¹, Simon M. Tierney^{1,3}, Rachael A. King^{1,2}, Karen Meusemann^{4,5,6}, Christoph Mayer⁶, Andreas Zwick⁴, Steven J.B. Cooper^{1,2} and Andrew D. Austin¹

¹Australian Centre for Evolutionary Biology and Biodiversity, School of Biological Sciences, The University of Adelaide, Adelaide, SA; ²Evolutionary Biology Unit, South Australian Museum, Adelaide, SA; ³Hawkesbury Institute for the Environment, Western Sydney University, Penrith, NSW; ⁴Australian National Insect Collection, CSIRO National Research Collections Australia, Canberra, ACT; ⁵Evolutionary Biology and Ecology, Institute for Biology I, University of Freiburg, Freiburg, Germany ⁶Centre for Molecular Biodiversity Research, Zoological Research Museum Alexander Koenig, Bonn, Germany

Groundwater-dependent ecosystems in the Australian arid zone comprise highly diverse populations of endemic invertebrates with complex evolutionary histories. However, exploitation of groundwater for mining, agricultural and domestic uses represents a significant threat to these important faunal communities. Most taxa are likely short-range endemics, ancient 'relict' species and act as essential bioindicators of ecosystem health and function. Therefore, a more detailed understanding of their systematics is fundamental for effective conservation management. *Haloniscus* isopods, in particular, are known from a number of groundwater systems across the arid zone, but the majority of species remain undescribed and their species diversity for many locations is poorly known, with molecular datasets so far limited to single genetic markers. We aimed to investigate the evolution and systematics of *Haloniscus* from three disparate groundwater-dependent ecosystems using a next-generation sequencing approach, and to describe new species from Great Artesian Basin springs in South Australia. Transcriptome data were utilised to develop a custom ortholog set (469 genes) and bait design for targeted sequence capture to explore *Haloniscus* diversity. This gene set will significantly increase the number of genetic markers available for isopod phylogenetics and has the potential to be used more broadly for future monitoring and management of threatened species. Here we present details on the methodological processes undertaken and discuss our preliminary phylogenetic and morphological findings.

Where to draw the line? Defining stygobitic amphipod species for conservation and management

W-1-8

Rachael A. King^{1,2}, Stephen J.B. Cooper^{1,2}, Nicholas Murphy³, William F. Humphreys⁴ and Andrew D. Austin¹

¹Australian Centre for Evolutionary Biology and Biodiversity and School of Biological Sciences, The University of Adelaide, Adelaide, SA; ²South Australian Museum, Adelaide, SA; ³La Trobe University, Bundoora, Vic; ⁴Western Australian Museum, Welshpool, WA

Amphipod crustaceans are a dominant faunal group in Australian subterranean aquatic habitats, however we have very few comprehensive phylogenetic analyses to inform systematics and classification. Our recent collective phylogenetics research, focused across Western Australia and South Australia, has shown that numerous diverse molecular lineages exist within several groundwater associated amphipod groups. These results indicate a significant expansion in the numbers of identified potential amphipod taxa and thus may influence the conservation and management of groundwater. Yet, defining species within the Australian groundwater amphipoda has been problematic. We have observed difficulties in 1) aligning and comparing certain sequence data, 2) providing informative outgroups for comparisons and 3) a paucity of samples available for both morphological and molecular analyses. These complications have in part created variable datasets from which we hypothesise species. Our recent work reflects a best evidence approach to species delimitation and is a rigorous assessment of the data given the unique, ancient and poorly known subterranean fauna involved. This research highlights that defining species is rarely straightforward; however the value in defining new species for conservation and management purposes is essential.

Molecular evolution of ‘eye genes’ in blind beetles – evidence for neutral evolution of phototransduction genes

W-1-9

Barbara Langille¹ Terry Bertozzi^{1,2} Simon Tierney¹ William Humphreys^{1,3} Andrew Austin¹ and Steven Cooper^{1,2}

¹University of Adelaide, Adelaide, SA; ²Evolutionary Biology Unit, South Australian Museum, Adelaide, SA; ³Western Australian Museum, WA; The University of Western Australia, WA

Neutral evolution theory predicts that genes specific to the development/function of eyes in subterranean animals will evolve under relaxed selection, ultimately becoming pseudogenes. Independently evolved subterranean beetle (Dytiscidae) species of Western Australia have converged on eye loss, providing a powerful system to explore changes to the genome with respect to troglomorphic characters. Using next generation sequence data, we investigated the molecular evolution of ‘eye genes’ of subterranean beetle species to test if they are evolving neutrally. We used transcriptome data from five beetle species (three subterranean and two surface) to design baits for hybrid enrichment of 60 pigmentation and phototransduction genes from 31 subterranean and surface species. Using a command line based approach, sequences were mapped and aligned to a concatenated reference containing the 60 genes. Subsequently, coding regions of each gene were translated into their amino acids and an assessment was made of functionality. Of the 60 ‘eye genes’, 7 showed evidence for a lack of transcription or pseudogenization in subterranean species relative to surface species. Most subterranean species either showed a parallel loss of *nina c*, UV opsin, and ciliary opsin, or our baits failed to capture them. Most arrestins, longwave opsin and *trpl* were recovered, however mutations rendered their protein most likely non-functional suggesting they have evolved neutrally into pseudogenes. Our study provides evidence for the parallel loss of key phototransduction genes, lending support to the neutral theory of regressive evolution.

Student Presenter

The ecological advantage of heterospory in *Selaginella* and *Isoetes*

W-1-10

Kurt B. Petersen and Martin Burd

School of Biological Sciences, Monash University, Clayton, Vic

Heterospory was a pivotal evolutionary innovation in the history of land plants, but the ecological advantages that favoured its origin are poorly understood. The appearance of heterospory first occurred in the Devonian where it is associated with early land plant ecosystems becoming increasingly complex. The differentiation of spore size and sex enabled adult sporophytes to provide extra nutrients to megaspores. These nutrients are unused by the gametophyte and only exploited by the developing sporophyte. The aim of these studies was to infer the functional ecology of heterospory in two free-sporing heterosporous plant genera. We focused on the two lycopod genera, *Selaginella* and *Isoetes*. For these two genera we estimated single gene phylogenies and assembled habitat data and spore size data. Our results show that *Selaginella* invests in larger megaspores in darker, competitive habitats and *Isoetes* invests into larger megaspores in low nutrient aquatic habitats. We also observed smaller microspores in high productivity and plant dense environments. The size reduction in microspores likely is caused by forest pollen filtering effects which have been observed in angiosperms. The increase of megaspore size in extant competitive environments agrees with the origin of heterospory in the Devonian fossil record. We suggest that heterospory is favourable in competitive habitats with high uncertainty of establishment.

Student Presenter

Sexual conflict and coevolution of sexually antagonistic armature in the ripple bug genus *Nesidovelia* (Veliidae)

W-1-11

Nikolai Tatarnic^{1,2}, Mitchell Hodgins³, Tom A. Weir⁴ and Gerasimos Cassis³

¹Western Australian Museum, Perth, WA; ²The University of Western Australia, WA; ³University of New South Wales, NSW; ⁴Australian National Insect Collection, CSIRO, ACT

Sexual conflict can be a significant driving force in the evolution of sexual dimorphism. Here we undertake a comparative study of male and female secondary sexual traits in the Australian ripple bug genus *Nesidovelia* (Insecta: Hemiptera: Veliidae). By analysing video recordings of mating attempts in *N. peramoena*, we document vigorous premating struggles in this species, and through comparative morphological examination of this and other species of *Nesidovelia*, we identify male and female antagonistic traits that are likely to interact and show patterns of coevolution. Although sexual conflict has not been explored in the Veliidae, based on their biology and our behavioural observations, we infer similar selective pressures as in their sister-clade, the water striders (Gerridae), for which ample evidence of sexual conflict exists. Using Bayesian comparative methods and a phylogeny of *Nesidovelia*, we show coevolution of male and female secondary sexual traits in a pattern consistent with sexually antagonistic coevolution. With their aggressive precopulatory struggles and elaborate male and female morphologies, veliids are an ideal model for studies of sexual conflict and sexually antagonistic coevolution.

Lunch

Wednesday, 12:30–13:15

Palaeoendemics

W-2-2

Greg Jordan

School of Biological Sciences, University of Tasmania, Hobart, Tas

This about the old and new—it is about relict plants (specifically palaeoendemics), but the approach is new. Parts of the punchline of the story reflect long held views, but others (especially the synthesis of ideas) are new.

This talk presents formal analyses of seed plant palaeoendemics at both a global level and a regional level from a hotspot (Western Tasmania). The analysis is based on current distributions and dated phylogenies. Locally, palaeoendemics show very strong, environmentally driven spatial structure—being linked to low fire frequency habitats in equable, wet climates. They are more linked to open vegetation than rainforest. Globally, palaeoendemics show similar environmental predictors (plus topographic complexity) and a greater association with forest. The palaeoendemic hotspots are the wet tropics of NE Queensland, New Caledonia and Western Tasmania, and other regions often considered as hotspots of “ancient lineages” whatever that means are lesser hotspots. Fossil evidences indicates that the palaeoendemics mostly (and perhaps all) represent clades that have undergone major contraction.

I explain these patterns as the effect of a combination of contraction of mesic lineages in response to increases in aridity, freezing climates and fire during the Neogene and Quaternary. However, the resulting patterns are underpinned by the combination of two biogeographic/evolutionary characteristics: (1) high level of phylogenetic niche conservatism for the environmental characteristics mentioned explaining why the clades have failed to adapt to modern environments, and (2) dispersal limitation causing the clades to become geographically isolated (that is, they are trapped within refugial areas).

Vera A. Korasidis and Malcolm W. Wallace

School of Earth Sciences, The University of Melbourne, Vic

The Eocene-Miocene brown coals of the Gippsland Basin in Australia represent one of the best southern hemisphere peatland rainforest records of climate, floral evolution and fire. Changing paleotemperatures produced major vegetation shifts within the peatlands from the Middle Eocene through to the Middle Miocene. An increased abundance of gymnosperms, including *Lagarostrobos*, is recorded in the warm Middle and Late Eocene and Middle Miocene coals. In contrast, the coals of the Oligocene and Early Miocene are characterized by a greater abundance of southern beech (*Nothofagus*) and cooler climate podocarps such as *Dacrycarpus*. The major floral shifts recorded in the Latrobe Valley coals also appear to correlate with the carbon isotopic compositions recorded for each coal seam. In particular, increases in gymnosperm abundance during warmer periods likely amplified the heavier $\delta^{13}\text{C}$ values associated with the Eocene and Middle Miocene coals. The close correlation between the $\delta^{13}\text{C}$ of the Gippsland brown coals and global benthic marine records also indicates a strongly coupled marine-terrestrial system. Detailed palynological analysis suggests that the distribution of charcoal and sclerophyllous flora within the coals is entirely controlled by facies and the paleoenvironments within the peatland, and does not result from drier climates as has been previously suggested. Charcoal and sclerophyllous flora are associated with emergent and meadow marsh environments that produced darker lithotypes. Counter-intuitively, these low-nutrient, fire-prone marsh environments that fringed the ever-wet rainforests of the Latrobe Valley peatlands appear to represent an ideal setting for Australia's modern fire-adapted flora to evolve in.

Student Presenter

Anne-Marie Patricia Tosolini and Penda Sisopha

School of Earth Sciences, The University of Melbourne, Vic

Ecosystems in deep time can be determined from plant–insect interactions, preserved by insect feeding/oviposition marks on fossil leaves. Insect feeding diversity during the Eocene was significantly higher in South America compared to North America, but there is little recorded from contemporaneous Australian biotas. The Christophel Collection, Melbourne Museum, Australia, used in this study, was collected from six discrete clay lenses overlying the Anglesea brown-coal measures during 1970–90s. Mummified and compression leaves come from two laterally equivalent sites: “Site I” and “Site II”. A Middle *Nothofagidites asperus* Zone, from palynological dating gave probable middle Eocene age. A diverse tropical flora includes 6 conifer (Podocarpaceae), 3 cycad and 19 angiosperm species. Leaf Margin Analysis has determined warmer climates (MAT 17°C), corresponding to the Middle Eocene Climatic Optimum. Previously recorded leaf mines came from Site I. New preliminary studies of fossil leaves record 78 leaf Damage Types (DT) belonging to 8 Functional Feeding Groups (FFG) including: 12 hole feeding; 7 margin-feeding; 9 skeletonisation; 7 surface-feeding; 4 piercing-and-sucking; 2 oviposition; 13 mining and 24 galling. Site I leaves are richer in galling, dominated by mature-insect feeding, such as margin- and hole-feeding, and lacks oviposition. In comparison, Site II has a greater intensity and diversity of damage. Plant taxonomy is crucial to understanding evolution of these plant–insect interactions within terrestrial ecosystems. Flora dominated by Lauraceae at Site I, combined with smaller leaf size and higher percentage of serrate margin leaves, may indicate plant strategies to avoid insect damage. *Myrtaceaphyllum* was only recorded from Site II and had a higher occurrence of surface, mining and skeletonisation feeding, evidence that these leaves were a favourable host for insect larvae. High diversity and inter-dependent plant–insect relationships reflect evolution of complex foodwebs in these tropical, high-latitude terrestrial ecosystems during the Eocene greenhouse, and can be used as an analogue for future climate change effects on ecosystems.

What role can palaeobotany play in integrating systematics for conservation and ecology?

W-2-5

Andrew Rozefelds

Queensland Museum, Brisbane, Qld

The distribution and conservation status of the modern Australian flora is the temporal legacy of climatic and environmental changes over many millions of years. The fossil record provides unique data that can (a) provide critical insights into the taxonomic groups present at the species level, (b) provide evidence on the spatial arrangement and the changing vegetation community patterns over time, and also (c) provide a temporal framework for understanding the timing of these changes. Fossil data is therefore important because it provides a long term temporal scale useful in studying change in plant communities and vegetation in Australia. Using examples from recent studies on the Vitaceae, *Lygodium* (Schizaeaceae), Casuarinaceae and Euphorbiaceae of northern Australia it is possible to demonstrate that the fossil record can provide significant taxonomic insights into the history of the modern Australian flora, which can also influence our understanding of the systematics and history of some modern plant groups. Interpretation of these plant remains helps interpret the palaeoecology of these fossil sites which can then be compared with contemporary ecological systems. These collective insights can also help frame our understanding of the conservation status of the modern flora and also provide surprising insights into the autecology of the modern Australian flora and associated fauna. Palaeontological data therefore provides a unique perspective on ecological and conservation issues which are unlikely to have been conceived if you were reliant solely upon neoecological data.

Cretaceous to Recent araucarian forests in New Zealand— evidence from pollen, wood, leaves, amber and biotic inclusions

W-2-6

John G. Conran¹, Daphne E. Lee², Uwe Kaulfuss², Alexander R. Schmidt³,
Jennifer M. Bannister², Jon K. Lindqvist², Mathew R. Vanner², Elizabeth M.
Kennedy⁴ and Dallas C. Mildenhall¹

¹School of Biological Sciences, The University of Adelaide, SA; ²Geology Department, University of Otago, Dunedin, New Zealand; ³Department of Geobiology, University of Göttingen, Göttingen, Germany; ⁴GNS Science, Lower Hutt, New Zealand

Araucarian forest trees have a long record in New Zealand from the Late Cretaceous through to the living *Agathis australis* forests of northern North Island. Araucarian wood with anatomical preservation is present at several localities of Palaeocene, Eocene, Oligocene and Miocene age. Araucarian foliage has been known from Late Cretaceous sites since the 1880s, and leaves of *Agathis* with preserved cuticle occur at several Oligocene–Miocene localities. The earliest sites with amber are Late Cretaceous in age and droplets, layers and blocks of amber occur in lignite, sandstone and mudstone from Cenozoic sites throughout New Zealand. Commonly bubble-filled and opaque, the amber was considered devoid of fossils. However new preparation techniques applied to thousands of methodically screened samples has revealed numerous three-dimensionally-preserved organisms and considerable biological and ecological complexity. There is an impressive diversity of arthropod fossils, including species from the arachnid orders Acari, Araneae and Pseudoscorpiones and at least 14 families of Hexapoda in the orders Collembola, Hemiptera, Psocoptera, Hymenoptera, Coleoptera, Lepidoptera, and Diptera, together with nematodes (soft-bodied soil and litter metazoans) and a variety of mould fungi. Ecologically, the organisms include predators such as spiders (including web remains with prey), tiny carnivores such as pseudoscorpions, diverse soil-dwelling mites, detritivores such as springtails, biting and gall midges, fungus gnats and chironomids, parasitoid and other wasps, ants, carpet and other beetles, bark lice and lepidopteran wing scales. This is the first major amber deposit with an abundance of biological inclusions from the Southern Hemisphere and the first of confirmed araucarian origin. These fossils expand the global record and evolutionary history of many arthropod and fungal groups, providing new insights into antecedents of the modern New Zealand terrestrial biota.

Robert S. Hill

Environment Institute, The University of Adelaide, Adelaide, SA

Australian plant fossils provide a great record of past environmental change, and in particular, of aridification and increasing frequency and intensity of fire. Many predictions have been made of intensifying fire into the future and there is some evidence that this may be occurring already. Such predictions suggest that Australian vegetation may be exposed to fire conditions more severe than anything they have evolved to cope with, and if this is true then we have challenging times ahead. However, the fossil record demonstrates the long term resilience of the Australian vegetation, and provides clear evidence of plant taxa with a capacity to adapt to change—the major questions now are how well can we expect plants to cope with rapid change in the relatively short term, and will we as a species survive well during this time of probable major change?

The fossil record of *Syzygium* and *Metrosideros* (Myrtaceae) in the Cenozoic of South Eastern Australia

W-2-8

Myall Tarran¹, Peter G. Wilson² and Robert S. Hill¹

¹School of Biological Sciences, University of Adelaide; ²Royal Botanic Garden, Sydney

New fossils of *Syzygium* (Lilly Pilly's) described from mummified leaves at the Miocene of Kiandra, NSW, are the first described fossil record of the genus in Australia, and may even have affinities to the subgenus *Acmena*. This research lays foundations for identification of further *Syzygium* fossil leaves, so that we can begin to trace the evolution and paleobiogeography of this important Australasian rainforest genus.

Furthermore, our research has revealed a long fossil record of *Metrosideros* (Rata's and Pohutukawa's) in Australia, where the genus is extinct today, and no fossil record of the genus had previously been recorded. Our research indicates an Australian origin for the genus, now one of the most widespread flowering genera in the Pacific.

Student Presenter

Species delimitation and morphometric analysis of *Anthotium humile* (Goodeniaceae)

W-2-9

Keelin J. Smith¹, Timothy A. Hammer¹, Kevin R. Thiele^{1,2}, Pauline F. Grierson¹ and Kelly A. Shepherd²

¹School of Biological Sciences, The University of Western Australia, WA; ²Western Australian Herbarium, Department of Biodiversity, Conservation and Attractions, WA

The *Anthotium humile* R.Br. species complex comprises a small group of taxa endemic to the Southwest Australian Floristic Region (SWAFR). The complex includes *A. humile*, a widespread and morphologically variable species, and two putative taxa, informally known as *A. sp. Darling Range* and *A. sp. Peaceful Bay*, the former of which is listed as a poorly known (Priority 1) taxon of conservation concern in Western Australia. This research project sought to determine whether these putative taxa should be accepted and formalised as distinct from *A. humile* (and if so, at what rank), and to assess the variation within *A. humile* itself. An integrative approach was undertaken incorporating a morphometric analysis based on 43 floral and leaf characters, an elliptical fourier analysis of floral morphology, and a molecular phylogenetic analysis using cpDNA (*trnL-F*) and nrDNA (ITS). The molecular phylogeny does not support the formalisation of *A. sp. Darling Range* and *A. sp. Peaceful Bay* as distinct species. Two clades of *A. humile* (A and B) were supported; Clade A was well supported and placed sister to *A. junciforme* (de Vriese) D.A.Morrison, while Clade B fell within a clade including *A. rubriflorum* Benth. and *A. odontophyllum* L.W.Sage. Progress continues on the morphometric and elliptical fourier analyses exploring morphological variation between Clades A and B of *A. humile* and to determine if the latter is supported as distinct from *A. odontophyllum* or if the current circumscription of this Priority 3 conservation species should be expanded. This study significantly increases our understanding of this poorly understood genus, which will in turn inform future conservation prioritisation and management strategies for *Anthotium* in particular and for the SWAFR more broadly.

Student Presenter

W.R. (Bill) Barker and Ed Biffin

State Herbarium of South Australia, Adelaide SA

Morphological and molecular analysis founded on a revisional study have clarified a remarkable diversification of a clade of *Lindernia* confined to northern and eastern Australia extending into adjacent New Guinea. The clade is defined by a synapomorphy of specialised sub-epidermal glands. Its species, many newly described, exhibit a diversity of pollination strategies involving changes to corolla shape and structure and modifications of the stamens. There are also examples of floral mimicry, niche specialisation and sympatry of closely allied species. The generic placement of the clade has been confirmed by a completed molecular study which extends global view of generic limits in the Linderniaceae (Biffin leader with Barker, Liang and Wannan).

Resolution of taxonomic limits in *Haloragis serra* and the *Haloragis exalata* species complex

W-2-11

Peter G. Wilson and Margaret Heslewood

National Herbarium of New South Wales, Royal Botanic Garden Sydney, Sydney, NSW

Our molecular analysis of a taxon from Geehi, NSW, putatively allied to the *Haloragis exalata* species complex determined that specific status was warranted, leading to recognition of *H. milesiae*. However, the same analyses revealed that members of the *H. exalata* species complex failed to resolve from accessions of the morphologically similar *H. serra* within that limited dataset. The *H. exalata* complex includes two infraspecific taxa listed as vulnerable at state and federal levels and resolution of taxonomic boundaries in the two species may impact conservation strategies for these taxa.

With funding from the Bush Blitz Tactical Taxonomy Grant programme we have expanded sampling of these two problematic taxa through their ranges in NSW, Queensland and Victoria, as well as sampling other selected Haloragaceae. We have compiled a dataset combining nuclear (ITS, ETS) and chloroplast (trnK intron and the atpB-rbcL and psbA-trnH intergenic spacer regions) DNA sequence data to address species delimitation of *H. exalata* and *H. serra*, and to determine the affinities of *H. milesiae*. While most accessions from sampled species form discrete though often unsupported clades, there is little clarity within the *H. exalata*/*H. serra* group, excepting several geographic subclades and reasons for this will be discussed. The closest affinities of *H. milesiae* appear to lie outside the *H. exalata* species complex.

Keynote Talk

Plenary – Horace Lamb

13:15–13:55

Herbarium data – global biodiversity and societal botanical needs for novel research

W–P–12

Shelley A. James

National Herbarium of New South Wales, Sydney NSW

Building on several centuries of botanical research based on herbarium specimens gathered around the globe through time, a new era of discovery, synthesis, and prediction using digitised collections data has begun. Aggregated, open access botanical and associated biological, environmental, and ecological data sets, from genes to the ecosystem, can be used to document, predict, and remediate the impacts of global change on organisms, communities, and society. There is a need for advocacy for botanical collections and their expansion. This includes continued and sustainable digitisation, adding non-traditional data fields and annotations, and creating born-digital field data. Such activities enable the rapid access of rich, digitally available datasets for research, education, informed decision-making, and other scholarly and creative activities.

Researchers are receiving enormous benefits from data aggregators like Global Biodiversity Information Facility (GBIF), iDigBio, the Atlas of Living Australia (ALA), and Biodiversity Heritage Library, but collaboration and data infrastructure are needed when working with large and disparate data sets. Tools for data discovery, visualisation, representation, and analysis, along with skills training, are increasingly important for inspiring novel research and, in turn, improving the intrinsic value of the physical and digital botanical collections.

move into concurrent sessions

14:00–

Phylogenetic niche conservatism and release in *Acacia* W-1-13

Matt A.M. Renner¹, Charles Foster², Joe Miller³ and Dan Murphy⁴

¹National Herbarium of NSW, Royal Botanic Garden, Sydney, NSW; ²University of Sydney, Sydney, NSW;

³National Science Foundation, Arlington, VA, USA; ⁴Royal Botanic Garden, Melbourne, Vic

This talk will consider some questions that can be asked of Australian lineages by combining well-sampled molecular phylogenies with spatial data available through AVH and ALA, with reference to *Acacia*. Within *Acacia* rainfall patterns explain most of the separation between species in a multidimensional climate space. Combining this space with the *Acacia* phylogeny identifies some interesting interactions between phylogeny and climate, suggesting both phylogenetic niche conservatism and release contribute to the distribution of diversity across the Australian continent.

Phylogenomics and island radiation – applying Anchored Hybrid Enrichment to *Leptospermum scoparium* (Myrtaceae) W-1-14

Matt Buys¹, Richard Winkworth², Peter de Lange³, Peter Wilson⁴, Alan Mellon⁵, Emily M. Lemmon⁶, Sean Holland⁶, Nora Mitchel⁷ and Beccy Ganley¹

¹New Zealand National Forestry Herbarium, NZ Forest Research Institute (Scion), Rotorua, New Zealand; ²Institute of Fundamental Sciences, Massey University, Palmerston North, New Zealand; ³Dept. of Environmental and Animal Sciences, UNITEC, Auckland, New Zealand; ⁴Royal Botanic Garden Sydney, Australia; ⁵Dept. of Scientific Computing, Florida State University, Tallahassee, USA; ⁶Dept. of Biological Science, Florida State University, Tallahassee, USA; ⁷Dept. of Ecology and Evolutionary Biology, University of Connecticut, USA

In New Zealand plant species radiations have attracted much attention. Recent evolutionary studies have shown that the morphological diversity characteristic of these radiations is not matched by genetic diversity at commonly studied marker loci. However, it is often assumed that morphological diversity would be matched if sufficient genetic data could be collected. *Leptospermum scoparium* is a morphologically highly variable species found in mainland Australia, Tasmania and New Zealand. In New Zealand this species has been described as containing up to six morphologically-based varieties, although currently only two — *L. scoparium* var. *scoparium* and *L. scoparium* var. *incanum* — are typically recognised. A comprehensive molecular phylogenetic exploration of diversity in New Zealand *L. scoparium* has not previously been reported. In the present study we used a recently developed technique called Anchored Hybrid Enrichment to acquire sequence data from c. 485 orthologous low-copy nuclear loci for 27 New Zealand and 3 Australian accessions of *L. scoparium* as well as representatives of several other *Leptospermum* species. The final concatenated data matrix contained in excess of 32×10^6 nucleotide positions of which more than 53000 were parsimony informative. Trees constructed using RAxML, ASTRAL-II and SVDQuartets converged on broadly similar topologies. Here we discuss the implications of our results in terms of the morphological diversity and taxonomic status of named entities in New Zealand *L. scoparium*.

Can NGS data resolve relationships in a recently-radiated genus? An example using the cycad genus *Cycas*

W-1-15

Nathalie Nagalingum

California Academy of Sciences, San Francisco, CA, USA

Relationships below the genus level have long been difficult to infer in cycads, principally due to the recent rapid radiation of the species and because of the reliance on few, relatively slowly evolving, uninformative markers. Next Generation Sequencing (NGS) data in the form of RADseq (Restriction-site Associated DNA sequencing) holds promise for resolving these relationships through the vast number of rapidly evolving nuclear markers. Focusing on *Cycas*, the largest cycad genus with over 100 species, a RADseq phylogeny was generated for three-quarters of species, covering the range of *Cycas* in Asia, Australia, Madagascar, India, and the southwestern Pacific Ocean islands. The phylogeny generated using RADseq provides resolution and support for species relationships, allowing assessment of biogeographic patterns and of the current classification within the genus for the first time.

Lars Nauheimer¹, Michael Gruenstaedl² and Thomas Borsch²

¹Australian Tropical Herbarium, James Cook University, Cairns, Qld; ²Systematic Botany and Plant Geography, Freie University, Berlin, Germany

Plastid genomes are an important resource for phylogenetic studies in plants. They are relatively easy to sequence, but contain less genetic information than most nuclear marker and Sanger sequencing datasets often fail to discriminate between closely related species. High-throughput sequencing techniques have become so affordable that whole plastome sequencing can be used to generate datasets that are larger by a magnitude. The increased availability of plastome sequences also enables to change the view from single isolated loci to whole plastomes and compare gene content, gene order, and changes in sizes of genome regions to understand plastome rearrangements in an evolutionary context.

Nymphaeales is an order of early diverging angiosperms and consists of c. 70 species in three families, Nymphaeaceae, Cabombaceae, and Hydatellaceae. Former phylogenetic analyses in Nymphaeales relied on few chloroplast markers as well as the nuclear ITS and could not resolve the relationships of several clades. The monophyly of Nymphaeaceae and of *Nymphaea* could not be confirmed or rejected. The position of the genus *Nuphar* remained ambiguous, which either groups with Nymphaeaceae or with Cabombaceae. Similarly, the genus *Victoria* was either recovered as embedded in *Nymphaea* or as separate.

Here we applied high-throughput sequencing to *de-novo* assemble and annotate whole plastomes of seven species in the Nymphaeales. We compared gene content, gene order, and the expansion of the inverted repeat regions with other early angiosperm lineages (Amborellales and Austrobaileyales). Further we performed phylogenomic analyses to resolve relationships in the Nymphaeales based on a 77-gene alignment. The assembly and annotation process revealed several erroneous annotations in published GenBank records. Gene content is conserved in Nymphaeales with the only differences in regard to the extent of the inverted repeats and the duplication of certain genes. *Trithuria* species have enlarged inverted repeats leading to larger plastome sizes up to 180k bp.

Phylogenomic analyses confirmed the position of *Victoria* as embedded in *Nymphaea* rendering the genus non-monyphyletic. However, the position of *Nuphar* in regard to other Nymphaeaceae and Cabombaceae remained ambiguous demonstrating the limitations of plastome datasets to resolve rapid radiations.

Probing the State's flora—a hybrid enrichment approach for vascular plants

W-1-17

Ed Biffin¹, Kor-jent van Dijk² and Michelle Waycott^{1,2}

¹State Herbarium of South Australia, Adelaide, SA; ²School of Biological Sciences, University of Adelaide, SA

Recent advances in DNA sequencing technologies hold great promise for collections based research. Probe based hybrid enrichment of targeted genome wide markers has emerged as an efficient and cost effective approach in systematics studies. For many of these studies, probes have been developed to target a set of loci for a specific taxon, but the utility of these at higher levels is uncertain. Here, we describe the development of a probe-based hybrid enrichment approach targeting both nuclear and plastid genomes with the aim of recovering comparable data sets across vascular plants. One objective of this approach is to facilitate the development of a DNA reference library for all vascular plants in the South Australian flora with application, for example, in metabarcoding and forensics as well as supporting the key role of the herbarium in systematics and biodiscovery.

Afternoon Break

Wednesday, 15:15–15:45

Wrap up and prizes—Horace Lamb

15:45–16:15

The ancestral flower of angiosperms and its early diversification

W-2-13

Hervé Sauquet^{1,2}, Maria von Balthazar³ and Jürg Schönenberger³

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

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

³Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria

Recent advances in molecular phylogenetics and a series of important palaeobotanical discoveries have revolutionised our understanding of angiosperm diversification. Yet, the origin and early evolution of their most characteristic feature, the flower, remains poorly understood. In particular, the structure of the ancestral flower of all living angiosperms is still uncertain. Here we report model-based reconstructions for ancestral flowers at the deepest nodes in the phylogeny of angiosperms, using the largest data set of floral traits ever assembled. We reconstruct the ancestral angiosperm flower as bisexual and radially symmetric, with more than two whorls of three separate perianth organs each (undifferentiated tepals), more than two whorls of three separate stamens each, and more than five spirally arranged separate carpels. Although uncertainty remains for some of the characters, our reconstruction allows us to propose a new plausible scenario for the early diversification of flowers, leading to new testable hypotheses for future research on angiosperms.

Host specificity in the New Zealand mistletoe *Korthalsella salicornioides* (Viscaceae)

W-2-14

Jennifer Tate¹, Sofie Pearson¹, Megan van Etten², Amir Sultan² and Alastair Robertson²

¹Institute of Fundamental Sciences, Massey University, Palmerston North, New Zealand; ²Institute of Agriculture and the Environment, Massey University, Palmerston North, New Zealand

Parasitic plants are naturally restricted in their distributions, especially if they depend on few species as hosts. *Korthalsella salicornioides* (Viscaceae) is an endemic New Zealand mistletoe that has two primary hosts on the North and South Islands: *Leptospermum scoparium* and *Kunzea robusta* (Myrtaceae). Microsatellite markers were developed from a shotgun genomic MiSeq run and were analysed to determine genetic variation within populations and if host-specific mistletoe genotypes were present on plants parasitising *Leptospermum* vs. *Kunzea* hosts. Eleven markers were genotyped in 272 *K. salicornioides* individuals from 16 populations. Across all populations few alleles were identified, and within-population assessment of genetic variation indicated that many populations have low levels of genetic diversity and high proportions of homozygotes. Despite the presence of few alleles, a high degree of genetic differentiation between most populations was detected and was found to reflect host genera. The low levels of genetic variation within populations is particularly concerning due to the recent discovery of myrtle rust in New Zealand.

Juliet Wege

Western Australian Herbarium, Department of Biodiversity Conservation and Attractions, Perth, WA

Western Australia’s diverse flora and extensive spatial scale make documenting, assessing and managing threatened and poorly known species an extremely challenging task. This task continues to grow—in the past 10 years, almost 1000 taxa have been added to the *Threatened and Priority Flora list for Western Australia* and the number of ‘Data Deficient’ taxa (those listed as Priority 1–3 under Western Australian Conservation Codes) has disproportionately increased. These changes have been driven by taxonomic research, including targeted studies on species of high conservation significance. While this research effort has reduced the overall number of undescribed (informally-named) taxa in Western Australia, the number of undescribed conservation-listed taxa has slightly increased, reflecting a high rate of species discovery. Collaborations between taxonomists and conservation personnel or industry representatives, and citizen scientist initiatives (not to mention the initiative of citizen scientists) are helping to resolve the taxonomy or conservation status of select taxa. An overarching *eFlora of Western Australia* is needed to facilitate conservation of the State’s unique plant biodiversity, which continues to be threatened by multiple processes.

Bronwen Keighery¹ and Gregory Keighery²

¹Agonis Botanical Consultants, Subiaco, WA; ²Department of Biodiversity Conservation and Attractions, Perth, WA

The interface of systematics and conservation is normally thought of as delimiting taxa that may be unrecognised and/or rare, but an adequate taxonomy allows many more conservation outcomes than this. The Perth area is probably the best-collected and recorded region of the Western Australia biodiversity hotspot. The high level of systematic study of the flora has defined 680 native vascular plant species, most of which have historical and recent collections. Having a more than adequate baseline systematics of the species present has allowed a quantitative assessment of change and loss of taxa and populations over time of the area. Over 20% of the recorded flora of the Perth area is now locally or regionally extinct, and 2 taxa are globally extinct.

While taxonomy should focus on delimitation of taxa, conservation as a science and practice should always be broader and based on loss of communities, species, populations (especially ecotypes) and genetic variation. With the concurrence of adequate herbarium collections, systematic studies and survey we have determined that Perth has over 200 of its native plants that have historic, genetic or geographical significance. This allows guidance for the conservation and management of this unique flora by the use of appropriate species and provenance as part of this management.

Rainbows end—orchid systematics and conservation in SW Western Australia

W-2-17

Gregory Keighery¹ and Mark Brundrett²

¹Department of Biodiversity, Conservation and Attractions, Kensington, WA; ²Department of Biodiversity, Conservation and Attractions, Swan Region, Crawley, WA

The proliferation of orchid species in south-western Western Australia (SWWA) from about 100 to over 400 in the past twenty years shows little sign of slowing. Currently taxonomic complexity within species complexes appears infinite and splitting into very narrowly defined species is unlikely to resolve identification or conservation problems, as many populations do not fit well into any remaining species.

Unfortunately both genetic and morphological evidence strongly suggest that there is little to justify such extreme splitting. Many of the newly described taxa are unable to be separated morphologically or have workable keys provided by their proponents. Currently differences in flowering times, pollinators, geographical ranges and habitats are being used to justify these species, but these are all prone to breakdown when subject to close study. Also these differences correspond more closely to ecotypes and are not conserving the crown taxa as required by systematics.

Currently of the 346 recognised SWWA Orchid taxa 192 have significant taxonomic issues, and of those 95 listed as conservation taxa 64 have similar issues. We suggest that narrow taxonomic delimitation of these species are not serving conservation or systematics. These poorly defined species consume resources but are not conserving many significant taxa, populations or genetic variation. Further they will consume limited taxonomic resources in the resolution of these issues.

Afternoon Break

Wednesday, 15:15–15:45

Wrap up and prizes—Horace Lamb

15:45–16:15

Genetic distance and pollen morphology in *Nothofagus* — a pilot study

Yelarney K. Beer¹, Robert S. Hill¹ and Michelle Waycott^{1,2}

¹School of Biological Sciences, University of Adelaide, Adelaide, SA; ²State Herbarium of South Australia, Adelaide, SA

Nothofagus (Nothofagaceae) has an extensive fossil record, particularly pollen. This important record forms the basis of our understanding of the evolutionary history and timing of this iconic genus. The four extant pollen types display strong taxonomic affinity at the subgeneric level, but, the affinities of four recognised fossil pollen types remains largely speculative. To learn more, a pilot study was undertaken to assess the utility of shape analysis for the classification of extant pollen, with the view to applying it to fossil morphs in the future. The study taxon, *Brassospora*, is the most species-rich extant subgenus and is found on New Caledonia and New Guinea, and there is evidence (genetics, cupules) that these geographic regions comprise two closely-related-but-distinct lineages/clades. The results of this study suggest that the pollen of the two clades may also be distinctive. A larger study incorporating all four extant subgenera is ongoing and will be combined with genomic data from next gen sequencing to assess the relationship between genetic distance/similarity and the morphological similarity of pollen as part of a PhD project.

Student Presenter

Disjunct populations of the halophyte liverwort *Monocarpus sphaerocarpus* show no sequence variation

Christine Cargill¹, Cécile Gueidan², Josephine Milne³ and Laura Forrest⁴

¹Australian National Herbarium, CANBR, Canberra, ACT; ²Australian National Herbarium, CSIRO-NCMI, Canberra, ACT; ³Royal Botanic Gardens Victoria, Melbourne, Vic; ⁴Royal Botanic Gardens Edinburgh, UK

Populations of the complex thalloid liverwort *Monocarpus sphaerocarpus* (Monocarpaceae) found in a disjunct distribution across southern Australia were sequenced to investigate whether plants found in eastern Australia were a different species from those found on the west coast of Australia, in line with potential differences in spore morphology. Sequences from five plastid gene regions were generated from specimens collected from several populations found in the states of Victoria, South Australia and Western Australia and spore morphology was reviewed using light and scanning electron microscopy. All individuals belonged to a single genotype on the basis of the five plastid markers *psbA-trnH*, *trnL-F*, *rbcL*, *rpoC1*, and *rps4-trnA*S. Moreover, observed morphological differences were not consistent with geographical origin and more likely indicative of infraspecific variation or difference in spore maturity when collected. These results support the recognition of only a single species in Australia. This finding may indicate gene flow between populations across southern Australia. But how can isolated populations exchange genes over a distance of almost 4000 km? One theory is via transportation by wading birds who frequent such habitats but also migrate across the southern part of the continent. Propagules may be transported on their feet or feathers or may be accidentally ingested while birds are feeding, and dispersed over long distances.

Cycad foliage, conifer cones, palm and Araliaceae flowers, weevils and cicadas – some highlights of the Miocene Hindon Maar *Konservat-Lagerstätte*, New Zealand

John G. Conran¹, Daphne E. Lee², Uwe Kaulfuss², Jennifer M. Bannister² and Dallas C. Mildenhall³

¹School of Biological Sciences, The University of Adelaide, SA; ²Geology Department, University of Otago, Dunedin, New Zealand; ³GNS Science, Lower Hutt, New Zealand

Hindon Maar is the second Miocene *Konservat-Lagerstätte* deposit to be described from southern New Zealand. The maar complex consists of four sediment-infilled subcircular basins that are partly eroded maar-diatreme volcanoes associated with the Waipiata Volcanic Field. New ⁴⁰Ar/³⁹Ar dates obtained from basanites associated with the maar give an age of c. 15 Ma, which supports an early to mid-Miocene age derived from palynomorphs. Preliminary excavations in two of the volcanic craters have exposed laminated diatomite and/or sponge-rich carbonaceous mudstone that have yielded exceptionally well-preserved fossils, particularly plants, insects and fish. The most common plant macrofossils are leaves with cuticular preservation, including many with insect damage. A species of cycad is present, together with foliage of several conifers including some polleniferous male cones. Monocots include the liane *Ripogonum* and palms which are represented by dispersed pollen, a flower with *in situ* pollen, and phytoliths. Leaves of basal dicots and eudicots include representatives of at least 10 families including several species of Araliaceae, Lauraceae (*Litsea*), Monimiaceae (*Laurelia*), Myrtaceae and Myrsinaceae. Most of the 20 or so flower compressions collected to date are assigned to Araliaceae on flower structure and pollen type. However, the macrofloral leaf assemblage is overwhelmingly dominated by several species of Nothofagaceae. Also, abundant in terms of numbers and diversity are insects, which currently comprise c. 190 specimens belonging predominantly to the orders Hemiptera, Hymenoptera, Trichoptera, Thysanoptera and Coleoptera, with weevils particularly diverse. The maar lakes were surrounded by *Nothofagus*/podocarp/mixed broadleaf forest growing under humid, warm temperate conditions. The remarkable preservation of soft-bodied fossils makes this a *Konservat-Lagerstätte* of global significance.

Systematics and host associations of Australian *Acizzia* (Hemiptera: Psyllidae) from the host plant genus *Dodonaea*

Alana Delaine, Gary Taylor and Andrew D. Austin

Department of Genetics and Evolution, University of Adelaide, Adelaide, SA

Often referred to as Jumping Plant-Lice, the Hemiptera: Psylloidea are small sap-sucking insects which are represented by over 3850 species worldwide and consist of eight families. The Australian fauna comprises all eight families from over 400 recorded species, with an unresolved richness of potentially more than 200 species. There is a major disjunct between species that have been discovered but which have yet to be formally described, with research suggesting that up to 70% of Australia's invertebrate fauna remains undescribed, and a vast number of these undescribed species belonging to the *Acizzia*, a genus of Psyllidae, which comprises in excess of 35 species. Examining and documenting the diversity of this poorly studied group of Australian insects using both morphological and molecular techniques will result in the morphological descriptions, identification keys, a molecular phylogeny and COI barcode sequence data of a monophyletic group within the genus *Acizzia* that is host specific to the plant genus *Dodonaea*.

This application of systematics and molecular species delimitations can assist in the formal descriptions of species, greatly adding to the richness of Australia's described insect diversity.

Student Presenter

Argophyllum (Argophyllaceae) in Australia – another example of edaphic speciation

Anthony Bean and Paul Forster

Queensland Herbarium, Department of Science, Information Technology and Innovation, Brisbane
Botanic Gardens, Toowong, Qld

The genus *Argophyllum* occurs in Australia and New Caledonia with currently c. 13 species recognised; ten of these are in New Caledonia. Revision of the genus in Australia has revealed at least five additional undescribed species. All Australian species are edaphic specialists and occur on rocky substrates of different geological origin, usually on the edges of rainforest where they mainly occur in narrow ecotonal vegetation communities. The greatest diversity of *Argophyllum* species in Australia is in the Wet Tropics bioregion and southern parts of the Cape York Peninsula bioregion with two outlying species: *A. lejourdanii* in the Townsville area and *A. nullumense* from Eungella south to northern New South Wales.

Insights into early social evolution from the only known social bee in the mega-diverse family Colletidae

Lucas Hearn¹, Michael Schwarz¹, Mark Stevens², Michael Gardner¹ and Olivia Davies¹

¹School of Biological Sciences, Flinders University, SA; ²South Australian Museum, University of South Australia, SA

The bee family Colletidae occurs on all continents except Antarctica and is highly diverse with five subfamilies and over 2000 species. The Australian hylaeine bee *Amphylaeus morosus* is the only species of the short tongued bee family Colletidae to exhibit social behaviour, and represents a key species for understanding the earliest stages of social evolution in insects. Colonies can contain up to three females but there is no evidence of reproductive hierarchies or kin recognition among nestmates. Previous studies have shown that benefits of social nesting appear to be small and relatedness among nestmates is also low. Furthermore, cell provisioning patterns of *Amphylaeus morosus* suggest that conflict over oviposition and foraging efforts could lead to individuals adopting uncooperative strategies. We show that nest switching is common in early spring prior to cell provisioning and suggests that kin selection is not an important factor maintaining sociality in this species. *Amphylaeus morosus* appears to conform to a growing number of other species where casteless social behaviour involves small benefits and low dispersal costs that do not allow potentially dominant females to monopolise reproduction by threatening eviction from the colony. However, the possibility for surreptitious cheating during oviposition raises major questions for how casteless societies can persist.

Student Presenter

Can a habitat shift from arid to temperate biomes explain the loss of sociality in gall-forming *Acacia* thrips?

Justin Holder and Michael P. Schwarz

Flinders University, College of Science and Engineering, SA

Australian gall-forming thrips on *Acacia* have received considerable attention because they contain multiple 'eusocial' species, characterised by the presence of a soldier caste that is specialised to defend galls from potential invaders, particularly kleptoparasitic thrips in the genus *Koptothrips*. All eusocial gall-forming thrips occur in xeric biomes. However, one gall-forming thrips, *Kladothrips rodwayi*, has colonised temperate habitats and has also lost the soldier caste. We hypothesise that loss of the soldier caste is due to seasonally extended and less episodic conditions for *Acacia* early phyllode growth, when galls are formed. Extended opportunities for gall initiation should mean that gall kleptoparasites are less able to track their hosts phenology and lead to lower rates of parasitism, and therefore fewer benefits for a defensive soldier caste. We test this hypothesis by comparing rates of kleptoparasitism in two habitats for *K. rodwayi*, a benign region where *Acacia* phyllode growth should be extended and kleptoparasitism rates low, and a marginal region where phyllode growth should be more episodic and parasitisation rates high. We argue that marginal cost and benefit ratios are important for understanding social evolution very diverse taxa, including thrips.

Student Presenter

Biogeography in the Australian Monsoon Tropics—distribution and diversification of andromonoecious *Solanum* and other sympatric lineages

Christopher T. Martine¹, Jason T. Cantley², *Peter C. Jobson³ and Angela J. McDonnell¹

*Presenting; ¹Biology Department, Bucknell University, Lewisburg, PA, USA; ²San Francisco State University, San Francisco, CA, USA; ³Northern Territory Herbarium, Alice Springs, NT

Using an andromonoecious clade of *Solanum* subgenus *Leptostemonum* as an initial proof of concept, we examine the link between climate oscillations over the past 2 million years and the distribution, evolution and diversification of multiple plant lineages of sandstone flora of the Australian Monsoon Tropics (AMT). The project is part of a larger lab-wide study of the biogeographic history of c. 10 angiosperm lineages in the AMT meant to provide insight on floristic evolution in the AMT, examine the role of sandstone escarpments as habitat refugia for some taxa, evaluate biogeographic barriers in regional angiosperms, and inform conservation efforts in the region.

Similarities and differences in phylogeographic patterns between two clades of monitor lizards

Stephen C. Donellan^{1,2}, Gabrielle H. Openshaw³, Mitzy R. Pepper³, *Carlos J. Pavón-Vázquez³ and J. Scott Keogh³

*Presenting; ¹South Australian Museum, Adelaide, SA; ²Australian Centre for Evolutionary Biology and Biodiversity, University of Adelaide, SA; ³Division of Ecology and Evolution, Research School of Biology, Australian National University, ACT

Monitor lizards (genus *Varanus*) are a remarkable group of reptiles that includes dwarf and giant species. They are particularly diverse in Australia, which is home to 32 of the 79 currently recognised species. We investigated the phylogeographic structure of two species belonging to the subgenus *Odatria* (*V. acanthurus* and *V. tristis*) based on mtDNA sequences. We constructed phylogenetic trees for each species and preliminarily delimited species with probabilistic methods. Remarkably, *V. acanthurus* is not monophyletic. While a more robust assessment of the species boundaries is still pending, our results make clear that there is notable geographic structure within each group. The *V. acanthurus* clade shows more fine-scale geographic structure than the *V. tristis* clade. This is probably associated with the saxicolous habits of *V. acanthurus* and the relatively high vagility of *V. tristis*. Interestingly, for both taxa a clade from tropical Australia is sister to a clade from the arid and semiarid regions. Within the arid/semiarid clade, a sub-clade from the Pilbara region is sister to a group with a wide distribution in arid Australia. Projects in progress include high throughput SNP sampling with DArTseq and more rigorous evaluations of the phylogeographic structure and species limits.

Student Presenter

Why did heterospory evolve?

Kurt B. Petersen and Martin Burd

School of Biological Sciences, Monash University, Clayton, Vic

The primitive land plant life cycle featured the production of spores of unimodal size, a condition called homospority. The evolution of bimodal size distributions with small male spores and large female spores, known as heterospory, was an innovation that occurred repeatedly in the history of land plants. The importance of desiccation-resistant spores for colonisation of the land is well known, but the adaptive value of heterospory has never been well established. It was an addition to a sexual life cycle that already involved male and female gametes. Its role as a precursor to the evolution of seeds has received much attention, but this is an evolutionary consequence of heterospory that cannot explain the transition from homospority to heterospory (and the lack of evolutionary reversal from heterospory to homospority). Very few arguments concerning the selective forces favouring heterospory have been proposed, a paucity of attention that is surprising given the importance of this innovation in land plant evolution. We highlight two ideas that may lead us to a better understanding of why heterospory evolved. First, models of optimal resource allocation which suggest that an evolutionary increase in spore size could reach a threshold at which small spores yielding small, sperm-producing gametophytes would return greater fitness per unit of resource investment than would large spores and bisexual gametophytes. With the advent of such microspores, megaspores would evolve under frequency-dependent selection. This argument can account for the appearance of heterospory in the Devonian, when increasingly tall and complex vegetative communities presented competitive conditions that made large spore size advantageous. Second, heterospory is analogous in many ways to anisogamy. Indeed, heterospory is a kind of re-invention of anisogamy within the context of a sporophyte-dominant land plant life cycle. The evolution of anisogamy has been the subject of important theoretical and empirical investigation. Recent work in this area suggests that mate-encounter dynamics set up selective forces that can drive the evolution of anisogamy. We suggest that similar dispersal and mating dynamics could have underlain spore size differentiation. The two approaches offer predictions that are consistent with currently available data but could be tested far more thoroughly. We hope to re-establish attention on this neglected aspect of plant evolutionary biology and suggest some paths for empirical investigation.

Student Presenter

A preliminary key to the genera of Australian jumping spiders (Aranaea: Salticidae)

Barry J. Richardson¹, R. Whyte² and Marek Żabka³

¹Australian National Insect Collection, CSIRO, ACT; ²Queensland Museum, South Brisbane, Qld; ³Siedlce University of Natural Sciences and Humanities, Siedlce, Poland

This LUCID-based key is intended to meet the needs of naturalists, biologists and taxonomists who wish to identify Australian jumping spiders. The character set has high redundancy allowing users to begin with whatever observable characters are available to them when using a high-powered hand lens or a low-powered microscope.

An information sheet attached to each genus provides a list of known species and information on evolutionary relationships, distribution, habits, a simplified diagnosis, and some key references. A series of diagrams and photographs (of living and preserved specimens) are provided.

Plant–bee networks in Fiji suggest that an endemic bee is a super-generalist that aids exotic weed spread and that introduced bees are much more benign

Sarah E. Hayes¹, Morgan Staines¹, Nikki Francis¹, Mark I. Stevens^{2,3} and *Michael P. Schwarz¹

*Presenting; ¹Flinders University, Adelaide, SA; ²South Australian Museum, Adelaide, SA; ³University of South Australia, Adelaide, SA

Various studies argue that co-adapted plants and their pollinators can form an invader complex when co-introduced into new regions, allowing them to rapidly establish even when suitable native pollinators are absent. However, it has also been argued that for islands with few pollinators, those species should evolve into ‘super-generalists’ that may be able to pollinate a wide variety of introduced plants. Fiji has only a single but highly abundant native bee, *Homalictus fijiensis*, in lowland regions. We show that this bee is a super-generalist, with a wider host plant range than introduced bee species, including the honeybee. Although it is not a buzz pollinator, it is able to pollinate introduced plants with poricidal anthers via pollen larceny. *H. fijiensis* is likely to make Fiji highly vulnerable to the spread of exotic weeds, including those that normally require specialised buzz pollinators. We argue that quarantine procedures in island ecosystems need to be especially stringent if local pollinator diversity is low. We also argue that for island biogeography theories, super-generalist pollinators could accelerate the recruitment of new plants species in ways that are not currently modelled.

Assessing the conservation status and genetic diversity of two endemic freshwater crayfish *Euastacus spinifer* and *Euastacus australasiensis* using molecular approaches

Cara Van Der Wal^{1,2}, Shane T. Ahyong^{2,3}, Simon Y.W. Ho¹ and Nathan Lo¹

¹School of Life and Environmental Sciences, University of Sydney, NSW; ²Australian Museum Research Institute, Australian Museum, NSW; ³School of Biological, Earth and Environmental Sciences, University of New South Wales, NSW

Freshwater crayfish (Decapoda: Parastacidae) are experiencing significant human-mediated impacts, ranked among the five most endangered animal groups. Australia is home to approximately 140 species of crayfish, of which the genus *Euastacus* is endemic. *Euastacus* are of significant conservation concern, due to a number of key threats including climate change, habitat loss and illegal harvesting. Previous morphological studies have highlighted the difficulties associated with species delimitation in *Euastacus*, owing to both small and large morphological differences between species. As a result, it is presently unclear whether these colour and morphological differences reflect intraspecific or interspecific variation. To address this knowledge gap this study will investigate the genetic diversity, population structure and phylogeny of *Euastacus spinifer* and *Euastacus australasiensis* using DArTseq, in order to assess their biodiversity and conservation status within New South Wales. This group is understudied, and therefore, our aim is to provide accurate and necessary information to promote correct conservation and management policies in New South Wales. We hypothesise that the currently recognised distribution of *E. spinifer* and *E. australasiensis* is inaccurate. Instead we predict that these species may actually represent species-complexes present in range-restricted, fragmented habitats. This result would radically alter their current conservation status, likely adding multiple species to the highest IUCN threat categories.

Student Presenter

A last word...

The conference organising committee comprised:

Co-convenors—Andy Austin (The University of Adelaide) and Michelle Waycott (The University of Adelaide and State Herbarium of South Australia)

Steve Cooper (South Australian Museum)

Rachael King (The University of Adelaide)

Molly Whalen (Flinders University)

Jürgen Kellermann (State Herbarium of South Australia and The University of Adelaide)

Yelarney Beer (The University of Adelaide)

Barbara Langille (The University of Adelaide)

Simon Tierney (The University of Adelaide/University of Western Sydney)

Ably supported by:

Ainsley Calladine (State Herbarium of South Australia)

Emma O'Loughlin (The University of Adelaide)