



**BOTANIC
GARDENS
OF SYDNEY**

Research Centre for Ecosystem Resilience (ReCER)

PUBLICATIONS 2020 - 2021

Foreword

The Research Centre for Ecosystem Resilience (ReCER) is part of the Australian Institute for Botanical Science (AIBS) and it is based at the Royal Botanic Garden Sydney. It was founded in 2020 with a brief to develop innovative science and technology to investigate the factors impacting the distribution and assembly of plant species, and consequently inform the conservation and restoration of resilient ecosystems.

The ReCER team undertakes research and collaborates across multiple areas including genomics, landscape and conservation genetics, ecological restoration, climate modelling, flora biogeography, evolution, and microbiome diversity. The knowledge obtained from this research is disseminated in a number of different ways including reports, book chapters and academic papers. Here we bring together selected abbreviated abstracts of these publications for the 2020-2021 calendar years.

ReCER staff, students or research associate authors are indicated in bold.

2021

Conserving the genetic diversity of condemned populations: Optimizing collections and translocation

Jason Bragg, Sam Yap, Trevor Wilson, Enhua Lee and Maurizio Rossetto

Evolutionary Applications 14(5): 1225–1238.

DOI:10.1111/eva.13192

We consider approaches for conserving genetic diversity from plant populations whose destruction is imminent. We do this using SNP genotype data from two endangered species, *Pimelea spicata* and *Eucalyptus* sp. Cattai. For both species, we genotyped plants from a 'condemned' population and designed ex situ collections, characterizing how the size and composition of the collection affected the genetic diversity preserved. Consistent with previous observations, populations where genetic diversity was optimized captured more alleles than populations of equal size chosen at random. This benefit of optimization was larger when the propagation population was small. That is, small numbers of individuals (e.g., 20) needed to be selected carefully to capture a comparable proportion of alleles to optimized populations, but larger random populations (e.g., > 48) captured almost as many alleles as optimized populations. We then examined strategies for generating translocation populations based on the horticultural constraints presented by each species. In *P. spicata*, which is readily grown from cuttings, we designed translocation populations of different sizes, using different numbers of ramets from each member of propagation populations. We then performed simulations to predict the loss of alleles from these populations over 10 generations. Large translocation populations were predicted to maintain a greater proportion of source population alleles than smaller translocation populations, but this effect was saturated beyond 200 individuals. In *E. sp. Cattai*, we examined strategies to promote the diversity of progeny from a conservation planting scenario with 36 individuals. This included the optimization of the spatial arrangement of the planting, and supplementing the diversity of the condemned population with individuals from additional sites. In sum, we studied approaches for designing genetically diverse translocations of condemned populations for two species that require contrasting methods of propagation, illustrating the application of approaches that were useful in different circumstances.



Current status of *Phytophthora* in Australia

T. Burgess, J. Edwards, A. Drenth, T. Massenbauer, J. Cunnington, R. Mostowfzadeh-Ghalamfarsa, Q. Dinh, **E. Liew**, D. White, P. Scott, P.A. Barber, E. O'Gara, J. Ciampini, K.L. McDougall, and Y.P. Tan
Persoonia 47: 151–177.

DOI:10.3767/persoonia.2021.47.05

Among the most economically relevant and environmentally devastating diseases globally are those caused by *Phytophthora* species. In Australia, production losses in agriculture and forestry result from several well-known cosmopolitan *Phytophthora*

species and infestation of natural ecosystems by *Phytophthora cinnamomi* have caused irretrievable loss to biodiversity especially in proteaceous dominated heathlands. For this review, all available records of *Phytophthora* in Australia were collated and curated, resulting in a database of 7 869 records, of which 2 957 have associated molecular data. Australian databases hold records for 99 species, of which 20 are undescribed. Eight species have no records linked to molecular data, and their presence in Australia is considered doubtful. The 99 species reside in 10 of the 12 clades recognised within the complete phylogeny of *Phytophthora*. The review includes discussion on each of these species' status and additional information provided for another 29 species of concern. The first species reported in Australia in 1900 was *Phytophthora infestans*. By 2000, 27 species were known, predominantly from agriculture. The significant increase in species reported in the subsequent 20 years has coincided with extensive surveys in natural ecosystems coupled with molecular taxonomy and the recognition of numerous new phylogenetically distinct but morphologically similar species. Routine and targeted surveys within Australian natural ecosystems have resulted in the description of 27 species since 2009. Due to the new species descriptions over the last 20 years, many older records have been reclassified based on molecular identification. The distribution of records is skewed toward regions with considerable activity in high productivity agriculture, horticulture and forestry, and native vegetation at risk from *P. cinnamomi*. Native and exotic hosts of different *Phytophthora* species are found throughout the phylogeny; however, species from clades 1, 7 and 8 are more likely to be associated with exotic hosts. One of the most difficult challenges to overcome when establishing a pest status is a lack of reliable data on the current state of a species in any given country or location. The database compiled here for Australia and the information provided for each species overcomes this challenge. This review will aid federal and state governments in risk assessments and trade negotiations by providing a comprehensive resource on the current status of *Phytophthora* species in Australia.

AusTraits, a curated plant trait database for the Australian flora.

Daniel Falster, Rachael Gallagher *et al.* including **Jason Bragg, Robert Kooyman and Maurizio Rossetto.**

Scientific Data 8: 254.

[DOI:10.1038/s41597-021-01006-6](https://doi.org/10.1038/s41597-021-01006-6)

We introduce the AusTraits database - a compilation of values of plant traits for taxa in the Australian flora (hereafter AusTraits). AusTraits synthesises data on 448 traits across 28,640 taxa from field campaigns, published literature, taxonomic monographs, and individual taxon descriptions. Traits vary in scope from physiological measures of performance (e.g. photosynthetic gas exchange, water-use efficiency) to morphological attributes (e.g. leaf area, seed mass, plant height) which link to aspects of ecological variation. AusTraits contains curated and harmonised individual- and species-level measurements coupled to, where available, contextual information on site properties and experimental conditions. This article provides information on version 3.0.2 of AusTraits which contains data for 997,808 trait-by-taxon combinations. We envision AusTraits as an ongoing collaborative initiative for easily archiving and sharing trait data, which also provides a template for other national or regional initiatives globally to fill persistent gaps in trait knowledge.

Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic *Fusarium* that Includes the *Fusarium solani* Species Complex

David Geiser, Abdullah Al-Hatmi, *et al.* including **Edward Liew.**

Phytopathology 111: 1-64

[DOI:10.1094/PHYTO-08-20-0330-LE](https://doi.org/10.1094/PHYTO-08-20-0330-LE)

Scientific communication is facilitated by a data-driven, scientifically sound taxonomy that considers the end-user's needs and established successful practice. In 2013, the *Fusarium* community voiced near unanimous support for a concept of *Fusarium* that represented a clade comprising all agriculturally and clinically important *Fusarium* species, including the *F. solani* species complex (FSSC). Subsequently, this concept was challenged in 2015 by one research group who proposed dividing the genus *Fusarium* into seven genera, including the FSSC described as members of the genus *Neocosmospora*, with subsequent justification in 2018 based on claims that the 2013 concept of *Fusarium* is polyphyletic. Here, we test this claim and provide a phylogeny based on exonic nucleotide sequences of 19 orthologous protein-coding genes that strongly support the monophyly of *Fusarium* including the FSSC. We reassert the practical and scientific argument in support of a genus *Fusarium* that includes the FSSC and several other basal lineages, consistent with the longstanding use of this name among plant pathologists, medical mycologists, quarantine officials, regulatory agencies, students, and researchers with a stake in its taxonomy. In recognition of this monophyly, 40 species described as genus *Neocosmospora* were recombined in genus *Fusarium*, and nine others were renamed *Fusarium*. Here the global *Fusarium* community voices strong support for the inclusion of the FSSC in *Fusarium*, as it remains the best scientific, nomenclatural, and practical taxonomic option available.

FloraBank Guidelines Module 5: Seed sourcing.

Peter Harrison, Martin Breed, Linda Broadhurst, Margaret Byrne, Siegfried Krauss, **Marlien van der Merwe**, Melissa Miller and **Maurizio Rossetto**

In book: Florabank Guidelines - best practice guidelines for native seed collection and use (2nd edition). Florabank Consortium Australia.

<https://www.florabank.org.au/guidelines/?link=Module5>

Determining where seed should be sourced is among the primary decisions for ecological restoration projects. Local provenancing has been widely adopted, but alternative strategies address concerns associated with habitat fragmentation, maintaining or maximising genetic diversity, and climate change. The choice of provenance strategy depends on many factors, but the overarching objective is to pursue a seed sourcing strategy that delivers short- and long-term success in a changing environment. A generalised decision tree is provided for selecting a potential provenance given the state of the local provenance and the site being restored.



Molecular phylogeography reveals two geographically and temporally separated floristic exchange tracks between Southeast Asia and northern Australia

Elizabeth Joyce, Caroline Pannell, **Maurizio Rossetto**, **Sam Yap**, Kevin Thiele, **Peter D Wilson** and Darren Crayn

Journal of Biogeography 48(5): 1213-1227.

DOI: [10.1111/jbi.14072](https://doi.org/10.1111/jbi.14072)

Aim. Exchange of plant lineages between Australia and Southeast Asia has 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. To address this, we conducted a molecular phylogeographic case study to identify exchange tracks between Australia and Southeast Asia. **Location.** India, Southeast Asia, Australia and Pacific islands. **Taxon.** The widespread tropical monsoonal tree species *Aglaia elaeagnoidea* (Meliaceae). **Methods.** We conducted a DArTseq phylogeographic study of 141 herbarium and silica-dried samples sourced from across the range of *A. elaeagnoidea*. We analysed 176,331 single nucleotide polymorphisms (SNPs) across 90,456 loci using multivariate, admixture, genetic differentiation and coalescent methods to characterise phylogeographic and phylogenetic patterns. These analyses were considered in the context of an environmental niche model for the last glacial maximum. **Results.** Two exchange tracks were identified: one from New Guinea to Cape York Peninsula in north-east Australia, and a second from Timor-Leste to the Kimberley Plateau of north-west Australia. The Cape York Peninsula track is contemporary, characterised by ongoing genetic exchange, whereas the Kimberley Plateau track is historic, facilitated by multiple past exposures of the Arafura Shelf during the Pleistocene. Overall, we suggest that phylogeographic patterns of *A. elaeagnoidea* have resulted from a combination of repeated range expansion and contraction cycles concurrent with Quaternary climate fluctuations and stochastic dispersal events. **Main conclusions.** This study provides the first molecular phylogeographic evidence for two floristic exchange tracks between northern Australia and Southeast Asia. It also highlights the influence of Quaternary climate fluctuations on the complex biogeography of the region, and supports the idea that the Kimberley Plateau and Cape York Peninsula in northern Australia have separate biogeographic histories.

Cryptic diversity found in Didymellaceae from Australian native legumes

Elizabeth Keirnan, Yu Pei Tan, Matthew Laurence, **Allison Mertin**, **Edward Liew**, Brett Summerell, Roger Shivas

MycoKeys 78: 1-20.

DOI: [10.3897/mycokeys.78.60063](https://doi.org/10.3897/mycokeys.78.60063)

Ascochyta koolunga (Didymellaceae, Pleosporales) was first described in 2009 (as *Phoma koolunga*) and identified as the causal agent of *Ascochyta* blight of *Pisum sativum* (field pea) in South Australia. Since then *A. koolunga* has not been reported anywhere else in the world, and its origins and occurrence on other legume (Fabaceae) species remains unknown. Blight and leaf spot diseases of Australian native, pasture and naturalised legumes were studied to investigate a possible native origin of *A. koolunga*. *Ascochyta koolunga* was not detected on native, naturalised or pasture legumes that had leaf spot symptoms, in any of the studied regions in southern Australia, and only one isolate was recovered from *P. sativum*. However, we isolated five novel species in the Didymellaceae from leaf spots of Australian native legumes from commercial field pea regions throughout southern Australia. The novel species were classified on the basis of morphology and phylogenetic analyses of the internal transcribed spacer region and part of the RNA polymerase II subunit B gene region. Three of these species, *Nothophoma garlbiwalawarda* sp. nov., *Nothophoma naiawu* sp. nov. and *Nothophoma ngayawang* sp. nov., were isolated from *Senna artemisioides*. The other species described here are *Epicoccum djirangnandiri* sp. nov. from *Swainsona galegifolia* and *Neodidymelliopsis tinkyukuku* sp. nov. from *Hardenbergia violacea*. In addition, we report three new host-pathogen associations in Australia, namely *Didymella pinodes* on *S. artemisioides* and *Vicia cracca*, and *D. lethalis* on *Lathyrus tingitanus*. This is also the first report of *Didymella prosopidis* in Australia.



Ecology and Conservation of a Living Fossil: Australia's Wollemi Pine (*Wollemia nobilis*)

Berin Mackenzie, Steve Clarke, Heidi Zimmer, **Edward Liew**, Maureen Phelan, Catherine Offord, Lisa Menke, David Crust, **Jason Bragg**, Hannah Mcpherson, **Maurizio Rossetto**, David Coote, **Jia-Yee Yap**, Tony Auld.

In book: Imperilled: The Encyclopedia of Conservation.

DOI:10.1016/B978-0-12-821139-7.00188-4

The iconic Wollemi Pine (*Wollemia nobilis*) is a critically endangered Australian conifer and one of the world's rarest trees with only 46 mature individuals remaining in the wild. The species is regarded as a "living fossil" and was discovered on the brink of extinction following a natural historical decline. While its discovery has enabled crucial intervention for its long-term conservation, it has also created novel threats. *Wollemia nobilis* is facing extinction in the wild due to its highly restricted distribution, extremely small population size, and ongoing impacts from exotic pathogens, inappropriate fire regimes, unauthorized site visitation, and anthropogenic climate change. A highly successful, collaborative program combining in situ management, ecological research and monitoring with public education and ex situ conservation strategies, such as translocation and commercial cultivation, is enhancing the species' long-term survival. The extended longevity and slow growth and maturation of wild Wollemi Pine present unique challenges to effective in situ conservation, including the multidecadal timescales required to deliver certain conservation objectives. The continued success of the conservation program depends on strong forward planning, intergenerational commitment and collaboration, and ongoing public support.

Phylogeny of *Lantana*, *Lippia*, and Related Genera (Lantaneae: Verbenaceae)

Patricia Lu-Irving, Ana Bedoya, Fátima Salimena, Tânia Dos Santos Silva, Lyderson Vaccini, Cássia Bitencourt, Verónica Thode, Pedro Cardoso, Nataly O'Leary, and Richard Olmstead.

American Journal of Botany 108 (8): 1354–73.

DOI: [10.1002/ajb2.1708](https://doi.org/10.1002/ajb2.1708)

PREMISE: *Lantana* and *Lippia* (Verbenaceae) are two large Linnean genera whose classification has been based on associated fruit traits: fleshy vs. dry fruits and one vs. two seed-bearing units. We reconstruct evolutionary relationships and the evolution of the two fruit traits to test the validity of these traits for classification. **METHODS:** Previous studies of plastid DNA sequences provided limited resolution for this group. Consequently, seven nuclear loci, including ITS, ETS, and five PPR loci, were sequenced for 88 accessions of the *Lantana*/*Lippia* clade and three outgroups. **RESULTS:** Neither *Lantana* nor *Lippia* is monophyletic. *Burroughsia*, *Nashia*, *Phyla*, and several *Aloysia* species are included within the clade comprising *Lantana* and *Lippia*. We provide a hypothesis for fruit evolution and biogeographic history in the group and their relevance for classification. **CONCLUSIONS:** Fleshy fruits evolved multiple times in the *Lantana*/*Lippia* clade and thus are not suitable taxonomic characters. Several sections of *Lantana* and *Lippia* and the small genera are monophyletic, but *Lippia* section *Zappania* is broadly paraphyletic, making circumscription of genera difficult. *Lippia* sect. *Rhodolippia* is a polyphyletic group characterized by convergence in showy bracts. Species of *Lantana* sect. *Sarcolippia*, previously transferred to *Lippia*, are not monophyletic. The clade originated and diversified in South America, with at least four expansions into both Central America and the Caribbean and two to Africa. The type species of *Lantana* and *Lippia* occur in small sister clades, rendering any taxonomy that retains either genus similar to its current circumscription impossible.

Conserving Refugia: What Are We Protecting and Why?

Maurizio Rossetto and **Robert Kooyman**

Diversity 13(2): 67

DOI:10.3390/d13020067

Refugia play an important role in contributing to the conservation of species and communities by buffering environmental conditions over time. As large natural landscapes worldwide are declining and are increasingly threatened by extreme events, critical decision-making in biological conservation depends on improved understanding of what is being protected by refugia and why. We provide three novel definitions for refugia (i.e., persistent, future, and temporary) that incorporate ecological and evolutionary dynamics into a land management decision framework and are applicable across changing temporal and spatial settings. Definitions are supported by identification, core value, and management strategy criteria to assist short- and long-term decision-making. We illustrate these concepts using the World Heritage Gondwana Rainforests (WHGR) of eastern Australia, briefly exploring the spatial and temporal factors that can inform the development of conservation management strategies following the extreme fire events of 2019–2020. For the WHGR, available knowledge can be used to protect critical assets by recognizing and implementing buffer zones and corridor connections, and by undertaking emergency translocations of target species into safe areas that will act as future refugia. More broadly, we suggest that the identification and protection of ecological and evolutionary processes across varying temporal and spatial scales is central to securing improved biodiversity conservation outcomes.

A conservation genomics workflow to guide practical management actions

Maurizio Rossetto, Jia-Yee Samantha Yap, Jedda Lemmon, David Bain, Jason Bragg, Patricia Hogbin, Rachael Gallagher, Susan Rutherford, Brett Summerell and Trevor Wilson

Global Ecology and Conservation 26:e01492

DOI:10.1016/j.gecco.2021.e01492

Owing to decreasing costs and increased efficiency, it is now conceivable that conservation genomic information can be used to improve the effectiveness of recovery programs for many, if not most, threatened plants. We suggest that a simple genomic study be viewed as an initial step in conservation decision-making, as it informs long-term recovery efforts in various ways. We present biodiversity managers and conservation biologists with a simple, standardized workflow for genomic research that can guide efficient collection, analysis and application of genomic information across disparate threatened plants. Using two case studies, 'Banksia vincentia' and *Daphnandra johnsonii*, we demonstrate how a single round of genotyping by sequencing – a one-time cost – produces multiple directly applicable benefits, and how generating genomic information as early as possible can enhance conservation outcomes. We argue for a shift away from asking whether genomic information is needed or justified, and a shift towards consideration of the questions that need to be addressed. Such questions should aimed at cost-effectively guiding multiple practical aspects of a threatened plant's management plan. The workflow presented here should help relevant stakeholders design a sampling strategy that directly suits their questions and needs.

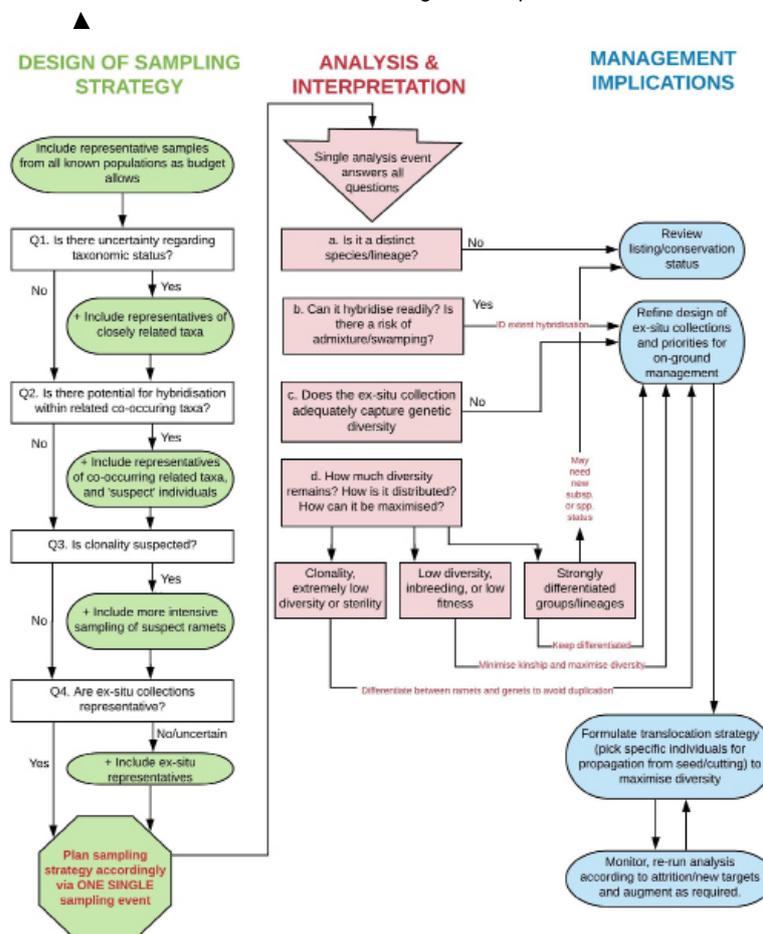
Looks can be deceiving: speciation dynamics of co-distributed *Angophora* (Myrtaceae) species in a varying landscape

Susan Rutherford, Justin Wan, Joel Cohen, Doug Benson, and Maurizio Rossetto

Evolution 75(2): 310-329.

DOI:10.1111/evo.14140

Understanding the mechanisms underlying species divergence remains a central goal in evolutionary biology. Landscape genetics can be a powerful tool for examining evolutionary processes. We used genome-wide scans to genotype samples from populations of eight *Angophora* species. *Angophora* is a small genus within the eucalypts comprising common and rare species in a heterogeneous landscape, making it an appropriate group to study speciation. We found *A. hispida* was highly differentiated from the other species. Two subspecies of *A. costata* (subsp. *costata* and subsp. *euryphylla*) formed a group, while the third (subsp. *leiocarpa*, which is only distinguished by its smooth fruits and provenance) was supported as a distinct pseudocryptic species. Other species that are morphologically distinct could not be genetically differentiated (e.g., *A. floribunda* and *A. subvelutina*). Distribution and genetic differentiation within *Angophora* were strongly influenced by temperature and humidity, as well as biogeographic barriers, particularly rivers and higher elevation regions. While extensive introgression was found between many populations of some species (e.g., *A. bakeri* and *A. floribunda*), others only hybridized at certain locations. Overall, our findings suggest multiple mechanisms drove evolutionary diversification in *Angophora* and highlight how genome-wide analyses of related species in a diverse landscape can provide insights into speciation.



Genetic guidelines for acquiring and maintaining collections for ex situ conservation.

Marlien van der Merwe, Maurizio Rossetto, Linda Broadhurst, David Coates.
In book: Plant Germplasm Conservation in Australia: strategies and guidelines for developing. Australian Network for Plant Conservation.
<https://www.anpc.asn.au/plant-germplasm/>

Phylogeography of the wide-host range panglobal plant pathogen *Phytophthora cinnamomi*

Shankar Shakya¹, Niklaus Grünwald, Valerie Fieland, Brian Kraus, Jerry Weiland, Cristiana Maia, André Drenth, David Guest, **Edward Liew**, Colin Crane, Tun-Tschu Chang, Chuen-Hsu Fu, Nguyen Minh Chi, Pham Quang Thu, Bruno Scanu, Eugenio Sanfuentes von Stowasser, Álvaro Durán, Marília Horta Jung, Thomas Jung
Molecular Ecology 30: 5164–5178.
<https://doi.org/10.1111/mec.16109>

Various hypotheses have been proposed regarding the origin of the plant pathogen *Phytophthora cinnamomi*. *P. cinnamomi* is a devastating, highly invasive soilborne pathogen associated with epidemics of agricultural, horticultural and forest plantations and native ecosystems worldwide. We conducted a phylogeographic analysis of populations of this pathogen sampled in Asia, Australia, Europe, southern and northern Africa, South America, and North America. Based on genotyping-by sequencing, we observed the highest genotypic diversity in Taiwan and Vietnam, followed by Australia and South Africa. Mating type ratios were in equal proportions in Asia as expected for a sexual population. Simulations based on the index of association suggest a partially sexual, semiclonal mode of reproduction for the Taiwanese and Vietnamese populations while populations outside of Asia are clonal. Ancestral area reconstruction provides new evidence supporting Taiwan as the ancestral area, given our sample, indicating that this region might be near or at the center of origin for this pathogen as speculated previously. The Australian and South African populations appear to be a secondary center of diversity following migration from Taiwan or Vietnam. Our work also identified two panglobal, clonal lineages PcG1-A2 and PcG2-A2 of A2 mating type found on all continents. Further surveys of natural forests across Southeast Asia are needed to definitively locate the actual center of origin of this important plant pathogen.

Allele Surfing and Holocene Expansion of an Australian Fig (*Ficus*—Moraceae)

Brendan Wilde, Susan Rutherford, Jia-Yee Samantha Yap, and Maurizio Rossetto
Diversity 13: 250.
[DOI:10.3390/d13060250](https://doi.org/10.3390/d13060250)

The creek sandpaper fig of southeastern Australia, *Ficus coronata* Spin, is culturally significant to Australian traditional owners who made use of the leaves to smooth timber and ate the fruit. The species is thought to have a long history on the continent, with some suggesting a Gondwanan origin. However, distributional patterns and overall ecology suggest a recent expansion across suitable habitats. We used landscape genomic techniques and environmental niche modelling to reconstruct its history and explore whether the species underwent a recent and rapid expansion along the east coast of New South Wales. Genomic analysis of 178 specimens collected from 32 populations throughout the species' New South Wales distribution revealed a lack of genetic diversity and population structure. Some

populations at the species' southern and western range limits displayed unexpected diversity, which appears to be the result of allele surfing. Field work and genetic evidence suggest a Holocene expansion which may have increased since European colonisation. We also present a novel method for detecting allele surfing—MAHF (minor allele at highest frequency).

2020

Spatial, Climate and Ploidy Factors Drive Genomic Diversity and Resilience in the Widespread Grass *Themeda triandra*.

Collin Ahrens, Elizabeth James, Adam Miller, Ferguson Scott, Nicola Aitken, Ashley Jones, **Patricia Lu-Irving**, Justin Borevitz, David Cantrill & Paul Rymer.
Molecular Ecology 29 (20): 387-3888.

<https://onlinelibrary.wiley.com/doi/10.1111/mec.15614>
Global climate change poses a significant threat to natural communities around the world, with many plant species showing signs of climate stress. Grassland ecosystems are not an exception, with climate change compounding contemporary pressures such as habitat loss and fragmentation. In this study, we assess the climate resilience of *Themeda triandra*, a foundational species and the most widespread plant in Australia, by assessing the relative contributions of spatial, environmental and ploidy factors to contemporary genomic variation. Reduced-representation genome sequencing on 472 samples from 52 locations was used to test how the distribution of genomic variation, including ploidy polymorphism, supports adaptation to hotter and drier climates. We explicitly quantified isolation by distance (IBD) and isolation by environment (IBE) and predicted genomic vulnerability of populations to future climates based on expected deviation from current genomic composition. We found that a majority (54%) of genomic variation could be attributed to IBD, while an additional 22% (27% when including ploidy information) could be explained by two temperature and two precipitation climate variables demonstrating IBE. Ploidy polymorphisms were common within populations (31/52 populations), indicating that ploidy mixing is characteristic of *T. triandra* populations. Genomic vulnerabilities were found to be heterogeneously distributed throughout the landscape, and our analysis suggested that ploidy polymorphism, along with other factors linked to polyploidy, reduced vulnerability to future climates by 60% (0.25-0.10). Our data suggests that polyploidy may facilitate adaptation to hotter climates and highlight the importance of incorporating ploidy in adaptive management strategies to promote the resilience of this and other foundation species.



Identifying evolutionary lineages in the *Elaeocarpus obovatus* complex: population genetics and morphometric analyses support a new subspecies, *Elaeocarpus obovatus* subsp. *umbratilis*, from northern Queensland, Australia

Yumiko Baba, **Maurizio Rossetto** and Darren Crayn

Australian Systematic Botany 33(4): 346-379

DOI:10.1071/SB18054

With the aim to solve long-standing problems of taxonomic delimitation within the *E. obovatus* species complex (*E. obovatus* G. Don, *E. arnhemicus* F. Muell., *E. sp.* Mt Bellenden Ker (L.J. Brass 18336) Qld Herbarium and *E. coorangooloo* J.F. Bailey & C.T. White), diversity and relatedness were assessed using a combined population genetics and morphometric approach among 181 and 102 individuals respectively. Simple sequence-repeat (SSR) markers were analysed with clustering methods, analysis of molecular variance (AMOVA) and STRUCTURE. The morphometric data were analysed using cluster and classification and regression tree (CART) methods. The morphometric and genetic analyses together resolve discrete groups corresponding to *E. arnhemicus*, *E. coorangooloo*, *E. obovatus* and *E. sp.* Mt Bellenden Ker. *Elaeocarpus arnhemicus* is clearly distinct from all other entities on most of the morphometric and genetic analyses. By contrast, *E. sp.* Mt Bellenden Ker and *E. obovatus* were not clearly separated from each other in many morphometric analyses, but can be distinguished clearly by the strongly curved pedicels in early bud and hairy ovary, and, to a lesser extent, by the frequent occurrence of two racemes per axil and cuneate leaf bases, and on the results of the genetic analyses. *Elaeocarpus coorangooloo* exhibits considerable genetic admixture with the other entities, but it is morphologically distinct. SSR profiles suggested that *E. arnhemicus* and *E. obovatus* may be tetraploid, whereas the other entities are diploid. This study has clarified the taxonomic limits of the currently recognised species *E. arnhemicus*, *E. obovatus* and *E. coorangooloo* and supports recognition of *E. sp.* Mt Bellenden Ker at subspecies rank, described herein as *E. obovatus* subsp. *umbratilis* Y. Baba & Crayn. A key to all taxa and revised accounts of *E. arnhemicus*, *E. obovatus* subsp. *obovatus* and *E. coorangooloo* are provided.

Optimizing the genetic composition of a translocation population: incorporating constraints and conflicting objectives.

Jason Bragg, Peter Cuneo, Ahamad Sherieff and **Maurizio Rossetto**

Molecular Ecology Resources 20(1): 54-65

DOI: 10.1111/1755-0998.13074

Translocations of threatened species can reduce the risk of extinction from a catastrophic event. For plants, translocation consists of moving individuals, seeds, or cuttings from a native (source) population to a new site. Ideally a translocation population would be genetically diverse and consist of fit founding individuals. In practice, there are challenges to designing such a population, including constraints on the availability of material, and tradeoffs between different goals. Here, we present an approach for designing a translocation population that identifies sets of founders that are optimized according to multiple criteria (e.g., genetic diversity), while also conforming to constraints on the representation of different founders (e.g., propagation success). It uses flexible inputs, including SNP genotypes, matrices of similarity between individuals, and vectors of phenotype data. We apply the approach to a critically endangered plant, *Hibbertia puberula* subsp. *glabrescens*

(Dilleniaceae), which was genotyped at thousands of SNP loci. The goals of minimizing genetic similarity among the founding individuals and maximizing genetic diversity were largely complementary: populations optimized for one of these criteria were near-optimal for the other. We also performed analyses in which we minimized genetic similarity among founding individuals while imposing selection (against hypothetical deleterious alleles, and against undesirable phenotypes, respectively), and here characterized sharp tradeoffs. This was useful in allowing the benefits of selection to be weighed against costs in terms of genetic similarity. In summary, we present an approach for designing a translocation population that allows flexible inputs, the imposition of realistic constraints, and examination of conflicting goals.

Evolutionary constraints and adaptation shape the size and colour of rainforest fruits and flowers at continental scale

Chloe EL Delmas, **Robert Kooyman** and **Maurizio Rossetto**

Global Ecology and Biogeography 29(5): 830-841

DOI:10.1111/geb.13065

Aim: Large-scale patterns in flower and fruit traits provide critical insights into selection processes and the evolutionary history of plant lineages. To isolate and identify the role of selective pressures including different plant-animal interactions, and the factors driving trait evolution, we investigate convergence and divergence between flower and fruit traits in shared environments. Location: Australia to Southeast Asia. Time period: Eocene (~45 My) to Present. Major taxa studied: Woody angiosperm rainforest species (2248 species, 133 families). Methods: Using a continental scale data set for all woody angiosperm species in the Australian rainforest (1816 free-standing and 432 climbing species) we compare the colour and size of fleshy fruits and flowers in relation to life form (trees/shrubs and vines), species biogeographic histories and origins (Sunda vs. Sahul), and bio-regional distributions. Results: Fleshy fruits in the Australian rainforest are mostly small, with a diversity of colours (<30mm; 81%), while flowers are mostly small (<10mm; 65%) and whitish (~80%). Compared to trees and shrubs, climbing species showed a higher proportion of red fleshy fruits, and large coloured flowers. Small whitish flowers were dominant across lineages from different biogeographic origins (Sunda-Sahul) and geographical regions, while both small and large fleshy fruits retained a range of disperser attractant colours. Main conclusions: Continental scale size and colour characteristics of flowers and fleshy fruits differed despite sharing environments with similar abiotic selective pressures through time. Plant-animal interactions including pollination and dispersal likely mediate different evolutionary outcomes for plant traits, and reflect both adaptation and evolutionary constraints.



Open Science principles for accelerating trait-based science across the Tree of Life

Rachael Gallagher, Daniel Falster *et al.* including **Maurizio Rossetto**.
Nature Ecology & Evolution 4: 294-303.

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Synthesizing trait observations and knowledge across the Tree of Life remains a grand challenge for biodiversity science. Species traits are widely used in ecological and evolutionary science, and new data and methods have proliferated rapidly. Yet accessing and integrating disparate data sources remains a considerable challenge, slowing progress toward a global synthesis to integrate trait data across organisms. Trait science needs a vision for achieving global integration across all organisms. Here, we outline how the adoption of key Open Science principles—open data, open source and open methods—is transforming trait science, increasing transparency, democratising access and accelerating global synthesis. To enhance widespread adoption of these principles, we introduce the Open Traits Network (OTN), a global, decentralised community welcoming all researchers and institutions pursuing the collaborative goal of standardising and integrating trait data across organisms. We demonstrate how adherence to Open Science principles is key to the OTN community and outline five activities that can accelerate the synthesis of trait data across the Tree of Life, thereby facilitating rapid advances to address scientific inquiries and environmental issues. Lessons learned along the path to a global synthesis of trait data will provide a framework for addressing similarly complex data science and informatics challenges. A decentralized community is introduced that aims to standardize and integrate species trait data across organismal groups, based on principles of Open Science.

Quantifying the distribution and threat of *Phytophthora cinnamomi* in New South Wales: implications for its management in natural vegetation

Keith McDougall, **Edward Liew**.

Cunninghamia 20: 153–181.

DOI:10.7751/cunninghamia.2020.20.008

Phytophthora cinnamomi is an oomycete (water mould) with a large host range. It infects plants through their roots and in some cases will kill them. The pathogen is readily dispersed in soil and water, over short distances by its swimming spores and over large distances by humans. While *Phytophthora cinnamomi* has been well-studied in other parts of Australia, its distribution and impact are poorly known in New South Wales (NSW). In the current study we compiled existing data on *Phytophthora cinnamomi* occurrence and filled spatial gaps in sampling. We found about 1000 records of *Phytophthora cinnamomi* presence in over 5000 tests of soil and root material, and collected a further 457 samples from areas where no sampling had previously been done. The resulting data set enabled modelling of *Phytophthora cinnamomi* habitat suitability using the software program MaxEnt with climate and soil spatial layers. We found that coastal areas and adjacent tablelands were most suitable for the pathogen, although some areas within that may be unsuitable because of soil properties. We then modelled assets (threatened species) potentially affected by *Phytophthora cinnamomi* to produce a layer of risk. Using projected climate layers, we found that habitat suitability and risk will decline in parts of northern NSW by 2070 but be amplified in the south. New susceptible species in places such as the Australian Alps are likely to be exposed to the pathogen in the future. We offer advice for managing *Phytophthora cinnamomi* in NSW. Management is difficult where the effects of this pathogen are often inconspicuous and its distribution is widespread. However, basic hygiene to limit spread to susceptible assets will have great benefit regardless.

The global abundance of tree palms.

Robert Muscarella, Thaise Emilio *et al.* including **Robert Kooyman**.
Global Ecology and Biogeography. 29 (9): 1495-1514.

DOI: 10.1111/geb.13123

Aim. Palms are an iconic, diverse and often abundant component of tropical ecosystems that provide many ecosystem services. Being monocots, tree palms are evolutionarily, morphologically and physiologically distinct from other trees, and these differences have important consequences for ecosystem services (e.g., carbon sequestration and storage) and in terms of responses to climate change. We quantified global patterns of tree palm relative abundance to help improve understanding of tropical forests and reduce uncertainty about these ecosystems under climate change. **Location.** Tropical and subtropical moist forests. **Time period.** Current. **Major taxa studied.** Palms (Arecaceae). **Methods.** We assembled a pantropical dataset of 2,548 forest plots (covering 1,191 ha) and quantified tree palm (i.e., ≥ 10 cm diameter at breast height) abundance relative to co-occurring non-palm trees. We compared the relative abundance of tree palms across biogeographical realms and tested for associations with palaeoclimate stability, current climate, edaphic conditions and metrics of forest structure. **Results.** On average, the relative abundance of tree palms was more than five times larger between Neotropical locations and other biogeographical realms. Tree palms were absent in most locations outside the Neotropics but present in $>80\%$ of Neotropical locations. The relative abundance of tree palms was more strongly associated with local conditions (e.g., higher mean annual precipitation, lower soil fertility, shallower water table and lower plot mean wood density) than metrics of long-term climate stability. Life-form diversity also influenced the patterns; palm assemblages outside the Neotropics comprise many non-tree (e.g., climbing) palms. Finally, we show that tree palms can influence estimates of above-ground biomass, but the magnitude and direction of the effect require additional work. **Conclusions.** Tree palms are not only quintessentially tropical, but they are also overwhelmingly Neotropical. Future work to understand the contributions of tree palms to biomass estimates and carbon cycling will be particularly crucial in Neotropical forests.

Pathogenic, Morphological, and Phylogenetic Characterization of *Fusarium solani* f. sp. *cucurbitae* Isolates From Cucurbits in Almería Province, Spain

Ana Pérez-Hernández, Liliana Rocha, Elena Porcel-Rodríguez, Brett Summerell, **Edward Liew** and Julio Gómez-Vázquez

Plant Disease 104: 1465–1476 .

DOI: 10.1094/PDIS-09-19-1954-RE

Fusarium solani f. sp. *cucurbitae* (syn. *Neocosmosporum cucurbitae*) is one of the most devastating soilborne pathogens affecting the production of cucurbits worldwide. Since its first detection in Almería Province in Spain in the spring of 2007, it has become one of the main soilborne pathogens affecting zucchini production. It has also been reported on melon, watermelon, and squash rootstocks in Spain, representing a high risk of dissemination in the area. The objectives of this study were to investigate the incidence and distribution of this disease in southeastern Spain and characterize isolates collected over 5 years. These strains were characterized on the basis of greenhouse aggressiveness assays on a range of cucurbit hosts, morphological characteristics, and elongation factor 1- and RNA polymerase II second largest subunit phylogenies. All pathogenic isolates were highly aggressive on zucchini plants, causing a high mortality rate a few weeks after inoculation. The rest of the cucurbit hosts showed differential susceptibility to the pathogen, with cucumber being the least susceptible. Plants belonging to other

families remained asymptomatic. Morphological characterization revealed the formation of verticillate monophialides and chlamydospores forming long chains, characteristics not described for this forma specialis. Phylogenetic studies of both the individual loci and combined datasets revealed that all pathogenic isolates clustered together with strong monophyletic support, nested within clade 3 in the *F. solani* species complex.

Survey, identification and genetic diversity of *Phytophthora capsici* causing wilt of chilli (*Capsicum annuum* L.) in Bhutan

Ganja Rai, **Edward Liew**, David Guest

European Journal of Plant Pathology 158: 655–665.

DOI: [10.1007/s10658-020-02108-4](https://doi.org/10.1007/s10658-020-02108-4)

Chilli (*Capsicum annuum* L.) is one of the most important crops in Bhutan, but currently production is seriously affected by a wilt disease. Although chilli wilt was first reported in Bhutan in 1995, the causal pathogen has never been formally identified. The aim of this study was to identify the causative agent of wilt epidemics on chilli in Bhutan and to investigate the morphological and genetic variations in the pathogen. A survey of the disease was conducted in all three chilli growing regions of Bhutan in 2018 and the pathogen isolated from 54 diseased plants. Morphological and PCR evidence identified the pathogen as *Phytophthora capsici* in 100% of the diseased plants. All isolates were of the A1 mating type. Four random amplified micro-satellite (RAMS) markers were employed to assess genetic variation among the 54 isolates of *P. capsici* collected. Genetic analysis showed 26 loci from all four primers and 65.4% of the isolates were polymorphic. Shannon's index of diversity (I) for the *P. capsici* isolates collected was 0.42, indicating that the pathogen population is highly clonal. These findings have significant implications for the development of sustainable disease management strategies including resistant genotypes in Bhutan.

Perceptions of Similarity Can Mislead Provenancing Strategies—An Example from Five Co-Distributed Acacia Species

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Diversity 12(8): 306

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Ecological restoration requires balancing levels of genetic diversity to achieve present-day establishment as well as long-term sustainability. Assumptions based on distributional, taxonomic or functional generalisations are often made when deciding how to source plant material for restoration. We investigate this assumption and ask whether species-specific data is required to optimise provenancing strategies. We use population genetic and environmental data from five congeneric and largely co-distributed species of Acacia to specifically ask how different species-specific genetic provenancing strategies are based on empirical data and how well a simple, standardized collection strategy would work when applied to the same species. We find substantial variability in terms of patterns of genetic diversity and differentiation across the landscape among these five co-distributed Acacia species. This variation translates into substantial differences in genetic provenancing recommendations among species (ranging from 100% to less than 1% of observed

genetic variation across species) that could not have been accurately predicted a priori based on simple observation or overall distributional patterns. Furthermore, when a common provenancing strategy was applied to each species, the recommended collection areas and the evolutionary representativeness of such artificially standardized areas were substantially different (smaller) from those identified based on environmental and genetic data. We recommend the implementation of the increasingly accessible array of evolutionary-based methodologies and information to optimize restoration efforts.

Phytophthora root rot: its impact in botanic gardens and on threatened species conservation

Brett Summerell, **Edward Liew**

Sibbaldia 18: 89-104.

<https://journals.rbge.org.uk/rbgesib/article/view/290/229>

Phytophthora root rot is one of the most devastating diseases of perennial plants worldwide, affecting plants in food production, amenity plantings and in natural ecosystems. The impact of these diseases in botanic gardens can be substantial and can affect how a site may be used for months and years ahead. Management is critically dependent on avoidance of the introduction of the pathogen and effective hygiene protocols are key to achieving this. Additionally, botanic gardens have a key role to play in protecting plants and enhancing conservation outcomes through surveillance, education and *ex situ* conservation programmes, as well as through the recognition that they can be critical as sentinel sites to detect new incursions of pests and diseases. The impact of several *Phytophthora* species on the in situ and ex situ management of the critically endangered *Wollemia nobilis* (Wollemi pine), which is highly susceptible to Phytophthora root rot, is used to highlight the need to ensure management of these pathogens is a critical component of threatened species recovery and management.

The susceptibility of seven threatened species to *Phytophthora gregata* and the aetiology of the disease caused by it

Justin Wan, Keith McDougall and **Edward Liew**

Australian Journal of Botany 68, 595–601 .

DOI: [10.1071/BT20062](https://doi.org/10.1071/BT20062)

Collar rot associated with the pathogen *Phytophthora gregata* T. Jung, M.J.C. Stukely & T. Burgess was recently observed on a subalpine wetland shrub, *Pimelea bracteata* Threlfall, in Kosciuszko National Park, New South Wales. The symptomatic collars of infected plants in the field may mean that *P. gregata* infects via the collar rather than through roots, as many other *Phytophthora* species do. In the glasshouse, we tested the susceptibility of seven threatened wetland species to *P. gregata*. Flooding and stem wound inoculations were applied as treatments. Based on symptoms and reisolations, we found that *Boronia deanei* ssp. *acutifolia* Duretto, *Correa baeuerlenii* F. Muell., *Pultenaea parrisiae* J.D. Briggs & Crisp and *Pimelea bracteata* were susceptible to *P. gregata*. These species were infected following both flood and stem inoculation, and all but *C. baeuerlenii* displayed very poor health under both treatments; stem wound inoculated *C. baeuerlenii* plants tended to be less affected than root inoculated plants. The pathogen could not be reisolated from the roots and collars of inoculated plants of *Callistemon purpurascens* S.M. Douglas & S. David, *Grevillea acanthifolia* ssp. *paludosa* Makinson & Albr., and *Pultenaea aristata* Sieber ex DC. This is the first test of the

susceptibility of eastern Australian native plants to *P. gregata* and the first to investigate the aetiology of the disease caused by this emerging threat. Given the growing body of evidence of the effects of a range of *Phytophthora* species on native plants, we suggest that the Key Threatening Process listing be broadened to include all destructive *Phytophthora* species.

Efficacy of chemical and biological agents against pepper blight (*Phytophthora capsici* Leonion) in East Asia: a meta-analysis of laboratory and field trial data

Justin Wan, Edward Liew

Journal of Plant Pathology 102: 835–842.

DOI: [10.1007/s42161-020-00519-0](https://doi.org/10.1007/s42161-020-00519-0)

Pepper blight caused by *Phytophthora capsici* Leonion is one of the most economically important plant diseases worldwide. In East Asia, pepper blight is a serious disease that is capable of decimating entire chili crops resulting in high economic losses. Management strategies undertaken to control the disease include the use of chemical and biological agents alongside soil fumigation and improved cultural practices. In recent years, biological agents are considered to be preferable to the use of chemicals due to the lower risk of resistance evolution and harm to the environment. Using meta-analysis, we synthesised the literature on the efficacy of different types of controls on pepper blight in East Asia. The studies were almost all conducted in Korea and China. We found that phenylamides (FRAC group 4), *Xenorhabdus* sp., *Pseudomonas* sp., and plant extracts were generally more effective against the pathogen in pepper; while soil amendments, *Bacillus* sp., *Chryseobacterium* sp., unidentified antagonists, and carboxylic acid amides (FRAC group 11) tend to be less effective. Overall, chemical agents were 50% more effective than biological agents. However, the benefits of using biological agents may outweigh the reduction in efficacy, particularly if used as a part of mixed treatments. Interestingly, control agents were 58% more effective on the disease in Korea compared to China, highlighting potential differences among pathogen genotypes or the resistance of cultivars to disease. Avenues for future research on biological forms of control and novel control strategies for plant pathogens are discussed.

Genus-level change in aggressiveness with continuous invasions: a phylogenetically-informed Bayesian quantile regression

Justin Wan, Edward Liew

Biological Invasions volume 22: 1931–1946.

DOI: [10.1007/s10530-020-02229-1](https://doi.org/10.1007/s10530-020-02229-1)

Phytophthora is a genus of oomycete plant pathogens consisting of numerous invaders of production and natural systems. To date, only few studies assessed how invasions change over time, and none have examined changes in invasive genera consisting of multiple species. With increasing globalisation, pathogens invade and adapt to new environments and hosts. After establishment, the aggressiveness of pathogens could decrease due to biotic and abiotic factors. Conversely, highly pathogenic genotypes should continuously replace less pathogenic ones. Here, we compiled the disease development data of *Phytophthora* species from published data and reports that span 105 years to assess how aggressiveness has changed over time. For each aggressiveness trial, we recorded the year of pathogen isolation and a measure of pathogenicity, as

well as local environmental variables. Phylogenetic multi-level quantile regression was used to analyse the relationships between aggressiveness and time across pathogen taxa under different environmental conditions. We found that aggressiveness decreased over time. This holds true if only the most commonly isolated taxa, and the most recent isolates, were considered. Highly aggressive pathogens from agriculture and natural ecosystems decreased significantly. However, pathogens from nurseries generally became more aggressive over time, particularly among the most common species. *Phytophthora* diseases overall are highly pathogenic and have potential to cause outbreaks, especially given that the common species were more aggressive under higher temperature variability. Through a multi-level approach, we uncover how the aggressiveness of pathogens changes globally at the genus-level with continuous emergence and invasion.

First example of hybridisation between two Australian figs (Moraceae)

Brendan Wilde, Susan Rutherford, Marlien van der Merwe, Megan Murray and Maurizio Rossetto

Australian Systematic Botany 33(5): 436–445.

DOI: [10.1071/SB19048](https://doi.org/10.1071/SB19048)

The chance discovery of an unusual *Ficus* specimen near Katherine in the Northern Territory prompted an investigation into hybridisation between two morphologically distinct endemic Australian sandpaper figs, *Ficus aculeata* A.Cunn. ex Miq. and *F. coronulata* Miq. In this study, genome-wide scans and morphological measurements were used to investigate the perceived hybridisation by using herbarium and freshly collected samples. Most of the putative hybrids displayed a wide variety of intermediate morphology and some individuals had characteristics consistent with the description of a third species, *F. carpentariensis* D.J.Dixon. Both genomic and morphometric results provided evidence of naturally occurring hybridisation events within *Ficus*. Additionally, the findings from this study showed possible taxonomic issues within the Northern Australian sandpaper figs that warrant further investigation.

Biotic exchange leaves detectable genomic patterns in the Australian rain forest flora

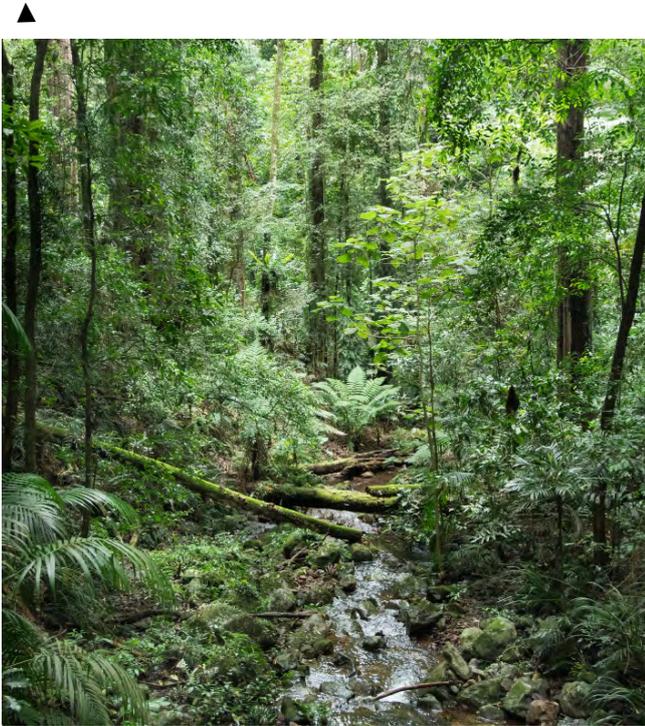
Sam Yap, Marlien M van der Merwe, Andrew Ford, Robert James Henry and Maurizio Rossetto

Biotropica 52(4): 627–635.

DOI: [10.1111/btp.12776](https://doi.org/10.1111/btp.12776)

The movement (or invasion) of plant lineages from Sunda (the Malay Archipelago) into Sahul (mainland Australia) has resulted in a present-day Australian rain forest flora of mixed ancestries. Floristic integration increased during the Quaternary when continental vegetation was subjected to recurrent expansion/contraction cycles. To date, this expansion history has yet to be investigated through multi-species, landscape-level genetic analyses within tropical Northern Australia, presumably the main point of contact for Sunda lineages. Here, we characterize and compare the dynamics of 53 species of Sunda and Sahul ancestry co-distributed across the Australian Tropics and Subtropics. We use whole chloroplast genomic datasets to obtain comparable measures of species-level diversity and estimate community dynamics through time across multiple rain forest sites. Unlike Sahul-derived species, Sunda-derived species show consistently low genomic diversities, with recent accumulation rates for Sunda species being detected across all sites, confirming recent arrival and expansion across eastern Australia. A subset of

Sunda-derived species with continental distributions consistently exhibited highest diversity at the most northerly site sampled, suggesting north to south colonization processes. The same species, however, differed in the levels of genomic differentiation between the Tropics and Subtropics, suggesting that continental expansion occurs at different temporal scales, with some species experiencing a northern time lag before a southern expansion along the east coast of Australia.



Unpublished reports

Conservation genomics of *Rhodamnia rubescens* and *Rhodomyrtus psidioides* in support of management. March 2022

Conservation genomics of *Pittosporum* sp. Coffs Harbour. Phase 1: September 2021, Phase 2: March 2022

Conservation genomics of *Syzygium paniculatum* Part 1: Population structure and reproductive patterns. October 2021

Conservation genomics of *Eidothea hardeniana* in support of management and translocation activities. December 2021

Conservation genomic project on *Caesia parviflora* var. *minor*. Part 1: November 2021

Fontainea oraria conservation genomics report. October 2021

Conservation genomics of *Persoonia pauciflora* in support of management and translocation activities. June 2021

Conservation genomics of *Zieria covenyi* in support of management and translocation activities. December 2020

Conservation genomics of *Prostanthera densa* and *P. marifolia*: species status, management and translocation advice. November 2020

Conservation genomics of *Astrotricha crassifolia* in support of management and translocation activities. October 2020

Conservation genetics of *Uromyrtus australis* (Peach Myrtle): species status, management and translocation advice. January 2020