MIND THE GAP

AUSTRALASIAN SYSTEMATIC BOTANY SOCIETY 2018 CONFERENCE

3-7 December 2018

Brisbane Botanic Gardens Mt Coot-tha, Australia

systematics.ourplants.org

CONTENTS

Welcome 3
Sponsors and supporters 4
Registration 5
Social program 5
Tour of Queensland Herbarium 5
Accessing the Queensland Herbarium collections 6
Workshop at the State Library of Queensland 6
Field Trip to Springbrook National Park 6
Awards and Presentations 7
ASBS student reimbursement 7
Systems exhibition 8
Venues 9
Conference Program Overview 11
Conference Program 12
Abstracts 18
Organising Committees and Delegates 74

Australasian Systematic Botany Society

Secretary: Jennifer Tate, secretary.asbs@gmail.com

ASBS website: www.asbs.org.au

Conference website: systematics.ourplants.org

Conference organised by the Queensland Herbarium

Cover illustration: Bunya Pine (*Araucaria bidwillii*) by Will Smith, Queensland Herbarium (CC BY 4.0)

WELCOME

FOREWORD

On behalf of the Organising Committee, I am delighted to welcome you to the 2018 Australasian Systematic Botany Society Conference in Brisbane, organised by the Queensland Herbarium.

Our theme, 'Mind the Gap', aims to highlight gaps in the field of systematics be they biogeographic, taxonomic, data, etc. You have helped us put together an exciting program covering all aspects of systematics and some related disciplines, including those by our Queensland based plenary speakers: Prof. Paulo Vasconcelos, a Geologist specialising in Geochemistry, Geology and Geomorphology, and Assoc. Prof. Alison Shapcott a Conservation Geneticist who integrates her work with other disciplines including systematics. I am eager to hear about the Genomics for Australasian Plants initiative, as well as the latest from Taxonomy Australia.

ASBS conferences are always a fantastic platform for students to wow us with their research and this year will be no different. On the final day of proceedings, the two students who impressed the most will receive awards for best oral presentation and best poster. Another honour to be awarded during the conference is the Nancy T. Burbidge medal. It goes to… you'll have to wait until Wednesday to find out! But it is to a well deserving botanist who has made a significant contribution to Australasian systematics.

Some missed out on the workshop and fieldtrip because the response was so great. For those that do attend, you will not be disappointed. The workshop is a collaboration between herbarium journal editors and the Australian Biological Resources Study to refresh and upskill our community in taxonomic reviews. It will be a great opportunity to share knowledge and boost reviewers our editors can call upon. The fieldtrip to Springbrook in the World Heritage Gondwana Rainforests of Australia has something for everyone: beautiful views, endemic species, various habitats (from heath to rainforest), and a fudge shop.

The *Systems* art exhibition will be in the Queensland Herbarium foyer from 4 to 14 December. Please admire this art meets biodiversity exhibition that Melissa Fletcher and the South-East Queensland artists have created. *Systems* will be launched at the conference welcome reception along with a botanical beer brewed for ASBS by local brewery Fritzenberger. If you miss out, try it on tap in their Brisbane pub.

Home to the Queensland Herbarium, the Brisbane Botanic Gardens Mt Coot-tha is a beautiful venue to hold the conference. It is situated at the base of the iconic Mt Coot-tha and only 15 minutes from the CBD. If you arrive early, are staying around after or need a break from conferencing then I encourage you to stroll around the gardens, relax and appreciate Queensland's premier subtropical botanic garden.

I wish you an enjoyable conference. I hope you take home new ideas and inspiration from the program and enjoy reconnecting with colleagues and friends, and make some new ones too.

Gillian Brown, Conference Convenor, Queensland Herbarium December, 2018

ACKNOWLEDGEMENT OF TRADITIONAL OWNERS AND COUNTRY

We acknowledge that Aboriginal peoples and Torres Strait Islander peoples are the Traditional Owners of this country and they retain their relationship and connection to the land, sea and community.

We pay our respects to all Traditional Owners, and to the Elders past, present and in the future for land and sea on which we work, live and walk.

SPONSORS AND SUPPORTERS

MIND THE GAP 2018 WAS SUBSTANTIVELY SUPPORTED BY

Australasian Systematic Botany Society

Brisbane City Council

ourplants.org

Queensland Herbarium, Department of Environment and Science

Queensland Museum, Department of Environment and Science

SPONSORSHIP THROUGH FUNDING WAS PROVIDED BY

Australian Biological Resources Study (ABRS)

environment.gov.au/science/abrs

ABRS provides national leadership and support for the discovery, naming and classification of Australia's living organisms.

BGI Australia

bgi-australia.com.au/

BGI is a global leader in genomics research and applications focusing on healthcare, agriculture, environment and conservation with a goal to use genomics to benefit mankind.

CSIRO Publishing

publish.csiro.au/

Australian Systematic Botany is an international journal devoted to the systematics, taxonomy, and related aspects of biogeography and evolution of all algae, fungi and plants, including fossils.

Atlas of Living Australia (ALA)

ala.org.au

The ALA is a collaborative, national project that aggregates biodiversity data from multiple sources and makes it freely available and usable online.

Fritzenberger

fritzenberger.com

We do frites, we do burgers and...wait, you'll need something to wash that down with! Like a beer! We brew in-house this means our beers are fresh and on point for taste. We love non-traditional brewing processes and experimenting with new ingredients. This with our regular guest tap policy keep our tap line-up Fritzen fantastic!

REGISTRATION

Registration will be available at the Welcome Reception on Monday evening and in the AUDITORIUM Tuesday – Thursday from 8am. Name tags will be provided on the day for the Workshop at the venue.

Please ensure you provide your PowerPoint file to the registration desk for uploading *by 8.30am* on day of your presentation. Presentations can also be uploaded during the Welcome Reception on the Monday evening and from 8am on Tuesday morning. Please bring your presentation file on USB stick, as PowerPoint file downloads will be slow on the council Wi-Fi.

Catering breaks will all be held in the undercover area off the left side of the AUDITORIUM. Please refrain from eating food that is labelled with particular dietary requirements, as this is for those participants who noted this on their registration.

A water fountain is available next to the AUDITORIUM, as well as in the QUEENSLAND HERBARIUM foyer.

Rest rooms are available next to the AUDITORIUM, as well as the QUEENSLAND HERBARIUM foyer. Additional facilities can be found in the Botanic Gardens café as well as in the gardens themselves. Refer to the map provided in your conference bag.

If you have any questions, or if problems arise during the conference, please speak to a conference organiser or helper (look for their different coloured name tags). Staff at the Herbarium reception desk can assist with non-conference related questions or can relay information to the Organising Committee.

You can find these marked on the Brisbane Botanic Gardens Mt Coot-tha venues map on page 9.

SOCIAL PROGRAM

WELCOME RECEPTION AND LAUNCH OF SYSTEMS EXHIBITION

The Welcome Reception and launch of *Systems* art exhibition starts at 5pm, until 8pm on Monday 3 December at the QUEENSLAND HERBARIUM.

You can find the QUEENSLAND HERBARIUM marked on the Brisbane Botanic Gardens Mt Coot-tha venues map on page 9.

CONFERENCE DINNER

The Conference Dinner starts at 6.30pm Wednesday 5 December at the Botanic Gardens Wedding and FUNCTION CENTRE.

You can find the FUNCTION CENTRE marked on the Brisbane Botanic Gardens Mt Coot-tha venues map on page 9.

TOUR OF QUEENSLAND HERBARIUM

There is a tour of the QUEENSLAND HERBARIUM by the Director, Dr Gordon Guymer, at 5.10pm Wednesday 5 December. The tour starts in the Herbarium foyer and takes approximately half an hour.

Places are limited so please sign up at the registration desk by midday Wednesday 5 December.

You can find the QUEENSLAND HERBARIUM marked on the Brisbane Botanic Gardens Mt Coot-tha venues map on page 9.

ACCESSING THE QUEENSLAND HERBARIUM COLLECTIONS

The QUEENSLAND HERBARIUM will be open the weekend before and during the conference between 9am and 5pm by appointment. If you would like to examine specimens in the collection please contact Queensland.Herbarium@qld.gov.au so we can facilitate your visit.

Please note that you will not be able to bring paper products into the collections without them going through our freezer for 7 days. We will provide det./conf./annotation slips and scrap paper for you to make notes on if needed.

You can find the QUEENSLAND HERBARIUM marked on the Brisbane Botanic Gardens Mt Coot-tha venues map on page 9. Report to reception on arrival and one of our staff will take you to the collections.

WORKSHOP AT THE STATE LIBRARY OF QUEENSLAND

The Conference Workshop, on how to referee taxonomic manuscripts, is from 9am to 5pm Monday 3 December in the INNOVATION LAB on level 1 of THE EDGE, at the State Library of Queensland.

Please arrive at 8.45am for a 9am sharp start. At 4.30pm (or thereabouts) we will transit to the QUEENSLAND HERBARIUM for the Welcome Reception and launch of *Systems* art exhibition

You can find the INNOVATION LAB marked on the State Library of Queensland venue map on page 10.

FIELD TRIP TO SPRINGBROOK NATIONAL PARK

Continuing with our ‘Mind the Gap’ theme, the 2018 ASBS conference field trip will take us to Springbrook and to the precipice of the remains of the Mt Warning caldera. The ancient lava flows of this giant shield volcano are swathed in bryophyte-laden subtropical and temperate rainforests, criss-crossed by swift-running streams. These closed communities are flanked by wet sclerophyll forests of towering eucalypts and brush box. Such forests possess a wide variety of understorey vegetation ranging from tall shrub lands to heath communities. The many lookouts and walking tracks of the area provide ample scope for visitors to experience a wide range of plant communities atop the basalt and rhyolite slopes and ridges.

As Springbrook has amongst the highest rainfall in South-east Queensland, participants should come prepared with a rain jacket and/or umbrella. Weather conditions can change rapidly. In December, temperatures can vary from being warm to hot during the day with the possibility of severe thunderstorms, to windy, overcast and cool enough for some to need coats. Other personal gear required includes a hat, sturdy shoes, sunnies, long sleeves and a water bottle.

Only those with an appropriate permit will be allowed to collect plants. Please bring this with you on the field trip if you intend to collect. Contact the Springbrook National Park Rangers beforehand to let them know of your intentions. We will provide basic collecting equipment (e.g. secateurs, presses, paper) but please do discuss your plans with us by COB Wednesday 5 December.

The field trip will depart the QUEENSLAND HERBARIUM at 7.15am on Friday 7 December. It takes approximately 1·5 – 2 hours to reach Springbrook, where we will spend the day. Lunch, morning and afternoon teas are provided. We will depart in time to reach Toowong for dinner (cost not included) by 6-6.30pm. Please ensure you have accommodation booked for this evening.

You can find the QUEENSLAND HERBARIUM marked on the Brisbane Botanic Gardens Mt Coot-tha venues map on page 9.

AWARDS AND PRESENTATIONS

The Pauline Ladiges Award for best oral presentation and the Young Career Scientist for best poster award are proudly supported by *CSIRO Publishing*. Eligible presenters will be assessed by the ASBS Council members over the course of the conference and presented on the final day of proceedings.

The Nancy T. Burbidge Medal is the highest award of the Australasian Systematic Botany Society. First presented in 2001, it was established as a way for the Society to honour those who have made a longstanding and significant contribution to Australasian systematic botany. This year’s presentation and Nancy T. Burbidge Memorial Lecture will be delivered on the morning of Wednesday 5 December.

ASBS STUDENT REIMBURSEMENT

Student members of the society are eligible for a refund of their registration if they present at the conference and have submitted an application to council 4 weeks before the conference.

SYSTEMS EXHIBITION

Systems is an exhibition that celebrates the diverse and curious biological systems of Australia's living world.

Presented alongside the 2018 ASBS conference, *Mind the Gap*, this exhibition showcases South East Queensland-based artists who take inspiration from living systems, revealing links between art, science and nature. From ecosystems and biodiversity, to the intangible interconnections between humans and nature, *Systems* draws attention to a broad range of themes in a variety of artistic mediums such as jewellery, sculpture, installation and print.

Artists featured: Renata Buziak, Donna Davis, Nicola Hooper, Alinta Krauth, Rachael Lee, Sandra Pearce, Paula Peeters, Clare Poppi, Tanya Scharaschkin and Svetlana Trefilova.

Systems is curated by Melissa Fletcher and supported by the Queensland Herbarium.

Systems will be launched during the conference Welcome Reception and is on display in the QUEENSLAND HERBARIUM foyer from 4 – 14 December (9am – 5pm, weekdays only).

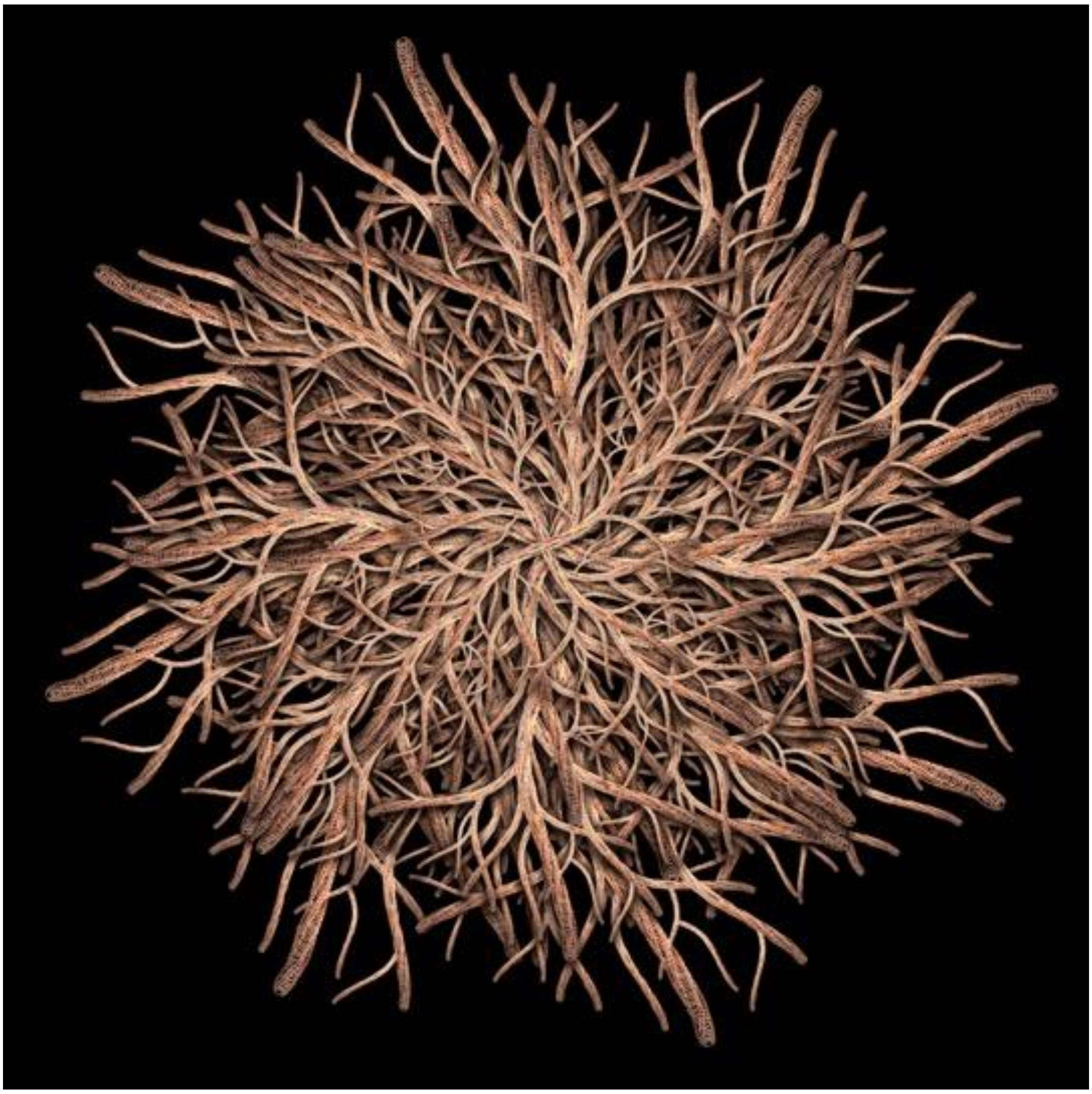


Image: Donna Davis, *Matrix 1*, 2016. Pigment print on Hahnemuhle fine art rag. Courtesy of the artist.

VENUES

The main conference venues are located within the Brisbane Botanic Gardens Mt Coot-tha, Toowong. Activities held elsewhere are Monday's Workshop (State Library of Queensland, South Brisbane) and Friday's Field Trip (Springbrook National Park, departing from and returning to the Queensland Herbarium).

BRISBANE BOTANIC GARDENS MT COOT-THA VENUES

The main conference venues are located within the Brisbane Botanic Gardens Mt Coot-tha, 152 Mount Coot-tha Road, Toowong:

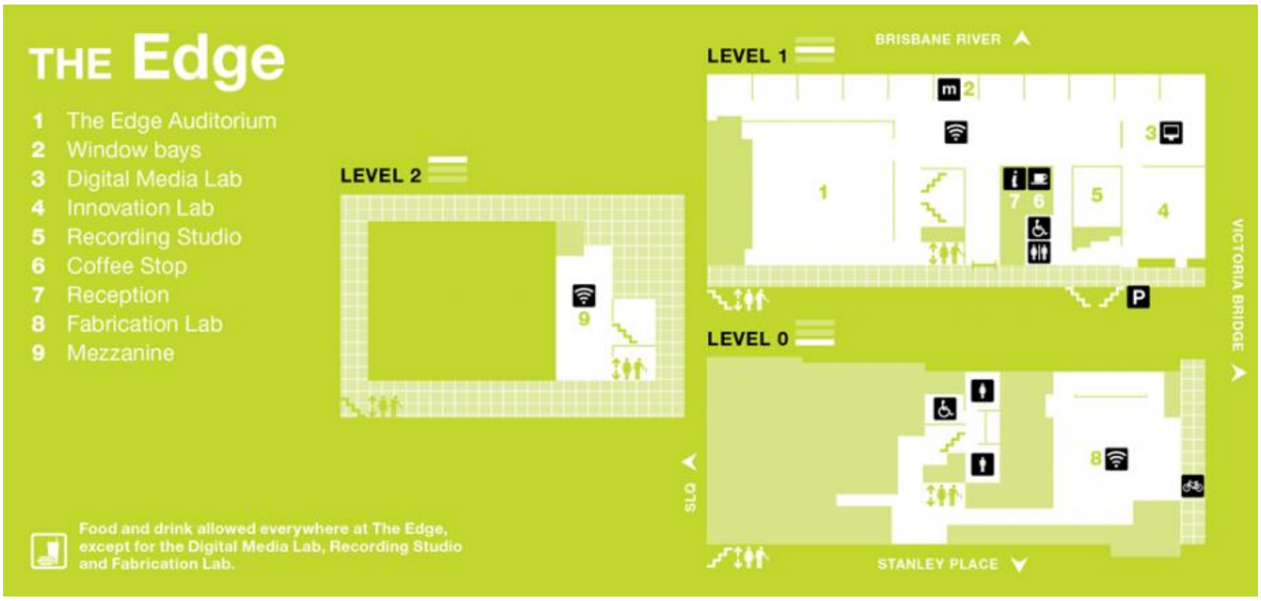
- Conference presentations, Tuesday to Thursday, are in the Brisbane City Council AUDITORIUM
- The QUEENSLAND HERBARIUM is hosting the ASBS Council Meeting, Welcome Reception and *Systems* art exhibition, and is the departure/return location for the Field Trip.
- Conference dinner is at the BOTANIC GARDENS FUNCTION CENTRE on Wednesday

You can get to the Brisbane Botanic Gardens Mt Coot-tha by car (free parking), bus (471, 598, 599), bike (bikeways nearby) or taxi/uber. Find more transport information at www.brisbane.qld.gov.au/facilities-recreation/parks-venues/parks/brisbane-botanic-gardens-mt-coot-tha/getting-gardens.

Brisbane City Council Wi-Fi is available (free) in the AUDITORIUM. There is no public Wi-Fi available in the QUEENSLAND HERBARIUM.

STATE LIBRARY OF QUEENSLAND VENUE

The Conference Workshop is in the INNOVATION LAB on level 1 of THE EDGE at the State Library of Queensland, Cultural Precinct, Stanley Place, South Brisbane. Please arrive at 8.45am for a 9am start.



Food and drink allowed everywhere at The Edge, except for the Digital Media Lab, Recording Studio and Fabrication Lab.

You can get to the State Library of Queensland by car (paid parking), bus, train, ferry, bike, foot or taxi/uber. The Cultural Precinct is on the opposite side of the Brisbane River from the CBD. Find more transport and venue information at www.slq.qld.gov.au/visit-us and www.slq.qld.gov.au/visit-us/venues.

Free Wi-Fi is available in the INNOVATION LAB, State Library of Queensland.

CONFERENCE PROGRAM OVERVIEW

SUNDAY

9:00 to 17:00	ASBS Council meeting

DAY 1 - MONDAY

9:00 to 17:00	Workshop: How to referee taxonomic manuscripts: State Library of Queensland
17:00 to 20:00	Welcome Reception and launch of *Systems* art exhibition

DAY 2 - TUESDAY

8:30	Introduction and Housekeeping
8:45	Welcome to Country and opening addresses
9:15	**Session 1**: Sharing botanical wealth: engagement, benefit sharing and the Nagoya Protocol
10:30	Morning Tea
11:00	**Session 1** (continued)
12:00	Lunch
13:00	**Session 2**: Insights from long ago: palaeobotany informing systematics
14:15	**Session 3**: MacPherson–Macleay, other gaps and overlaps: biogeography of Australasia
14:45	Afternoon Tea
15:15	**Session 3** (continued)
16:00	**Session 4**: Poster Presentations
16:45	Housekeeping
17:00 to 18:00	ASBS Annual General Meeting

DAY 3 - WEDNESDAY

8:30	Housekeeping
8:40	N.T. Burbidge medal introduction by ASBS President
8:45	N.T. Burbidge medal recipient address
9:45	Taxonomy Australia
10:15	Poster chat
10:30	Morning Tea
11:00	**Session 5**: Phylogenetic and Taxonomic progress 1
12:30	Lunch
13:30	**Session 6**: Phylogenetic and Taxonomic Progress 2
15:15	Afternoon Tea
15:45	**Session 7**: Botanical Diversity and Utilisation
17:00	Housekeeping
17:10 to 17:40	Queensland Herbarium Tour
18:30	Conference Dinner

DAY 4 - THURSDAY

8:30	Housekeeping
8:45	**Session 8**: Informed decision making – conservation genetics of threatened flora
10:30	Morning Tea
11:00	**Session 9**: Phylogenetic and Taxonomic progress 3
11:45	**Session 10**: Information Gaps in the age of Genomics 1
12:30	Lunch
13:30	**Session 11**: Information Gaps in the age of Genomics 2
15:30	Afternoon Tea
16:00	Conference Summation and Presentation of Student Prizes
16:30	Next ASBS conference presentation
16:40 to 17:00	Conference Close

DAY 5 - FRIDAY

7:00 to 18:30	Field trip to Springbrook departing QLD Herbarium

CONFERENCE PROGRAM

Student presenters are indicated with an * in the Program

SUNDAY 2 DECEMBER 2018 F.M.BAILEY ROOM (HERBARIUM)

9:00-late	ASBS Council meeting

MONDAY 3 DECEMBER 2018 MULTIPLE LOCATIONS

8:45 for 9:00-17:00	Workshop: How to referee taxonomic manuscripts: STATE LIBRARY OF QUEENSLAND
17:00-20:00	Welcome Reception and launch of *Systems* art exhibition: QUEENSLAND HERBARIUM

TUESDAY 4 DECEMBER 2018 AUDITORIUM (BOTANIC GARDENS)

8:30-8:45	Introduction and Housekeeping
8:45-9:15	Welcome to Country, Welcoming Address and Opening of Conference

SESSION 1: SHARING BOTANICAL WEALTH: ENGAGEMENT, BENEFIT SHARING AND THE NAGOYA PROTOCOL

SESSION CHAIR: KATHARINA NARGAR

9:15-10:00	Queensland Biodiscovery Act Julia Playford
10:00-10:15	Indigenous Engagement with Science Gerry Turpin
10:15-10:30	Ka rere nga purapura a Matariki; the seeds of the Pleaides are falling Nick Roskruge

10:30-11:00 MORNING TEA

11:00-11:15	Nagoya Protocol on Access Benefit Sharing: implications for herbaria and systematics research Shelley James; Gillian Brown, Antony Kusabs, Karina Knight, Josephine Milne, Dhahara Ranatunga
11:15-11:30	Increasing fungal literacy in Australasia: lessons from Universities to communities Teresa Lebel; Sapphire McMullan-Fisher, Sandra Abell
11:30-12:00	Sharing botanical wealth panel discussion

12:00-13:00 LUNCH

SESSION 2: INSIGHTS FROM LONG AGO: PALAEOBOTANY INFORMING SYSTEMATICS

SESSION CHAIR: ALEXANDER SCHMIDT-LEBUHN

13:00-13:45	*Plenary Address*: Imposing geochronological constraints on the stratigraphic record of life Paulo Vasconcelos

13:45-14:00 Newly discovered syncarpous fruits from the Oligocene Capella locality suggest links to Moraceae
Andrew Rozefelds

14:00-14:15 A comprehensive fossil calibration database for estimating angiosperm divergence times
Hervé Sauquet; Santiago Ramírez-Barahona, Susana Magallón

SESSION 3: MACPHERSON–MACLEAY, OTHER GAPS AND OVERLAPS: BIOGEOGRAPHY OF AUSTRALASIA

SESSION CHAIR: MATT RENNER

14:15-14:30 Mind the Gap – Extinction pulse at Eocene–Oligocene boundary drives diversification dynamics of the Australian temperate flora
Francis Nge*; Ed Biffin, Kevin Thiele, Michelle Waycott

14:30-14:45 Evolution of *Geosiris* (Iridaceae): historical biogeography and plastid-genome evolution in a genus of non-photosynthetic tropical rainforest herbs disjunct across the Indian Ocean
Elizabeth Joyce*; Darren Crayn, Vivienne Lam, Wesley Gerelle, Sean Graham, Lars Nauheimer

14:45-15:15 AFTERNOON TEA

15:15-15:30 Phylogeography of *Spyridium parvifolium* (Rhamnaceae) across south-eastern Australia
Catherine Clowes*; Michael Bayly, Gillian Brown

15:30-15:45 Gaps and Overlaps in the South-East Australian Mallee: Systematics and Phylogeography of Mallee-Boxes
Patrick Fahey*; Michael Bayly, Frank Udovicic, David Cantrill

15:45-16:00 The SAD model - an uplifting tale of how migration stimulated the diversification of the Malesian flora
Darren Crayn; Elizabeth Joyce

SESSION 4: POSTER PRESENTATIONS

SESSION CHAIR: GILL BROWN

16:05-16:10 Using large-scale ecological data to support taxonomic decisions in difficult species complexes in *Ptilotus* (Amaranthaceae)
Timothy Hammer*; Paul Macintyre, Ladislav Mucina, Kevin Thiele

16:10-16:15 Phylogeographic congruence in *Lindernia* (Linderniaceae) with biotic regions across northern Australia
Bill Barker; Ed Biffin

16:15-16:20 Clarification of species limits of *Prostanthera cineolifera* R.T.Baker & H.G.Sm. (Lamiaceae) essential for conservation
Ruth Palsson*; Jeremy Bruhl, Rose Andrew, Ian Telford, Trevor Wilson

16:20-16:25 Integrative taxonomic revision of *Melichrus* R.Br. (Ericaceae subfam. *Epacridoidae*)
Helen Kennedy*; Jeremy Bruhl, Darren Crayn, Rose Andrew, Ian Telford

16:25-16:30 ddRAD-seq identifies a recurrent *Dicksonia* tree fern hybrid
Lara Shepherd; Patrick Brownsey, Chris Stowe, Leon Perrie

16:30-16:35 Population genetic analysis to inform conservation of the endangered Isis Tamarind, *Alectryon ramiflorus* (Sapindaceae)
Robert Lamont; Steven Ogbourne, Gabriel Conroy, Joel Nichols

16:35-16:40 In defence of phrase names
Ian Telford; Jeremy Bruhl

16:40-16:45 Blindspots in the rainforest – a case study of *Elaeocarpus* (Elaeocarpaceae) in Fiji
Yumiko Baba; Marika Tuiwawa

16:45-17:00 Housekeeping

17:00-18:00 ASBS Annual General Meeting

WEDNESDAY 5 DECEMBER 2018 AUDITORIUM (BOTANIC GARDENS)

8:30-8:40 Housekeeping

8:40-8:45 *N.T. Burbidge medal introduction by ASBS President*

8:45-9:45 N.T. Burbidge medal recipient address

9:45-10:15 Taxonomy Australia
Kevin Thiele

10:15-10:30 Poster chat (poster presenters to be available to discuss their work)

10:30-11:00 MORNING TEA

SESSION 5: PHYLOGENETIC AND TAXONOMIC PROGRESS 1

SESSION CHAIR: TANYA SCHARASCHKIN

11:00-11:15 Resolving of the backbone of *Ptilotus* and establishing a new taxonomic framework for the aervoid clade (Amaranthaceae)
Timothy Hammer*; Xiao Zhong, Catherine Colas des Francs-Small, Paul Nevill, Ian Small, Kevin Thiele

11:15-11:30 If it's yellow, let it mellow: Investigating toxicity variation in southern Australian yellow-staining *Agaricus* in a phylogenetic context
Amelia-Grace Boxshall*; Teresa Lebel, Damien L. Callahan, Todd McLay, Joanne Birch

11:30-11:45 Taking an integrative approach to resolve the *Xerochrysum bracteatum* species complex
Tim Collins*; Alexander N. Schmidt-Lebuhn, Rose L. Andrew, Ian R.H. Telford, Jeremy J. Bruhl

11:45-12:00 The 'Taxonomic Gap' and progress towards a 'Global Flora'
Russell Barrett

12:00-12:15 How to look again at *Spermacoce* and *Borreria* (Rubiaceae): is morphological evolution in Australian *Spermacoce* key to our understanding of generic limits?
Kerry Gibbons; Marco Duretto

12:15-12:30 Speciation theory and species delimitation using *Eucalyptus* as a model
Susan Rutherford

12:30-13:30 LUNCH

SESSION 6: PHYLOGENETIC AND TAXONOMIC PROGRESS 2

SESSION CHAIR: SHELLEY JAMES

13:30-13:45 Australian grass diversity: phylogenetic overview, global comparisons and future direction
Tanya Scharaschkin

13:45-14:00 Vale *Velleia* (and others) – the final chapter of our *Goodenia s.l.* saga
Kelly Shepherd; Rachel Jabaily

14:00-14:15 How many species of toropapa (*Alseuosmia*) are disguised in the bush?
Lara Shepherd; Andrew Townsend, Peter de Lange, Leon Perrie

14:15-14:30 OMG *Boronia* (Rutaceae) is polyphyletic: coping with large well supported clades that contain few morphologically useful characters
Marco Duretto; Margaret Heslewood, Mike Bayly

14:30-14:45 Taxonomic revision of the *Myosotis australis* group (Boraginaceae) in Australia, New Zealand and New Guinea
Heidi Meudt; Jessie Prebble, Michael Thorsen

14:45-15:00 Treating *Tephrosia* (Fabaceae) for the eFlora of Australia: project progress and plans
Ryonen Butcher

15:00-15:15 Plant traits for everyone – A proposal for a new multi-purpose minimum trait set
Russell Barrett; Hervé Sauquet

15:15-15:45 AFTERNOON TEA

SESSION 7: BOTANICAL DIVERSITY AND UTILISATION

SESSION CHAIR: LARA SHEPHERD

15:45-16:00 Preliminary floristic patterns observed in the Kakadu sandstone flora
Peter Jobson; Jason Cantley, Angela MacDonnell, Chris Martine

16:00-16:15 How many species of *Rottboelliinae* (Poaceae) are there in Australia?
Melodina Fabillo; Tanya Scharaschkin

16:15-16:30 Archaeobotanical sense-making: an Australian archaeologist's journey with plants
Brit Asmussen

16:30-16:45 Chasing duplicates beyond the century, across the world and throughout the vault: but mind the gaps
Austin Brown

16:45-17:00 Checking it twice: an update on the National Species List (NSL)
Anna Monro; Brendan Lepschi, Anne Fuchs

17:00-17:05 Housekeeping

17:10-17:40 Queensland Herbarium Tour, starting from QUEENSLAND HERBARIUM foyer

18:30 CONFERENCE DINNER

18:30 ASBS Conference Dinner at the BOTANIC GARDENS FUNCTION CENTRE,
Brisbane Botanic Gardens Mt Coot-tha, Toowong.

THURSDAY 6 DECEMBER 2018 AUDITORIUM (BOTANIC GARDENS)

8:30-8:45 Housekeeping

SESSION 8: INFORMED DECISION MAKING – CONSERVATION GENETICS OF THREATENED FLORA

SESSION CHAIR: HERVÉ SAUQUET

8:45-9:30 *Plenary Address*: Conservation of Australian Plants with a focus on northern Australia especially Queensland
Alison Shapcott

9:30-9:45 *Reedia spathacea* F.Muell.: Phylogeography and population structure
Jessica Bruce*; Annette Koenders, Kristina Lemson, Quinton Burnham, Margaret Byrne, Pierre Horwitz

9:45-10:00 Conservation genetics of threatened native olives (genus *Notelaea*) in southern Queensland
Chapa Manawaduge*; Matthew Phillips, Susan Fuller

10:00-10:15 How did it go? A genetic analysis of the *Gossia gonoclada* recovery program
Laura Simmons; Tamara K. Taylor

10:15-10:30 Congruent geographic structuring in *Macrozamia* and their pollinating thrips
Alicia Toon; Lyn Cook

10:30-11:00 MORNING TEA

SESSION 9: PHYLOGENETIC AND TAXONOMIC PROGRESS 3

SESSION CHAIR: SUSAN RUTHERFORD

11:00-11:15 The evolution and biogeography of Australian Asparagales
Joanne Birch; Daniel Murphy, Neville Walsh, John Conran, Terry Macfarlane, J. Chris Pires, Bee Gunn

11:15-11:30 Using phylogenetics to investigate continental, biome and habitat shifts and radiations in *Phlegmariurus* (Lycopodiadiaceae)
Ashley R. Field; Thaís Elias Almeida, Lucie Bauret, Weston Testo

11:30-11:45 Australasian orchid diversification in space and time: phylogenetic insights from *Dendrobiinae* (Orchidaceae)
Katharina Nargar; Claire Micheneau, Kamolphat Atsawawaranunt, Lars Nauheimer, Mark A. Clements

SESSION 10: INFORMATION GAPS IN THE AGE OF GENOMICS 1

SESSION CHAIR: TODD MCLAY

11:45-12:30	Genomics for Australian plants: developing genomic resources for the Australian plant community Linda Broadhurst, **Margaret Byrne**, David Cantrill, **Darren Crayn**, Anna Fitzgerald, Graham King, Jen Taylor, Mabel Lum (The Steering Committee and project management on behalf of the Genomics for Australian Plants Consortium)

12:30-13:30 LUNCH

SESSION 11: INFORMATION GAPS IN THE AGE OF GENOMICS 2

SESSION CHAIR: JO BIRCH

13:30-14:00	Evolution of *Oryza* as Revealed by Genomics **Robert Henry**
14:00-14:15	A hybrid-enrichment bait capture kit for *Hibisceae*, trialled on Australian *Hibiscus* section *Panduriformes* **Todd McLay**; Mike Bayly, Jennifer Tate, Sarah Mathews
14:15-14:30	Phylogenomics of Australian *Gnaphalieae* (Asteraceae) using target enrichment **Alexander Schmidt-Lebuhn**; Jess Bovill, Ian Lester
14:30-14:45	Using sequence capture to infer gymnosperm phylogeny **Nathalie Nagalingum**; Lorena Endara, Steffi Ickert-Bond, Gordon Burleigh
14:45-15:00	Resolving complex evolutionary relationships in the sun orchids (*Thelymitra*, Orchidaceae) – insights through molecular phylogenetics and phylogenomics **Lars Nauheimer**
15:00-15:30	Conservation genomics for taxon delimitation and management of rare and threatened plants **Margaret Byrne**; Rachel Binks, Carol Wilkins, Donna Bradbury, Adrienne Markey

15:30-16:00 AFTERNOON TEA

16:00-16:30	Conference Summation and Presentation of Student Prizes
16:30-16:40	Next ASBS conference presentation
16:40-17:00	Conference Close

FRIDAY 7 DECEMBER 2018 MEET AT FRONT OF HERBARIUM

7:00-18:30	Field trip to Springbrook Departing from and returning to QUEENSLAND HERBARIUM

ABSTRACTS

In presentation order

TUESDAY 4 DECEMBER 2018 AUDITORIUM (BOTANIC GARDENS)

SESSION 1 TUESDAY 9:15-10:00

QUEENSLAND BIODISCOVERY ACT

Julia Playford

Queensland Department of Environment and Science

Biodiscovery makes a valuable contribution to the State’s economy. The Queensland Government is committed to stimulating and streamlining biodiscovery in Queensland and encouraging investment in the State’s bioeconomy.

The *Biodiscovery Act 2004* regulates the take and use of Native Biological Material from state lands and Queensland waters for biodiscovery. A recent review of the Act, combined with international progress on access and benefit sharing protocols, has identified areas of potential reform to ensure Queensland continues to lead Australia by providing a contemporary regulatory framework for biodiscovery.

Key issues emerging from the Review include implementation of the Nagoya Protocol and the rights of Aboriginal and Torres Strait Islander people regarding the use of their resources and traditional knowledge for biodiscovery, definitions of key terms and the regulatory framework for access and benefit sharing.

Reform of the Act will enable Queensland’s biodiscovery industry to collaborate and trade internationally, such as with the European Union and India, which requires demonstration of compliance with the Nagoya Protocol on access and benefit sharing; and, ensure the benefits of biodiscovery are shared appropriately.

SESSION 1 TUESDAY 10:00-10:15

INDIGENOUS ENGAGEMENT WITH SCIENCE

Gerry Turpin[1,2]

[1]Queensland Herbarium; [2]Australian Tropical Herbarium

Prior to European colonisation, Australia was a continent with over 500 different clan groups or nations and more than 250 languages. For thousands of years Australian Indigenous peoples have lived on and managed this country, shaping the landscapes and environments, and adapting to changing climates. The knowledge that has been accumulated through intimate and sustained connections to the land had been passed down orally through generations, existing in stories, paintings, song and dance. A more recent term recognising this knowledge is Indigenous Biocultural Knowledge (IBK).

Globally, IBK is well recognised, accepted and respected in contemporary biodiversity conservation and management. In Australia, Indigenous and non-Indigenous scientists are working together to create meaningful and more equitable collaborations between knowledge systems. However, there is still a lack of understanding and reluctance to recognise IBK and explore ways that it can be respectfully employed with Western Science to benefit communities and society.

This talk will look at the historical aspect and present day of Indigenous Engagement, including steps on constructive engagement.

Gerry is an Mbabaram man from north Queensland and a renowned Ethnobotanist. He has been employed by the Queensland State Government for about 30 years and has previously been involved in the Queensland Herbarium’s Vegetation Surveys and Regional Ecosystem Mapping Project in Queensland.

Gerry manages the Tropical Indigenous Ethnobotany Centre at the Australian Tropical Herbarium, in partnership with James Cook University, DES and CSIRO, and has worked with many Traditional Owner groups on Cape York and other parts of Queensland. He is a member of the Ecological Society of Australia Board of Directors with the role of Indigenous Engagement. As an Indigenous ethnobotanist Gerry has a strong cultural commitment to facilitating effective partnerships that support Indigenous communities to protect, manage and maintain their cultural knowledge on the use of plants.

KA RERE NGA PURAPURA A MATARIKI; THE SEEDS OF THE PLEAIDES ARE FALLING

Nick Roskruge

Massey University

As the Nagoya Protocol on Access to Genetic Resources establishes itself as a key consideration for botanists and botanically centric researchers around the world, the limited understanding of what constitutes an indigenous interest in their science is even more apparent. In New Zealand the traditional knowledge systems of Māori are compromised by various contemporary factors yet are now receiving a resurgence in understanding as the science community attempts to gain insight to another realm of knowledge. The whakatāuki or Māori proverb recited here tells us of the understanding that traditional knowledge is now coming into recognition for the value, support and insight it can give to those who strive to protect our natural world.

One of the commonalities among indigenous cultures is the relationship between mankind and the natural world. For Māori this is represented in their relationship to the primal parents - Ranginui and Papatūānuku - who were derivatives of the spiritual realm and begat a generation assigned responsibility for the relationships, care and utility of our natural world. To be Māori is to believe to be descended from this primal relationship and to continue the obligation of kaitiakitanga the spiritual world requires; the care and respect for our natural world for all future generations. This is a serious obligation and is supported by many generations of mātauranga or traditional knowledge which is both spatially and temporally orientated. Traditional forms of taxonomy provide the very base of this knowledge, primarily informing relationships between natural features; flora, fauna, people and place. These systematics further inform relationships across species, families, the animate and inanimate, and is a very personal system which is inclusive of mankind rather than exclusive. The proverb - Ka rere ngā purapura a Matariki - helps to create a contextual explanation of this mātauranga in the 21st century. Matariki or the Pleiades is said to be the repository of knowledge, especially as it relates to our relationship to the botanical world. The falling of seeds represents the knowledge as it finds its way to gain uptake and therefore contribute to the next generation, and the next. Our Earth mother Papatūānuku promised our sustenance. She retains all the secrets of her being and will always support those who respect her. Ko Papatūānuku te matua o te tangata; she is the parent of the human race.

Nick Roskruge is an ethnobotanist and horticulturist by training and currently head of Maori and Pacific Agribusiness at Massey University in New Zealand. He is of Te Atiawa and Ngati Porou descent, chairs the National Maori collective Tahuri Whenua, sits on a range of committees and entities representing Maori Interests and was a Fulbright Scholar in 2013 with indigenous development at Cornell University in Upstate New York. More recently Nick has been involved in a number of projects with taxonomic interests as well a supervising Maori and Pasifika students in food security and related topics. Nga mihi atu.

MORNING TEA 10:30-11:00

NAGOYA PROTOCOL ON ACCESS BENEFIT SHARING: IMPLICATIONS FOR HERBARIA AND SYSTEMATICS RESEARCH

Shelley James[1]; Gillian Brown[2], Antony Kusabs[3], Karina Knight[4], Josephine Milne[5], Dhahara Ranatunga[6]

[1]National Herbarium of NSW, Royal Botanic Gardens and Domain Trust; [2]Queensland Herbarium; [3]Museum of New Zealand Te Papa Tongarewa; [4]Western Australian Herbarium; [5]Royal Botanic Gardens Victoria; [6]Auckland War Memorial Museum

The Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization (ABS) to the Convention on Biological Diversity is an international agreement which came into effect on 12 October 2014. It aims to ensure the sharing of benefits arising from the utilization of genetic resources in a fair and equitable way. It is a supplementary agreement to the Convention on Biological Diversity ratified by 111 countries, and has a strong legal framework.

Australia is a signatory to the Nagoya Protocol, but as yet has not yet ratified nor provided country-specific advice on interpretation and implementation of the protocol. The New Zealand Parliament is unlikely to become a signatory to the Nagoya Protocol due to a Treaty of Waitangi Claim (WAI 262) and subsequent 2011 Waitangi Tribunal Report "Ko Aotearoa tenei: a report into claims concerning New Zealand law and policy affecting Māori culture and identity". While the impacts on herbaria and botanical research are as yet unclear, what is certain is that herbarium specimens collected after 12 October 2014 fall under Nagoya Protocol regulations, and Australian and NZ herbaria are beginning to implement procedures in order to document the legal acquisition and use of specimens and their associated genetic resources. Documenting permit details, Prior Informed Consent and Mutually Agreed Terms for specimen collecting events, regardless of the immediate use of specimens for genetic research or non-commercial use, and the request for use of herbarium specimens for molecular destructive sampling, are beginning to come under scrutiny.

The Managers of Australasian Herbarium Collections (MAHC) will share their knowledge, the guidelines being developed, and community needs to help with understanding and need for conformity to the Nagoya Protocol and WAI 262 recommendations.

INCREASING FUNGAL LITERACY IN AUSTRALASIA: LESSONS FROM UNIVERSITIES TO COMMUNITIES

Teresa Lebel[1]; Sapphire McMullan-Fisher[2], Sandra Abell[3]

[1]Royal Botanic Gardens Victoria, [2]FunFungi Ecology, [3]Australian Tropical Herbarium

Active teaching about the fungal kingdom has gradually been decreasing in Universities. Mycology lectures have greatly decreased, coupled with a general shift away from organismal biology reducing the ‘intriguing’ and ‘naturalist’ first stage observational skills of students. However, curiosity and knowledge seeking is increasing through community based groups, socially funded workshops and forays, and the use of social media (e.g. Facebook fungal appreciation groups, photography, restoration projects, etc.).

From our experiences in teaching both tertiary students and the enthusiastic general public, we have noticed that: University students take information and try to retain it for regurgitation rather than applying the knowledge or concepts. In contrast community groups, particularly land management groups, take new ideas and immediately try to apply them to their day-to-day management actions. Ideally students should quickly learn concepts and features that might indicate relationships to other related species, together with possible interactions between other organisms, thus determining how knowledge of fungi can be applied to the management of diversity and function of natural systems.

This is likely to be partly a reflection of the experience and maturity of ‘community’ participants compared with the younger students, who are often still in a ‘school’ mentality. However, more, and younger people are joining these community-based attempts to seek knowledge about fungi. This is where social media, and applications such as mushroom observer and iNaturalist have had significant impacts on access to fungal knowledge, particularly mushrooms.

We present some suggestions on providing successful fungal education to different audiences, including activities, and also share our favourite resources.

Dr Teresa Lebel is a Senior Mycologist at the Royal Botanic Gardens Victoria, and Honorary Associate of the Victorian Poisons Information Centre, School of BioSciences at The University of Melbourne, and Landcare Research New Zealand. She is an authority on the taxonomy, systematics and ecology of Australasian truffle-like fungi and their mushroom, punk or cup relatives. Current studies focus on the affinities, placement and evolution of fungi with truffle-like fruitbody forms across all macrofungal lineages, and establishing a DNA library of barcodes from type and other material from fungarium collections.

SESSION 1 TUESDAY 11:30-12:00

SHARING BOTANICAL WEALTH PANEL DISCUSSION

Notes

LUNCH 12:00-13:00

Plenary Address

IMPOSING GEOCHRONOLOGICAL CONSTRAINTS ON THE STRATIGRAPHIC RECORD OF LIFE

Paulo Vasconcelos

University of Queensland

SESSION 2 TUESDAY 13:45-14:00

NEWLY DISCOVERED SYNCARPOUS FRUITS FROM THE OLIGOCENE CAPELLA LOCALITY SUGGEST LINKS TO MORACEAE

Andrew Rozefelds

Queensland Museum

Fruits composed of a many individual fruitlets that are united into a complex structure can be described as a syncarpium or a sorosus (*sensu* Spjut, 1994). Spjut (1994) considered that sorosi occur in diverse, and phylogenetically unrelated families, such as in the monocots Araceae, Bromeliaceae, Cyclanthaceae, Pandanaceae, and dicots Balanophoraceae , Bataceae, Chloranthaceae, Cornaceae, Moraceae, Rafflesiaceae, Rubiaceae and Urticaceae. Permineralised fruits from the Oligocene Capella locality consists of many fruitlets, and the seeds occur in the upper portion of each fruitlet. The fruitlets form connate radiating segments, which are interpreted as being derived from the perianth. These radiating segments extend from the centre to the margin of the fruit and adjacent perianth apices appear to be fused apically, forming an irregular pentagonal-hexagonal imbricate surface which shows no consistent phyllotactic pattern. It was possible to exclude the monocot families and Balanophoraceae because the arrangement of seeds in the fruits of these families typically exhibit a regular phyllotaxy, which is less evident in the Pandanaceae. The structure of the fruit and seed shape in the fossil differs from that in Rafflesiaceae. The fossil also has a complex internal structure consisting of connate radiating thin elements that are closely aligned together and in this respect the fossils differs from the internal fruit morphology of Cornaceae, Chloranthaceae, Rubiaceae, Bataceae and Urticaceae. The morphology of the syncarpous fruits is considered to lie with the Moraceae, although fruits with five radiating sections in the fruit are not known from this family.

Spjut, R.W. (1994). A systematic treatment of fruit types. Memoirs of the New York Botanical Gardens, vol 70. New York.

Andrew's research interests are varied but a central focus has been on the history and evolution of Australia's rainforests through the study of both living and fossil plants. Study of the fossil record gives us a unique opportunity to understand the history and tempo of plant evolution, which in turn provides insights into how Australia's vegetation has changed over time.

SESSION 2 TUESDAY 14:00-14:15

A COMPREHENSIVE FOSSIL CALIBRATION DATABASE FOR ESTIMATING ANGIOSPERM DIVERGENCE TIMES

Hervé Sauquet[1]; Santiago Ramírez-Barahona[2], Susana Magallón[2]

[1]National Herbarium of NSW, Royal Botanic Gardens and Domain Trust; [2]Universidad Nacional Autónoma de México

Calibration using multiple fossil age constraints is the keystone of molecular dating studies using relaxed clock models. In recent years, several papers have called for better practices and higher standards of justifying fossil calibrations. However, these have not yet been applied widely to angiosperms. In addition, the number of fossil calibrations used in angiosperm molecular dating studies remains very small compared to the extraordinary diversity of known fossil taxa. While not every fossil constitutes as suitable and robust calibration, this underutilization has raised many concerns from the palaeobotanical community. Here, we present a first step towards solving these two problems by presenting a dataset of 238 fossil calibrations. These provide independent age constraints on 210 distinct nodes of the angiosperm phylogeny, including the oldest reliable records for 146 families. This dataset builds upon a previous set of 137 calibrations from a recent study and additional published lists of calibrations proposed for magnoliids, monocots, and asterids. Recently described fossil taxa of particular significance for specific clades were also added. Each fossil calibration was entirely revised for phylogenetic assignment and absolute age, and a detailed structured justification is provided for each record. Importantly, separate quality scores are associated with each aspect of the justification. This approach allows us to include many important fossils whose relationships have not yet been tested through total evidence phylogenetic analyses. These constraints may represent ‘early but risky’ calibrations that users of our dataset may want to filter out and exclude, depending on the goals of the analyses. We demonstrate the potential application of this dataset by presenting results from relaxed molecular clock analyses of angiosperms using a new dataset of seven markers and 1209 species sampled from all currently recognized orders (64) and families (436). These analyses provide the first comprehensive set of comparable estimates for stem ages of every angiosperm family and crown-group ages for 384 (88%) of them, showing that most families started to diversify in the Paleogene (23-66 million years ago). These results appear to be robust to various assumptions made on the crown-group age of angiosperms as a whole, which remains highly uncertain. We hope that our angiosperm calibration database will represent a useful resource for the community. Our aim is to improve it over time and release multiple versions in the future, taking into account feedback and new studies.

I am an evolutionary biologist and systematic botanist with a broad interest in macroevolution. A key focus of my research is to unravel and better understand large-scale patterns in the evolution of flowers, combining molecular phylogenies and databases of plant morphology. I obtained my PhD in 2003 in Paris, worked as a postdoc in Stockholm, Sydney, and Kew, then as an Associate Professor at Université Paris-Sud from 2009 to 2017. I now work as a Systematic Botanist at the Royal Botanic Gardens and Domains Trust.

SESSION 3 TUESDAY 14:15-14:30

MIND THE GAP – EXTINCTION PULSE AT EOCENE–OLIGOCENE BOUNDARY DRIVES DIVERSIFICATION DYNAMICS OF THE AUSTRALIAN TEMPERATE FLORA

Francis Nge[1]; Ed Biffin[1], Kevin Thiele[2], Michelle Waycott[1]

[1]University of Adelaide; [2]Biosystematics and Taxonomy Plan

The diversification dynamics of the Australian temperate flora remains largely unexplored. Here, we investigate whether differences in species richness in the southwest (SWA) and south-east (SEA) regions of the Australian continent can be attributed to higher net diversification, more time for species accumulation, or a combination of both.

We assembled dated molecular phylogenies for 21 dominant plant families found across mesic temperate Australia, encompassing both SWA and SEA regions, and applied a series of diversification models to investigate responses across different groups and time scales.

We show that higher species richness in SWA can be attributed to a higher net rate of lineage diversification and more time for species accumulation. Different pulses of diversification were retrieved for the two regions. An extinction pulse across all major plant lineages was noted in the southeast at the Eocene– Oligocene boundary (c. 34 Ma), compared with the southwest which continued to diversify during that period.

Our study demonstrates the importance of historical diversification pulses and differential responses to global events as drivers of present day diversity.

Student presenter

Francis is a PhD Candidate at the University of Australia and State Herbarium of South Australia. His current research project focuses on the diversification and evolution of Australian temperate plants, with a focus on Rhamnaceae, Myrtaceae, and Proteaceae.

SESSION 3 TUESDAY 14:30-14:45

EVOLUTION OF *GEOSIRIS* (IRIDACEAE): HISTORICAL BIOGEOGRAPHY AND PLASTID-GENOME EVOLUTION IN A GENUS OF NON-PHOTOSYNTHETIC TROPICAL RAINFOREST HERBS DISJUNCT ACROSS THE INDIAN OCEAN

Elizabeth Joyce[1]; Darren Crayn[1], Vivienne Lam[2], Wesley Gerelle[2], Sean Graham[2], Lars Nauheimer[1]

[1]Australian Tropical Herbarium; [2]Department of Botany, University of British Columbia

Mycoheterotrophs–plants that acquire carbon from root-associated soil fungi–often have highly degraded plastomes, reflecting relaxed (or released) selective constraints on plastid genes following the loss of photosynthesis. *Geosiris* Baill. is the only mycoheterotrophic genus in the family Iridaceae and comprises two species in Madagascar (*G. aphylla* Baill.) and nearby islands (*G. albiflora* Goldblatt & J.C.Manning), and a third recently discovered species in NE Australia (*G. australiensis* B.Gray & Y.W.Low). Here we characterise the plastome of *G. australiensis* and *G. aphylla* to compare patterns of gene retention and loss in relation to autotrophic and other mycoheterotrophic taxa, test the monophyly of the genus and its position in Iridaceae, and investigate its historical biogeography. The assembled plastomes of *Geosiris* were also compared to published and newly-generated plastomes of autotrophs and other mycoheterotrophs. Both examined *Geosiris* species have reduced plastome sizes, reflecting loss of approximately half their plastid-encoded genes. Most intact genes experience levels of purifying selection indistinguishable from photosynthetic relatives, but when analysed together there was a small but significant reduction in purifying selection in retained non-photosynthetic genes, consistent with general relaxation of selection. *Geosiris australiensis* has a more degraded plastome and has undergone a major structural change by transferring almost all genes from the small single copy region to the inverted repeats.

Geosiris is confirmed as monophyletic and is placed in Iridaceae as the sister group of a large clade comprising Aristeoideae, Nivenioideae, and Crocoideae. Ancestral range reconstruction and dating analyses suggest the early divergences in Iridaceae took place in the late Cretaceous and Palaeocene in Australia (then part of Gondwana). Initial divergence of *Geosiris* occurred around 53 Ma, with a subsequent diversification c. 30 Ma. Africa (including Madagascar) is reconstructed as the most likely ancestral area of the genus, implying a major range expansion event (either by transoceanic dispersal or migration along the northern rim of the Indian Ocean) back to Australia after the divergence of *G. aphylla* and *G. australiensis* in the Oligocene. The independent evolutionary history of these two species is associated with multiple differences in plastome degradation. Our study highlights the dynamic evolutionary history of *Geosiris*, contributes to the characterisation of mycoheterotrophic plastomes, and furthers our understanding of plastome structure and function.

Student presenter

I am a PhD candidate from the Australian Tropical Herbarium and James Cook University. My main research focus is on the exchange of plant lineages between the Sunda and Sahul continental shelves throughout the Cenozoic, and how this influenced the evolution of the northern Australian flora.

AFTERNOON TEA 14:45-15:15

PHYLOGEOGRAPHY OF *SPYRIDIUM PARVIFOLIUM* (RHAMNACEAE) ACROSS SOUTH-EASTERN AUSTRALIA

Catherine Clowes[1]; Michael Bayly[1], Gillian Brown[2]

[1]University of Melbourne; [2]Queensland Herbarium

Spyridium parvifolium is a widespread and morphologically variable shrub from south-eastern Australia. It has a disjunct distribution, separated by Bass Strait (between Victoria and Tasmania including the Furneaux Island) and divided across the South Australian Murray Basin. The species is discontinuously distributed throughout Victoria with populations dotted across the state. Seventy-two complete chloroplast genomes of *S. parvifolium* were sequenced from across the species distribution range and morphological forms. Results from Maximum Parsimony and Bayesian Analysis both reveal clear geographic patterns. We found a strong genetic disjunction into South Australia, with samples from this state deeply divergent not only from those in other states but also from each other (north to south). Samples from the inland side of the Great Dividing Range (GDR) are distinct, and populations south of the GRD and north/east of the Gippsland Basin are differentiated. Despite the apparent disjunction across Bass Strait, we found recent gene flow between populations of *S. parvifolium* located in south-western/south-central Victoria and those in Tasmania and Flinders Island.

Student presenter

Catherine is currently completing a PhD at the University of Melbourne focused on genetic diversity within *Spyridium parvifolium*. She completed a Bachelor of Science (Honours) at The University of Melbourne with her honours project focused on the *Acacia longifolia* group. She has also completed a Diploma of Secondary Education (Science) (Geography) at Monash University and a Bachelor of Applied Science (Environmental Management) (Biology) at Deakin University. Prior to beginning her PhD Catherine worked as a Consultant Botanist with Biosis Pty Ltd.

SESSION 3 TUESDAY 15:30-15:45

GAPS AND OVERLAPS IN THE SOUTH-EAST AUSTRALIAN MALLEE: SYSTEMATICS AND PHYLOGEOGRAPHY OF MALLEE-BOXES

Patrick Fahey[1]; Michael Bayly[1], Frank Udovicic[2], David Cantrill[2]

[1]University of Melbourne; [2]National Herbarium of Victoria, Royal Botanical Gardens Victoria

The Interglacial Refugium Hypothesis (IRH) states that some species that were widespread in glacial periods retracted to and survived in refugia during interglacial periods. While there has been less investigation of this hypothesis than the more common pattern of glacial refugia, evidence has been building that the scattered distributions of certain arid adapted species in the southern hemisphere may fit with the IRH. During my PhD I am aiming to undertake molecular phylogeographic studies of box eucalypts with disjunct distributions in south-east Australia to investigate if their pattern of genetic diversity is consistent with the IRH. To test this, I will use high-throughput sequencing and phylogenetic analyses, along with habitat modelling and molecular dating to test hypotheses regarding the environmental factors driving the distribution of the target species both in the past and present. Target species for the study are all members of *Eucalyptus* section *Adnataria* Pryor & Johnson (Boxes): *E. behriana* F.Muell. (Bull Mallee), *E. viridis s.l.* (Green Mallee), *E. polybractea* (Blue Mallee), and *E. baueriana* Schauer (Blue Box). The first two taxa are mallee-boxes of semi-arid regions and form the first section of my project, while *E. baueriana* is a tree of higher rainfall areas and will be investigated subsequent to this. Given the poor dispersal ability of eucalypts, it is unlikely that long-distance colonisation events have played a major role in establishing the disjunct populations of the focal species, with a historically wider distribution and subsequent contraction and vicariance due to environmental change being a stronger hypothesis. In this presentation I will be providing a background to my project and presenting my results to date.

Student presenter

Having completed my Honours year investigating a new species of *Chloris* (windmill grass) at The University of Queensland in 2017, in 2018 I have made the move to Melbourne to take up a PhD reconstructing the phylogeography of a number of *Eucalyptus* species.

SESSION 3 TUESDAY 15:45-16:00

THE SAD MODEL - AN UPLIFTING TALE OF HOW MIGRATION STIMULATED THE DIVERSIFICATION OF THE MALESIAN FLORA

Darren Crayn; Elizabeth Joyce

Australian Tropical Herbarium, James Cook University

Investigating diversification processes in tropical ecosystems is vital for understanding how they were assembled and informing conservation decisions. Megadiverse Malesia lies at the convergence of the Sunda and Sahul continental shelves, which collided from c. 23 Ma. This convergence wrought profound geological change and resulted in a major exchange of previously isolated Sundanian and Sahulian floras, yet our understanding of how the Sunda-Sahul Floristic Exchange (SSaFE) influenced the evolution of the Malesian flora has advanced little in 50 years. To investigate this, we conducted a comparative analysis of patterns in diversification across 13 trans-Wallacean plant clades for which molecular chronograms were available. Log lineage-through-time (LTT) plots were constructed for each clade, and a linear mixed model was applied to test the effect of Sunda-Sahul disjunctions on diversification. We found substantial variation in diversification patterns between clades exchanged in the SSaFE, yet there are common trends on a floristic scale. We show that floristic dispersal between Sunda and Sahul was correlated with a significant increase in diversification (19%), a novel finding. The results also shed light on the dynamism of the SSaFE and its contribution to the diversification of the Malesian flora. Patterns of dispersal and diversification changed through time and comprise three distinct phases, which we propose to formalise as the SAD model; the Saturation Phase (c. 20–14 Mya), the Admixture Phase (c. 14–8 Mya), and the Diversification Phase (c. 8–2 Mya). We discuss the potential geological and climatic factors correlating with each phase, and suggest that New Guinea had a particularly important role in the Admixture and Diversification phases of the SSaFE. The SAD model of diversification provides a working hypothesis for future research, and provides insight into the dynamic and important role the SSaFE played in the evolution of the Malesian flora.

As Director of the Australian Tropical Herbarium (a CSIRO-JCU-Qld Govt-Aust. Govt. joint venture), Darren's role is roughly equal parts management/leadership and research. The latter involves studies of the origins, evolution and classification of plants and deals broadly with the questions: how many plant species exist, where do they occur, how are they related, and how have they evolved? Current research foci include the systematics and evolution of Ericaceae and Elaeocarpaceae, the Sunda-Sahul floristic exchange and its impact on the assembly of northern Australian biomes, and the biodiversity and conservation of tropical montane floras.

SESSION 4: POSTER PRESENTATIONS TUESDAY 16:05-16:10

USING LARGE-SCALE ECOLOGICAL DATA TO SUPPORT TAXONOMIC DECISIONS IN DIFFICULT SPECIES COMPLEXES IN *PTILOTUS* (AMARANTHACEAE)

Timothy Hammer; Paul Macintyre, Ladislav Mucina, Kevin Thiele

School of Biological Sciences, University of Western Australia

Ecological traits provide many characters that are not, or are only informally, evaluated in traditional taxonomy. Such traits may provide supporting evidence for lineage separation, particularly among closely related taxa, and help elucidate the role of natural selection on their populations and evolution. *Ptilotus* (Amaranthaceae) is a genus of ~120 species distributed throughout Australia, with the centre of diversity in arid Western Australia. The genus is thought to have diverged from its closest relatives, distributed from Africa to S. Asia, after reaching Australia in the early Miocene, after which it underwent rapid adaptive radiation. Within *Ptilotus* are a series of species complexes that for many years have been difficult to resolve, leading to taxonomic instability. Morphological taxonomic concepts of two such species complexes within *Ptilotus* were tested by using georeferenced specimen datasets from the Australasian Virtual Herbarium, coupled with high-resolution environmental layers, and analysed with Maxent and CART modelling. In both cases, putative taxa delimited by morphological characters were found to have strong geographical and environmental partitioning, lending support to their recognition as separate species and providing examples of the reciprocity of ecology and morphology and the importance of ecological data in modern taxonomy. With the increasing availability of large, aggregated, online, georeferenced specimen datasets coupled with high-resolution environmental layers (e.g. those available on the Atlas of Living Australia), we expect the formal integration of ecology and morphology in taxonomic studies to become more common.

Student presenter

I am a PhD Candidate and an inaugural Forrest Scholar at the University of Western Australia. My thesis covers the systematics, taxonomy and biogeography of the 'aervoid' clade within Amaranthaceae, which includes the Australian genera *Ptilotus* (mulla mulla), *Kelita* and *Omegandra* and the African-Asian genera *Aerva* and *Nothosaerva*.

PHYLOGEOGRAPHIC CONGRUENCE IN *LINDERNIA* (LINDERNIACEAE) WITH BIOTIC REGIONS ACROSS NORTHERN AUSTRALIA

Bill Barker; Ed Biffin

State Herbarium of South Australia

The globally widespread genus *Lindernia* has a major radiation in northern Australia with remarkable morphological diversity, which has led to recent recognition of subgenera and sections and formal establishment of many new species. Character transformations within the Australia-New Guinea endemic subg. *Didymadenia* with c. 40 species include: perennial vs. annual habit; erect vs. procumbent habit; glabrous vs. eglandular or glandular pubescence; paniculate vs. racemose vs. solitary flowers; reduction of anthers from two pairs to one; exsertion or inclusion of the anther pairs; reduction of anther cells from two to one, by fusion or loss; loss of the abaxial staminal spurs that typify the family; development of a corolla flap embracing the adaxial stamens; compression or abrupt dilation of the normally gradually dilated corolla tube; stout vs. slender capsules; small vs. large seeds.

Morphological and molecular data, the latter using matK and trnH-psbA markers, show extraordinary congruence (presented at last ASBS conference).

Two major clades in recent evolution being largely confined to Arnhem Land and the Kimberley (with a subsequent extension to Arnhem Land). (Other clades having wider range, possibly reflecting past radiations). Distribution patters of species in subg. Didymadenia show congruence with the biotic regions across northern Australia proposed by Edwards et al. (2017).

CLARIFICATION OF SPECIES LIMITS OF *PROSTANTHERA CINEOLIFERA* R.T.BAKER & H.G.SM. (LAMIACEAE) ESSENTIAL FOR CONSERVATION

Ruth Palsson[1]; Jeremy Bruhl[1], Rose Andrew[1], Ian Telford[1], Trevor Wilson[2]

[1]University of New England; [2]National Herbarium of NSW, Royal Botanic Gardens and Domain Trust

Prostanthera cineolifera R.T.Baker & H.G.Sm. is considered Data Deficient by the NSW Office of Environment and Heritage (OEH) “as its taxonomy needs to be reviewed”, and listed as a “Vulnerable” under both Commonwealth and NSW legislation. The current mapped distribution of *P. cineolifera* is fragmented across three areas: (i) the type location is near Pokolbin in the Lower Hunter Valley; (ii) St Albans, in the Lower Hawkesbury catchment; and (iii) two outlying collections from the North Coast of NSW (AVH 2018). We have found that plants from these three areas are morphologically distinct. Specimens of *Prostanthera* from the localities in the Upper Hunter Valley including Wingen Maid and Sandy Hollow, have previously, variously been determined as *P. cineolifera*, *P. lanceolata* Domin or *P. ovalifolia* R.Br. There is confusion about the taxonomic limits of *P. cineolifera*. Until the taxonomic limits and the distribution of *P. cineolifera* are known, a recovery strategy for the species cannot be prepared, let alone acted upon. Preliminary results from a morphometric analysis indicate: (i) the North Coast of NSW populations are *P. lanceolata*—a seemingly ‘good’ species mostly lumped into *P. ovalifolia*; (ii) the St. Albans populations are most likely *P.* sp. Hawkesbury (B.J.Conn 2591); (iii) the Wingen Maid and Sandy Hollow populations are *P. cineolifera*; and (iv) there are populations of *P. cineolifera* in Goulburn River NP and Wollemi NP. *Prostanthera cineolifera* is confined to the Hunter Valley but with a much wider distribution than currently recorded. Molecular data will be integrated with the morphological data to assist finalizing the species limits of *P. cineolifera*.

Student presenter

Ruth Palsson is a masters student at the University of New England. She is studying the species limits of *Prostanthera cineolifera* on a Saving Our Species and UNE funded project.

SESSION 4: POSTER PRESENTATIONS TUESDAY 16:20-16:25

INTEGRATIVE TAXONOMIC REVISION OF *MELICHRUS* R.BR. (ERICACEAE SUBFAM. *EPACRIDOIDAE*)

Helen Kennedy[1]; Jeremy Bruhl[2], Darren Crayn[3], Rose Andrew[2], Ian Telford[2]

[1]Department of Agriculture and Water Resources; [2]University of New England; [2]Australian Tropical Herbarium, James Cook University

The Ericaceae Juss. subfamily Epacridoidae Arn. is an overwhelmingly Australasian clade of more than 500 species of sclerophyllous, shrubs to trees typically found on acidic, oligotrophic soils in temperate climates. The group has been the subject of extensive phylogenetic research over the last 20 years that has established generic limits that reflect monophyly and provide the taxonomic foundation for remaining species-level research. As such, a recent ABRS grant was awarded to make progress toward a Flora of Australia account for the subfamily. Included in this project is a revision of the genus *Melichrus* R.Br.

Melichrus is a group of small shrubs endemic to Australia, with a broad eastern Australian distribution and a more geographically constrained presence in southern Western Australia. Species of *Melichrus* from Western Australia and the eastern states of Australia form sister clades, allowing the proposed study to focus on the eastern Australian clade, while a collaborative partner researches the western clade.

In eastern Australia, *Melichrus* occurs from the coast to mid-western districts in all three mainland states. The genus was last revised by Betsy Paterson (now Betsy Jackes) in 1958. She included four species in eastern Australia: *M. adpressus*, M. erubescens, *M. procumbens* and *M. urceolatus*. Five additional putative species are now recognised by the Queensland (BRI) and the N.C.W. Beadle (NE) herbaria. A further six putative species separated at NE need testing. *Melichrus adpressus* and *M. urceolatus* appear to have been widely misapplied.

We outline our morphological and molecular study, which will thoroughly test and describe species diversity in eastern Australian *Melichrus*.

Student presenter

Helen is an early-career plant scientist specialising in systematics. In her current role as a botanical diagnostician for the Department of Agriculture and Water Resources she identifies plant material and assesses its risk to the biosecurity of Australia. She plans to commence her doctoral research in March at the University of New England. This will shift her focus to research on the origins, evolution and classification of *Melichrus*, with the aim to contribute to the description and preservation of natural diversity.

SESSION 4: POSTER PRESENTATIONS TUESDAY 16:25-16:30

DDRAD-SEQ IDENTIFIES A RECURRENT *DICKSONIA* TREE FERN HYBRID

Lara Shepherd[1]; Patrick Brownsey[1], Chris Stowe[2], Leon Perrie[1]

[1]Museum of New Zealand Te Papa Tongarewa; [2]Urtica Inc. Ecological Monitoring and Consultancy

Natural hybridization is common in many ferns and contributes to fern evolution and speciation. However, hybrids are rare between the ~30 species of *Dicksonia* tree ferns. Here we examine the relationships of the three New Zealand *Dicksonia* species to a newly-discovered *Dicksonia* that does not fit the current taxonomy of the genus. Our microsatellite genotyping and ddRAD-seq data indicate that this form is a recurrent F1 hybrid that has formed between *D. fibrosa* and *D. lanata* subsp. *lanata*. This is the first confirmed record of natural interspecific hybridization in *Dicksonia* and provides another example of hybridization between deeply diverged fern lineages, with the two parent species estimated to have diverged 55-25 Ma. Our chloroplast sequencing indicates asymmetric chloroplast inheritance in the hybrid with *D. lanata* subsp. *lanata* always contributing the chloroplast genome.

Lara is an evolutionary biologist who uses genetic techniques to study the evolution of New Zealand's flora and fauna. Current research projects include examining Māori cultivation and translocation of New Zealand plants and the development of non-destructive sampling methods for museum specimens.

SESSION 4: POSTER PRESENTATIONS TUESDAY 16:30-16:35

POPULATION GENETIC ANALYSIS TO INFORM CONSERVATION OF THE ENDANGERED ISIS TAMARIND, *ALECTRYON RAMIFLORUS* (SAPINDACEAE)

Robert Lamont; Steven Ogbourne, Gabriel Conroy, Joel Nichols

University of the Sunshine Coast

Apart from several isolated individuals left by chance along roadsides following extensive clearing for agriculture, *Alectryon ramiflorus* is known from only two small vine scrub remnants near Childers in southern Queensland, which contain a total of approximately 200 trees. To examine levels of genetic diversity and differentiation among populations, we used next generation sequencing (NGS) and bioinformatics to identify polymorphic microsatellites in silico, reducing both the time and cost of marker development. We found low levels of diversity (mean A = 4.92; mean HE = 0.50) and moderate levels of differentiation suggesting restricted gene flow (mean FST = 0.104). This study identified two distinct populations, which possess different genetic signatures, with low levels of genetic diversity present in both populations. To ensure long term conservation of the species, we recommended that (a) both populations should be more actively protected due to the unique genetic make-up of each site, and (b) translocation sites to southern areas using genetic capture from both populations are established.

Dr Robert Lamont undertook his PhD in ecological genetics at the University of the Sunshine Coast investigating polyploidy, apomixis, hybridisation and cryptic speciation in an association of microspecies belonging to the genus, *Allocasuarina* (She-Oaks). Rob’s research as a molecular ecologist specialises in the development and characterisation of microsatellite markers, chloroplast and mitochondrial DNA sequencing, cytogenetics, and genetic data analysis, and is focused on the conservation genetics and fire ecology of threatened plant and animal species.

IN DEFENCE OF PHRASE NAMES

Ian Telford; Jeremy Bruhl

University of New England

Phrase names (tag names in New Zealand) provide a convenient means of segregating and labelling putative new species prior to formal publication. The term was adopted in 1992 by the Australian Herbarium Information Systems Committee (HISCOM) to clarify the ambiguities inherent in the use of ‘sp. aff.’. Currently, if accepted by the APC Working Group and CHAH, the name is listed in the Australian Plant Census with the aim of standardisation of such informal names, which we applaud. Use of APC-approved phrase names appears to be uneven across Australian herbaria. We will consider the pros and cons of phrase names, together with suggestions for improved communication among herbaria and end-users.

As curator of NE, Ian Telford is involved in ensuring best practice in herbarium management. His interests are in the biology, systematics and biogeography of Cucurbitaceae and Phyllanthaceae, as well as taxonomy and biogeography of various groups including Asteraceae tribe Gnaphalieae, *Prostanthera*, *Phebalium* and *Melichrus*.

SESSION 4: POSTER PRESENTATIONS TUESDAY 16:40-16:45

BLINDSPOTS IN THE RAINFOREST – A CASE STUDY OF *ELAEOCARPUS* (ELAEOCARPACEAE) IN FIJI

Yumiko Baba[1]; Marika Tuiwawa[2]

[1]Auckland Museum Tāmaki Paenga Hira; [2]South Pacific Regional Herbarium, University of The South Pacific

A local flora often serves as a starting point looking for research questions bounded by geography. This is particularly true in the case of 'Flora Vitiensis Nova'. The five volumes of the flora were published between 1979- 1991 and each account has highlighted the knowledge gaps in both geographical and morphological coverage of the collections. For example, 19 of the 22 of *Elaeocarpus* species included in 'Flora Vitiensis Nova' are endemic, but eight of these species were known only from the type specimen or type locality. Since the publication of the flora, extensive UN led surveys have been conducted to help close the knowledge gaps identified in the flora.

A herbarium based specimen inventory for *Elaeocarpus* was carried out at the South Pacific Regional Herbarium (SUVA) in August 2018 to collect base-line data with the aim of updating the *Elaeocarpus* account. This revealed that the number of collections for many *Elaeocarpus* species has not increased since the 1960s and there remain serious knowledge gaps regarding species circumscriptions and geographical coverage. While global phylogenetic studies of *Elaeocarpus* propelled by the rapidly advancing molecular techniques are continuing, the success of these studies is likely to be hindered by a lack of field survey and collections.

The aim of this poster is to highlight some of the impediments to ongoing studies in the genus, including phylogenetic, evolutionary and taxonomic research, which stem from inadequate field surveys and collections. This, also affects our understanding of both the basic ecology and conservation status of these taxa. This problem is not restricted to *Elaeocarpus*, nor to Fiji, but reflects a wider, global trend.

Dr Yumiko Baba is the Associate Curator at the herbarium of Auckland Museum Tāmaki Paenga Hira, New Zealand. Her research interests include taxonomy, systematics and documenting plant biodiversity in both tropical and temperate regions. She studied taxonomy and systematics of the tree genus *Elaeocarpus* in Australasia for her PhD, and this genus has become her life-long research interest.

ASBS GENERAL MEETING 17:00

WEDNESDAY 9:45-10:15

TAXONOMY AUSTRALIA

Kevin Thiele

Taxonomy Australia, Australian Academy of Science

The taxonomy and biosystematics decadal plan (see www.science.org.au/support/analysis/decadal-plans-science/discovering-biodiversity-decadal-plan-taxonomy) was successfully launched in late April 2018. While the plan, and the process leading to its development, was a great success for our community, having a good strategic plan for the next decade is not in itself enough to bring about the change our community needs (particularly in new investments and enhanced resourcing). For this reason, a key recommendation of the plan was the establishment, in both Australia and New Zealand, of peak bodies to advocate and implement the decadal plan. In Australia, we have established Taxonomy Australia for this purpose. While it has not yet been publicly launched, governance arrangements for Taxonomy Australia are in place, a membership model has been agreed, and work has commenced on a website that we hope will be engaging, inspiring and informative. A key task for Taxonomy Australia is to reposition our discipline and our work – exploring the biosphere, discovering its species, and understanding its evolution – as a science that is both cool and impactful. This repositioning is key to successful advocacy for the sector. This presentation will provide an update on Taxonomy Australia and its proposed role, functions and work plan, and seek guidance from the community on making Taxonomy Australia and the decadal plan successful and effective agents of positive change.

MORNING TEA 10:30-11:00

RESOLVING OF THE BACKBONE OF *PTILOTUS* AND ESTABLISHING A NEW TAXONOMIC FRAMEWORK FOR THE AERVOID CLADE (AMARANTHACEAE)

Timothy Hammer[1], Xiao Zhong[2], Catherine Colas des Francs-Small[2], Paul Nevill[3], Ian Small[2], Kevin Thiele[1]

[1]School of Biological Sciences, University of Western Australia; [2]ARC Centre of Excellence in Plant Energy Biology, University of Western Australia; [3]ARC Centre for Mine Site Restoration, School of Molecular and Life Sciences, Curtin University

The informally named ‘aervoid’ clade includes the Australian genera *Ptilotus* R.Br. (~120 spp.), *Kelita* A.R.Bean (1 sp.) and *Omegandra* G.J. Leach & C.C.Towns (1 sp.) and the African-Asian genera *Aerva* Forssk. (11 spp.) and *Nothosaerva* Wight (1 sp.). Previous studies using Sanger sequences failed to fully resolve the backbone of this clade and between the major clades of *Ptilotus*, but showed evidence for the paraphyly of *Aerva* with respect to *Ptilotus.* The aims of the present study were to: (1) elucidate relationships between genera and within *Ptilotus* using a phylogenomic approach; (2) identify morphological characters within each genus to help delimit generic boundaries; and (3) provide an updated taxonomic framework for the aervoids. A well-supported coding DNA sequence (CDS) phylogeny was constructed for 36 aervoid and 5 outgroup species based on 69 gene sequences derived from assembled whole-plastid genomes. The CDS tree was used to constrain relationships on a larger phylogeny based on Sanger-sequenced ITS and matK for 135 taxa, comprising near-comprehensive sampling within the aervoids. Both datasets were analysed using maximum likelihood and Bayesian inference. Morphological characters were assessed from herbarium specimens. The resulting phylogeny resolves the intergeneric relationships and is used along with identified morphological characters to support a new taxonomic framework for the aervoids, including new genera and new combinations.

Student presenter

I am a PhD Candidate and an inaugural Forrest Scholar at the University of Western Australia. My thesis covers the systematics, taxonomy and biogeography of the 'aervoid' clade within Amaranthaceae, which includes the Australian genera *Ptilotus* (mulla mulla), *Kelita* and *Omegandra* and the African-Asian genera *Aerva* and *Nothosaerva*.

SESSION 5 WEDNESDAY 11:15-11:30

IF IT'S YELLOW, LET IT MELLOW: INVESTIGATING TOXICITY VARIATION IN SOUTHERN AUSTRALIAN YELLOW-STAINING *AGARICUS* IN A PHYLOGENETIC CONTEXT

Amelia-Grace Boxshall[1]; Teresa Lebel[2], Damien L. Callahan[3], Todd McLay[4], Joanne Birch[1]

[1]University of Melbourne; [2]Royal Botanic Gardens Victoria; [3]Deakin University; [4] CSIRO, Centre for Australian National Biodiversity Research

Humans have an irresistible urge to eat mushrooms. Unfortunately, certain species are difficult to distinguish, and mushroom-related poisoning affects 200-300 Victorians every year. *Agaricus xanthodermus*, commonly known as 'the yellow-stainer', is responsible for most of these poisonings. However, this species appears to exhibit variation in toxicity: consumption of these mushrooms results in gastrointestinal irritation in some cases but not others. Reaction severity has also been reported to vary. We inferred the evolutionary relationships of yellow-staining *Agaricus* lineages (sections *Arvenses*, *Minores*, *Leucocarpi*, *Agaricus*, *Hondenses*, *Xanthodermatei*) and investigated the evolution of toxicity in the context of the resulting phylogeny. We investigated whether phenol, the constituent responsible for yellow-stainer toxicity, varied in concentration and tested characters for association with toxicity. We used Sanger and targeted amplicon sequencing to generate sequence data from two markers (ITS, tef1-α). Seventy-eight individuals, representing 29 yellow-staining species were included in phylogenetic analyses. The phylogeny was reconstructed using maximum likelihood and Bayesian inference criteria and utilised gas chromatography-mass spectrometry to quantify phenol concentration in freshly collected samples. Phylogenetic results support two new Australian species within section *Xanthodermatei* and indicate that taxonomic revision may be required within the section. *Agaricus xanthodermus* was supported as monophyletic. Phenol was only detected within section *Xanthodermatei*, but we observed considerable variation in phenol concentration associated with substrate and location which may contribute to the observed variation in symptoms.

Student presenter

Grace completed a Bachelor of Science (Plant Sciences) at the University of Melbourne in 2016 and is due to complete her Master of Science (BioSciences- Plant Sciences) at the University of Melbourne in late 2018. Grace was the recipient of a 2017 Hansjorg Eichler Research Grant for her master's research project focusing on the mushroom genus *Agaricus*.

SESSION 5 WEDNESDAY 11:30-11:45

TAKING AN INTEGRATIVE APPROACH TO RESOLVE THE *XEROCHRYSUM BRACTEATUM* SPECIES COMPLEX

Tim Collins[1]; Alexander N. Schmidt-Lebuhn[2], Rose L. Andrew[1], Ian R.H. Telford[3], Jeremy J. Bruhl[3]

[1]University of New England; [2]CSIRO, Centre for Australian National Biodiversity Research; [3]N.C.W. Beadle Herbarium, University of New England

Long-standing taxonomic uncertainty exists around the *Xerochrysum bracteatum* species complex. Widely recognised *Xerochrysum* phrase-name taxa have remained without formal description for many years, and we hypothesise that there are nine additional putative species to be tested. Morphological characters used to delimit species of *Xerochrysum* have depended upon the available herbarium specimens, many of which are incomplete in regards to lower leaves and growth form. Taxonomic characters have been mainly based on, and limited to, phyllary, leaf and stem indumentum and style appendages.

Integrating multiple lines of evidence, derived from diverse data sources, can provide robust cross-validation of species delimitation. We are approaching species delimitation in the *Xerochrysum bracteatum* species complex and more broadly across the genera *Xerochrysum* and the closely related *Coronidium*, by integrating morphological, molecular and karyological analyses. This approach is made possible by augmenting existing herbarium specimens and online databases with new fieldwork involving collection of high quality specimens and samples, including fruits for cultivation of seedlings; being used for cytology, DNA and as a 'common glasshouse experiment' for morphology and life history.

We will present details of the processes involved in integrating the different lines of investigation and some of the initial results from fieldwork, fruit and seedling morphology, and flow cytometry.

Student presenter

Tim completed his BSc Honours project examining the taxonomy of *Eucalyptus magnificata* in 2016. In 2017 Tim began a PhD research project "Integrated taxonomic revision of *Xerochrysum* and *Coronidium* (Gnaphlieae; Asteraceae).

THE ‘TAXONOMIC GAP’ AND PROGRESS TOWARDS A ‘GLOBAL FLORA’

Russell Barrett

National Herbarium of NSW, Royal Botanic Gardens and Domain Trust

With four editions of the Angiosperm Phylogeny Group classification of plant families, we should be approaching a global consensus and thus stability of names at this level. By implication, names below the rank of family should become increasingly stabilised as the rapid accumulation of novel genetic data allow phylogenetic relationships to be rigorously tested.

Increasing stabilisation presents excellent opportunities for international collaborations to test remaining uncertainties such as genera with widely disjunct distributions that are likely to have independent phylogenetic origins. Many groups that have historically proven intractable on morphology alone (e.g. Cleomaceae), can finally be made sense of based on sound phylogenetic hypotheses on which to base new interpretations of morphological homology.

There is no question that our scientific knowledge is advancing rapidly, but is taxonomy lagging behind? The pace of taxonomic change is a double-edged sword. End users do not like change, and especially do not like change that is premature or poorly justified. For these reasons, adoption of new names will also likely have a lag time while name changes are assessed for scientific merit and end-user utility. On the flip-side, if taxonomic change lags too far behind our understanding of phylogenetic relationships, we stand accused of neglecting our work. Making sound changes should increase long-term stability, reducing long-term criticism.

The public and political reputation of science in general is at an all-time low, and we cannot afford to let a minority of views detract from the significant advances that are being made globally in the field of plant systematics. Publication of a large number of nomenclatural changes in a special issue of The Global Flora has raised many questions that the international botanical community must both grapple with and respond to. I will summarise global concerns that have been raised over ‘The Global Flora’, why this is not a publication that can be ignored, and flow-on effects for international collaborations.

Dr Russell Barrett is a systematic Botanist at the New South Wales herbarium. He has a broad range of research interests in plant systematics, ecology and conservation. His current work combines traditional taxonomy and molecular methodology to increase our understanding of the Australian flora. He has a keen interest in the public promotion of scientific discoveries, and practical applications for research outcomes.

SESSION 5 WEDNESDAY 12:00-12:15

HOW TO LOOK AGAIN AT *SPERMACOCE* AND *BORRERIA* (RUBIACEAE): IS MORPHOLOGICAL EVOLUTION IN AUSTRALIAN *SPERMACOCE* KEY TO OUR UNDERSTANDING OF GENERIC LIMITS?

Kerry Gibbons; Marco Duretto

National Herbarium of NSW, Royal Botanic Gardens and Domain Trust

Spermacoce L. *s. lat*. (Rubiaceae: Spermacoceae) has a pantropical and subtropical distribution, with a centre of diversity in the Americas and many species in Africa and Australia. In its narrowest circumscription, *Spermacoce* included only those species with one dehiscent and one indehiscent mericarp, with *Borreria* G.Mey. erected to accommodate species with other types of capsule dehiscence. Under this generic concept, all Australian species were placed in *Borreria*. In recent decades, a broader circumscription of *Spermacoce* has generally been adopted, with only some South American taxonomists accepting *Borreria*. Preliminary international molecular phylogenetic studies have shown that *Spermacoce*, when broadly circumscribed, is polyphyletic, unless many morphologically distinct and well accepted genera are also included. Studies of South American species suggest floral, seed and palynological characters might be more useful than capsule dehiscence in delimiting genera. A group of species with included stamens and stigmas, 'type 1' pollen and other characters shared with *Spermacoce s. str*. form a well-supported clade together with *Spermacoce s. str.*, and are now accepted in *Spermacoce* by South American authors. The one Australian species included in previous studies was nested was within this clade. Our much broader sampling confirms that Australian species sampled to date are monophyletic and nested in this *Spermacoce* clade, although most of our weedy species might be better recognised in *Borreria*. Yet in the morphologically diverse Australian *Spermacoce*, there are both species that, morphologically and palynologically, fit well within this group, and species that bear a closer resemblance to those in the *Borreria* clade. We look again at morphological characters that might be useful in delineating genera and explore the utility of ancestral character reconstructions to our understanding of the taxonomy of the group.

I am a plant systematist currently working on the Australian members of the tribe Spermacoceae (Rubiaceae), predominantly the genera *Spermacoce*, *Hedyotis* and *Oldenlandia*. I am also interested in Loganiaceae. My work combines molecular phylogenetic and morphological approaches to resolve taxonomic problems.

SPECIATION THEORY AND SPECIES DELIMITATION USING *EUCALYPTUS* AS A MODEL

Susan Rutherford

National Herbarium of NSW, Royal Botanic Gardens & Domain Trust

Speciation is a central process in evolutionary biology and is fundamental to the origins of biodiversity. While there has been considerable progress in evolutionary research over the last 150 years, understanding the many different aspects of speciation remains a major challenge. I focus on a group of closely related eucalypts called the green ashes (*Eucalyptus* subgenus *Eucalyptus* section *Eucalyptus*). The green ashes include tall trees on fertile soils (such as *Eucalyptus regnans*), as well as medium trees and mallees on low nutrient soils (e.g. the small mallee, *E. cunninghamii*). An interdisciplinary approach was used to investigate speciation mechanisms in the green ashes. Phylogenetic analyses based on genome-wide scans revealed that species boundaries within the green ashes were not always consistent with classifications based on morphology and there was evidence of hybridisation and gene flow across lineages. Population genetic analyses suggested that the green ashes were at varying stages of speciation, with some species being highly genetically differentiated, while others were at earlier stages on the speciation continuum. A common garden study revealed that inter-specific differences in seedling traits were significant, and that some traits (e.g. leaf width) were highly plastic across resource treatments for many species. I suggest that an interdisciplinary approach combining phylogenomics, population genomics and a common garden experiment can provide insights into speciation mechanisms and species delimitation in a group of closely related taxa. This type of approach may be useful in not only understanding the evolutionary history of the green ash eucalypts, but could also provide insights into speciation mechanisms of other groups of organisms.

My research interests centre on evolutionary biology and botany. I am especially interested in speciation, hybridisation, species boundaries and plant response to changes in environment. I recently completed my Ph.D., where I used a range of methods (e.g. phylogenetics, population genetics, morphology, functional traits, species distributional data and common garden experiments) to investigate speciation mechanisms in the green ash eucalypts. Currently, I am based at the Royal Botanic Garden Sydney where I continue to work on evolution in eucalypts.

LUNCH 12:30-13:30

SESSION 6 WEDNESDAY 13:30-13:45

AUSTRALIAN GRASS DIVERSITY: PHYLOGENETIC OVERVIEW, GLOBAL COMPARISONS AND FUTURE DIRECTION

Tanya Scharaschkin

Botanical Research, Art and Training

Poaceae are the fifth-largest family of angiosperms, by species number with approximately 11,500 species in 768 genera worldwide. Current phylogenetic classification places these species in 12 subfamilies. Four subfamilies contain most of the global grass diversity, in terms of percentage of grass species, these are Panicoideae (28%), Pooideae (35%), Bambusoideae (14%) and Chloridoideae (14%). The remaining 9% of species occur in eight subfamilies, namely Aristidoideae , Danthonioideae, Micrairoideae, Oryzoideae, Arundinoideae, Puelioideae, Pharoideae and Anomochlooideae. This study examines the phylogenetic placement of all Australian species of Poaceae. The approximate 1340 species of Poaceae native to Australia are from 10 of the 12 subfamilies, with no representatives from Puelioideae and Anomochlooideae. The majority of the grasses belong to three subfamilies: Panicoideae (35%), Pooideae (28%) and Chloridoideae (20%). Most of the non-native grasses in Australia belong to the subfamily Pooideae. 39% of Australian genera are monotypic, 48% have between two to 10 species and only 3% of genera have more than 50 species. Comparison are made with global trends and implications for future directions of research relevant to systematics, efloras and understanding of Australia’s native grass diversity as well as management implications of non-native species are discussed.

Dr Tanya Scharaschkin is a free-lance botanist and artist with over 30 years of teaching experience. Tanya is interested in plant systematics (Poaceae, Annonaceae) and plant structure. Her research has focused on phylogeny reconstruction, character evolution, historical biogeography. She is particularly interested in studying plant anatomy and developing protocols for sectioning, staining ad light microscopy. Tanya worked at The Queensland University of Technology from 2006 to 2017, where she supervised numerous students including 4 PhDs as principal supervisor and 4 as associate supervisor and 7 Honours project. She currently lives and works in Tasmania.

VALE *VELLEIA* (AND OTHERS) – THE FINAL CHAPTER OF OUR *GOODENIA S.L.* SAGA

Kelly Shepherd[1]; Rachel Jabaily[2]

[1]Western Australian Herbarium; [2]Colorado College

Close scrutiny of *Goodenia* (Goodeniaceae) and allied genera in the ‘core Goodeniaceae’ over recent years has clarified our understanding of this iconic group. While expanded sampling (> 90% of described species), sequencing of multiple regions, and an NGS reinforced backbone clearly support *Goodenia s.l.* as monophyletic and distinct from *Scaevola* and *Coopernookia*, there appear to be no synapomorphic characters that uniquely characterise this morphologically diverse clade. Within *Goodenia s.l.* there is strong molecular support (nuclear, chloroplast and mitochondrial) for three major clades (clade A including *Selliera*, clade B, and clade C including *Velleia*, *Verreauxia*, and *Pentaptilon*) and various subclades. This led to earlier suggestions for the possible recognition of a number of supported clades as new genera, while retaining *Velleia*, *Verreauxia*, and *Pentaptilon* as distinct. Through ongoing work it has become evident that this is impractical as conflict remains between subclades of the morphologically diverse clade C, likely due to recent radiation, possible hybridisation and incomplete lineage sorting. In light of this, it is proposed that a combination of morphological characters should be used to circumscribe an expanded *Goodenia* to include the embedded genera. Preparation of a new infrageneric classification is underway that aims to recognise the supported subclades within *Goodenia s.l.*

Dr Kelly Shepherd is a Senior Research Scientist based at the Western Australian Herbarium. She is a taxonomist currently working on a range of plant groups in Western Australia, focusing on naming and describing new species of conservation concern. A full bio can be found at science.dpaw.wa.gov.au/people/?sid=241

SESSION 6 WEDNESDAY 14:00-14:15

HOW MANY SPECIES OF TOROPAPA (*ALSEUOSMIA*) ARE DISGUISED IN THE BUSH?

Lara Shepherd[1]; Andrew Townsend[2], Peter de Lange[3], Leon Perrie[1]

[1]Museum of New Zealand Te Papa Tongarewa; [2]Department of Conservation; [3]Unitec Institute of Technology

Alseuosmia (toropapa) is the fourth largest endemic plant genus in New Zealand in terms of number of species, with 6 species currently recognised. This genus has been confusing botanists for over 100 years because it shows extreme variation in leaf shape – even between plants considered to be the same species from a single location. To add to the confusion, the leaves of some toropapa plants show a remarkable resemblance to completely unrelated species, which has been suggested to be an example of mimicry. The taxonomy of the group needs urgent review with some of the morphological forms mostly found in unprotected forest remnants. We report on the morphological diversity detected during our fieldwork and our preliminary ddRAD-seq results.

Lara is an evolutionary biologist who uses genetic techniques to study the evolution of New Zealand's flora and fauna. Current research projects include examining Māori cultivation and translocation of New Zealand plants and the development of non-destructive sampling methods for museum specimens.

OMG *BORONIA* (RUTACEAE) IS POLYPHYLETIC: COPING WITH LARGE WELL SUPPORTED CLADES THAT CONTAIN FEW MORPHOLOGICALLY USEFUL CHARACTERS

Marco Duretto[1]; Margaret Heslewood[1], Mike Bayly[2]

[1]National Herbarium of NSW, Royal Botanic Gardens and Domain Trust; [2]University of Melbourne

Boronia (Rutaceae) is a scleromorphic genus of 160 species confined to Australia and New Caledonia. It is characterised by usually having opposite decussate leaves, 4-merous diplostemonous flowers, carpels being fused only along the style, and explosively dehiscent fruit. These features are common in Rutaceae and a defining morphological apomorphy for the genus is apparently lacking. *Boronia* is classified into eight sections with seven endemic to Australia and one, section Boronella, endemic to New Caledonia.

Previous molecular analyses have placed *Boronia* as sister to a large clade containing many rainforest genera that are mostly confined to Australasia, as well as the scleromorphic genera, *Zieria* and *Neobyrnesia*.

The monophyly of *Boronia* has not been critically tested even though it has been the subject of generic studies where it was assumed to be monophyletic. Although it was included in several larger studies of generic relationships within Rutaceae, it has never been represented by more than two sections.

Here, maximum parsimony and Bayesian inference analyses were performed using three plastid markers (psbA-trnH, trnL-F and rbcL) and two nuclear markers (ITS, ETS) for 120 species in 38 genera of the Australasian clade of subfamily Amyridoideae. This included 58 species of *Boronia* representing all eight sections plus two of the four species placed incertae sedis.

These analyses indicate *Boronia* is polyphyletic with section *Cyanothamnus* sister to a *Melicope-Acronychia* clade and this clade sister to a *Zieria-Euodia* clade. *Boronia*, less section *Cyanothamnus*, remains in the isolated position sister to the *Melicope-Cyanothamnus-Euodia* clade. These clades are strongly supported by molecular data but lack obvious morphological apomorphies. *Cyanothamnus*, an Australian endemic, will be reinstated.

The Australasian clade within subfamily Amyridoideae contains five distinct lineages adapted to sclerophyllous environments as well as three or four distinct rainforest lineages suggesting a complicated history of biome transition in the Australasian flora.

SESSION 6 WEDNESDAY 14:30-14:45

TAXONOMIC REVISION OF THE *MYOSOTIS AUSTRALIS* GROUP (BORAGINACEAE) IN AUSTRALIA, NEW ZEALAND AND NEW GUINEA

Heidi Meudt[1]; Jessie Prebble[2], Michael Thorsen[3]

[1]Museum of New Zealand Te Papa Tongarewa; [2]Manaaki Whenua - Landcare Research; [3]ERA Ecology

Approximately 90 species of *Myosotis* (Boraginaceae, forget-me-nots) occur worldwide, with about half comprising a southern hemisphere lineage, where New Zealand is a centre of diversity with related species in Australia, New Guinea, and southern South America. One of the species groups in this lineage is the *Myosotis australis* group, which comprises several published species and informal tag-named entities in Australia, New Zealand and New Guinea and whose species limits and taxonomy is unclear. In this talk, the following questions will be addressed: What species comprise the *M. australis* group? What are the species limits and geographic distribution of *M. australis s.s.?* Can *M. australis* be distinguished from the other native Australian species, *M. exarrhena*, and from the non-native species, *M. discolor*? Is there evidence for recognising New Guinean plants as a distinct species from *M. australis* (*M. saruwagedica*)? Does New Zealand harbour multiple species in the *M. australis* group? Is there evidence for recognising any of the tag-named entities as new species or subspecies? To answer these questions, we performed statistical analyses of up to 80 morphological and pollen characters from multiple herbarium specimens of all published species and informal tag-named entities of the *Myosotis australis* species group sampled from throughout its geographical range. These data were analysed separately and together with data from other southern hemisphere *Myosotis* groups from previous publications using ordination, multidimensional scaling and mclust analyses totalling over 450 *Myosotis* specimens (including 126 newly sampled here).

Heidi Meudt completed her PhD in Botany in 2004 at the University of Texas at Austin, and since 2006 is a Research Scientist in Botany at Te Papa. She was also an Alexander von Humboldt Experienced Research Fellow at the University of Oldenburg, Germany from 2012-2014. Her main research focus is on the taxonomy and evolution of southern hemisphere plants, particularly Plantaginaceae and Boraginaceae. Her research integrates data from morphology, DNA, pollen, chromosomes and other data to revise the taxonomy and better understand the geographical, morphological and phylogenetic patterns of species, especially New Zealand species radiations.

SESSION 6 WEDNESDAY 14:45-15:00

TREATING *TEPHROSIA* (FABACEAE) FOR THE EFLORA OF AUSTRALIA: PROJECT PROGRESS AND PLANS

Ryonen Butcher

Western Australian Herbarium

Tephrosia Pers. is a widespread and common component of the northern Australian flora, yet its taxonomy is largely unresolved and few identification tools exist. In part this results from relatively poor knowledge of the flora of northern Australia (e.g. few specimens of many taxa; collection gaps; unstudied morphological diversity), in part from the size of the genus, and in part from fragmentation of previous effort. The genus has not been treated Australia-wide since Bentham's *Flora Australiensis*.

With c. 140 native taxa recognised in northern and central Australia, *Tephrosia* (Fabaceae: Millettieae) is the largest legume genus in Australia excepting *Acacia* Mill. While 21 names (16 tax. nov.) have been published for Australian taxa since 1977, 62 phrase names (c. 45% of all taxa) are presently recognised in the APC—*Tephrosia* has one of the highest proportions of phrase-named taxa of any large genus in Australia. Siloed research has built local expertise but led to taxonomic duplication and inter-state inconsistencies. Herbarium visits have identified 15 informally-named taxa as having multiple names across institutions; most are now reconciled in the APC, but AVH maps show some informal taxa have distributions truncated at state borders, indicating inaccurate synonymies and occurrence statements in the APC still. Additional 'in-house' names and concepts also require consolidation.

Recent collaborative research has resulted in substantial growth in knowledge, especially in Western Australia. In particular, many informally named taxa are now well-characterised and resolved across state borders. This has provided the springboard for this project, which proposes to:

- formally name and describe the c. 40 phrase-named taxa that occur in Western Australia and the Northern Territory—this includes taxa that are shared between these regions and neighbouring states,
- provide a revisionary eFlora of Australia treatment for all taxa in Western Australia and the Northern Territory (c. 90), and
- construct a key to all taxa in Australia (c. 150).

This project will establish the framework for the treatment of *Tephrosia* in Queensland (& New South Wales) in the future—60% of APC-listed taxa occur in Queensland and c. 35% are endemic, including 26 phrase-named taxa. These numbers are a reflection of long-term taxonomic effort there. This presentation will give an overview of the project and progress to date, highlight a number of areas where resolution of taxa is hampered by gaps in knowledge and data delivery, and discuss future directions.

Ryonen Butcher is a plant taxonomist at the Western Australian Herbarium, and has concentrated on the resolution and description of species in south-west Western Australia, primarily from the families Proteaceae, Fabaceae and Elaeocarpaceae. She is presently employed on an ABRS research grant to investigate the pan-tropical genus *Tephrosia* (Fabaceae) in northern and central Australia. Ryonen is a member of the 'Nuytsia' editorial team, and an ASBS councillor.

SESSION 6 WEDNESDAY 15:00-15:15

PLANT TRAITS FOR EVERYONE – A PROPOSAL FOR A NEW MULTI-PURPOSE MINIMUM TRAIT SET

Russell Barrett; Hervé Sauquet

National Herbarium of NSW, Royal Botanic Gardens and Domain Trust

We are targeting a single, unique standard trait set fitting many applications at once. ‘Trait-thinking’ has long been the basis of cladistics and more recently evolutionary ecology, but has somehow remained quite disconnected from taxonomic practice. In addition, consistent recording of plant morphological traits is rarely undertaken with multiple users in mind. As taxonomists, we regularly document plant traits for taxonomic papers and flora treatments. Each publication typically contains terminology highly specific to the taxonomic group, thus making comparative use difficult. By assessing traits at the source (collection-based), we can develop a trait set that is beneficial to both macroevolution and taxonomy (including identification and online delivery through portals such as ALA and EoL). Such trait sets are also likely to provide a baseline for “next-generation” taxonomic descriptions.

We believe that we can improve and move beyond current taxonomic practice without necessarily replacing the current model. We propose adoption of a new Minimum Angiosperm Trait Set (MATS) to be scored both in the field at a collection level, and herbarium studies at specimen or species level. Ideally, traits can be scored directly into an app linked directly to an online database, or recorded on printed ‘scorecards’ for remote use. We have developed a draft list of 50 morphological characters that can be consistently scored for most angiosperms. A key factor is that those collecting the trait data can do so with minimal effort, which we hope will encourage adoption as standard practice. Importantly, these traits have been selected and defined to be scored without requiring expert knowledge of specific clades and thus should also fit the purpose of both teaching and citizen science applications. An additional key advantage of a uniformly-scored set of traits using standard vocabulary is considerable facilitation of automated extraction, re-use, and delivery to online databases, regardless of the electronic format by which traits are collected and published.

We present concrete examples of improved descriptions in a variety of formats (i.e., extended descriptions, trait lists, matrices). This will demonstrate that more complete species descriptions, explicitly reporting traits assumed to be constant at the genus or higher level, are possible and beneficial. If adoption of a MATS is successful, secondary and tertiary trait sets can be developed for clades that do require more specialist terminologies or finer divisions of characters to enable reliable application to species level.

Dr Russell Barrett is a systematic Botanist at the New South Wales herbarium. He has a broad range of research interests in plant systematics, ecology and conservation. His current work combines traditional taxonomy and molecular methodology to increase our understanding of the Australian flora. He has a keen interest in the public promotion of scientific discoveries, and practical applications for research outcomes.

AFTERNOON TEA 15:15-15:45

SESSION 7 WEDNESDAY 15:45-16:00

PRELIMINARY FLORISTIC PATTERNS OBSERVED IN THE KAKADU SANDSTONE FLORA

Peter Jobson[1]; Jason Cantley[2], Angela MacDonnell[3], Chris Martine[3]

[1]Northern Territory Herbarium, Alice Springs; [2]San Francisco State University, California, USA; [3]Bucknell University, USA

The Kakadu National Park is internationally recognised for its high endemism, particularly in its highly dissected plateaux. Using specific species groups that are restricted to sandstone derived soils of the Australian Monsoon Tropics (andro-monoecious *Solanum*, *Boronia* sect. *Valvatae*, *Acacia* sect. *Lycopodiifoliae*, *Grevillea* Heliosperma group, *G.* Agrifolia group, and *Hibbertia*) two distinct distribution groupings are observed. One pattern divides the Kakadu plateaux into a north and south distribution; the second pattern subdivides the plateaux into three – Northern Outliers, Central and Southern Kakadu. These patterns shall be tested using SNPs via a ddRADSeq approach.

Peter Jobson is a Senior Botanist & Curator at the Northern Territory Herbarium, Alice Springs. His interests lie in arid Australian flora, legumes of Australia (particularly the egg-and-bacon peas) and the biogeography of the Australian Monsoon Tropics. He is also known for his knitting prowess and for wearing an Ultilikilt at conferences. Despite appearances, he hasn't bitten anyone for over 48 years now.

SESSION 7 WEDNESDAY 16:00-16:15

HOW MANY SPECIES OF *ROTTBOELLIINAE* (POACEAE) ARE THERE IN AUSTRALIA?

Melodina Fabillo[1,2]; Tanya Scharaschkin[1,3]

[1]Queensland University of Technology; [2]Queensland Herbarium; [3]Botanical Research, Art and Training

Rottboelliinae is one of nine subtribes of the tribe Andropogoneae (Poaceae). The number of taxa recognised in Rottboelliinae varies with taxonomic treatments from 10 to 16 genera and 99 to110 species. Taxonomic instability appears to be due to overlapping variability in gross morphological characters used to delimit genera and species and the lack of comprehensive taxon sampling in previous phylogenetic studies.

In Australia, Rottboelliinae is represented by approximately 20 species in 6-7 genera that occur mainly in mesic eucalypt woodlands and savannahs. Seven of these species are endemic to Australia and two are declared rare and endangered. *Hemarthria* shows great morphological diversity, raising questions of whether it includes cryptic species or is a single variable species. Morphological characteristics of *Eremochloa, Thaumastochloa* and *Mnesithea* do not consistently agree with taxonomic descriptions and identification using published keys is problematic.

The primary objective of this study was to test previous hypotheses of relationships and taxonomic decisions regarding generic delimitation in Rottboelliinae and species delimitation in the Australian taxa. In order to resolve taxonomic issues, the phylogenetic position of all known taxa belonging to the subtribe was determined using the following strategies: comprehensive taxon sampling, multi-locus sequencing, and careful examination of key morphological characters of representative vouchers.

Phylogenetic results based on separate and combined analyses of chloroplast sequence data (partial *ndh*F gene, *rbc*L gene, *trn*L-F intron and intergenic spacer) using Bayesian inference, maximum likelihood and parsimony provide results that indicate that the subtribe Rottboelliinae, as currently circumscribed, is not monophyletic. There is strong to moderate statistical support for the monophyly of some genera (e.g., *Eremochloa, Glyphochloa*).

Some morphological characters previously used to delimit genera and species in Rottboelliinae (e.g., position of sessile spikelet, presence or absence of wings in the lower glume) appear to be useful in generic and species delimitation whilst others (e.g., leaf sheath condition, length of wings in the lower glume, length of joints) are uninformative or homoplasious.

Recommendations for taxonomic and conservation status changes of Australian Rottboelliinae as a result of our study will be discussed including: describing one new species of Australian *Eremochloa* and 2-3 new species of *Thaumastochloa* and reassessing the endangered and rare status of the Australian species of *Eremochloa* and *Mnesithea*. This study is the first comprehensive phylogenetic study of Rottboelliinae at a global and Australian level.

Dr Melody Fabillo is a plant biologist (particularly interested in studying systematics of Australian grasses) and science educator with a curious mind for scientific, technical and administrative processes related to advancing research, teaching and learning techniques. Currently enjoys work as a Technical Officer at the Queensland Herbarium.

ARCHAEOBOTANICAL SENSE-MAKING: AN AUSTRALIAN ARCHAEOLOGIST'S JOURNEY WITH PLANTS

Brit Asmussen

Queensland Museum

Archaeologists seek to reveal the detail of human lives through the excavation of sites and the analysis of artefacts and physical remains from those sites, including plant remains. By combining multiple lines of evidence, detailed and surprising glimpses of plant use can be revealed. Here I present the approaches undertaken in the study of Aboriginal Macrozamia seed utilisation, from Aboriginal accounts, linguistics, data-mining historical archives, using archaeological quantitation and experimental techniques, and analysis of the spatial and temporal history of use and relationship to past climate change, and indicate how these kinds of studies can be of benefit to multiple users and audiences.

Brit Asmussen is the Senior Curator of Archaeology in the Indigenous Cultures Program at the Queensland Museum, Southbank. She researches in Australian Archeology, investigating Aboriginal animal and plant management and use, taphonomy, zooarchaeology, ethnobotany and experimental archaeology and Aboriginal agency in objects held in museum collections.

CHASING DUPLICATES BEYOND THE CENTURY, ACROSS THE WORLD AND THROUGHOUT THE VAULT: BUT MIND THE GAPS

Austin Brown

Royal Botanic Gardens Victoria

Identification of plant holotypes and isotypes in our contemporary taxonomic world is relatively straight forward, due to strict adherence to the International Code of Nomenclature for publishing new names, to the computerisation of records and distributions, and to extensive data-basing and digital imagery undertaken by more and more herbaria. Not so, in the good old days. What started as a search for the source of a grass holotype at LE (Komarov Botanical Institute, St. Petersburg) ended up (well, hardly ended yet) with a compilation of information from over 300 herbarium sheets: the partial product of little more than a dozen years collecting in Tasmania by Ronald Gunn for William Hooker in England. Although Gunn collected all manner of plants, algae, moss, lichen, shells and even birds, the current study was restricted to a search for Agrostid grasses (i.e. *Agrostis*, *Deyeuxia*, *Dichelachne*, *Echinopogon*, *Lachnagrostis*, *Pentapogon* and *Polypogon*) collected by Gunn and his friends from 1832–1846. The result was the discovery of 80–90 gatherings with usually two to four duplicates each (occasionally many more), scattered across a dozen herbaria (particularly in Europe) and many having passed through two or more hands before their final resting place. The confusion of Gunn's habit of numbering taxa, instead of collections, or the use of multiple numbers for the same taxon, was compounded by gaps in collection details (i.e. date and location), the mixing of collections on the same herbarium sheets (sometimes with little guide to which is which), multiple determinations and name changes (or none), gaps in information attached to the distribution of duplicates by Hooker and Lindley (e.g. no collector name or collection/taxon number) and the renumbering of collections (either by design or mistake). Added to all this was the fact that many collections were not databased or were filed under a variety of names, even within the same herbarium. Nevertheless, with a great deal of cross-checking, speculation, jig-saw puzzling, general detective work and invaluable help from friendly fellow botanists, most collections could be identified with their original gathering.

With a long-term career in soil science and a long-time passion in plants (particularly grasses) and animals, Austin has a broad ranging interest in ecology, taxonomy, conservation and history of all things biological and their environments.

CHECKING IT TWICE: AN UPDATE ON THE NATIONAL SPECIES LIST (NSL)

Anna Monro; Brendan Lepschi, Anne Fuchs

Centre for Australian National Biodiversity Research

The aim of the National Species Lists (NSL) project is to provide a central point of access for the names of plants, fungi and animals in Australia and an accepted taxonomy for all of these groups. The NSL data provide the taxonomic framework for all projects within the Atlas of Living Australia infrastructure, including the Australasian Virtual Herbarium, the eFlora of Australia profiles, and the Online Zoological Collections of Australian Museums. This update will cover both the expanding content of the National Species Lists and the information systems used to manage these data. The presentation will highlight existing resources of use to the systematic botany community and will outline work in progress to improve these tools and to develop new ones. Topics will include how to search and export data for use in research, cite the taxon concepts presented, and embed NSL identifiers in your own datasets.

SESSION 8 THURSDAY 8:45-9:30

Plenary Address

CONSERVATION OF AUSTRALIAN PLANTS WITH A FOCUS ON NORTHERN AUSTRALIA ESPECIALLY QUEENSLAND

Alison Shapcott

University of the Sunshine Coast

The field of conservation genetics has grown and diversified so where are we now, where are the gaps and where might we be heading? Conservation genetics primarily developed from a conservation application of population genetics. Two of the major themes have been: species wide identification of patterns of diversity and inbreeding and using these to identify conservation priorities and, testing for the genetic impacts of fragmentation. These are being used to guide conservation but increasingly restoration and species recovery. The use of conservation genetics has also been employed to assist with fine scale species delineation where there is taxonomic ambiguity since the conservation unit has mostly been at the species level. However, while many studies have been undertaken on many taxa there are many gaps in both the taxa, reproductive biology, life forms and habitats. While many general hypotheses hold there is much variation and generalisations are hard to make making it difficult and expensive for conservation assessments. Selection of study taxa has largely been driven by EPBC act legislation and various industry interests as part of their legal obligations with additional taxa targeted by restoration groups. Thus many of the common species are less well known than the endangered species making context difficult. The field is becoming increasingly applied in a field that is filled with subjective value judgements. New developments in molecular methodology is opening up new tools to address new questions and promises for an expansion in the types of questions being asked and the breadth of the field is expanding. Queensland examples will be used to illustrate these topics.

SESSION 8 THURSDAY 9:30-9:45

REEDIA SPATHACEA F.MUELL.: PHYLOGEOGRAPHY AND POPULATION STRUCTURE

Jessica Bruce[1]; Annette Koenders[1], Kristina Lemson[1], Quinton Burnham[1], Margaret Byrne[2], Pierre Horwitz[1]

[1]Edith Cowan University; [2]Department of Biodiversity and Conservation, Western Australia

Reedia spathacea F.Muell is a critically endangered species of sedge (Cyperaceae) found in the peat swamps of the Jarrah Forest and Warren Biogeographical Regions of Western Australia. *Reedia* has been identified as a Gondwanan relict species on the basis of some morphological and genetic evidence. Characteristics of relictual taxa in the south-west include being of Gondwanan or Pangaean origin, thus having become restricted to mesic habitats from a previously wider distribution and retaining some ancestral morphological states. They also are expected to have high beta genetic diversity with relatively low alpha diversity and deep phylogenetic distinction from sister taxa. Exploration of these criteria through microsatellite analyses will be presented. If this study supports the recognition of *Reedia* as a highly-restricted relict then the genetic consequences of historical population decline or extinction can be addressed.

Student presenter

Jessica has a degree in conservation and wildlife biology from ECU, and remained with the university to complete her masters research. She has a keen interest in comparative phylogeography, threatened species conservation and how the two can work together in management practice.

SESSION 8 THURSDAY 9:45-10:00

CONSERVATION GENETICS OF THREATENED NATIVE OLIVES (GENUS *NOTELAEA*) IN SOUTHERN QUEENSLAND

Chapa Manawaduge; Matthew Phillips, Susan Fuller

Queensland University of Technology

The genus *Notelaea* (family Oleaceae) is endemic to Australia and consists of 12 species, of which two are currently listed as threatened. *Notelaea ipsviciensis*, with only 17 mature trees distributed within less than 2 km^2 in South-East Queensland, is listed as critically endangered while *N. lloydii* is listed as vulnerable due to its restricted distribution encompassing approximately 3700 km^2 in South-East Queensland. *Notelaea lloydii* occurs in sympatry at the only site where *N. ipsviciensis* is found and *N. ipsviciensis* exhibits intermediate morphology between *N. lloydii* and *N. ovata* raising speculation that it is a natural hybrid of the two. A recent genetic study on *N. ipsviciensis* supports its hybrid origin from *N. lloydii* and *N. ovata* ancestors. In a hybridization event, if the hybrid does not exhibit reduced fitness relative to parental taxa, it may ultimately displace pure populations of one or both parental taxa. Therefore, it is of critical conservation importance to evaluate the levels of genetic diversity and genetic structure of parental populations to determine whether they are at a risk of extinction due to displacement by hybrids. Furthermore, *N. lloydii* occurs in few small disjunct populations in South-East Queensland. Given the high degree of urbanisation and vegetation clearance, it is possible that intra-specific gene flow is limited between these small and isolated populations and inbreeding may be a significant risk. Thus to inform conservation management strategies, it is essential to evaluate the levels of genetic diversity within populations and the genetic differentiation and gene flow among populations of *N. lloydii*. Furthermore, despite being recognized as distinct species, there are some ambiguities surrounding the phylogenetic relationships among *Notelaea* species. Considering all these gaps, we aim to conduct a population genetic analysis of these threatened *Notelaea* spp. as well as a phylogenetic analysis of the genus *Notelaea* as a part of a broader study on the conservation biology of the endemic and threatened species in southern Queensland. Results to date include sample collection and DArTseq (SNPs) analysis of 94 individuals of *N. lloydii* (from seven populations), *N. ipsviciensis*, *N. ovata* and *N. longifolia*. Principal coordinate analysis of 61,392 loci has revealed a high degree of genetic structure among *N. lloydii* populations indicating little contemporary gene flow among isolated populations. Phylogenetic analyses have been conducted using both SNPs and Sanger sequencing data and preliminary results will be presented and discussed.

Student presenter

Chapa Manawaduge holds BSc (Hon.) special degree in Botany from University of Peradeniya, Sri Lanka. Her Honours research project was on the taxonomy and the conservation of the genus *Aponogeton* in Sri Lanka that resulted in the discovery of new species. She has been awarded a QUT Postgraduate Research Award and HDR Tuition Fee Sponsorship to undertake a PhD project at QUT on the conservation biology of threatened native olives in southern Queensland.

HOW DID IT GO? A GENETIC ANALYSIS OF THE *GOSSIA GONOCLADA* RECOVERY PROGRAM

Laura Simmons[1,2]; Tamara K. Taylor[3]

[1]Genecology Research Centre, University of the Sunshine Coast; [2]Queensland Herbarium; [3]Environmental Futures Research Institute, Griffith University

Gossia gonoclada is an endangered tree that is restricted to extremely limited areas of remnant riparian rainforest in highly urbanised south-east Queensland. A recovery program was undertaken in the 1990's with the aim of arresting the decline of the species in the wild and maintaining viable *in situ* populations and included conservation genetic studies to inform propagation and planting of recovery populations. Natural attrition of individuals, concern of clonal spread and the significant threat of the invasive fungal plant pathogen myrtle rust, has prompted a re-assessment of the natural and recovery *G. gonoclada* populations to inform further recovery efforts.

21 polymorphic microsatellite markers developed from ddRADseq libraries were utilised to genotype each natural (23 of 26 remaining plants) and recovery (79 offspring) individual and assess genetic variation, diversity and levels of inbreeding in the natural and recovery populations (17 total).

Unique genotypes were identified, which will be useful in matching pedigrees with myrtle rust resistance information. Wild plants have retained moderate levels of species genetic variation across all populations (*As* = 3.2) and we found little evidence of clonal spread within source populations with little genetic clustering or isolation of wild individuals and populations. All of the recovery populations had moderate to high levels of excess heterozygosity; however, these were similar to the largest wild population and expected given the limited gene pool for the previous recovery plan. The genetic diversity of the species has been captured in the recovery actions and is spatially well spread, with representation of the genotypic composition of the wild populations and increased average levels genetic diversity in recovery populations compared to the wild populations. Future restoration programs should focus on sourcing propagating material from genetically diverse wild and offspring individuals and continuing to capture the full genetic representation of *G. gonoclada*.

SESSION 8 THURSDAY 10:15-10:30

CONGRUENT GEOGRAPHIC STRUCTURING IN *MACROZAMIA* AND THEIR POLLINATING THRIPS

Alicia Toon; Lyn Cook

University of Queensland

Like many cycads, species of Australian *Macrozamia* have intimate associations with insect pollinators: species are pollinated by weevils, thrips, or both weevils and thrips. The genus displays a push-pull pollination system in which pollen cones produce a chemical that attracts the pollinator but heating of the cone during the day forces the pollinator to leave, only to return later when the cone cools. Such a system is comparable to well-known angiosperm-pollinator interactions, such as figs and fig-wasps, yucca and yucca moths, and certain orchids and the male wasps they sexually deceive. Pollinators in these systems affect gene flow in the plants they pollinate to the extent they have been implicated in speciation. Here, we use genetic markers to assess population structure within and among species of thrips-pollinated *Macrozamia* in southeast Queensland. We find a significant match between genetic structure in the cycads and that of their thrips pollinators, and a mismatch with the current taxonomy of the cycads. Our results show that pollinators of Macrozamia might have an important role in population connectivity and, potentially, speciation in this genus.

I study interactions among species and how they contribute to biodiversity and biogeography of Australian animals and plants. My current focus includes cycads and their pollinating insects, bird and bee pollination of pea plants and galling insects and their host plants.

MORNING TEA 10:30-11:00

SESSION 9 THURSDAY 11:00-11:15

THE EVOLUTION AND BIOGEOGRAPHY OF AUSTRALIAN ASPARAGALES

Joanne Birch[1]; Daniel Murphy[2], Neville Walsh[2], John Conran[3], Terry Macfarlane[4], J. Chris Pires[5], Bee Gunn[2]

[1]University of Melbourne; [2]Royal Botanic Gardens Victoria; [3]University of Adelaide; [4]Department of Biodiversity, Conservation and Attractions, Western Australia; [5]University of Missouri Columbia

Asparagales comprise one third of all monocots (14 families, 1,122 genera, ca. 36,205 species) including Orchidaceae and economically important taxa (e.g. asparagus, onion and many ornamental plants). Despite the significant non-Orchidaceae diversity in Australia (9 families; 48 genera; ca. 327 species), phylogenetic studies to-date have neglected sampling of Australian taxa, including only placeholder genera. As a result, understanding of the evolution of the extreme morphological heterogeneity present within asparagoid families is limited. Australian Asparagales taxa are found across a striking range of habitats. A phylogenetic study of character evolution among genera holds potential to provide insights into the evolution of habitat-associated adaptive traits, such as the evolution of desiccation-tolerance strategies and geophytism.

Phylogenetic relationships of Australian Asparagales were inferred to provide a context for understanding the morphological and ecological diversity of the order. All native Australian genera were sampled and species level diversity was represented by 200 individuals. Genome skimming libraries were generated and high throughput sequencing technology (Illumina 2000) was used to generate sequence data. Whole chloroplast genomes were de-novo assembled, mapped to reference and aligned, and the phylogeny was inferred using the maximum likelihood criterion in RAxML. Data for key morphological and ecological characters were reconstructed onto the phylogeny using Fitch parsimony.

The asparagoid phylogeny we have generated based on genomic data supports monophyly of existing Asparagales subfamilies and, for the first time for many genera, has allowed assessment of the monophyly and relationships of Australian taxa. Morphological and ecological diversity of Australian genera will be examined in a phylogenetic context, towards assessment of taxonomic status, focusing on genera with putatively overlapping boundaries and those containing extreme morphological heterogeneity. Character evolution in Australian Asparagales and implications for evolution of Asparagales-dominated vegetation will be discussed in light of these results.

Dr Joanne L. Birch holds a teaching and research position in the School of BioSciences at the University of Melbourne and is the Curator of the University of Melbourne Herbarium (MELU). Her research investigates of evolution and diversification of plant lineages from the Australasian and Pacific floras. Current studies focus on monocotyledon systematics and biogeography including of Australian Asparagales and Australasian Poa (Poaceae–Poeae).

SESSION 9 THURSDAY 11:15-11:30

USING PHYLOGENETICS TO INVESTIGATE CONTINENTAL, BIOME AND HABITAT SHIFTS AND RADIATIONS IN *PHLEGMARIURUS* (LYCOPODIADIACEAE)

Ashley R. Field[1,2]; Thaís Elias Almeida[3], Lucie Bauret[4], Weston Testo[5]

[1]Queensland Herbarium; [2]Australian Tropical Herbarium, James Cook University; [3]Universidade Federal do Oeste do Pará, Brazil; [4]Xishuangbanna Tropical Botanical Garden, China; [5]University of Florida, USA.

Phlegmariurus is an ancient genus in the family Lycopodiaceae with a modern diversity of 250 species spread across the wet tropics, wet subtropics and wet temperate zones globally. We explore hypotheses about the biogeographic radiation, biome shifts and transitions between the epiphytic and terrestrial niches in *Phlegmariurus* using phylogenetic data from Sanger-sequencing and target-sequence-capture from a comprehensive global sampling. We infer that *Phlegmariurus* is most likely of Gondwanan origin, and that it diverged from the Laurasian *Huperzia* and Gondawan *Phylloglossum* in the Mesozoic. *Phlegmariurus* has subsequently diverged into Neotropical and Palaeotropical radiations in the Eocene, with the Neotropical radiation repeatedly dispersing both eastwards and westwards into the Palaeotropics to the present. Conversely, the Palaeotropical radiation has dispersing into the Neotropics only once. The orogenesis of the Andes is likely to have been a primary driver of the shift of *Phlegmariurus* back into the terrestrial niche and its subsequent hyperdiversification and local endemism in the montane Neotropics. In contrast, the Palaeotropical radiation remains predominated by epiphytes from tropical rainforests, with secondary terrestrialisation being comparatively rare and restricted to a few facultative species in the temperate zones. Long distance dispersal and specialisation within the epiphytic habitat appear to be important factors in the diversification of *Phlegmariurus* in the Palaeotropics with multiple dispersals reaching even the most remote forested Oceanic islands of the Pacific.

Dr Ashley Field is a Senior Botanist at the Queensland Herbarium based at the Australian Tropical Herbarium. Ashley's research focuses on the systematics, evolutionary diversification and conservation biology of ferns and lycophytes. Ashley completed PhD studies at James Cook University on the genus *Phlegmariurus*, contributes to the Pteridophyte Phylogeny Group and Geneology of Flagellate Plants projects and is a Queensland Smithsonian Fellow.

SESSION 9 THURSDAY 11:30-11:45

AUSTRALASIAN ORCHID DIVERSIFICATION IN SPACE AND TIME: PHYLOGENETIC INSIGHTS FROM *DENDROBIINAE* (ORCHIDACEAE)

Katharina Nargar[1,2]; Claire Micheneau[1], Kamolphat Atsawawaranunt[3], Lars Nauheimer[1], Mark A. Clements[4]

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Subtribe Dendrobiinae (Epidendroideae) contains one of the five largest orchid genera, *Dendrobium* Sw., with over 1,500 mostly epiphytic species. The high species number together with the extraordinary morphological and ecological diversity of Dendrobiinae has rendered the understanding of evolutionary relationships, systematics, and spatio-temporal evolution of the subtribe challenging. Even though significant progress has been made over the past two decades using molecular systematics, phylogenetic inferences have mainly relied on few molecular markers yielding limited insights within this hyperdiverse orchid group.

Here we present the results of a combined analysis of a 75 protein-coding plastid loci dataset for 143 *Dendrobium* samples and 28 outgroup samples and a 4-loci dataset (ITS, xdh, matK, ycf1) for 849 additional *Dendrobium* samples. The resulting supermatrix contained 1020 samples, including 485 *Dendrobium* species representing all 27 sections within the genus. Phylogenetic inferences were carried out in RAxML and MrBayes. For divergence time estimations, the data set was pruned to include one sample per species and four loci (ITS, xdh, matK, ycf1), constraining the topology according to the results obtained from the phylogenetic analysis based on the supermatrix of 75 loci. Divergence time estimations were conducted using fossil and secondary calibration points in BEAST. Ancestral range estimations were carried out based on the BEAST chronogram applying the dispersal-extinction-cladogenesis model as implemented in BioGeoBEARS. The study provides detailed insights into evolutionary relationships in Dendrobiinae and their evolution in time and space, in particular within the Australasian region. Implications for a taxonomic revision of Dendrobiinae will be discussed.

Dr Katharina Nargar is a molecular systematist and evolutionary biologist with a research focus on tropical plant biodiversity. Her research interests lie in understanding the diversification of species-rich tropical plant groups in time and space, and the underlying factors that shaped today's diversity. Since 2010 Katharina has worked at the Australian Tropical Herbarium where she leads the orchid research program. Katharina's current research projects employ genomic approaches to reconstruct phylogenetic relationships and the spatio-temporal evolution of Australia's major orchid lineages, in particular of Diurideae, Pterostylidinae, and Dendrobiinae.

GENOMICS FOR AUSTRALIAN PLANTS: DEVELOPING GENOMIC RESOURCES FOR THE AUSTRALIAN PLANT COMMUNITY

Linda Broadhurst, Margaret Byrne, David Cantrill, Darren Crayn, Anna Fitzgerald, Graham King, Jen Taylor, Mabel Lum

The Steering Committee and project management on behalf of the Genomics for Australian Plants Consortium

Australia's unique flora is the result of millions of years of isolated evolution prior to collision with the Asian continent and subsequent floral exchange. Since European settlement some 13% of native vegetation has been completely converted for land use, and a further 62% is subject to varying degrees of disturbance. Genomic approaches offer the possibility of unlocking the enormous information in nuclear genomes for plant evolutionary and conservation studies to significantly improve conservation management decisions.

The Genomics for Australian Plants Initiative is a nationally-inclusive collaboration led by researchers from the Australian State and National Herbaria and Botanic Gardens. The Initiative will be driven by the plant research community and brings together researchers, data specialists, state governments, commonwealth government agencies and plant conservation agencies with the aim of using genomics approaches to understand Australian native plants with cultural, economic, conservation and/or scientific value. The central resource for this initiative will be derived from herbaria and botanic gardens (living collections) around the country, adding significant value to the collections. The genome sequencing data will focus on reference genomes, phylogenomics and conservation genomics, and will contribute to the development of new research methods and capabilities that can be adopted by the national and international plant research communities.

LUNCH 12:30-13:30

EVOLUTION OF *ORYZA* AS REVEALED BY GENOMICS

Robert Henry

Queensland Alliance for Agriculture and Food Innovation

The genus *Oryza* has a pan tropical distribution with significant but poorly known diversity in Australia. High quality reference genome sequences are being developed for most species in *Oryza*. The AA genome clade from which rice (*Oryza sativa*) was domesticated extends to Australia. Chloroplast and nuclear phylogenies are not in agreement suggesting chloroplast capture between closely related taxa. *Oryza meridionalis* from northern Australia is the AA genome species most distant from rice. Rice was domesticated form *O. rufipogon* in Asia. Populations that have been considered *O. rufipogon* in Northern Australia can be readily distinguished from the Asian populations in both chloroplast and nuclear genomes. Their chloroplast genome is closer to that of *O. meridionalis* than that of *O. rufipogon*. However, the Australian and Asian populations are morphologically very similar. This system illustrates the challenges of relating genomic and taxonomic data. Analysis of the genomes of the wider genus suggests that evolution of the genus has involved a combination of divergence associated with geographic separation interspersed with multiple introgressions between widely separated populations.

Robert Henry conducts research on the development of new and improved products from plants. He is Professor of Innovation in Agriculture and Director of the Queensland Alliance for Agriculture and Food Innovation, at the University of Queensland. His research targets improved understanding of the molecular basis of the quality of products produced from plants and genome analysis to capture novel genetic resources for diversification of food and energy crops.

A HYBRID-ENRICHMENT BAIT CAPTURE KIT FOR *HIBISCEAE*, TRIALLED ON AUSTRALIAN *HIBISCUS* SECTION *PANDURIFORMES*

Todd McLay[1]; Mike Bayly[2], Jennifer Tate[3], Sarah Mathews[1]

[1] CSIRO, Centre for Australian National Biodiversity Research; [2]School of Biosciences, University of Melbourne; [3]Institute of Fundamental Sciences, Massey University

Target enrichment sequencing of hundreds of nuclear loci using baited hybrid-capture has emerged as the leading high-throughput sequencing method for resolving phylogenetic and population genetic scale questions in plants. While some generic bait kits exist, made-to-measure baits have been shown to perform better at shallow evolutionary scales. Our goal was to develop a bait kit to answer phylogenetic and taxonomic questions in Australian Hibisceae (Malvaceae). We identified low-copy nuclear genes from three Hibisceae transcriptomes; these were mapped to the *Gossypium raimondii* (diploid) genome to check exon/intron boundaries. Baits were designed from 689 genes and 1334 exons (a total of 355862 bp) using 3x tiling. The bait kit was tested with multiple samples of Australian *Hibiscus* section *Panduriformes* species, representatives of several other *Hibiscus* sections, and other Malvaceae genera. Sequence analysis was performed using HybPiper, the gene alignments were used for phylogenetic reconstruction with both concatenation and coalescent approaches, and the topologies of the nuclear and plastid phylogenies were compared. The results of this pilot study will test the taxonomy in Australian *Hibiscus* sect. *Panduriformes* and guide the experimental design of research into other Australian Hibisceae.

SESSION 11 THURSDAY 14:15-14:30

PHYLOGENOMICS OF AUSTRALIAN *GNAPHALIEAE* (ASTERACEAE) USING TARGET ENRICHMENT

Alexander Schmidt-Lebuhn[1]; Jess Bovill[1], Ian Lester[2]

[1]CSIRO, Centre for Australian National Biodiversity Research; [2]Australian National University

The everlasting paper daisy or cudweed tribe Gnaphalieae accounts for *c*. 500 species, or about half of the native Australian Asteraceae. Its local centres of diversity are in the south-west and south-east of Australia. The morphological and ecological diversity of the tribe is immense, ranging from the shrubs of the well-known genera *Cassinia* and *Ozothamnus* to minuscule ephemerals. Past studies have suggested that the Australasian clade of the Gnaphalieae is derived from a dispersal event from South Africa only *c*. 15 million years ago. It has been hypothesised that the Australian representatives first established in temperate to subtropical areas and subsequently radiated into the expanding arid zone.

Previous phylogenetic studies using traditional Sanger sequencing makers were, however, most successful in testing the status of individual, large to medium-sized genera. They were limited in their ability to provide significant support to the resolution of deeper relationships and to resolve species-level relationships at the shallowest phylogenetic levels, making it difficult to confidently address broader questions of evolutionary and biogeographic history.

We tested the use of a bait set designed for target enrichment of Conserved Ortholog Set (COS) loci in the Asteraceae family on Australian Gnaphalieae. Our first set of specimens combined broad but patchy sampling across the tribe with thorough sampling of a group of three genera hypothesised to be closely related, to test resolution at several phylogenetic depths. In addition to target enrichment of low-copy nuclear loci, we skimmed the sequence reads to assemble complete ribosome and chloroplast sequences.

Preliminary results show limited but strongly supported topological differences between nuclear and chloroplast data. Ribosomal and chloroplast phylogenies are generally strongly supported throughout, whereas COS loci provide relatively few informative characters in our study group and accordingly lower branch support. Concatenated and short-cut species tree analyses of COS loci resolve highly similar topologies.

Alexander is a CSIRO Research Scientist at the Australian National Herbarium in Canberra. His research focuses on the Asteraceae family, polyploidy, and user-friendly identification tools.

USING SEQUENCE CAPTURE TO INFER GYMNOSPERM PHYLOGENY

Nathalie Nagalingum[1]; Lorena Endara[2], Steffi Ickert-Bond[3], Gordon Burleigh[2]

[1]California Academy of Sciences; [2]University of Florida; [3]University of Alaska-Fairbanks

After decades of molecular phylogenetic analyses, many aspects of the gymnosperm phylogeny remain contentious. As part of the large “Genealogy of Flagellate Plants” project to resolve the genealogy of all flagellate plants, we are using a sequence capture approach to assemble a species-level phylogeny of gymnosperms from over 400 nuclear markers. Preliminary results indicate that the sequence capture approach is successful across gymnosperms—although we obtain the most nuclear loci from conifer taxa, and fewer loci from cycads and Gnetales. An alignment of the exon (probe) regions from over 450 gymnosperm taxa reveals a well-resolved backbone tree. Alignments that also include the flanking intron regions can resolve relationships among closely related species, such as within Araucariaceae, and provide insights into taxonomic and nomenclatural questions. However, relationships among species in other clades, such as within some cycad genera, remain unresolved.

SESSION 11 THURSDAY 14:45-15:00

RESOLVING COMPLEX EVOLUTIONARY RELATIONSHIPS IN THE SUN ORCHIDS (*THELYMITRA*, ORCHIDACEAE) – INSIGHTS THROUGH MOLECULAR PHYLOGENETICS AND PHYLOGENOMICS

Lars Nauheimer

Australian Tropical Herbarium, James Cook University

Thelymitra is a genus of terrestrial orchids in the tribe Diurideae and comprises c. 119 species occurring in Australasia, with the majority of species in Australia. Despite considerable taxonomic work over the past two decades, evolutionary relationships and species delimitation within *Thelymitra* are still poorly understood. For a first assessment of the infrageneric relationships within *Thelymitra*, we conducted a molecular phylogenetic study based on one nuclear and three plastid loci including the majority of species in the genus. The four loci data set resolved major clades, which corresponded largely to previously defined morphological groups. However, insights into the relationships within and between these major clades were limited due to low sequence variation in the markers studied. Furthermore, conflicting signal between the plastid and nuclear phylogenies was detected, which provided support for hybridization events involving plastid capture in the deeper evolutionary history of the genus as well as in more recent times. These reticulations played a major role in the diversification of *Thelymitra*; however; also present a great challenge in reconstructing evolutionary relationships. To obtain higher resolution and further insights into the complex history of *Thelymitra*, we applied high-throughput sequencing using target capture and restriction site associated markers (ddRAD) on a more extensive sampling. These two genomic approaches yielded molecular datasets with increased power in unravelling interspecific relationships, thus leading to phylogenetic reconstructions with higher resolution and providing further insights into the reticulate evolution of the sun orchids.

Dr Lars Nauheimer is postdoctoral research fellow at the Australian Tropical Herbarium in Cairns. His work focusses on understanding biodiversity of Australasian orchids using molecular phylogenetics and high-throughput sequencing techniques.

SESSION 11 THURSDAY 15:00-15:30

CONSERVATION GENOMICS FOR TAXON DELIMITATION AND MANAGEMENT OF RARE AND THREATENED PLANTS

Margaret Byrne; Rachel Binks, Carol Wilkins, Donna Bradbury, Adrienne Markey

Department of Biodiversity, Conservation and Attractions, Western Australia

Conservation of threatened plants requires a range of information to ensure appropriate management strategies. Genetics, and more recently genomics, can provide important information to inform such strategies, such as providing knowledge of genetic diversity and structure, identification of conservation units, assisting in resolution of taxon boundaries among closely related entities, and understanding hybridisation and hybrid taxa. While genetics is now recognised as providing critical information for conservation of threatened species, genomics provides greater analytic power, particularly in the context of resolution of cryptic taxa where the distinction between population level differentiation and species identification can be challenging.

Here we demonstrate the value of genomics in contributing to management of threatened species using several case studies. Genomic analysis of species of *Seringia* in the Kimberley have identified unexpected taxon relationships, identification of a hybrid taxon and evidence to support synonymising a currently recognised threatened species and a common species. Genomic analysis of *Banksia biterax*, a species with populations in three disjunct locations in south western Australia has confirmed significant genetic structure among the locations providing information to support management of two very small isolated populations. Genomic analysis of several related eucalypt species in south western Australia has identified clonality, limited genetic structure across a disjunct distribution of tree and mallee populations, and confirmation of putative parents of a species of hybrid origin.

Dr Margaret Byrne is recognised as a leading conservation scientist who has been at the forefront of applications of genetics and genomics in Australian plants to inform conservation of rare and threatened plants, and biodiversity conservation at landscape scales in relation to pollen dispersal, remnant viability and restoration. She is a member of the National Academy of Sciences Committee on Ecology, Environment and Conservation, and on the advisory boards of numerous state and national science initiatives, including the Western Australian Biodiversity Science Institute, Western Australian Marine Science Institution, Terrestrial Environmental Research Network, and Centre of Excellence in Environmental Decisions.

AFTERNOON TEA 15:30-16:00

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