



Newsletter

Australasian Systematic Botany Society

No. 182-183, June 2020



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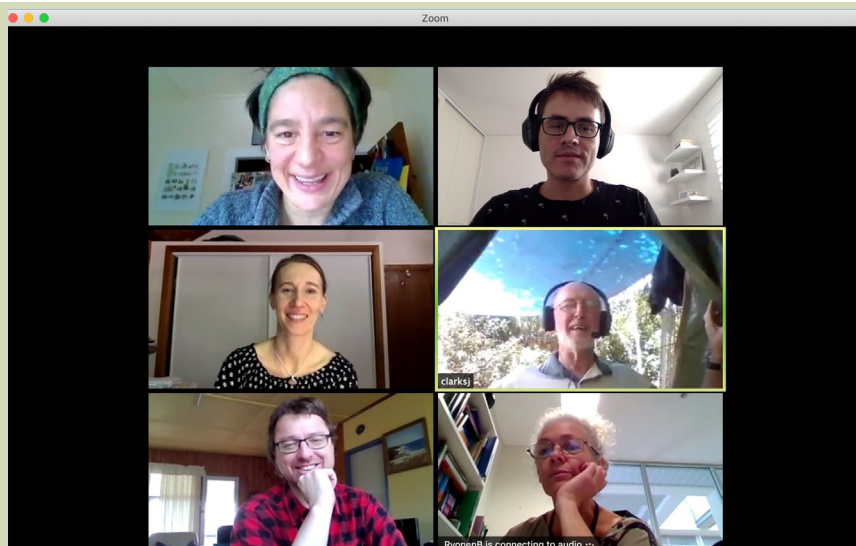
From the President

Dan Murphy

Since my previous President's report written in January, a great deal has happened and the world and many of our working and personal arrangements have radically shifted. At that time, I was based in Okinawa, Japan, for a few months, and perhaps had a vague awareness of COVID-19 reports in China; I think few could foresee what would become a global pandemic. In January, the Australian bushfires were front of mind and were dominating media in Australasia and beyond, and now, while the bushfires are still an important event, they seem something of a distant memory, as we are facing the global COVID-19 general shutdowns. Whole economies are heavily impacted as the limitations on interactions between people to try to control the spread of the disease are enforced to different extents across the world. I think it is very difficult to try to predict the subsequent new challenges that will no doubt arise, although it seems clear that there will be enormous economic and social distancing impacts for the months and potentially year(s) ahead, and the terrible impacts on whole regions through the death and illness of large numbers of people. Australia and NZ have successfully 'flattened the curve' of infections at this point in time, and as I write this Australasia is emerging from

lockdowns at different rates across the region.

In an email communication sent out in March I expressed the concerns and support on behalf of our Society council to all our members, and you will no doubt have received many similar messages sent out by other organisations; I believe these are important sentiments. The ASBS Council also want to reassure our members that, in a very practical sense, our business and activities are running mostly as per usual. We, as a society, are adapted to a dispersed model of governance and largely electronic communications in the main during the year. On 22 April we held a Council teleconference covering a large number of agenda items that had accumulated over the past 6 months (during the meeting we had only a relatively short interruption when removalists arrived at my house!). We are planning another shorter Council meeting soon, as a follow up and to discuss the planned ASBS conference. We tend to structure our year heavily around an annual conference, as we hold the Annual General Meeting there, and our yearly 'face-to-face' council meeting, both events are where a majority of the business of the society is resolved and transacted, not to mention a chance for many members to get together to meet friends and colleagues, listen to the latest science talks, attend workshops and fieldtrips, and have the opportunity to discuss our work in depth. I have stressed



Left: ASBS Councillors at the digital ASBS Council meeting earlier this year. Photo credit: Hervé Sauquet

several times in my reports that the ASBS conferences are a key aspect of the society, and at this point the planning for the next conference to be held in Cairns in November remains ongoing by the conference organising committee (an update on this is in this newsletter). The running and most of the decision making for ASBS conferences is in the hands of the local organisers, with support from Council and others, and at this time because of the constantly changing circumstances I feel there is probably only a 50:50 chance that a face-to-face conference will be possible by the end of 2020. However, we will ask the Cairns organising committee to make this decision (with support and advice from Council as required), and a decision will be needed in the next few weeks.

The implications of not holding an ASBS conference this year are not overly serious; other than the requirement to hold an AGM. Council is considering ways of holding the AGM within the Rules if travel restrictions are not relaxed and is sure it can come up with a solution; many societies will be in a similar situation. Alternatives to a 2020 ASBS conference will be discussed as required, but I do note that Kevin Thiele has recently organised a successful meeting for Taxonomy Australia completely online, which was mostly a series of virtual round-table meetings and webinars. I have not yet experienced an online scientific conference, but anyone who has spent days in teleconferences will tell you that these tele-meetings are more tiring than face-to-face meetings or seminars, and it may be worth the wait until we can all meet in Cairns. However, it could be interesting to trial a new type of meeting, one that, in the interests of reducing travel costs and environmental impacts (not to mention reduction of health risks), may be our future anyway?

I would like to remind members to keep an eye out for the call for nominations to ASBS Council positions. This call will be triggered when a date for the next AGM is decided upon. Under the ASBS Constitution, nominations for council roles are sought annually and I will have served my full term of six years on Council this year and therefore will be step-

ping down as of the next AGM. I am happy to discuss what being on the ASBS Council is like and what the different roles involve (as would all of our Council members). I strongly encourage any member interested in being involved to nominate, as I have found being on the ASBS Council to be a wonderful and collegial experience throughout, plus an excellent opportunity to meet many fellow society members and work towards very rewarding goals (like helping fund student and early-career scientific research).

In recent news for the society, we are finalising an agreement for ASBS to administer student travel grants on behalf of ABRs, and we will have more details about this scheme soon. We feel this will fill an obvious gap in the way our society can support our student members, and are very grateful to ABRs for their assistance and support. Elsewhere in the newsletter, John Clarkson has delivered a detailed report on the society's current financial position, and the news is positive. The society has weathered the recent financial turmoils of the global share market quite well so far, and in fact, John has even found a way to increase our funds at this time, via his work on resolving a refund of franking credits from the Australian Tax Office.

Finally, we are very grateful to our new newsletter editors, Lizzy Joyce and Alex George, for volunteering to fill the editor roles, and in doing so bringing their skills, experience and enthusiasm to the tasks ahead. Council has resolved for this year to ask our newsletter editors to deliver the newsletter in broadly the same format as in the past, however, we will be reviewing this at the end of the year and we may see some changes in the future. I am sure you will notice some exciting changes to the newsletter design in this issue already, although with continuity to the past also (for example the President still got to choose the taxon on the cover). Thanks very much Lizzy and Alex for taking on these important roles and bringing your clear plans for the newsletter to Council. The whole society is very grateful for your work and I look forward to seeing the new directions you take with delivering the newsletter to ASBS members.

New editorial team for the *ASBS Newsletter*

Lizzy Joyce

Last year Bill and Robyn Barker made the decision to step down from many years of service as editors of the *ASBS Newsletter*. It is with enthusiasm and a healthy dose of trepidation that I take over the role of newsletter Editor; Bill's and Robyn's are big shoes to fill. I'm very lucky to be working with a great editorial team, with Alex George as Associate Editor, John Clarkson as Section Editor for Book Reviews and Todd McLay as the Section Editor for News. As well as having complementary skill sets, I think we also represent a diversity of experience that will hopefully provide a good balance of tradition and new ideas to the newsletter.

In 2019 ASBS Secretary Hervé Sauquet conducted a survey about the future of the *ASBS Newsletter*. The findings of the survey (published in *ASBS Newsletter* No. 181 December 2019) showed that while many members would like to see the newsletter changed to an electronic version and the format changed,

a quarter (26%) of the membership still prefer to receive and read the newsletter in print format. As such, the print format has continued, but with a refreshed look and format, with the view to transition to an electronic-only format in the coming years. I hope you are pleased with the new look.

Finally, I encourage all ASBS members to consider contributing to the newsletter. For many years the newsletter has been a platform for debate, information, points of view and entertainment. I think it's an important part of the ASBS not just for communication, but also for maintaining a sense of collegiality amongst our members spread across Australasia and beyond. It is the contributions from members that make the newsletter. So, whether you're a student like me or an established researcher in our field, please don't hesitate to contact us if you have any items to contribute, ideas or feedback, or if you would like to join the editorial team (we could always use the help!).



Lizzy Joyce Editor

I'm a PhD candidate at the Australian Tropical Herbarium and James Cook University in Cairns. Far from the tropical rainforest of Queensland, I grew up in Perth and complet-

ed my undergraduate degree in Botany and Zoology at The University of Western Australia. I finished my Honours on the taxonomic resolution of the *Tetratheca hirsuta* (Elaeocarpaceae) complex, and from there became captivated with trying to understand the taxonomy and the origins and evolution of the Australian flora. After a few years working in botanical and ornithological consulting and studying visual art at the Central Institute of Technology, I moved to Cairns to start my PhD.

I am currently in the last year (will I regret having that in writing!?) of my PhD where I'm trying to understand the influence of the Sunda–Sahul floristic exchange on the evolution of the Asian and northern Australian flora. I'm taking a multi-lineage, multi-scale approach, using floristic, phylogeographic and phylogenetic data to characterise the spatio-temporal patterns of the Sunda–Sahul floristic exchange and the underlying mechanisms driving these patterns.



Alex George
Associate Editor

I was born in East Fremantle, Western Australia, in 1939 and educated at Applecross State School, Wesley College, and The University of Western Australia, graduating with a Bachelor of Arts in 1963. To this I added a major in Botany in 1964. In 1959 I joined the Western Australian Herbarium as a laboratory assistant, later taxonomist, and worked there until early 1981. I then spent twelve years in Canberra as foundation Executive Editor of the Flora of Australia project with the Australian Biological Resources Study. In 1993 I returned to Perth to set up a consultancy as a botanist, editor and indexer, and am now semi-retired.

Field work has taken me throughout Australia. My plant collections total more than 18,000 numbers and include many new discoveries. My major interests in classification have been Western Australian orchids, *Banksia*, *Dryandra* and *Synaphea* (Proteaceae), *Verticordia* and *Calothamnus* (Myrtaceae), and the endemic family Gyrostemonaceae. I have named more than 300 new plants and several new genera. I also have a strong interest in botanical history. I have published some 200 botanical papers and (as sole or joint author) 14 books. Besides 14 volumes of the Flora of Australia I have edited 50 books and indexed 25.

Left: At Kew in 2005 at the end of my second ABLO term with people who were on the staff during my first term in 1968, (from left) Martin Sands, Bernard Verdcourt, Steve Renvoise, Sylvia Philips, Ray Harley and Dick Brummitt. Photo credit: Andrew McRobb.

I have had a long association with the Royal Botanic Gardens, Kew, being the only botanist to have served two terms there as Australian Botanical Liaison Officer, the first in 1968, the second in 2004–05. I was President of The Kew Guild in 2010–11.

In the 1970s I was a member of the Conservation Through Reserves Committee that reviewed conservation reserves throughout Western Australia, leading to the establishment of a number of new national parks and reserves.

My other interests include gardening, photography, music, travel, reading and aviation (I held a private pilot's licence for 20 years). In 2000–01 I was President of the Royal Society of Western Australia. In 2004 I was awarded the Nancy Burbidge Medal of the Australasian Systematic Botany Society, and in 2009 received an Honorary Doctor of Science by Murdoch University. In 2012 I became a Member of the Order of Australia. In 2015 I was awarded the Wildflower Society Award of the Wildflower Society of Western Australia.

In my last editorial (*Newsletter* 25, Dec. 1980), I asked members to 'support the next Editor by continuing to write useful, informative, thought-provoking or just interesting articles'. I think that the intervening 156 numbers of the *Newsletter* are evidence that they have done just that. A huge amount of information is now recorded in its pages. Little did I think then that 40 years later I would once again be helping to produce it, but I repeat that request. More than ever, in this uncertain time, it is a vital link between members, serving to bring our community together as was a prime reason for the formation of the Society.



John Clarkson

Section Editor – Book Reviews

Having had a short biography published in the *Newsletter* when I joined Council for the first time, when Lizzy wrote and asked for another for an article introducing her new editorial team, I immediately thought of Stephen Fry. Fry published two autobiographies and a memoir between 1997 and 2014 and he's 7 years younger than me. How many times can you tell the story of a life? Then I realised my original bio appeared in *Newsletter* number 78 in March 1994. That's 26 years ago. I dare say quite a few current members of ASBS were not even born then. I had a look at the membership database and about 70% of the current members joined the Society after that. Quite a few things have happened to me and the Society since then, so a few notes are probably warranted.

In those 26 years I have been fortunate to have been a member of Council when many important decisions were made. I've have had the privilege of serving in all executive positions and had the great honour of having

Life Membership of the Society conferred on me in 2010. It is perhaps the Treasurer's role that has given me, and still does give me, the greatest satisfaction. My first term ran from 1996 to 1999. I took over from Peter Wilson. Tim Entwisle was the President at the time. This was just after Marlies Eichler made the first of many extremely generous donations to the Research Fund in memory of her husband Hansjörg. Council had to decide how to put these funds to good use and, although I had no real claim to any financial acumen, it fell to me as Treasurer to help make these decisions. I am pleased to say the decisions made at that time, through the sound management of successive Treasurers and Councils, stood the Society in good stead for many years. Marlies died in January 2011 leaving a large part of her estate to the Research Fund. During my second term as Treasurer from 2013 to 2017, with the help of the Society's Financial Advisory Committee, the challenge was to find an investment strategy for what by then amounted to slightly over 1.1 million dollars. During that second term, it gave me great pleasure to be a member of the Council that decided to name the Society's Post Doctorate Fellowship in honour of Marlies. Now I am back for a third term and enjoying helping Council develop a strategy to manage the Research Fund through the financial downturn brought about by the coronavirus pandemic (and chasing up members who have not paid their annual dues ;)).

In 1994, I was living in Mareeba and had what I considered my dream job — then in 1997 John Howard's government sold the first tranche of its Telstra shares. Proceeds from the sale were used to set up the National Heritage Trust (NHT) which provided funds for environmental and natural resource management projects across the country. The following year, as projects were rolled out, I was seconded from the Queensland Herbarium (BRI) to Queensland Parks and Wildlife Service (QPWS) to provide botanical input to a number of interesting studies focused on Cape York Peninsula, a place where I had spent a large part of my working life and knew a little bit about. The work was inter-

esting and challenging and I was working with a great team of people from many disciplines in a place that I cared a lot about. When the NHT work ended, my position was permanently transferred from BRI to QPWS. Since then I have been involved in all manner of studies that required a botanical input. In the early 1980s, I was one of the first to draw attention to the weed threat posed by *Hymenacne amplexicaulis*, an introduced ponded pasture species. Since then I have worked to promote the ecologically responsible use of introduced plants and to encourage early identification and response to environmental weeds. I am currently a member of a small QPWS team that helps plan how weed and

pest animal issues are dealt with on national parks across Queensland.

As my day to day work has taken me away from plant systematics, being actively involved with ASBS has been one of the ways I have managed to maintain some connection with the discipline I love. I also manage to participate vicariously by providing what help I can to botanists visiting Far North Queensland. In my spare time I am still working towards a revision of the Australian members of the genus *Erythroxylum*, but publication will probably have to wait until I eventually retire — a notion I toy with from time to time.



Todd McLay
Section Editor – News

I am a New Zealander, and studied at Massey University in Palmerston North for my undergraduate and Master's degree. My Master's project was on the population genetics of *Dactylanthus taylorii*, an endemic holoparasite that is declining due to the flowers being a special delicacy of brushtail possums. I moved to Australia in 2012 to undertake a PhD at The University of Melbourne. My PhD research used a variety of next-generation

sequencing methods to explore the evolution of grass trees, *Xanthorrhoea*, a project I chose because I thought grass trees looked cool. In 2017 I moved to Canberra to work on the phylogeny and taxonomy of native hibiscus at the Australian National Herbarium, funded by ABRIS. At the start of 2020 I moved back to Melbourne as the Pauline Ladiges Plant Systematics Research Fellow, joint between the Royal Botanic Gardens Victoria and The University of Melbourne.

I was admittedly very naive as to what the Australian flora looked like, beyond gum trees and miles of red desert that you are exposed to by Australian tourism ads, but I have since grown to love it just as much as I love the New Zealand flora. I am really interested in everything to do with plant evolution and taxonomy, but my ongoing projects include phylogenomics and taxonomy of Australian *Hibisceae* (Malvaceae), a Eucalypt Australia funded project on the phylogeny and phylogeography of northern eucalypts including *Corymbia* and *Eucalyptus* (Myrtaceae), continuing work on *Xanthorrhoea* (Asphodelaceae), as well as a variety of projects on orchids, *Monotoca* (Ericaceae), and native citrus (Rutaceae). I am also particularly interested in the development and application of high-throughput sequencing methods, and various bioinformatic and analytical methods to best use such data.

Taxonomy Australia national meeting goes digital

Kevin Thiele

In the last *ASBS Newsletter* I reported on a planned national meeting to be held in Adelaide in mid-March, to develop a scope and detailed plan for an ambitious science mission to discover and document all remaining Australian species in a generation.

The meeting didn't eventuate quite as planned — it was cancelled the day before it was due to start (!), because of the rapidly-escalating COVID-19 pandemic and rapidly-evolving national lockdown, which would have prevented most attendees from getting to Adelaide.

But — every challenge is an opportunity, and the Taxonomy Australia Steering Committee and I immediately began planning an online meeting to replace the planned face-to-face one. And this, I believe, was a great success.

Over three weeks from late April to early May, more than 200 people joined in and contributed to this online meeting, which included video presentations, discussion boards, Zoom roundtables, and webinars. Participants came from all around Australia and around the world, and from all taxonomic disciplines

from plants, algae and fungi to mammals, insects and micro-organisms both terrestrial and marine. And the best thing? We were all a bunch of taxonomists, thinking hard about taxonomy and its future. The collegiality, good will and sense of community were palpable.

The most concrete current outcome of the meeting is a series of wrap-up presentations from each of ten roundtable (breakout) discussions covering different aspects of taxonomy and its future. We discussed the role of morphology and DNA in modern taxonomy, considered how best to structure field campaigns around an all-species mission, discussed new and emerging technologies and their role and prospects, tried to envisage collections of the future, and many more. The wrap-ups are available at <https://www.taxonomyaustralia.org.au/part-4-roundtable-wrapups> (and you can read more about the meeting and its plan and outcomes at <https://www.taxonomyaustralia.org.au/our-mission>).

A great meeting is one thing. Outcomes are quite another, and delivering outcomes from the national meeting is the main activity for Taxonomy Australia at the moment. Over the next weeks we will be developing a synthesis, including both short-term and long-term actions, and ones that can be done now (needing only a little will and a good work ethic) to ones that will require substantial investment and funding.

In parallel, Deloitte Access Economics is working on a preliminary cost-benefit analysis for an all-species mission. With luck and hard work, by the end of June we will have a clear, costed plan and an estimate of the benefits that will accrue from discovering and documenting our remaining Australian species.

Our next step once this work is done will be to develop an advocacy plan and to begin advocating our mission — and hence taxonomy — to governments, industry and the community.

In summary — not even a global pandemic crisis can hold us taxonomists down. More next *Newsletter*.

Left: What attending the Phylogenetics Taxonomy Australia roundtable zoom meeting looks like during COVID-19. Photo credit: Hervé Sauquet



ABRS grants awarded, plus Euclid, Flora and Bush Blitz news

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The successful grants for the 2020–21 round of the National Taxonomy Research Grant Program were approved by the Minister for the Environment, Sussan Ley, in late March. In total, 17 grants were funded, including postgraduate study top-ups, postdoctoral fellowships, early career researcher grants, alongside the more traditional three-year research projects. Congratulations to all successful applicants.

ABRS will be looking for a new member in the Flora Team in the next couple of months, as Zoe Knapp has moved to the Partnerships team of Parks Australia. We'd like to thank Zoe for her significant role in establishing the eFlora and hope she enjoys her new role. We also welcome Bob Makinson to the team, who will be spending the next six months working with Phillip Kodela on editing and publishing some of the recently-submitted treatments for the eFlora.

Flora of Australia

Since December 2019 the Flora team is reduced in number but continues to oversee the 2019 Flora Writers Project contracts and other incoming contributions to the Flora of Australia (FoA). Treatments recently published or revised online: Hymenophyllaceae, Ecdeiocolaceae, Elaeagnaceae, *Punica* (Lythraceae), *Chionachne*, *Eulalia*, *Germainia*, *Hackelochloa*, *Heteropogon*, *Mnesithea*, *Pseudopogonatherum*, *Rottboellia*, (Poaceae – Andropogoneae p.p.), *Anthocercis* (Solanaceae), *Desmocladus* (Restionaceae), Sapindaceae p.p. and miscellaneous taxa from various other families. ABRS thanks the

many contributors involved with these treatments.

Please contact the ABRS (address above) with any feedback about the FoA content and platform functionality, or if you would like to contribute new taxon profiles or update existing descriptions. This could include anything from adding complete treatments to adding profiles for taxa from your research papers. There is also much opportunity for updating and editing treatments loaded from the hard copy floras, reconciling the information with currently accepted taxonomic concepts.

Euclid – online Eucalyptus key

The new Euclid key (4th edition) was released in March (<https://apps.lucidcentral.org/euclid>). It is available on the web, and as an app for Apple and Android phones. At the moment, it has had over 500 downloads from the app stores, which is great to see. Matt Taylor at Identica was instrumental in getting the new edition published, and it wouldn't have been finished without the contributions from key botanist Andrew Slee (Australian National Herbarium), technical support from Robyn Lawrence, and project management by Anthony Whalen (ABRS).

Bush Blitz

The scheduled Bush Blitz to Rungulla National Park (Qld) in April was cancelled, due to COVID-19. However, the Bush Blitz team has been hard at work, teaming up with iNaturalist to create the new Backyard Species Discovery Project. The project will allow people to explore the species in their local environments and have identifications verified by many of the scientists who would usually be out in the field on a Bush Blitz. Find out more about the exciting project here: <https://inaturalist.ala.org.au/projects/backyard-species-discovery-with-bush-blitz-australia>

Genomics for Australian Plants consortium update

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 www.genomicsforaustralianplants.com

 [@PlantsAus](https://twitter.com/PlantsAus)

The Genomics for Australian Plants (GAP) Framework Data Initiative aims to develop genomics resources to enhance our understanding of the evolution and to support the conservation of the unique Australian flora. The project was initiated by Bioplatforms Australia as a consortium in partnership with the Australian State and National Herbaria and Botanic Gardens. GAP has three major project streams: reference genomes, phylogenomics, and conservation genomics. Here we present a brief update on progress across each of these three streams since the last report in the ASBS newsletter (June 2019). In addition, we provide an update on the development of plant genomics training resources by the consortium. For a more entertaining overview of GAP and progress so far, please view the recording of David Cantrill's recent BioCommons presentation: <https://www.youtube.com/watch?v=x8cgUVQczJk>

Update list

1. Reference genomes pilot – *Acacia pycnantha* (golden wattle), *Telopea speciosissima* (waratah), *Areocleome oxalidea*
2. Phylogenomics: bioinformatics, pilot, and stage 1 of the Australian Angio sperm Tree of Life (AAToL)
3. Conservation genomics
4. Training

Reference genomes pilot

Plant genomes are particularly challenging due to their large size and high repeat content, and long sequencing reads are particularly useful for re-constructing large contiguous genomic regions. The reference genome pilot projects were designed to identify the potential challenges and pitfalls working with Australian native plants.

Acacia pycnantha

Team leader Dan Murphy, Royal Botanic Gardens Victoria

Sequence data has been obtained from three different genome-scale DNA sequencing platforms: Nanopore¹ (long reads), Illumina² (short reads) and Chromium 10x³ (linked reads). Combining data from these three different approaches overcomes the limitations of each, e.g. short read (100–300 bp fragments) Illumina data provide the highest accuracy but need to be 'scaffolded' on long read (but lower accuracy) Nanopore data to assemble repetitive DNA regions.

Nuclear genome assembly is almost complete—various assemblers have been used followed by polishing and scaffolding. The resulting contigs are now being assessed for

length, correctness, and other metrics. The team is preparing for genome annotation by comparing annotation tools, particularly regarding options to mask repeats such as transposable elements. Lab work is underway to obtain additional RNA-seq data to improve genome annotation. Assembly of chloroplast and mitochondrial genomes is in progress.

Telopea speciosissima

Team leader Jason Bragg, Royal Botanic Gardens Sydney

The living plant from which initial DNA samples were sourced was lost during the recent bushfires. The team are keeping an eye out for additional individuals that can be

sampled for Hi-C analysis, and that would be appropriate for propagation, and obtaining a voucher specimen.

- A Chromium 10x assembly is complete, best N50 is approximately 1.3 MB.
- Nanopore MinION long reads assembly update:
 - Flye finished, N50 ~2.5 MB
 - NECAT finished, N50, 10.7 MB
 - BUSCO at around 80% for both.
- Two runs of Nanopore PromethION have now been completed and Redbean assembler is running. The team is planning to test the Canu workflow on NCI, but if this doesn't work out, will use in house computer resources at RBG Sydney.



Above: *Telopea speciosissima*. Photographer David Lochlin CC BY 2.0

¹Nanopore sequencing is a technology that enables direct, real-time analysis of long DNA or RNA fragments. It works by monitoring changes to an electrical current as nucleic acids are passed through a protein nanopore. – <https://nanoporetech.com/>

²Illumina sequencing by synthesis (SBS) technology is the most widely adopted next-generation sequencing (NGS) technology, responsible for generating more than 90% of the world's sequencing data. It is a base-by-base sequencing approach that enables accurate data for a broad range of applications. – <https://sapac.illumina.com/science/technology/next-generation-sequencing/sequencing-technology.html>

³Linked-Reads is a sequencing technology developed by 10x Genomics, which leverages microfluidics to partition and barcode high-molecular weight DNA to generate a data type that provides contextual information of the genome from short-reads – <https://www.10xgenomics.com/linked-reads/>

Areocleome

Team leader Russell Barrett, Royal Botanic Gardens Sydney

The team encountered significant and ultimately insurmountable challenges in obtaining suitable plant material of *Areocleome*. The GAP Steering Committee decided to end the project after discussions with the project lead.

Unsurprisingly, the pilot projects presented a significant challenge to the teams, particularly the *Areocleome* project which was unable to continue after 15 months. Both the *Acacia* and *Telopea* teams have generated long and linked read data and are currently working towards generating additional data (e.g. RNA, Hi-C genome assembly data) to facilitate assembly and annotation of the genomes. Unfortunately, the *Telopea* plant chosen for the pilot perished in the recent bushfires, highlighting the need to prepare clonal material and ensure that strategies are in place to preserve nominated specimen plants for future sampling.

Other major hurdles that were not anticipated include the difficulty in obtaining suitable plant material in sufficient quantity due to heat stress in extreme weather conditions and timing of plant growth, and challeng-

es in extracting DNA suitable for long read sequencing. We found that DNA extraction can be quite difficult to optimise for different taxa. However, the quality of DNA extracted from the plant is very important for obtaining good quality, long sequencing reads, therefore it is worthwhile spending some time on the DNA extraction phase. The DNA extraction methods successfully used by the *Acacia* and *Telopea* group can be found at www.genomicsforaustralianplants.com/protocols/.

We have also learnt from challenges in the data generation and bioinformatics space. These include the type and combination of sequencing technologies to be used, compute challenges (capacity, access and configuration), and rapidly evolving tools available to assemble the genomes.

For more details on the lessons learnt, please visit <https://docs.google.com/document/d/1RNghfr5lvs2Bxo-CTCCfAW-Wq67g7oRs0ROYM6dCPyU/edit>

It is recommended that all teams considering submitting an EOI in future rounds familiarise themselves with the potential challenges and address these in their EOI submissions. An EOI for the second suite of projects will be circulated to the community shortly.

Phylogenomics

The GAP Phylogenomics project has the ambitious long-term goal of producing a sequence data resource and a published phylogenetic tree containing 95% of Australian angiosperm species and their sisters—the Australian Angiosperm Tree of Life (AAToL). This is to be achieved by supporting collaborators to achieve their research goals where they contribute to GAP Phylogenomics goals, and coordinating efforts across the community. Work will proceed in three stages as follows. GAP will prioritise completion of the first two stages. The third stage is beyond current resources.

1. In collaboration with the Plant and Fungal Tree of Life project (PAFTOL—[www.kew.org/science/our-science/projects/plant-](http://www.kew.org/science/our-science/projects/plant-and-fungal-trees-of-life)

[and-fungal-trees-of-life](http://www.kew.org/science/our-science/projects/plant-and-fungal-trees-of-life)), resolve the AAToL to genus level using one exemplar species of >95% of accepted Australian genera (per the Australian Plant Census (APC)—www.anbg.gov.au/chah/apc/) and related non-Australian taxa.

2. Generate phylogenomic datasets with denser sampling within genera to address questions of monophyly, evolution, and biogeography.

3. Resolve the AAToL to species level, complete for >95% of accepted Australian species.

In stage 1, target capture sequencing will use the Angiosperms353 bait set to leverage global datasets generated by PAFTOL and others, and to maximise re-use of GAP data. The Collaborative Agreement artic-

ulating the agreed conditions under which data products and know-how generated under PAFTOL and GAP are managed and utilised has been finalised and will be shared between the initiatives and made available on the GAP webpage shortly.

Lalita Simpson has been engaged as the Research Community Project Manager for the GAP phylogenomics project. In this role she will focus on the Australian Angiosperm Tree of Life (AAToL) project, co-ordinating sampling efforts among contributing teams to avoid redundancy in sampling efforts and ensure that the greatest coverage of Australian angiosperm genera is achieved. Lalita's bio: https://www.researchgate.net/profile/Lalita_Simpson.

Phylogenomics bioinformatics

Prepared by Alexander Schmidt-Lebuhn

A working group led by Alexander Schmidt-Lebuhn (Australian National Herbarium) has been established for the bioinformatics component of the phylogenomics project. This group will liaise with PAFTOL to determine and implement protocols to align and share approaches and data between GAP and PAFTOL. Some of the known challenges and opportunities, and progress in addressing them are outlined below:

- Dealing with paralogy: automated Hyb-piper pipeline used by Alexander and Todd McLay (RBG Victoria) is being tested on another dataset.
- Exploration of NextFlow to containerise bioinformatics scripts, making them easier to install on various platforms.
- Development of Draft Recommendations document for data analysis in GAP phylogenomics projects. The purpose of the recommendations document is to:
 - find agreement on preferred approaches to analysis of data (methods and software) for any consortium-level publications, and
 - provide recommendations to individual consortium members less familiar with the various options, while helping to identify potential training needs.

- Exploration of how crucial intermediate files, in particular assembly results including all paralogs, can be made available to the community.
- Discussion on what metadata should be available for each sample.

Phylogenomics pilot

We are currently undertaking a pilot study comparing the Angiosperms353 (see <https://academic.oup.com/sysbio/article/68/4/594/5237557>) and Waycott lab (South Australian Herbarium/University of Adelaide) target capture nuclear bait sets. Bait sets are oligonucleotide probe sets that are used to increase the concentration of the loci targeted for sequencing in raw libraries of fragmented DNA. The outcomes of this pilot will assist in the design of AAToL stages 2 and 3. Community participation in the pilot experiment through sharing of existing DNA libraries was invited through an EOI process:

- a. Six responses were received with 983 libraries representing >80 angiosperm families offered
- b. Pilot experiment plan:
 - 133 samples – head to head test of Angiosperms353 baits and Waycott baits
 - 8 samples – combination Angiosperms353 + Waycott baits
- c. Libraries have passed quality control and have been submitted for sequencing. Data generation will be completed by the end of May 2020.

Phylogenomics EOI: Stage 1—Australian Angiosperm Tree of Life (AAToL)

Community participation in Stage 1 of the AAToL project was invited through an EOI process:

- a. Six responses were received; all were accepted. 90% of Australian genera will be sampled in either the AAToL or the PAFTOL project, with 78% of Australian genera represented by an Australian species.
- b. Collectively, the six accepted EOI's include participants from major Australian herbaria

in all States and Territories (AD, BRI, CANB, CNS, DNA, HO, MEL, MELU, PERTH, NSW, UNE), rendering this a truly national project.

c. We are currently in the initiation stages for the physical sampling effort for the project. So far 1354 samples have been committed by participants.

Conservation Genomics

The Conservation Genomics component aims to provide genomic information to support conservation of the Australian flora. Conservation genomics covers a range of activities according to the management questions being addressed. The types of studies that best fit the objectives of GAP are those that seek to resolve species complexes containing suspected conservation-dependent species, as these address the GAP principles, i.e. use herbarium specimens, build capacity in herbaria and botanic gardens, provide genomic resources that can be used in future studies, improve knowledge of Australian plant diversity, have a direct conservation benefit, and can be implemented across Australia with a common approach.

A call for expressions of interest to participate in the Conservation Genomics project is currently open, closing July 6 2020. Details and EOI documents are available at www.genomicsforaustralianplants.com/conservation-eoi/

Training

As part of building capacity in the Australian plant genomics research community, the GAP project will develop relevant training resources, including online material and in-person workshops. The training committee meets regularly, and in consultation with the GAP Steering Committee has identified that topics around bioinformatics are in particular demand. A new plant genomics training page has been set up by Anna Syme with some primary resources; additional tutorials will be added during the project. We welcome your contributions and suggestions—more details at <https://plant-genomics.github.io/training/>. A genomics workshop will be presented at

the next ASBS meeting (Cairns), and an associated webinar is scheduled for December 2020, hosted by the Australian BioCommons. A Q&A forum for plant genomics questions is also being developed. We aim to be a conduit between expertise in the GAP project consortium and the wider plant research community, and will integrate training resources with some of the GAP project data to best highlight analytical approaches and concepts.

We gratefully acknowledge the support of the Ian Potter Foundation, the Royal Botanic Gardens Victoria Foundation, and the many institutions and researchers that have committed cash and in kind support to the project.

Editor's note: After this article was received for publication GAP announced a call out for expressions of interest for the GAP Reference Genomes project. EOIs are due July 6, 2020. More information can be found at: <https://www.genomicsforaustralianplants.com/reference-genomes-eoi/>

Update on ASBS 2020 conference, Cairns

The Organising Committee

Katharina Nargar, Darren Crayn, Ashley Field, John Clarkson and Frank Zich



Due to the COVID-19 outbreak and subsequent national and international travel restrictions, the ASBS conference 'Biodiverse futures — systematics in a changing world' originally scheduled for July this year in Cairns, was postponed to November 22-27 2020. However, uncertainties regarding the development of travel restrictions at national and federal level and by our home institutions are still remaining which may affect participation at this year's ASBS conference. Therefore, the ASBS organising committee will re-assess the situation at the end of May to determine whether the ASBS conference in Cairns can go ahead this November and if yes, in which format, as conventional face-to-face meeting or as virtual meeting. A further update will be provided on our ASBS conference webpage (<https://systematics.ourplants.org/>), the ASBS Facebook page (<https://www.facebook.com/groups/434955569922530/>) and circulated to ASBS members via email at the end of this month. Please feel free to [contact the organising committee](#) by email if you have any queries or comments. We sincerely apologise for any inconvenience and thank you for your understanding.

Australasian Systematic Botany Society Inc. Grants and Awards

Marlies Eichler Postdoctoral Fellowship

Applications close on 31st July 2020

We invite applications from members

Hansjörg Eichler Scientific Research Fund

Round 2 applications close on 14th September 2020

For eligibility and other information see the ASBS website
<http://www.asbs.org.au/asbs/research-funds/index.html>
 or contact Vice-President Heidi Meudt (vicepres.asbs@gmail.com)

ASBS now a registered charity

John Clarkson

Members might be interested to hear that the Society has recently been registered as a charity with the Australian Charities and Not-for-profit Commission. By applying when it did, the Society was responding to a recent announcement from the Australian Taxation Office that it was about to reform the Deductible Gift Recipient (DGR) system. The reform is aimed at providing assurance to donors to DGRs that their donations are being used for charitable purposes. The Society's case for charity status was based upon its support for education and its contribution to advancing the natural environment. The Society's Deductible Gift Recipient Status has been confirmed and remains unchanged.



Above: The Australian Charities and Not-for-profit Commission's "Registered Charity Tick" now able to be displayed by the ASBS

With registration secured, the Society is now in a position to claim franking credits earned on investments in the Research Fund. Charity registration was granted from 3rd December 2012, the date on which the ACNC was established, but subsequent correspondence with the ATO has seen the Society formally endorsed on the Australian Business Regis-

ter as income tax exempt from 1st July 2000 meaning the claim for a refund of franking credits can be back-dated to then.

This news could not have come at a better time. ASBS members would be aware of the downturn in the world economy brought about by the coronavirus pandemic. This could have had serious impacts on the Society's ability to fund the second round of this year's Hansjörg Eichler grants and the Marlies Eichler Fellowships. The first round of Hansjörg Eichler grants for 2020 was funded from cash reserves but for the October round the Society was to draw on the managed fund. This is something the Society had planned to do when the investment portfolio was restructured in 2017. The initial investment strategy had the first drawdown scheduled for April 2018 but generous donations from members, profits from the Brisbane conference and modest income from term deposits saw this postponed several times. If we can secure franking credits, budgeting suggests that the first draw down might now be postponed to October 2021 when, hopefully, the unit price will have risen above its current depressed value. Council would like to reassure members that it is keeping a very close watch on things and will keep you informed.

One final plea to members who have not paid their membership fee for this year. Please contact me soon. The end of this financial year is fast approaching and I'd very much like to close the books with everyone paid up. Stay safe.



Perspective

Why we need to manage lists of taxa as well as lists of the names of taxa

Kevin Thiele

In taxonomy, we have a long and, particularly in Australia, proud tradition of managing the names of taxa. The ABRS- and CHAH-managed Australian Plant Name Index (APNI) and Australian Plant Census (APC), both of which are representations of data in the National Species Lists (NSL), are world-leading, relatively efficient, quite effective, and widely used.

We usually think of APNI as being a listing of names and instances of names, and the APC as being a listing of accepted taxa. This is correct in the sense that the APC rounds up and assigns non-accepted names (synonyms) under accepted names, and in this sense an APC entry is a taxon.

However, ever since Linnaeus, we have been mixing up taxa with the names of taxa, which leads to confusion and limits our ability to properly manage our knowledge of Australia's biodiversity.

Our problem stems from one key issue — the name of a taxon is a very different thing from a taxon. Another way of saying this is that taxa and the names of taxa behave in very different ways when we do taxonomy.

Consider a taxon t with name x . Two situations commonly occur that illustrate the problem. In the first situation, t stays the same but its name changes from x to y . This can happen if, for example, an earlier valid name (y) is discovered and we choose not to conserve x . Our taxon t remains exactly the same in all respects: it has the same circumscription, the same specimens, the same traits; only its name changes.

The second common situation is the inverse of this: the taxon changes but its name stays the same. If a taxonomist splits t into two new taxa, u and v , and the type of the name x belongs in u , then u retains the name x , even though it has a different circumscription, comprises a different set of specimens, and has different traits — that is, is a different taxon — to the original taxon t .

As taxonomists, we're all entirely familiar with these situations, and scarcely notice that the behaviours described above are actually rather odd. We've been changing names for the same taxon, and using the same names for different taxa, since the very beginning of taxonomy, and have grown perfectly accustomed to the oddity.

But when managing information on biodiversity, particularly in digital form, these behaviours are not just odd, they are counter-productive. Imagine if the Australian Census (of people) were set up in such a way that it couldn't recognise that two people called John Smith are actually different people, or that when someone changes their name by deed poll they remain the same person. A Census unable to handle these cases would be a very problematic census indeed.

And yet, this is exactly what we do with respect to taxa and their names.

Two examples show why we handle biodiversity information badly when we cannot adequately discriminate a taxon from its name.

Consider a collection of images, with each image indexed in a database using its taxon name (or a taxon name identification number). If we have a set of images of taxon *t* indexed under its name *x*, and *x* changes to *y*, either our database breaks or we have to re-index all the images from *x* to *y*. This is not a good way to manage an image database.

For the second example, consider a set of specimens, all of which are believed to comprise a single species *t*, databased under the name (or nameID) *x*. The specimens are distributed around various herbaria in Australia, and their records are aggregated in the Australian Virtual Herbarium (AVH), which provides a distribution map. Then, a taxonomist discovers that what was believed to be a single species *t* is actually two species, *u* and *v*. Taxon *u* retains the name *x*, while taxon *v* is given a new name.

At the taxonomist's home herbarium, the specimens will probably be curated, and the records on AVH updated, so only specimens of taxon *u* now have the name *x*. However, this is unlikely to happen at all Australian herbaria simultaneously. For several (to perhaps many) years, some herbaria will apply the name *x* to the original taxon *t*, while others

will correctly apply it to the new taxon *u*. The problem is that until all herbaria are correctly curated, there may be virtually no way to tell which records on the AVH are of taxon *t* (that is, the *sens. lat.* taxon) and which are of taxon *u* (the *sens. str.* taxon). Any query of the AVH using the name *x* will yield uncontrollably ambiguous results until all herbaria are curated to the new taxonomy. This is exactly equivalent to a Census that is unable to distinguish two different John Smiths.

Two separate actions need to be taken to fix these problems.

The first is that our database managers need to change their databases to allow them to manage taxa as well as the names of taxa. This work is in progress in the NSL.

The second is that we taxonomists need to change our work practices, so that database managers can correctly manage their records when taxon circumscriptions change (or don't change, as the case may be).

Over centuries of practice, we've become very good at rigorously managing the names of taxa, and (fairly) clearly and unambiguously explaining in taxonomic papers what's happening to our taxon names. The nomenclature block at the beginning of a protologue does this in a well-standardised way.

But there is no equivalent standardisation for explaining in our taxonomic papers what has happened with our taxa. Changes in circumscription are usually buried in the Notes section of the protologue, and readers often need to infer changes to circumscriptions from discursive and relatively unstructured information, or worse still, the circumscriptional changes are not in the paper at all and require special knowledge to be noticed.

Once the NSL is properly managing both taxa and the names of taxa, and the AVH is able to discriminate taxa from their names, it will become critical to make the changes in our work practices so that these systems can

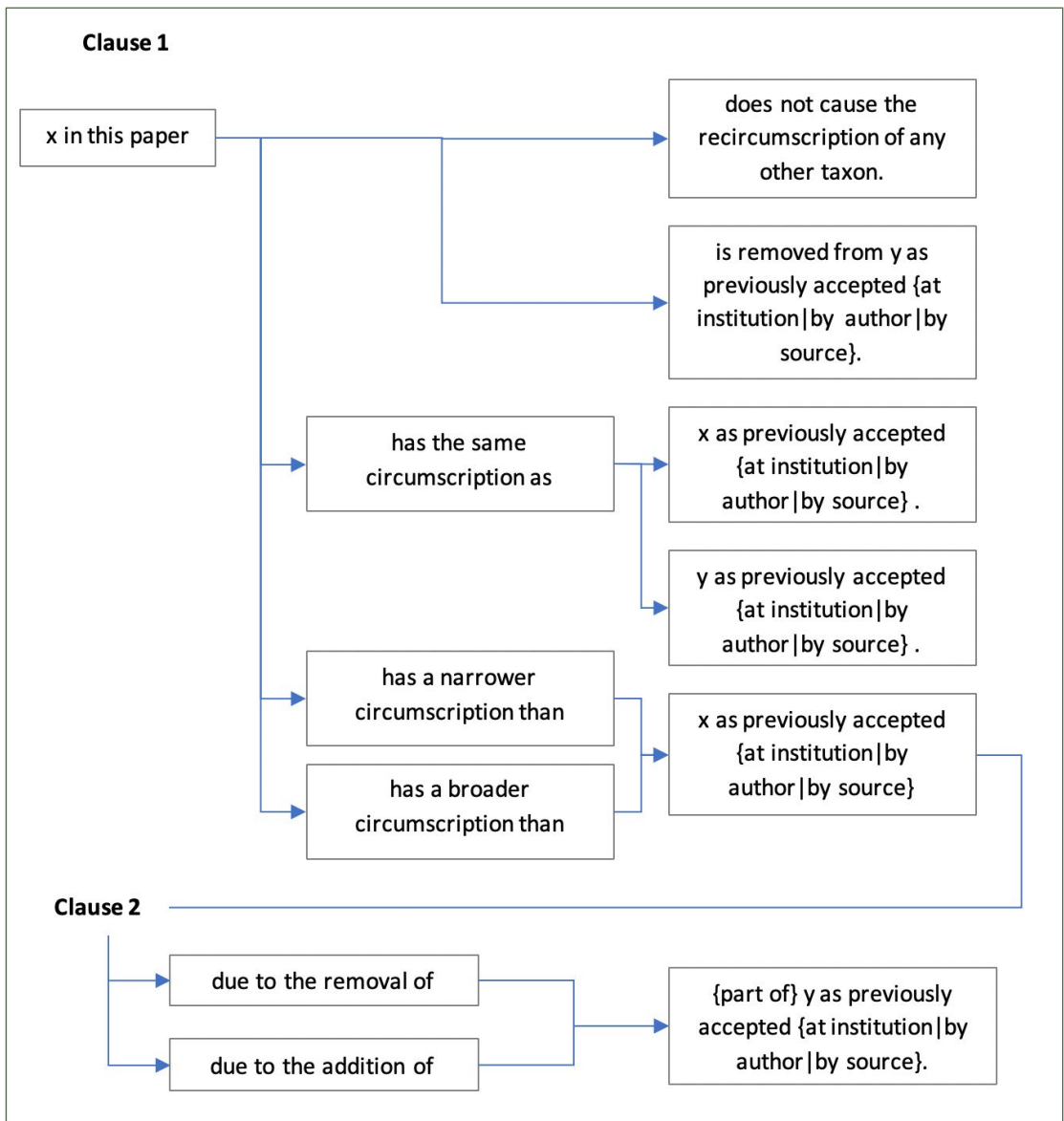
be properly managed.

I believe two changes are required, the first in our protologues, and the second on our det slips. In this paper I propose solutions to both. A community-wide discussion is needed to refine and finesse these, while work on the NSL and AVH is proceeding.

In protologues (or in the taxonomic papers that carry protologues), I believe we need to use a standard way to express changes to circumscriptions in a manner as clear and

rigorous as the way we express changes in nomenclature. Only if we do this will a database manager be able to know, for example, whether a new taxonID needs to be coined or an old taxonID needs to persist.

I propose here a set of standardised statements, preferably presented in a single block at the end of a taxonomic paper, which expresses changes in circumscriptions that are proposed in the paper. A schema could be as follows:



Using this schema, a series of standard statements would be included in every paper. An example from a submitted paper of mine is as follows:

Summary of taxon circumscriptions

Hibbertia polystachya Benth. in this paper has the same circumscription as *H. polystachya* Benth. as previously accepted at PERTH.

Hibbertia spicata F.Muell. in this paper has a narrower circumscription than *H. spicata* F.Muell. subsp. *spicata* as previously accepted at PERTH due to the removal of *H. asterella* K.R.Thiele, *H. subglabra* K.R.Thiele, *H. capensis* K.R.Thiele and *H. prolata* K.R.Thiele.

Hibbertia asterella K.R.Thiele sp. nov. in this paper is removed from *H. spicata* F.Muell. subsp. *spicata* as previously accepted at PERTH.

Hibbertia subglabra K.R.Thiele sp. nov. in this paper is removed from *H. spicata* F.Muell. subsp. *spicata* as previously accepted at PERTH.

Hibbertia capensis K.R.Thiele sp. nov. in this paper is removed from *H. spicata* F.Muell. subsp. *spicata* as previously accepted at PERTH.

Hibbertia prolata K.R.Thiele nom. nov. in this paper is removed from *H. spicata* F.Muell. subsp. *spicata* as previously accepted at PERTH.

Hibbertia leptotheca (J.R.Wheeler) K.R.Thiele comb. et stat. nov. in this paper has the same circumscription as *H. spicata* subsp. *leptotheca* as previously accepted at PERTH.

The schema above is simple, plain-language, readily understandable by both taxonomists and non-taxonomic readers and, most importantly, unambiguously records all changes in circumscription effected in the paper. This will allow managers of a database of Australian taxa to know, for example, that the taxonID for the taxon with the name *Hibbertia polystachya* remains the same, while a new taxonID is needed for the recircumscribed *H. spicata*, because it is not the same as *H. spicata* as previously accepted.

Importantly, the schema is flexible where necessary. In particular, it provides three ways to reference a taxon concept – as previously accepted at {institution}, as previously accepted by {author}, and as previously accepted by {source}. The first of these is quite loose and hence ambiguous; the second is better but still far from ideal, as it references a previous author or publication that may itself be ambiguous. Over time, the last form will become preferable (and may become mandated), and

the source will be the APC (once this adequately deals with taxa as well as the names of taxa).

I believe there are no impediments to the adoption of this schema (but would welcome comments as to how it can be improved).

The second change to our taxonomic practice deals with determinavit slips, and is contingent on a working APC with taxonIDs.

The aim of this change is to ensure that every specimen can be unambiguously assigned to a taxon (not just a taxon name), even in cases when two or more taxa have the same name. It is needed if we are to deal with the second example above, where a taxon is split into two taxa, one of which retains the same name (but has a different circumscription), and with specimens distributed across multiple herbaria.

Our problem is that we need to discriminate

between a record of the *sens. lat.* taxon and the *sens. str.* taxon. We cannot do this simply using a name, because the name is the same in both cases. The only way we can do this is to refer to a name and a taxon on the det slip. A convenient form may be as follows:

DETERMINAVIT

Hibbertia spicata F.Muell. : APC-126-656

Det: K.R.Thiele

15 Jan 2020

Such a determinavit will be familiar to every taxonomist, but has one extra element – the taxonID after the colon. When every taxon in the APC has a readily accessible taxonID, and when taxonIDs behave as taxonIDs rather than nameIDs, this system will become possible, and will place a very small extra burden on practicing taxonomists. Because in such an enhanced APC the taxonID for *H. stricta sens. lat.* (i.e. before the publication of my forthcoming paper) will be different from the taxonID of *H. spicata sens. str.* (i.e., after the paper), it will become possible to fix the problem discussed above. Note, of course, that the name alone cannot solve this problem, because it's a name of a taxon, not a taxon. Of course, whatever code is used to designate the taxon will need to be concise and easy to use for this purpose.

When does a taxon change its circumscription?

An issue in any system for dealing with taxa is the question of when a taxon circumscription changes. I believe this is best left to the judgment of the taxonomist making the change, rather than trying to specify a rules system based on e.g. specimens or publications.

Most cases will be clear and obvious. For example, if a taxon is split into two or more fairly equal-sized taxa, then clearly each daughter taxon has a different circumscription than the parent taxon, and all taxa are different (including the daughter and parent that share the same name). At the other extreme, if a single specimen that has been filed with a taxon but is clearly misplaced there, is removed to a new taxon, this will not imply

a change in circumscription of the taxon from which it is removed. Between these clear-cut cases, there will be boundary cases where discretion will need to be applied.

Note that this applies also at ranks above species. If a *de novo* species is added to *Grevillea*, I think it is reasonable to say that the circumscription of *Grevillea* has not changed – this is equivalent in some ways to some new specimens being added to a species. If, however, an existing species of *Grevillea* is moved to another genus, then the circumscription of *Grevillea* has changed. It would also clearly change if *Grevillea* were to be split into several genera (one of which would retain the name), or if other genera were merged into *Grevillea*.

A philosophical aside

It's interesting to consider how or why the lack of a clear distinction between taxa and their names has arisen. The reason may lie in our use of language: we regularly use taxon names as if they are the names of individuals rather than the names of classes.

If someone points to a tree and asks me what it is, I'm likely to answer 'That's *Banksia grandis*' or 'That's *Eucalyptus marginata*'. These statements are shorthand, of course: the fully explicit answer would be 'That's an individual of a taxon the currently accepted name of which is *Banksia grandis*'. Of course, none of us talk like this (and we'd probably lose friends if we did).

While this may seem like a trivial linguistic quibble, it may be that our loose use of language causes us to confuse taxa ('a taxon with the currently accepted name *B. grandis*') with their names ('*B. grandis*').

The problem is that a name may adequately stand in for an individual, but not for a member of a class. For example, the name 'John Smith' is a fairly adequate way to refer unambiguously to an individual called John Smith (notwithstanding that elsewhere there may be other John Smiths). If someone points to a man in a crowd and asks me who it is, I

can fairly accurately answer 'John Smith'. But a class name cannot unambiguously stand in for a member of the class to which it refers. This is why, if someone points to a horse and asks what it is, I'd answer 'a horse', not 'horse'. The 'a' indicates that I'm labelling a member of a class. But this is not how we usually answer when we're asked to identify a tree – the answer '*Banksia grandis*' is like 'John Smith' and 'horse', not like 'a horse'.

This causes confusion because a process that can happen to a class–subdivision into two new classes–cannot happen to an individual. Hence, loosely using taxon names as though they are the names of individuals rather than the names of classes obscures one of their most important properties and obscures the need to manage the classes (taxa) separately from the management of their names. This may be the root of the problem.

Summary

Taxa and their names are different things, have different behaviours, and need to be handled differently in our biodiversity data

systems. The difference is shown most clearly when a taxon remains the same but gets a new name, and when a taxon changes (that is, gets a different circumscription) but retains the same name. Our data systems such as the NSL do not currently include taxonIDs that behave in a way that adequately accounts for these cases.

As well as changing the way we deal with taxa and their names in our data systems, we also need to change some taxonomic work practices, to ensure that taxa can be adequately managed. One change involves including a set of standardised statements in taxonomic papers that clearly express changes in circumscriptions proposed in the paper. The other change involves a simple addition of a taxonID to det slips, so we can unambiguously assign a specimen to a taxon even when two taxa share the same name.

Both these changes can be made without substantial extra work, and will greatly increase the clarity and reduce ambiguity and error in taxonomic work and biodiversity data systems.



If it's yellow, let it mellow: investigating toxicity variation within southern Australian yellow-staining *Agaricus* L. in a phylogenetic context

Amelia-Grace Boxshall

University of Melbourne

In 2016, I took on a challenge: to work out what on earth was going on with the toxicity and taxonomy of a species of mushroom, *Agaricus xanthodermus* (Figure 1), which was apparently sometimes making people sick when they ate it and sometimes not. Innocent and new to fungi as I was, I had no idea that the questions posed by this mushroom genus in Australia would ensnare me for years to come...

Mushrooms of the approximately 420-species-strong genus *Agaricus* are rarely far from human lips. The genus is best known for its edible species, including the tame and domesticated *Agaricus bisporus* (the button mushroom, commonly found on supermarket shelves) and 'wild' species such as *A. arvensis* (the horse mushroom) and *A. campestris* (the field mushroom). However, *Agaricus* also contains poisonous species. Together, *A. xanthodermus* and other representatives of yellow-staining sect. *Xanthodermatei* are believed to be responsible for 89% of all poisonings arising due to deliberate ingestion of mushrooms in Victoria (Hender et al. 2000). Symptoms of poisoning include severe gastrointestinal irritation (Gill & Strauch 1984; Hender et al. 2000), with phenol identified as the likely cause of *A. xanthodermus* toxicity (Gill & Strauch 1984). Although, in a puzzling turn of events, there are numerous cases of *A. xanthodermus* being consumed without ill effects, including one case of the mushroom being cultivated for food in Austria (Genevier 1876; Kerrigan et al. 2005; Karunarathna et

al. 2016). As of 2016, no one knew why this species appeared to be sometimes poisonous and sometimes not.

To add to this mushrooming mystery, *Agaricus* morphology is highly variable. Although it is relatively straightforward to identify *Agaricus* to genus, collections are alarmingly difficult to identify to sectional or species level and are frequently misidentified, even by experts (Challen et al. 2003). Could the 'sometimes edible' reputation of *A. xanthodermus* be the result of consumers misidentifying edible, yellow-staining *Agaricus* species? Were there perhaps cryptic, edible species regularly being confused with *A. xanthodermus*? And were we even confident that what we call *A. xanthodermus* in Australia was the same the species as the Northern Hemisphere *A. xanthodermus*?

That last question isn't as unlikely as it sounds. Our understanding of fungi diversity in general in Australia remains hampered by the historical perception that all fungi taxa had cosmopolitan distributions (Thorsten Lumbsch et al. 2008). Although this view is no longer widely held, there remain large gaps in our knowledge of Australian fungal diversity, affinities, and biogeography. One of the current challenges for Australian mycologists is to identify which taxa are truly present in Australia (possibly as introductions) and which European and North American names have been misapplied to Australian taxa. Over the last ten years, our understanding of the evo-

Figure 1 (Left, p21): *Agaricus xanthodermus* button showing yellow-staining, a reaction which occurs in certain species after the mushroom tissue is cut, scratched or bruised. Photo credit: A.-G. Boxshall



Figure 2 (above): Grace in the field, carefully uprooting an *Agaricus* mushroom. Photo credit: T. Lebel.

lutionary history and taxonomy of *Agaricus* globally has been dramatically revised from three subgenera and eight sections to six subgenera and 25 sections (Zhao *et al.* 2011; Zhao *et al.* 2016; Chen *et al.* 2017; He *et al.* 2018; Parra *et al.* 2018). However, currently native *Agaricus* species in Australia remain incompletely known.

Project aims

The exact aims of my master's research can be broken down into the following questions:

- Which species of yellow-staining *Agaricus* are present in southern Australia and what are the relationships of these Australian *Agaricus* species?
- Does variation in phenol concentration account for variation in toxicity within *A. xanthodermus*?
- Is there a phylogenetic signal for toxicity in *Agaricus* and, if so, are there factors that are associated with phenol concentration?

Research

I conducted phylogenetic and chemical analyses as part of this research. I sampled 79

collections (43 field collections, 36 specimens from the National Herbarium of Victoria). Field collections were made opportunistically between August 2016 and June 2017 (Figure 2) and were aided by the general public via the social media page, FungiSight (www.facebook.com/fungisight). The genomic DNA was isolated from field and herbarium sampled individuals by me or Dr Teresa Lebel using the QIAGEN DNeasy Plant Mini Kit. The nuclear regions of DNA used for this project were translation elongation factor 1 alpha (*tef1- α*) and internal transcribed spacers 1 and 2 (ITS1, ITS2). Sequence data were generated using a revised targeted amplicon sequencing protocol developed by Dr Todd McLay (unpublished) and sequenced as 50% of an Illumina MiSeq run (600-cycle kit) generating 300 bp paired-end reads of the target amplicons. The contribution of funding from the Hansjörg Eichler Scientific Research Fund by way of the Australasian Systematic Botany Society facilitated the application of targeted amplicon sequencing to this project—a technique which had been applied to macrofungi only once before (Picking 2017) and which made it possible for me to generate genetic data for more individuals than would have been possible using standard Sanger sequencing. As a result, I was able to increase the coverage of *Agaricus* sectional and species diversity and produce a phylogeny which provided greater understanding of the evolution of yellow-staining and toxic *Agaricus* in southern Australia. An additional twenty-two sequences (11 ITS1&2, 11 *tef1- α*) were obtained using Sanger sequencing. After assembling and aligning the resulting sequences, I performed maximum likelihood analyses using RAxML-HPC2 (Stamatakis 2006, 2014) on the online CIPRES portal (Miller *et al.* 2010) and Bayesian Inference analyses in MrBayes 3.2.6 (Ronquist *et al.* 2012).

Dr Damien Callahan and I developed a new protocol for the extraction and GC-MS quantification of simple phenols (such as phenol and hydroquinone) from fungi (Boxshall *et al.* submitted). I then quantified the simple phenol content in twenty-eight fresh field collections representing seven species in-

cluding 52 mature specimens, 42 button specimens, 46 pileus sections and 46 stipe sections (Figure 3). The support of the Hansjörg Eichler Scientific Research Fund was instrumental in developing our new GC-MS protocol to quantify simple phenols in *Agaricus*. The funds enabled us to optimise the protocol, which is soon to be available (Boxshall *et al.* submitted). This funding also made it possible to quantify simple phenols from both early (button) and late (mature) stages of mushroom development to ensure variation associated with those developmental stages was accounted for in our analyses. Simple phenol concentration was quantified in edible *Agaricus bisporus* samples for comparison. (A few tips on our new extraction protocol: firstly, frozen mushrooms are surprisingly difficult to grind and seem to require the adoption of an extremely noisy, somewhat violent grinding technique; secondly, to avoid explosively misplacing your carefully weighed 50 mg samples of ground, frozen mushroom tissue, make sure the liquid nitrogen has fully evaporated BEFORE putting them in safe-lock Eppendorf tubes.) The resulting concentrations were analysed against characters such as tissue type, developmental stage, substrate, odour, and staining. I was aided by Dr Matt Symonds who analysed the dataset with Markov chain Monte Carlo generalised linear mixed models (GLMMs) as implemented using the R package MCMC-

glmm ver. 2.29 (Hadfield 2010) in R version 3.6.1 (R Core Team 2019).

Phenol concentrations were considered in a phylogenetic context by placing those concentrations onto the tips of the *Agaricus* phylogeny.

Results

By including GenBank sequences representing global *Agaricus* diversity, I was able to reconstruct 22 of the 25 currently recognised *Agaricus* sections. In this study, Australian taxa placed in nine sections and one unnamed clade: sections *Arvenses*, *Minores*, *Spissicaules*, *Subrutescentes*, *Nigrobrunnescentes*, *Sanguinolenti*, *Xanthodermatei*, *Hondenses*, *Bivelares*, and *Chitonoides*. This research places Australian taxa in sections *Spissicaules*, *Subrutescentes*, *Nigrobrunnescentes*, *Xanthodermatei*, *Hondenses*, *Bivelares*, and *Chitonoides* for the first time in addition to the six *Agaricus* sections from which Australian species were already known (Mitchell & Bresinsky 1999; Lebel & Syme 2012; Lebel 2013).

This study contributes to our understanding of the relationships and circumscriptions of Australian *Agaricus*. *Agaricus xanthodermus* samples were placed alongside Northern Hemisphere samples in a large, well-supported clade suggesting that the two are

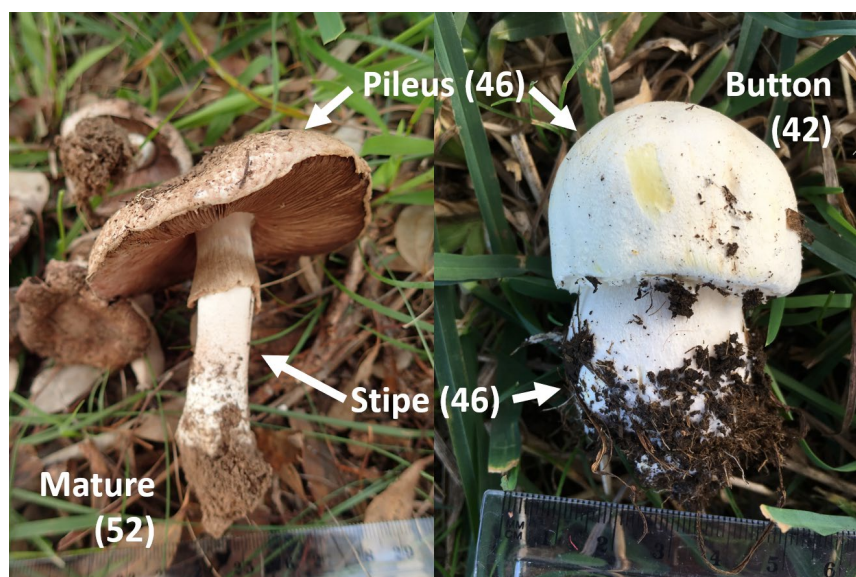


Figure 3 (left): Developmental stages and tissue types for chemical analyses in *Agaricus*. Ten species were collected for chemical analyses, which equated to 28 fresh field collections and one purchased *A. bisporus* 'collection'. Collections could contain a mature mushroom (left), a button mushroom (right) or both. Samples from both the pileus and stipe were analysed for each mushroom. The number of each type of sample is indicated in parentheses. Photo credit: A.-G. Boxshall and T. Lebel.

indeed the same species and confirming that *A. xanthodermus* has a widespread distribution extending across both hemispheres. The Northern Hemisphere species, *A. moelleri*, which differs from *A. xanthodermus* only in the presence of persistent, dark-coloured squamules (Kerrigan et al. 2005), was placed within the *A. xanthodermus* clade. This placement, considered alongside *Agaricus* morphology, suggests that *A. moelleri* might more accurately be considered a synonym of *A. xanthodermus*. *Agaricus endoxanthus*, which is otherwise present in North America (Florida) and South East Asia, is also present in Australia. Geographic clustering is observed within *A. endoxanthus*: the Australian and Thai samples formed a clade sister to the European and North American samples.

Within section *Xanthodermatei*, I identified three potentially undescribed species, whose diversity warrants further investigation. These species were placed within section *Xanthodermatei*; however, their morphological diversity is not accurately accounted for within known species. I look forward to hopefully making some more collections and investigating further!

After mapping the phenol concentration onto the tips of the phylogeny, I observed that section *Xanthodermatei* was characterised by poisonous phenol and hydroquinone production. The concentration of phenol produced in section *Xanthodermatei* was extremely variable. Within *A. xanthodermus*, the concentration of phenol produced in 50 mg of tissue varied between 0 mg kg⁻¹ and 52 mg kg⁻¹. The phenol concentrations detected are high enough to account for the toxicity of *A. xanthodermus* and other section *Xanthodermatei* representatives. Using the dosage calculations provide by the Agency for Toxic Substances and Disease Registry (ATSDR) (2008) and assuming the average human weighs 70 kg, an individual would need to consume only 613 g of yellow-staining *Agaricus* of average phenol content (16 mg kg⁻¹) or 188 g of the highest phenol concentration mushroom sample (52 mg kg⁻¹) to reach the minimum dosage for gastrointestinal irritation by phenol poisoning. Following our brief

surveys directed at mushroom foragers on social media, we found that foragers typically consumed approximately 180 g of foraged *Agaricus* in one sitting, although some foragers estimated that they consume up to 1.5 kg.

We were able to identify factors that were statistically significantly associated with higher phenol concentration within section *Xanthodermatei*. Higher concentrations of phenol were detected in pileus tissue, in mature mushrooms, and in mushrooms growing on woody substrates such as native litter and mulch (Boxshall et al. submitted). We also identified factors associated with poisonous simple phenol production, which could be used if a forager were looking at an unidentified *Agaricus* mushroom with no idea whether or not they should eat it. Mushrooms that smelt unpleasant or grew in lawns were more likely to produce poisonous phenol and hydroquinone. These factors correspond closely with characters associated with *A. xanthodermus* which possesses a distinctive chemical/phenol odour and shows a marked preference for urban habitats, especially lawn.

Every time I look back on my master's project, I'm astounded by how much I achieved. However, this project only highlights how much work needs to be done to understand this genus in Australia. I've committed to return to *Agaricus* once again for a PhD starting in mid-2020. In the meantime, we are currently working towards the publication of these results in two papers: one focusing on the chemistry and another focusing on the phylogeny. So, more *Agaricus* adventures to follow...

Acknowledgements

I am extremely grateful for the contributions made to this project by the ASBS Hansjörg Eichler Scientific Research Fund. In 2017, I received \$4,505 Hansjörg Eichler Scientific Research Fund which made it possible for me apply targeted amplicon sequencing techniques to this project and contributed towards the costs associated with my developing the new extraction protocol required

to perform chemical analyses.

This project would not have been possible without the support and guidance of my supervisors, Dr Jo Birch (University of Melbourne), Dr Teresa Lebel (now at the State Herbarium of South Australia) and Dr Damien Callahan (Deakin Burwood). Teresa also provided wonderful field photos and action shots. I'd like to acknowledge the contributions of the Australasian Mycological Society and The University of Melbourne Botany Foundation, Todd McLay, Rachael Fowler, Naveed Doomun, and my collectors and volunteers (Teresa Lebel, Sapphire McMullan-Fischer, Megan Rixon, Beau Picking, Fran Guard). And, of course, the members of the public who contributed to FungiSight.

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Understanding the role of the Sunda-Sahul floristic exchange in shaping Australia's northern flora

Lizzy Joyce

Australian Tropical Herbarium & James Cook University

In 2017 I was lucky enough to receive an ASBS Hansjörg Eichler Research grant to support my PhD research. Broadly, my PhD focuses on trying to understand the exchange of flora that has occurred between the Sunda continental shelf, Wallacea and the Sahul continental shelf (Figure 1) throughout the Cenozoic, and the influence that this has had on the evolution of the northern Australian flora. To investigate this theme I have a number of projects with specific questions, and the Hansjörg Eichler funds were used to support two of these projects. One project focuses on exchange tracks between Australia and Asia, and another aims to build on the knowledge of the spatio-temporal dynamics of floristic exchange between Sunda and Sahul by examining the evolution of Sapindalean lineages in the region. Here's an account of how those funds have been used and the progress I've made on those projects so far...

Exchange tracks between Asia and northern Australia

Exchanges of plant lineages between Australia and Southeast Asia have had a substantial impact on the evolution of Australia's northern, tropical flora, with important ramifications for its conservation and biosecurity. Despite this, floristic exchange tracks between northern Australia and Southeast Asia remain poorly understood. It is generally assumed that the major floristic exchange track between Australia and Southeast Asia lies between New Guinea and Cape York in north-east Australia, partly because the Torres Strait between these is the narrowest seaway (c. 150 km at its narrowest, with intervening islands) between the two regions

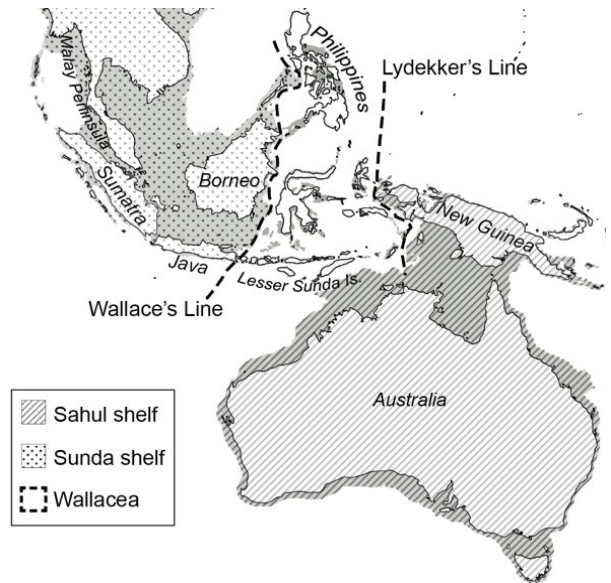


Figure 1 (above): Map of Wallacea, and the Sunda and Sahul continental shelves.

(Van Steenis 1934; Burbidge 1960; Specht 1981; Sniderman & Jordan 2011). Crisp *et al.* (1995) was the first to suggest that there may be a second floristic exchange track between New Guinea and the monsoon tropics of Australia in the Northern Territory and Western Australia based on cladistic biogeography of 11 clades, and a phylogenetic link between south-west Western Australia and the Lesser Sunda Islands was also identified (by Brown *et al.* 2011) in *Paraserianthes* (Fabaceae). However, the presence of two floristic tracks has never been formally tested in a phylogeographic study.

To test the presence of two exchange tracks into northern Australia, we conducted a phylogeographic case study on the widespread and variable tree *Aglaia elaeagnoidea*

(Meliaceae). We retrieved 176,331 single nucleotide polymorphisms (SNPs) from 90,456 loci for 141 herbarium and silica-dried samples (Figures 2 & 3) distributed across India, Southeast Asia, Australia and the Pacific Islands using DART-seq. Multivariate, admixture, genetic differentiation, and coalescent analyses were conducted on the SNP data to characterise phylogeographic and phylogenetic patterns in *A. elaeagnoidea*.

Our results indicate that there are two exchange tracks between northern Australia and Asia (Figure 4). One exchange track was identified between New Guinea and the Cape York Peninsula in north-east Australia, and another was identified between the Lesser Sunda Islands, Timor and the Kimberley region of north-west Australia. The former track is contemporary, characterised by ongoing genetic exchange, while the latter

track is historic, facilitated by exposures of the Arafura Shelf throughout the Pleistocene but not currently active. Overall, we suggest the phylogeography of *A. elaeagnoidea* has been produced by a combination of repeated expansion–contraction cycles concurrent with Quaternary climate fluctuations, as well as stochastic dispersal events. Further, our results suggest that *A. elaeagnoidea* as currently circumscribed is polyphyletic, and should be split, at minimum, into a western and eastern species. We're aiming to submit this study for publication later this year.

This phylogeographic study would not have been possible without the support of the ASBS, with the grant funding the costs of the lab work to extract DNA. It also enabled me to travel to Sydney to work with and learn from my collaborators Maurizio Rossetto and Sam Yap at the Royal Botanic Gardens, Sydney, on the analysis for this project.

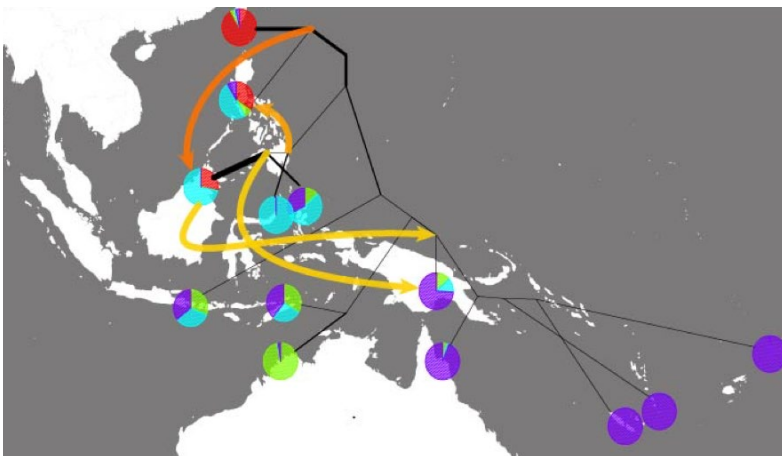


Figure 2 (above-left): sampling *Aglaia* herbarium specimens with collaborator Caroline Pannell.

Figure 3 (above-right): collecting *Aglaia elaeagnoidea* in a Kimberley rainforest patch in 2018.

Figure 4 (left): preliminary results showing population genetic structure across part of the distribution of *A. elaeagnoidea* from LEA analysis (pie charts). The pattern of population splitting and migration according to TreeMix analysis is superimposed

Sapindalean evolution dynamics across Wallace's Line

The Hansjörg Eichler research fund was also used to support my study on the evolution of Sapindales across the Sunda and Sahul shelves. A comparative phylogenetic approach is essential for understanding the spatio-temporal dynamics of the Sunda–Sahul floristic exchange (see Crayn *et al.* 2015). However, when comparing published phylogenies in the literature, the different methodologies used to generate and date those phylogenies can conflate the results and lead to inaccurate patterns.

To address this, we aim to produce a densely-sampled phylogeny of Sapindales to examine the patterns of exchange between Sunda and Sahul in one, large analysis. Sapindales is an order of angiosperms comprising approximately 6,550 species and 460 genera in 9 families (Anacardiaceae, Biebersteiniaceae, Burseraceae, Kirkiaceae, Meliaceae, Nitrariaceae, Rutaceae, Sapindaceae and Simaroubaceae). This order was chosen as it has a high number of genera and families that are shared across the Sunda and Sahul shelves, and encompasses a high diversity of life-forms, biomes and dispersal syndromes. The idea is that this phylogeny will enable us to get a better idea of the timing and directionality of the exchange, but also explore questions like: if a lineage jumps Wallace's Line, are they more likely to diversify? If you're bird-dispersed, are you more likely to jump across continental shelves? And, do you see differences in the spatio-temporal dynamics of exchange if you're a savannah lineage instead of a rain-forest lineage?

To produce this phylogeny, we formed a collaboration with the Plants and Fungi Tree of Life (PAFTOL) project at the Royal Botanic Gardens, Kew. In July 2019 I travelled to Kew to do the lab work for this project over four months, with the Hansjörg Eichler grant covering the cost of my accommodation. Thanks to PAFTOL and a

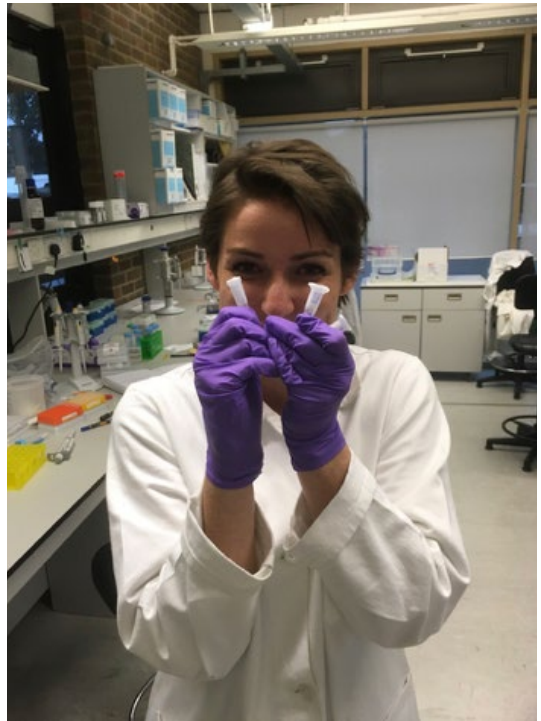


Figure 5 (top): Very excited to be holding these three tubes with my sequencing pools after months of work in the Jodrell Laboratory.

Figure 6 (bottom): How to glove a broken hand for the lab.

team of Sapindales researchers from around the world, I was able to sample and generate Angiosperm353 libraries for nearly 300 Sapindales genera. In combination with PAFTOL data already generated, this has given us sequences for c. 92% of Sapindales genera. As a bonus, I also came away with the skill of ambidextrous pipetting after acquiring a broken hand a month into my stay and having to pipette left-handed.

Now the exciting (and daunting) task of data analysis begins! Hopefully within the next 12 months we will have a picture of how the biogeography of Sapindales lineages across Sunda and Sahul has influenced their evolution, and vice versa.

I sincerely thank the ASBS for their financial support of these projects, as well as my wonderful advisors (Darren Crayn, Kevin Thiele and Katharina Nargar) and numerous collaborators. Thanks to these people and the Hansjörg Eichler grant I have been able to make progress in understanding the Sunda–Sahul exchange, and have had some of the most lucky and enriching experiences of my PhD; I have learned so much, gained new skills and met so many knowledgeable and inspiring plant scientists.

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Corrections to botanical Latin in Stearn and Short & George

Alex George

When Emma Short and I compiled our *Primer of Botanical Latin with Vocabulary* (2013) we came across a number of errors in the vocabulary in William Stearn's *Botanical Latin*, fourth edition (1992 and later reprints). I am always reluctant to draw attention to errors since they happen in many publications and are almost impossible to avoid, no matter how hard one tries. I am only too well aware of those in much of my own writing and editing and, indeed, several slipped through in our *Primer*. Sometimes, however, they may be noted so that, assuming they are read, they will not lead users astray or be perpetuated. Stearn himself wrote how difficult it is to avoid errors, and the list below in no way lessens my great respect for him and his many achievements. The abbreviations here are as used in his book. Those from our *Primer* follow.

Botanical Latin (1992)

accuratus should be part. A

blue correct in *Gk. comp.* cyano-

bristle last line, correct 247 to 277

cone ... correct **cone-like** strobilaceous

consuete correct customarily

culmen insert space in petiole bases

dicimus should be **decimus**

descended from *ortus* should be part. A

ditch and **ditio** move to correct alphabetical position, after **disturbed**

double *duplex* is adj. B

ectoascus should be s.m. II

exasperatus correct 226 to 266

excipule should be **exciple**

galbus should be **galbanus**

gibba move to correct alphabetical position, before **gibbosus**

gompho- correct in *Gk comp.*

gongylodes should be adj. C

hair-covering second-last line, correct *capilliformis*

humus should be s.f. II

illaqueans should be **illaquens**

ion-, correct second prefix to **iono-**

lignescens should be part. B

main mainly insert 'adv.' after *praecipue*

means correct *opes*

multiplex should be adj. B

niger line 2, correct **nigrifactus**

ops correct to **opes**, s. f. III pl.

percurrans should be part. B

phyllary correct TEGULA

pseudocyphylla correct to **pseudocyphella**

quamobrem in this sense is an adv.

redolens should be part. B

resine correct to **resin**

salugineus correct to **salsugineus**

scatens should be part. B

sciophilus correct to **sciaphilus** and place before **scilicet**

sinuato-dentatus line 5, correct **sinuosus**

solemniter correct to **sollemniter**

stilbeus ... **stilbiformis** should be adj. B

sulphate ... **sulphur yellow** correct to *sulphureus*

taeni line 7 correct tapeworm

tall last line correct *altus*

transsectio correct to **transectio**

trapping correct *illaquens*

twining lines 3–4, *dextrorsum* should be italic

veternus ... **vetus** should be adj. B

zygomorphis correct to **zygomorphic**

A Primer of Botanical Latin with Vocabulary 2013 (these were corrected in the second printing, 2014)

chromosome *chromosoma* correct to (noun n. 1)

ops correct to **opes**

periderm *periderma* correct to (noun n. 3)

soma correct to (noun n. 3 ...)

Western Australian books on exploration

Alex George

For the past ten years I have been a member of the Western Australian Exploration Diaries Project which aims to locate, transcribe and publish journals of all who explored new country in the colony from the time of settlement in 1826. A team of volunteers is undertaking the task, with the volumes published by Hesperian Press, Victoria Park. The journals are arranged in chronological order. A number of them mention plants, e.g. as components of the vegetation, as feed for their horses, as toxic or potentially so. Besides proof-reading, my involvement has been interpreting the plants mentioned, which requires knowledge of the flora, vegetation and distribution, a fascinating and sometimes challenging exercise. These are listed in an appendix to each volume (except vol. 1 for which the appendix appears in volume 2). In the early years especially, the explorers knew few scientific names (and many at this time were unnamed). Sometimes they likened a plant to one that they knew in Britain, e.g. a tree resembling weeping willow (*Agonis flexuosa*). They also learnt names from indigenous people met during the expeditions, e.g. Yeit that became Yate (*Eucalyptus occidentalis*). And they coined their own names, such as Raspberry Jam (*Acacia acuminata*), Cabbage Tree (*Nuytsia*), Cable Gum (*Eucalyptus salubris*) and York Nut (*Santalum spicatum*). Most volumes also include appendices on the fauna and ecology by Ian Abbott.

Published volumes of particular interest for flora and fauna

Western Australian Exploration vol. 1, December 1826 – December 1835, principal editor Joanne Shoovert (2005).

Western Australian Exploration 1836–1845, edited by Marion Hercock and Sheryl Milentis with Phil Bianchi (2011) [this also includes an appendix on plants for the previous volume].

The Western Australian Explorations of John

Septimus Roe 1829–1849, edited with an introduction by Marion Hercock (2014).

Samuel Grau Hübbe and the South Australia to Western Australia Stock Route Expedition 1895 – 1896, edited with an introduction by Andrew Guy Peake (2018) [this has no appendix but much of it is repeated in *To the Golden Land* where the plants are interpreted].

Journal of the Elder Scientific Exploring Expedition 1891–1892 by David Lindsay (2018).

Exploration Eastwards 1860–1869, edited by Peter J. Bridge and Kim Epton (2018).

To the Golden Land 1869–1896, edited by Peter J. Bridge (2018).

Volumes in preparation will cover exploration from 1846 to 1860, and in the Kimberley, Pilbara, Gascoyne and Nullarbor.

Previously published expeditions, but not part of this series, include new editions of D.Carnegie, *Spinifex and Sand*, J.Forrest, *Explorations in Australia*, G.Grey, *Expeditions in Western Australia, 1837–1839*, F.Hann, *Do Not Yield to Despair*, and E.Giles, *Australia Twice Traversed*.

Although not part of this series, two companion volumes are:

'Work Completed, Canning': *A comprehensive history of the Canning Stock Route [1906–2010]*, by Phil Bianchi (2013).

Woodlines of Western Australia: A Comprehensive History of the Goldfields Woodlines, by Phil Bianchi (2019). This includes an analysis of the species of trees cut for firewood and mine timber.

A complementary series by Lesley Brooker, also published by Hesperian, retraces some explorers' routes, with many maps and photographs of significant landmarks and plants. Under the general title *Explorers Routes Revisited*, these are:

Moore Expedition 1836

Drummond Expeditions 1841–1842

Clarkson Expedition 1864

Roe Expedition 1836

Giles Expedition 1875

Over the past 40 years or so Hesperian Press has published more than 550 titles, all relevant to Western Australia. A catalogue may be seen at www.hesperianpress.com.

Victory trees

Peter G. Wilson

Royal Botanic Gardens, Sydney

A few years ago, the Botanical Information Service at the Royal Botanic Gardens, Sydney, received a phone enquiry asking if a particular tree, growing on a Uniting Church property in the Sydney suburb of Belfield, was a 'Victory Tree'. An internet search found a series of articles in the Trove digitised newspaper archive that mention these trees. The Victory Tree program appears to have been initiated in the lead-up to Anzac Day 1920, although it wasn't until 1927 that all Australian States observed some form of public holiday on or around 25 April. The initiative came from the 'Young People's Department' of the Methodist Church with the earliest reference being in *The Methodist* newspaper in February 1920 with reference to a rally to be held in Newcastle on 22 March of that year. (1)



Perhaps the best summary is that given in *The Daily Telegraph* on Sat. 24 April 1920:

"In connection with the great demonstration to be held in the Town Hall during the forthcoming meetings of the General Conference, the Methodist Young People's Department has devised a scheme that is likely to be as popular as it is original, through the courtesy of the director of the Botanic Gardens, the department has been able to promise to every Methodist Sunday School in the State, on certain conditions, the presentation of a tree, to be known as the Victory tree. The conditions are that the tree shall be planted in church or parsonage grounds, and that it shall be known as the Victory tree. Its purpose is to keep in living memory of the children of to-day and future days the significance of the victory by which the freedom of their country was secured to them.

A further condition imposed is that at least once a year, as near to the commemoration of Anzac Day as is practicable, a thanksgiving service shall be held around the tree, when the Doxology shall be sung, and prayer offered. Every Sunday School, and there are 580 Methodist schools in the State, is being invited to accept a presentation tree on these conditions, and at the Town Hall demonstration It is anticipated that some 300 will be distributed. The remainder will be despatched to the country by mail." (2)

Here we see the role played by J.H.Maiden in supplying the trees. In an article in *The Methodist* in June 1920, there is this further comment concerning the kinds of trees being distributed:

"The trees are beautiful specimens of the kind most suitable for districts concerned, and the presentation of them is made possible by the kindness of Mr. Maiden, the Government Botanist." (3)

Here it is clear that the trees were selected for their suitability to sites across the State. An article in the *Sunday Times* of 20 June 1920 reported that "Victory trees planted to date exceed 100, and applications are still

Left: A Brush Box (*Lophostemon confertus*), growing at the Uniting Church site in Belfield

being received" and a later report, in 1926, noted that 200 trees had been distributed courtesy of Mr Maiden. The tree growing at the Uniting Church site in Belfield is a Brush Box (*Lophostemon confertus*, see photo) and only a few newspaper records mention the species planted at particular locations. One example is this report in *The Armidale Express and New England General Advertiser* of July 16, 1920, which reported the following:

"The weather was ideal for tree-planting, but not much good for open air standing, so the schoolroom was requisitioned, and some scores of people gathered to take part.

Rev. H. E. Andrews presided, and in a few words, explained the purport of the movement, and incidentally mentioned the indebtedness of the management to the kindness of Ven. Archdeacon Johnstone, who had very greatly helped in the acquisition of a suitable tree. He then called on Mr. W. Curtis, Mayor of Armidale, as churchman, first citizen, and expert horticulturist, to plant the tree.

The Mayor gave a most interesting talk about the little tree with a big name—*Cupressus Torulosa*—telling of its home in the Himalayas, of its tough texture, of its many uses, of its great height—even to 130ft. sometimes—and told how it is recorded that for over a century in earlier days, the great doors at St. Peter's at Rome were made of this timber." (4)

There are two brief mentions of particular trees

in *The Methodist* on Saturday 19 June and 31 July 1920: "At Tenterfield on Tuesday, 1st June, the Rev. Harold Wheen planted the Victory Tree (*Cedrus deodora* [sic]) in the church grounds, in the presence of a goodly number of children and officers of the school." (5) and "Rozelle Victory Tree planting by Mrs. J. Colwell was a pleasant function. The red fig was planted on the parsonage lawn". The fig was presumably a cultivar of *Ficus carica*. (6)

A fourth reference appears in the *Goulburn Evening Penny Post* on 23 May 1922, incorporating further patriotic sentiments:

"The 'Victory Tree,' a sturdy young oak, is one of a number given two years ago by Mr. Maiden, Government Botanist, the trees having been distributed by the Methodist Sunday-school Department on condition that they should each be planted in church grounds and a service held around them for several years at least. It is the intention of the local Methodists to carry on the services indefinitely so that coming generation may see in the spreading oak a living memorial of the British victory." (7)

References

- (1) Web ref: <https://trove.nla.gov.au/newspaper/article/155272377>
- (2) Web ref: <https://trove.nla.gov.au/newspaper/article/239622994>
- (3) Web ref: <https://trove.nla.gov.au/newspaper/page/15593174>
- (4) Web ref: <https://trove.nla.gov.au/newspaper/article/189277471>
- (5) Web ref: <https://trove.nla.gov.au/newspaper/article/155274656>
- (6) Web ref: <https://trove.nla.gov.au/newspaper/article/155273510>
- (7) Web ref: <https://trove.nla.gov.au/newspaper/article/99205215>

MEL News

Frank Udovicic

Teresa Lebel, Mycologist, resigned after more than twenty years at MEL. Teresa made great contributions to our knowledge of fungi (particularly truffle-like forms) in Australasia, and added significant value to our collections at MEL. She has been an excellent mentor to students, fine collaborator and exquisite baker. Unfortunately the border shutdowns have prevented a proper farewell, but we look forward to remedying that in the hopefully not too distant future. Our loss however is Adelaide's gain, as she took on the role of Senior

Botanist, Cryptogams, at the State Herbarium of South Australia (AD) from 30 March 2020. Tempering our sadness at Teresa's departure, was the confirmation that we were able to commence recruitment for a new Mycologist to form the other half of MEL's dynamic fungi duo with Tom May.

Our amazing Collections Branch passed a major milestone in early March - the official 30,000th Type specimen imaged for JSTOR Plants. The specimen just happened to be the isolectotype of *Berberis triacanthophora*, collected by Dr Augustine Henry in Sichuan Sheng, China, during his 1885-88 collecting trip.

News

Todd McLay

Online and in the media

Eucalyptus erythrocorys (red-capped gum) is the 2020 eucalypt of the year

The results of the Eucalypt of the Year competition (run by Eucalypt Australia) was announced on the 23rd of March, World Eucalypt Day, with *Eucalyptus erythrocorys* taking out the title this year. In second was *Eucalyptus regnans*, and third was *Corymbia citriodora*. Next time I think we should see how all the votes fall.

<https://www.eucalyptaustalia.org.au/eucalypt-of-the-year-2020/>

Below: The distinctive winner Illyarie (*Eucalyptus erythrocorys*). Photo credit: Eucalypt Australia

A new edition of EUCLID

An essential tool for eucalypt identification, the 4th edition of EUCLID was recently released. The LUCID based key includes descriptions for 934 species of eucalypts, including *Eucalyptus*, *Corymbia*, and *Angophora*. It is available online for free, or you can download it as an app on both Android and Apple platforms for \$19.95. It's the only app I've paid for.

Link to media release: <https://identic.com.au/blog/euclid-eucalypts-of-australia-fourth-edition-released/?fbclid=IwAR14r8oynE9VzEVRweeGAVH-siV-6bi9Nu6iifvGRNveUrQQ3pei6l6jB0l>

EUCLID online: <https://apps.lucidcentral.org/euclid/>

iTunes store: <https://apps.apple.com/au/app/euclid-eucalypts-of-australia/id1503451097>

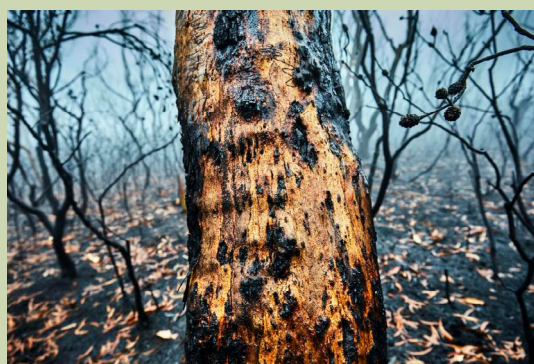
Google Play: <https://play.google.com/store/apps/details?id=com.lucidcentral.mobile.euclid>



South Australian herbarium blogs about the impact of bushfires on the state

Our friends at the State Herbarium of South Australia have been putting together a series of stories about the impact of the recent summer bushfires on the state. This particular post illustrates the utility of herbarium specimens for understanding how the bushfires have affected areas of high species richness or endemism.

<https://know.ourplants.org/fire/fire-blog-2-the-significance-of-the-2019-20-sa-bushfires/>



Repeated severe fires may put even the most fire-resilient species at risk

One of the more common and worrying rhetorics shared during the bush fire season was about how the Australian bush is built to withstand fire, needs fire, and will bounce back perfectly fine after fire, ignoring the frequency and intensity of fires we have been experiencing in the past ten years. This article reviews several papers studying the impacts of repeated, severe burns on eucalypt forests, and suggests that all-is-not-normal. In the Victorian high country, some sites with repeated burns experienced tree mortality of over 50% (in *Eucalyptus pauciflora*), near complete loss of *Eucalyptus delegatensis*, and decreased resprouting success.

<https://pursuit.unimelb.edu.au/articles/why-australia-s-severe-bushfires-may-be-bad-news-for-tree-regeneration.amp>

Left: Burned trunk in the bushfires earlier in 2020.
Picture credit: <https://pursuit.unimelb.edu.au>

Darren Crayn's TEDx: The Dark Matter of Biodiversity

Former ASBS president, Darren Crayn (James Cook University, Australian Tropical Herbarium) presented at a TEDx event at JCU, and spoke about taxonomy and what we do and don't know about the biodiversity of Australia and New Zealand. Well worth a watch, if only to learn a little more about *Geosiris australiensis*.

Link to the video: https://www.ted.com/talks/darren_crayn_the_dark_matter_of_biodiversity?fbclid=IwAR3GbGclZubOt6F-0SKSkc3El6D-aOX83HKt8Ncp47sWjOCN-3L7h_qorLJOI

Paper about *Geosiris australiensis*: <http://www.publish.csiro.au/sb/sb18028> (Joyce et al. 2019, *Australian Systematic Botany*)



Royal Botanic Gardens Sydney Science Seminars online

The RBG Sydney Seminar series, held at The Calyx in the heart of the Sydney Botanic Gardens, are now available online. These include both internal scientists and guest speakers. Talks are also streamed live through the RBG Sydney Facebook page. If you wish to receive announcements of (or be invited to present at) future seminars contact Hervé Sauquet at herve.sauquet@gmail.com.

<https://www.rbg Syd.nsw.gov.au/Science/Botanic-Gardens-Science-Seminar-Series>

SPNHC conference online

The Society For The Preservation Of Natural History Collections (SPNHC) conference is going to be held online this year. It is free to register, it will be held on Zoom, and there will be two different session blocks to cater for different time zones.

<https://www.eventbrite.com/e/spnhc-icom-nathist-2020-virtual-conference-tickets-103678569392>

Papers and publications

50 years of the Western Australian herbarium - *Nuytsia* special issue

What better way to celebrate 50 years of publishing new species than by publishing 50 new species in a year!

<https://florabase.dpaw.wa.gov.au/nuytsia/current>

A special issue on low-cost methods in plant science

Applications in Plant Sciences published a special issue with 11 papers focused on scientific research of plants with limited resources. Papers that may be of particular interest to the ASB crowd include strategies for reducing costs in target captures, ddRAD sequencing on herbarium specimens, and a protocol for chromosome counting (with videos!). All papers are open-access.

<https://bsapubs.onlinelibrary.wiley.com/doi/full/10.1002/aps3.11341>



Above: Hannah McPherson presenting at the RBG Sydney Seminar series. Photo credit: www.rbg Syd.nsw.gov.au/

BSA 2020 is going online

The Botanical Society of America conference was due to be held in Alaska in July this year, but will now be shifted entirely online. A new registration portal will be open soon.

<http://2020.botanyconference.org/>

A new family of angiosperms

It's not every day a new family of flowering plants is described. *Tiganophyton karasense* (Tiganophytaceae) is a small shrub from southern Namibia, that upon first glance was suspected to be a new species of *Salsola* (Amaranthaceae), but only after phylogenetic analysis were its relationships revealed to be with the Brassicales.

<https://www.mapress.com/j/pt/article/view/phytotaxa.439.3.1/39451>



Above: *Tiganophyton karasense*. Photo credit: W. Swanepoel

Many IUCN red list species have names that evoke negative emotions

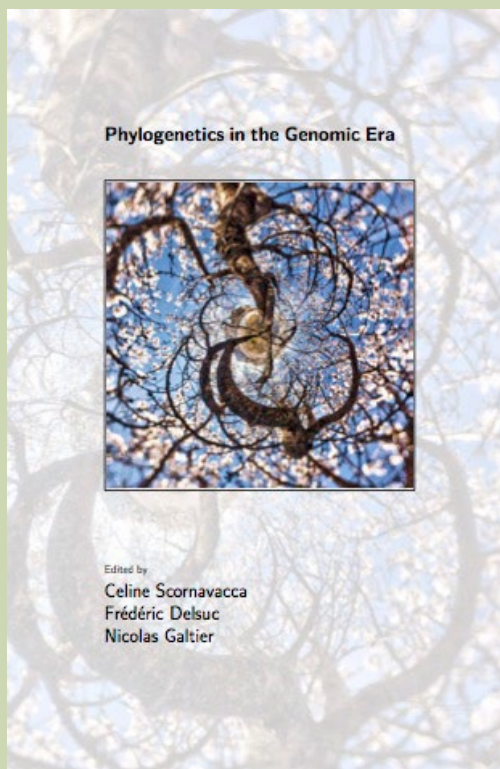
Gregg *et al.* (2020) performed a sentiment analysis by comparing IUCN red list species common names to databases that link words with human feelings, and their results may be useful when thinking about vernacular names for new taxa.

Link to paper: [Gregg *et al.* 2020, Human Dimensions of Wildlife](#)

Free book: Phylogenetics in the genomics era

If you are at all interested in phylogenetics, download this book now. It includes multiple chapters to ground oneself with phylogenetic theory, as well as 'How-to' chapters on several major phylogenetic tools, written by many of the pillars of the phylogenetics community. There is literally no reason to not have a copy.

Download the book: <https://hal.inria.fr/PGE/>



New 'Name that flower' book

'Name that flower' is an excellent companion resource for plant identification, and features information on plant reproduction, structure and function, and angiosperm classification. Descriptions of 46 families are accompanied by both line-drawings and coloured pages.

Buy the book: [Clarke & Lee \(2019\) Name that Flower. Melbourne University Press](#)

Marianne North's Australian paintings

This paper examines the English artist's paintings and writings together, to provide a narrative of the state of the Australian environment in the late nineteenth century, filtered through the themes of personal botanical discovery, colonial expansion and British imperialism.

Link to paper: [Dowe, J.L. \(2020\) Cunninghamia 20: 1–33 doi: 10.7751/cunninghamia.2020.20.001](#)

New edition of guide to botanical nomenclature

Plant Names is a guide to the use of scientific, commercial and common names for plants and the conventions for writing them, written by horticultural botanists Roger Spencer and Rob Cross at the Royal Botanic Gardens Victoria. This fourth edition is based on the recently updated *International Code of Nomenclature for Algae, Fungi, and Plants* and the *International Code of Nomenclature for Cultivated Plants*. It makes this technical information readily understandable to a range of readers, including botanists, publishers, professional horticulturists, nursery workers, hobby gardeners and anyone interested in plant names.

Buy the book: [Spencer & Cross \(2020\) Plant Names: A Guide to Botanical Nomenclature, 4th edn, CSIRO Publishing, Clayton.](#)

The newsletter

The ASBS newsletter keeps members informed of society events and news, and provides a platform for debate and discussion. The newsletter is published quarterly on the ASBS website and in print. Original articles, notes and letters (not exceeding ten published pages in length) are encouraged for submission by ASBS members.

Have an article or an idea for the newsletter?

Send it to Lizzy (Editor):
lizzy.joyce@my.jcu.edu.au,
or Alex (Associate Editor):
a.george@murdoch.edu.au

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Full page: \$200

Half page: \$100

Flyers: \$250

A 20% discount applies for regular advertisements. ASBS members are exempt from advertisement fees but not insertion costs for flyers (\$50). For advertising enquiries please contact the editor.

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The society

The Australasian Systematic Botany Society is an incorporated association of over 300 people with professional or amateur interest in botany. The aim of the society is to promote the study of plant systematics.

Membership is open to all interested in plant systematics. Members are entitled to attend general and chapter meetings, and to receive the ASBS *Newsletter*. Any person may apply for membership by filling in a membership application form available at <http://www.asbs.org.au/asbs/membership.html>, and forwarding it to the Treasurer. Subscriptions become due on 1 January each year.

The ASBS annual membership subscription is AUD \$45, and a concessional rate of AUD \$25 is offered to full-time students, retirees and unemployed people. Payment may be by credit card or by cheque made out to Australasian Systematic Botany Society Inc., and remitted to the Treasurer. All changes of address should be sent directly to the Treasurer as well.

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