

Research Centre for Ecosystem Resilience (ReCER)

Publications 2023

Foreword

The Research Centre for Ecosystem Resilience (ReCER) at the Botanic Gardens of Sydney uses innovative science and technology to investigate the factors impacting the distribution and assembly of plant species and informs 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 our research is disseminated in several different ways including academic papers, reports, book chapters and blog posts. Here we bring together abstracts of publications from the 2023 calendar year, including peer-reviewed publications led or co-authored by the ReCER team. ReCER staff, students or research associate authors are indicated in bold.

Many of our publications are open access and can be downloaded from the links provided below. Other publications and unpublished reports can be requested from the authors. Meet the ReCER team and subscribe to our quarterly e-Newsletter at <https://www.botanicgardens.org.au/recer>

Peer-reviewed publications

Reproductive characteristics, population genetics, and pairwise kinship inform strategic recovery of a plant species in a fragmented landscape.

Chantelle Doyle, Jia-Yee Samantha Yap, Jason Bragg, Maurizio Rossetto, Andrew Orme, and Mark Ooi

Conservation Science and Practice 4 (4) e12910

<https://doi.org/10.1111/csp2.12910>

Population genetics and understanding of mating systems provide fundamental information for conservation planning. Pairing these methods is a powerful tool in the study of threatened species, however, they are rarely applied in concert. We examined the mating system and used molecular genetics to measure pairwise kinship and the potential for inbreeding in *Hibbertia spanantha*, a critically endangered long-lived shrub endemic to the Sydney Basin, Australia, as a model for conservation planning of species in highly fragmented populations. In situ hand pollination experiments demonstrated that the species is preferentially outcrossing, with limited ability to self-pollinate (either autogamously or geitonogamously). Although population genetics confirmed high levels of kinship and clonality, there is currently enough population heterozygosity for successful open pollination, primarily through buzz pollination by Sweat Bees (*Lasioglossum [Chilalictus]*). High levels of clonality and population kinship in one population may be the cause of reduced fitness, identified because our outcrossing pollination treatment produced significantly more seeds with greater viability and seed mass than the open treatments. Differences in weight of filled (viable) seeds were identified between populations, although not treatments, where clonal dominance may be swamping pollinator foraging activities. Identification of species mating system, population reproductive capacity, and impacts of fragmentation on population genetic health provides a robust basis for strategic planning and conservation of this critically endangered species, including establishment of an ex situ population and genetic rescue through population augmentation. These methods are easily applicable and particularly relevant to other plant species with small populations or those occurring in fragmented systems.



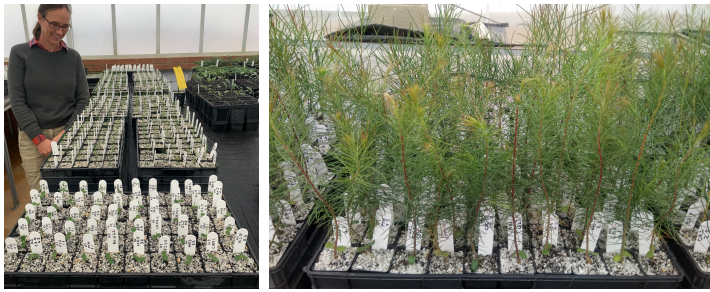
The efficacy of a range of hygiene measures for boot cleaning to protect natural vegetation from *Phytophthora cinnamomi*.

Edward Liew, Maureen Phelan & Keith McDougall

Scientific Reports. 13. 5825

<https://doi.org/10.1038/s41598-023-32681-7>

Phytophthora cinnamomi is an oomycete found in the soil and capable of invading the roots of a wide range of host plants globally, potentially killing them and affecting the ecosystems they inhabit. This pathogen is often inadvertently dispersed in natural vegetation on the footwear of humans. A range of equipment is often provided or recommended to be carried for cleaning footwear in places where *P. cinnamomi* poses a threat to biodiversity. These are typically a brush for mechanically removing soil and/or a disinfectant for killing the pathogen. Despite their widespread use, to our knowledge, the majority of hygiene measures have not been experimentally tested for their efficacy. In the current study, we tested whether two types of brush and the two most widely used disinfectants (70% methylated spirits and benzalkonium chloride) were effective in removing the pathogen from boots. We tested the brushes and disinfectants in two soil types and two moisture levels. All hygiene measures were found to be better than doing nothing, although some were only effective with sandy or dry soils. Benzalkonium chloride was largely ineffective as a spray but highly effective when used in a footbath. Brushing did not improve cleaning when used with 70% methylated spirits. None of the hygiene measures was completely effective for cleaning boots that had been in wet loamy soil. Our findings have important implications for management of this threat because some recommended hygiene practices are not doing what they claim.



Capturing Genetic Diversity in Seed Collections: An Empirical Study of Two Congeners with Contrasting Mating Systems.

Patricia Lu-Irving, Jason G. Bragg, Maurizio Rossetto, Kit King, Mitchell O'Brien and Marlien van der Merwe

Plants 12(3) 522

<https://doi.org/10.3390/plants12030522>

Plant mating systems shape patterns of genetic diversity and impact the long-term success of populations. As such, they are relevant to the design of seed collections aiming to maximise genetic diversity (e.g., germplasm conservation, ecological restoration). However, for most species, little is known empirically about how variation in mating systems and genetic diversity is distributed. We investigated the relationship between genetic diversity and mating systems in two functionally similar, co-occurring species of *Hakea* (Proteaceae), and evaluated the extent to which genetic diversity was captured in seeds. We genotyped hundreds of seedlings and mother plants via DArTseq, and developed novel implementations of two approaches to inferring the mating system from SNP data. A striking contrast in patterns of genetic diversity between *H. sericea* and *H. teretifolia* was revealed, consistent with a contrast in their mating systems. While both species had mixed mating systems, *H. sericea* was found to be habitually selfing, while *H. teretifolia* more evenly employed both selfing and outcrossing. In both species, seed collection schemes maximised genetic diversity by increasing the number of maternal lines and sites sampled, but twice as many sites were needed for the selfing species to capture equivalent levels of genetic variation at a regional scale.

Integrating seed microbiome knowledge into restoration and *ex situ* conservation of native Australian plants.

Allison Martin, Merize Philpott, Linda Blackall, Kris French, Edward Liew and Marlien M. van der Merwe

Australian Journal of Botany 71(7) 379–394.

<https://doi.org/10.1071/BT22109>

Context: Seeds harbour a diversity of microbes, which in some plants aid with germination and establishment. Seeds form a critical part in the lifecycle of plants and a role in many conservation and restoration activities. Aims: Because this is an emerging field in seed biology, we aim to highlight the key research gaps of interest to seed on the basis of restoration and *ex situ* conservation. Methods: We identify knowledge gaps associated with the seed endophytic microbiome of native Australian plants through undertaking a literature review. Additionally, culturing methods were used to identify the fungal seed endophytes of five native Australian species. Key results: We identified a diversity of taxa within the native seed and show three taxa that are common to all study hosts. Sampling seed from additional hosts at a site and additional sites of a host species showed new fungal diversity. Our literature review showed that little information is available on native seed microbiomes and we identified four key areas where research gaps exist, linking with seed-based restoration practices. Conclusions: We provide evidence that there is a complex and diverse seed microbiome within some Australian native plants and suggest ways that it could be integrated into restoration and conservation practices. Implications: We propose that by taking into consideration the presence of a seed microbiome and its potential impacts on plant health, seed microbiomes could be used as one method to restore microbial diversity into an ecosystem and to contribute to the seedling microbiome and plant health at restored sites.

Maintaining separate maternal lines increases the value and applications of seed collections.

Marlien M. van der Merwe, Jason Bragg, Richard Dimon, Patrick Fahey, Patricia Hogbin, Patricia Lu-Irving, Allison Martin, Maurizio Rossetto, Trevor Wilson and Jia-Yee Samantha Yap

Australian Journal of Botany 71(7), 406–419

<https://doi.org/10.1071/BT22136>

Context: Given the effort and resources that go into collecting and maintaining seed collections, it is crucial that we maximise their usefulness. Conservation, restoration and research rely heavily on good quality collections in order to establish new populations, create habitat, minimise extinction and address scientific questions. Aims: Although seed viability, excellent metadata and genetic representativeness make for good quality collections, we provide 10 detailed reasons why the maintenance of separate maternal lines further increases the quality and usefulness of seed collections. Key results: Maternal line seed collections can accommodate new information, this is especially important given the increasing longevity of seed collections. For example, maintaining separate maternal lines facilitates accommodation of taxonomic changes, minimises the impact of erroneous plant identifications, and facilitates separation of polyploid races, hybrids and inappropriate lineages. Separate maternal line collections also facilitate better estimates of the genetic diversity captured, and consequently better inform conservation translocations and the establishment of conservation gardens and seed orchards. Separate maternal line collections can also expedite breeding for specific traits, such as disease resistance or other selective challenges that impact on biodiversity conservation. New seed microbiome data show how only some maternal lines contain pathogenic fungi, reminding seed collectors and collections managers that contamination can be better contained by keeping each maternal line separate. Conclusions and implications: Maintaining separate maternal lines is a simple and effective way to increase the value of seed collections for multiple applications.



Applying simple genomic workflows to optimise practical plant translocation outcomes.

Maurizio Rossetto, Jason Bragg, Dianne Brown, Marlien van der Merwe, Trevor Wilson & Jia-Yee Samantha Yap

Plant Ecology 224, 8030816

<https://doi.org/10.1007/s11258-023-01322-4>

Translocation is an important conservation tool for reducing the probability of extinction of threatened plants. It is also becoming an increasingly common management practice, as habitats are destroyed and climate change pushes more plants beyond the limits of their tolerances. Here we outline the case for informing translocations with dedicated genomic data. We begin by describing principles for using genomic and genetic approaches to enhance the efficiency and success of translocation actions. This includes ensuring that translocated populations are adaptively representative, diverse, and composed (to the greatest possible extent) of unrelated individuals. We then use two Australian case studies to illustrate how these principles have been applied in practice and in a resource-efficient way. For *Prostanthera densa*, we describe how genomic data have quantitatively informed complex decisions, such as whether, and how extensively, to mix individuals from spatially isolated populations in translocated populations. For *Fontainea oraria*, genomic data have been used during post-translocation monitoring to confirm that newly established populations incorporate and recombine the little diversity that remained in wild individuals. Overall, we illustrate how a simple workflow can support the development and planning of genomic studies and translocation activities in tandem. In order to ensure greater adoption of translocation genomic workflows, funding bodies in charge of biodiversity management and conservation must direct the necessary resources towards them.

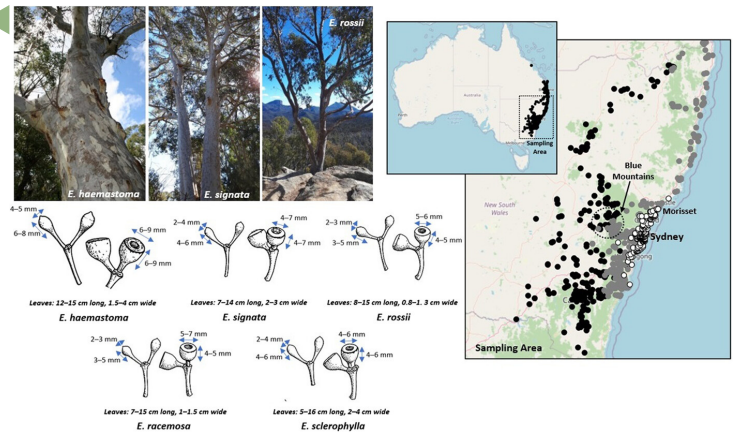
Where to draw the boundaries? Using landscape genomics to disentangle the scribbly gum species complex.

Susan Rutherford, Maurizio Rossetto, Jason Bragg & Justin Wan

American Journal of Botany 110(11): e16245.

<https://doi.org/10.1002/ajb.216245>

Premise: Species delimitation is an integral part of evolution and ecology and is vital in conservation science. However, in some groups, species delimitation is difficult, especially where ancestral relationships inferred from morphological or genetic characters are discordant, possibly due to a complicated demographic history (e.g., recent divergences between lineages). Modern genetic techniques can take into account complex histories to distinguish species at a reasonable cost and are increasingly used in numerous applications. We focus on the scribbly gums, a group of up to five closely related and morphologically similar "species" within the eucalypts. Methods: Multiple populations of each recognized scribbly gum species were sampled over a wide region across climates, and genomewide scans were used to resolve species boundaries. Results: None of the taxa were completely divergent, and there were two genetically distinct entities: the inland distributed *Eucalyptus rossii* and a coastal conglomerate consisting of four species forming three discernible, but highly admixed groups. Divergence among taxa was likely driven by temporal vicariant processes resulting in partial separation across biogeographic barriers. High interspecific gene flow indicated separated taxa reconnected at different points in time, blurring species boundaries. Conclusions: Our results highlight the need for genetic screening when dealing with closely related taxonomic entities, particularly those with modest morphological differences. We show that high-throughput sequencing can be effective at identifying species groupings and processes driving divergence, even in the most taxonomically complex groups, and be used as a standard practice for disentangling species complexes.



Seeing the forest through the trees: applications of species distribution models across an Australian biodiversity hotspot for threatened rainforest species of *Fontainea*.

Aaron Brunton, Gabriel Conroy, David Schoeman, Maurizio Rossetto, & Steven Ogbourne

Global Ecology and Conservation 42: e02376.

<https://doi.org/10.1016/j.gecco.2023.e02376>

Southern *Fontainea* (*Fontainea australis*) and Coastal *Fontainea* (*F. oraria*) are two closely-related, rare plant species endemic to the subtropical rainforests of central, eastern Australia. Both species have threatened conservation status, with their contemporary and projected distribution poorly known. We aimed to use species distribution models (SDMs) to identify (1) the potential range under current conditions, (2) suitable habitat area conserved in protected areas and (3) responses under future environmental conditions of the species. Using a presence-pseudo-absence approach, and a set of bioclimatic variables, combined with topographic factors, we modelled the spatial dynamics of Southern *Fontainea* and Coastal *Fontainea*. We present comparisons among regression (GLM) and Random Forest (RF) SDMs for current and projected future conditions under low (SSP 1-2.6) and high (SSP 5-8.5) emission scenarios for the period 2081-2100 from an ensemble of three CMIP6 climate models. On-ground surveys verified the contemporary distribution of Southern *Fontainea* across the study extent. GLM-and RF-based models identified similar areas of suitable habitat under current conditions, but both models indicated that less than half of the suitable Southern *Fontainea* habitat is under protected tenure. GLM-based SDMs suggest an expansion of suitable areas of Southern and Coastal *Fontainea* under both low-and high-emission climate projections. By contrast, RF-based SDMs indicated a moderate increase of suitable habitat under future climate projections. The steep slopes and gullies of the mountain ranges, which span the Queensland and New South Wales border of central, eastern Australia, seem likely to provide long-term, stable climate refugia for Southern *Fontainea*. Models generated under current conditions identified novel areas that could support undiscovered populations of Southern and Coastal *Fontainea*. These findings have significant conservation implications for the critically endangered Coastal *Fontainea*, which is projected to lose suitable habitat under a high-emission climate

Recognising Indigenous plant-use histories for inclusive biocultural restoration.

Emilie Ens, Maurizio Rossetto and Oliver Costello

Trends in Ecology & Evolution. 38 (10) 896-898

<https://doi.org/10.1016/j.tree.2023.06.009>

Indigenous Peoples have manipulated environments and species for millennia. However, restoration science often overlooks ancient human plant dispersal, niche construction, and selection pressures that may have resulted in plant 'cultural traits'. Concerted efforts to acknowledge Indigenous plant-use histories in restoration could help to abate the coextinction of species and cultures.

Taxonomic re-circumscriptions in the *Aglaia elaeagnoidea* complex (Meliaceae).

Elizabeth Joyce, Darren Crayn, Maurizio Rossetto, Jia-Yee Samantha Yap, Kevin Thiele and CM Pannell

Blumea Journal of Plant Taxonomy & Plant Geography 68: 26-38

<https://doi.org/10.3767/blumea.2023.68.01.02>

Aglaia is the most widespread and species-rich genus in Meliaceae, comprising 124 species. *Aglaia elaeagnoidea* has presented a long standing dilemma for taxonomists; it is highly morphologically and ecologically variable, and has a range extending across India, South east Asia, Australia and islands of the western Pacific Ocean. Previous work has examined molecular variation in the eastern part of the species 'range'; however, molecular variation in the western half of its distribution remained uncharacterised, precluding taxonomic resolution of the complex. In this study, we used DArT-seq analysis to investigate genetic structure in *A. elaeagnoidea* from India, Sri Lanka, Bangladesh, Thailand, Java and Bali. We find a strong genetic disjunction between Sri Lanka and Bangladesh, suggesting that western *A. elaeagnoidea* comprises two taxa. On the basis of these results, in combination with morphology and previous molecular work on eastern *A. elaeagnoidea*, we resolve *A. elaeagnoidea* into three species, retaining *A. elaeagnoidea* for the eastern (type) species, and reinstating *A. wallichii* for a species in Bangladesh, Thailand, Java and Bali, and *A. roxburghiana* for a species occurring in India and Sri Lanka. We provide descriptions for each taxon and a key to the species, thereby resolving a previously difficult species group in a notoriously complex genus.

Variation in leaf functional and plant defence traits of introduced *Eucalyptus* species across environmental gradients in their new range in Southern China.

Hui Liu, **Susan Rutherford**, **Justin Siu Hung Wan**, Jinhui Liu, Jin Zhang, Muhammad Rahil Afzal, Daolin Du and **Maurizio Rossetto**

Forests 14(5) 936.

<https://doi.org/10.3390/f14050936>

Due to the rapid development of China's economy, the demand for wood is steadily increasing. *Eucalyptus* species have been introduced in large quantities because of their fast growth, strong adaptability, and wide utility. To understand the phenological changes in introduced *Eucalyptus* in its new range, we carried out a field investigation to examine leaf functional and chemical defense traits of three introduced species (*E. saligna*, *E. grandis* and *E. robusta*) over latitudinal and altitudinal gradients in southern China. We sampled multiple stands of each species, and measured the leaf physical characteristics (e.g., leaf width, leaf thickness, and specific leaf area [SLA]), leaf nitrogen (N) and phosphorus (P) content, and phenolic compounds. We found that many functional traits (e.g., leaf size and thickness) decreased at lower latitudes, especially in *E. grandis*, possibly to reduce heat and water loss under higher temperatures. In *E. grandis*, we found that leaf P was lower at higher latitudes and altitude, and phenolics increased with elevation, while in *E. robusta*, both leaf N and P decreased with altitude. These findings suggested that both species were more conservative in resource allocation, with *E. grandis* possessing enhanced chemical defenses in response to the conditions experienced at higher elevations. In addition, we found the tree populations at the northern range limit of *E. robusta* had lower SLA, suggesting a more conservative growth strategy. In contrast, small populations in the northern part of the ranges of *E. grandis* had higher SLA, indicating range expansion at the edge of the species' geographic distribution. Overall, it is particularly important to consider intraspecific trait differences across wide geographic areas when studying the spread of invasive species in the new range.

Dispersal of *Phytophthora* species by off-road vehicles in New South Wales

Keith McDougall and **Edward Liew**

Australasian Plant Pathology 53(1)

DOI:10.1007/s13313-023-00961-5

Off-road vehicles are potential vectors for the spread of destructive plant pathogens such as *Phytophthora cinnamomi*. However, the retention of *Phytophthora* species in soil on vehicles used off-road does not appear to have been assessed empirically. We sampled soil from 22 off-road vehicles used in conservation management in New South Wales and tested samples for the presence of *Phytophthora* species. Two species (*P. cryptogea* and *P. aff. alticola*) were detected from three vehicles. Two of these three vehicles were regarded as being clean externally and had not been used off-road for more than one week. *Phytophthora* species can therefore survive in small amounts of soil on vehicles for extended periods, potentially facilitating the spread of these destructive pathogens. Cleaning is required of management vehicles entering areas of high conservation value vegetation to minimise the risk of spreading *Phytophthora* species. However, research is needed to find the most effective methods for removing soil

Phylogenomics reveals extreme gene tree discordance in a lineage of dominant trees: hybridization, introgression, & incomplete lineage sorting blur deep evolutionary relationships despite clear species groupings in *Eucalyptus* subgenus *Eudesmia*

Todd McLay, Rachael Fowler, **Patrick Fahey**, et al.

Molecular Phylogenetics and Evolution 187, 107869

DOI: <https://doi.org/10.1016/j.ympev.2023.107869>

Eucalypts are a large and ecologically important group of plants on the Australian continent, and understanding their evolution is important in understanding evolution of the unique Australian flora. Previous phylogenies using plastome DNA, nuclear-ribosomal DNA, or random genome-wide SNPs, have been confounded by limited genetic sampling or by idiosyncratic biological features of the eucalypts, including widespread plastome introgression. Here we present phylogenetic analyses of *Eucalyptus* subgenus *Eudesmia* (22 species from western, northern, central and eastern Australia), in the first study to apply a target-capture sequencing approach using custom, eucalypt-specific baits (of 568 genes) to a lineage of *Eucalyptus*. Multiple accessions of all species were included, and target-capture data were supplemented by separate analyses of plastome genes (average of 63 genes per sample). Analyses revealed a complex evolutionary history likely shaped by incomplete lineage sorting and hybridization. Gene tree discordance generally increased with phylogenetic depth. Species, or groups of species, toward the tips of the tree are mostly supported, and three major clades are identified, but the branching order of these clades cannot be confirmed with confidence. Multiple approaches to filtering the nuclear dataset, by removing genes or samples, could not reduce gene tree conflict or resolve these relationships. Despite inherent complexities in eucalypt evolution, the custom bait kit devised for this research will be a powerful tool for investigating the evolutionary history of eucalypts more broadly.

The influence of cone age & urbanisation on the diversity & community composition of culturable seed fungal endophytes within native Australian *Banksia ericifolia* L.f. subsp. *ericifolia*.

Merize Philpott, **Edward Liew**, **Marlien van der Merwe**, **Allison Mertin** and Kristine French

Journal of fungi 9, 706

<https://doi.org/10.3390/jof9070706>

Seed fungal endophytes play a crucial role in assisting the overall health and success of their host plant; however, little is known about the factors that influence the diversity and composition of these endophytes, particularly with respect to how they change over time and within urban environments. Using culturing techniques, morphological analyses, and Sanger sequencing, we identified the culturable seed fungal endophytes of *Banksia ericifolia* at two urban and two natural sites in Sydney, New South Wales, Australia. A total of 27 Operational Taxonomic Units were obtained from 1200 seeds. Older cones were found to contain, on average, more colonised endophytes than younger cones. Species richness was also significantly influenced by cone age, with older cones being more speciose. Between urban and natural sites, the overall community composition did not change, although species richness and diversity were greatest at urban sites. Understanding how these endophytes vary in time and space may help provide an insight into the transmission pathways used and the potential role they play within the development and survival of the seed. This knowledge may also be crucial for restoration purposes, especially regarding the need to consider endophyte viability in ex situ seed collection and storage in seed-banking practices.

Eucalyptus cryptica (Myrtaceae): a critically endangered new species

Trevor Wilson, Susan Rutherford, Jia-Yee Samantha Yap, Steven Douglas, Enhua Lee and Maurizio Rossetto

Australian Systematic Botany 36(5) 386-400

<https://doi.org/10.1071/SB22031>

Recognition that the critically endangered mallee *Eucalyptus* sp. *Cattai* (Gregson s.n. 28 Aug 1954) is a distinct species has been complicated by close morphological similarity between it and other members of *E.* subgenus *Symphymyrtus* section *Latoangulatae* series *Annulares*. Recent genomic evidence has demonstrated that it is distinct from other species. In this study, we provide *E.* sp. *Cattai* with the new species name, *E. cryptica* T.C.Wilson, S.Rutherford & S.M.Douglas, and use genomic scans of adults and seedlings to assist in its description and support its conservation by identifying hybrids. Accompanying the description of *E. cryptica* are images, diagnostic illustrations and an updated part of the *Eucalyptus* key for the Flora of New South Wales.

Analyzing trait-climate relationships within & among taxa using machine learning & herbarium specimens

Brendan Wilde, Jason Bragg, and William Cornwell

American Journal of Botany

<https://doi.org/10.1002/ajb2.16167>

Premise: Continental-scale leaf trait studies can help explain how plants survive in different environments, but large data sets are costly to assemble at this scale. Automating the measurement of digitized herbarium collections could rapidly expand the data available to such studies. We used machine learning to identify and measure leaves from existing, digitized herbarium specimens. The process was developed, validated, and applied to analyses of relationships between leaf size and climate within and among species for two genera: *Syzygium* (Myrtaceae) and *Ficus* (Moraceae). Methods: Convolutional neural network (CNN) models were used to detect and measure complete leaves in images. Predictions of a model trained with a set of 35 randomly selected images and a second model trained with 35 user-selected images were compared using a set of 50 labeled validation images. The validated models were then applied to 1227 *Syzygium* and 2595 *Ficus* specimens digitized by the National Herbarium of New South Wales, Australia. Leaf area measurements were made for each genus and used to examine links between leaf size and climate. Results: The user-selected training method for *Syzygium* found more leaves (9347 vs. 8423) using fewer training masks (218 vs. 225), and found leaves with a greater range of sizes than the random image training method. Within each genus, leaf size was positively associated with temperature and rainfall, consistent with previous observations. However, within species, the associations between leaf size and environmental variables were weaker. Conclusions: CNNs detected and measured leaves with levels of accuracy useful for trait extraction and analysis and illustrate the potential for machine learning of herbarium specimens to massively increase global leaf trait data sets. Within-species relationships were weak, suggesting that population history and gene flow have a strong effect at this level. Herbarium specimens and machine learning could expand sampling of trait data within many species, offering new insights into trait evolution.

Do Southeast Asia's Paleo-Antarctic trees cool the planet?

Peter Wilf and Robert Kooyman

New Phytologist 239: 1556-1566

<http://dx.doi.org/10.1111/nph.19067>

Many tree genera in the Malesian uplands have Southern Hemisphere origins, often supported by austral fossil records. Weathering the vast bedrock exposures in the everwet Malesian tropics may have consumed sufficient atmospheric CO₂ to contribute significantly to global cooling over the past 15 Myr. However, there has been no discussion of how the distinctive regional tree assemblages may have enhanced weathering and contributed to this process. We postulate that Gondwanan-sourced tree lineages that can dominate higher-elevation forests played an overlooked role in the Neogene CO₂ drawdown that led to the Ice Ages and the current, now-precarious climate state. Moreover, several historically abundant conifers in Araucariaceae and Podocarpaceae are likely to have made an outsized

contribution through soil acidification that increases weathering. If the widespread destruction of Malesian lowland forests continues to spread into the uplands, the losses will threaten unique austral plant assemblages and, if our hypothesis is correct, a carbon sequestration engine that could contribute to cooler planetary conditions far into the future. Immediate effects include the spread of heat islands, significant losses of biomass carbon and forest-dependent biodiversity, erosion of watershed values, and the destruction of tens of millions of years of evolutionary history.

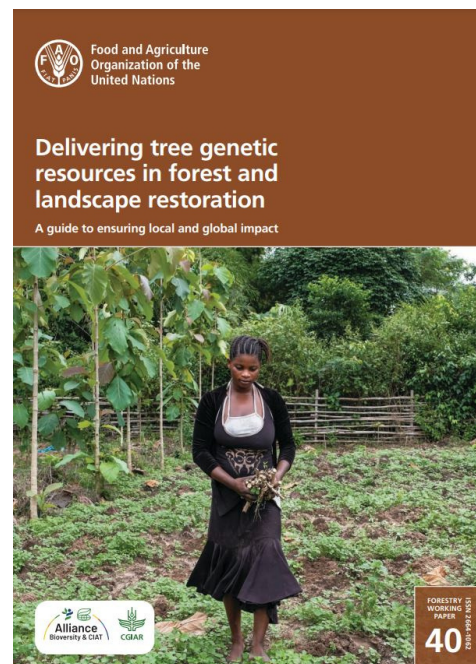
Other publications

Delivering tree genetic resources in forest and landscape restoration – A guide to ensuring local and global impact.

H Gaisberger, R Jalonen, et al. and **M Rossetto**.

Forestry Working Paper, No. 40. Rome, Food and Agriculture Organisation of the United Nations

DOI: [10.4060/cc8955en](https://doi.org/10.4060/cc8955en)



Chapter 2: Science Partnerships.

G Boggs, MF Breed, M Byrne, N Macgregor, SM Prober, **M Rossetto**, D Wrigley and R Young

Chapter 3: Planning

AJL Lynch, D Bickerton, K Bradby, L Broadhurst, M Byrne, N Gellie, N Hancock, PA Harrison, D Rogers, **M Rossetto**

In: Guidelines for embedded experiments in ecological restoration and management in Australia. CSIRO, Canberra

<https://wabsi.org.au/latest-research/guidelines-for-embedded-experiments-in-ecological-restoration-and-management-in-australia/>

The Shifting Rhetoric of Environmental Science in Australia: Acknowledging First Nations People and Country.

E. Ens, S. Russell, B. Campbell, S. Rysnik-Steck, **M. Fahey**, P. Cooke, R. Cawthorne and D. Sloane

In: Global Rhetorics of Science 2023. State University of New York Press.

<https://sunypress.edu/Books/G/Global-Rhetorics-of-Science>

Unpublished reports prepared for the NSW Saving our Species program

Conservation genomics of *Astrotricha roddii* in support of management.

Eilish McMaster, Jia-Yee Samantha Yap, Richard Dimon, Maurizio Rossetto

Conservation genomics of *Astrotricha roddii* in support of management. *Astrotricha roddii* is a rare shrub species that is only found along the border of Queensland and New South Wales. The NSW Department of Planning and Environment's (DPE) Saving our Species (SoS) initiative is managing the conservation of this endangered species. This study aimed to determine the taxonomic status of *A. roddii* and assess its genetic health to support its management. To achieve this, we conducted genomic analyses of all existing subpopulations of *A. roddii* in Northern NSW and a known population in QLD. We found that *A. roddii* is a genetically distinct species, consisting of two genetically distinct groups that have limited gene flow. Although genetic diversity is present in both groups, we also found evidence of inbreeding, which indicates that the existing populations are further endangered by current threats, such as exotic weed and pest infestations and increasing fire frequency. These threats will lead to further habitat degradation if not addressed, thus we endorse on-ground actions that preserve existing habitat and protect populations. In addition, to guide translocation planning, we provide recommendations for optimising genetic diversity in translocation populations for both genetic groups.

Conservation Genomics of *Diploglottis campbellii* and *Endiandra floydii* in support of management.

Jia-Yee Samantha Yap, Richard Dimon, Maurizio Rossetto

Diploglottis campbellii and *Endiandra floydii* are two endangered rainforest species that exist in small numbers in the far north coast of NSW. Translocation work has been funded to safeguard the current genetic diversity for both species. This study using high throughput genomic data was conducted to provide insights about each species' genetic health, address species taxonomic uncertainty and offer genomic based advice to support the translocation work. Major genomic insights include *E. floydii* and its morphologically similar species *E. wongawallanensis* being genetically distinct, both *D. campbellii* and *E. floydii* reported with low levels of genetic variation, and high levels of relatedness detected across all *D. campbellii* sites. For all studied species including *E. wongawallanensis*, higher levels of kinship were detected in sampled sites that were in the southern range where urban development is present. The results overall indicate the need for human intervention for these species that have low genetic variation remaining and at high risk of becoming extinct due to small population size. Actions recommended include implementing new translocation populations to boost numbers and facilitate mixing diversities from isolated and imperilled sites, and genetic rescue efforts to minimise further inbreeding particularly at the southern sites. The selection of individuals required to optimise genetic diversity for translocation efforts was calculated in consultation with the threatened species officer and is provided in this report. This study also genetically screened the ex-situ collection of *D. campbellii* at the Australian National Botanic Gardens in Canberra and revealed unexpected diversity that demonstrates the importance of including ex-situ material within the study.



Conservation genomics of *Hibbertia spanantha* in support of management.

Manuela Cascini, Chantelle Doyle, Jia-Yee Samantha Yap, Maurizio Rossetto

Hibbertia spanantha is a critically endangered shrub endemic to the Sydney Basin, Australia. The present conservation genomics study was undertaken as part of the ongoing monitoring of the species and is a follow-up of the research of Doyle et al. (2023). Samples were collected from the six wild populations, two of which are newly discovered, and from the translocation site in Ryde. The study aimed to elucidate the genomic characteristics, clonality, and kinship of the newly discovered populations, while also assessing the genetic diversity among translocated seedlings at Ryde. The findings from this investigation were used to inform conservation management strategies for the species, including the establishment of a new translocation site at Maroota.



Conservation Genomics of *Pherosphaera fitzgeraldii* in support of management.

Eilish McMaster, Jia-Yee Samantha Yap, Stephanie Chen, Maurizio Rossetto

Pherosphaera fitzgeraldii, commonly known as the Dwarf Mountain Pine, is endemic to the Blue Mountains of New South Wales, Australia, with a limited distribution and isolated subpopulations. Recent surveys have revealed selected populations are in decline, with notable threats including pollution, invasive weeds, and limited recruitment. To address these challenges, a comprehensive conservation genomics study was conducted as part of the Saving our Species (SoS) program, focusing on population health assessment and strategic recommendations for conservation. The genomic analysis of *Pherosphaera fitzgeraldii* revealed two distinct genetic groups, with one group comprising the Wentworth Falls and Undercliff subpopulations, while all other subpopulations belong to the second group. Limited gene flow, even among nearby subpopulations, suggests continued isolation may lead to further genetic differentiation. All subpopulations showed signs of inbreeding and genetic depletion due to historical limited gene exchange and small population sizes. We provide recommendations for site prioritisation, optimising the genetic diversity in ex-situ collections, and suggest conducting further genomic research to understand the species' sex determination mechanism for conservation purposes.

Conservation Genomics of *Polystichum moorei* in support of management.

Eilish McMaster, Jia-Yee Samantha Yap, Maurizio Rossetto

This study presents genomic insights into *Polystichum moorei*, an endangered fern species unique to Lord Howe Island. Through high-quality genome scans (DArTseq), we analysed the species' taxonomic status, genetic diversity and population structure, leading to recommendations for conservation management. Key findings include: *P. moorei* is genetically distinct from the co-occurring *Polystichum* species, *P. whiteleggei*, with no evidence of hybridization. There is genetic isolation between Erskine creek caves and Mt Lidgbird tablelands subpopulations of *P. moorei* due to limited gene flow. Reduced genetic diversity in *P. moorei* compared to *P. whiteleggei* and *P. proliferum* is attributed to its small population size and inbreeding. All three species (*P. moorei*, *P. proliferum*, and *P. whiteleggei*) exhibit non-diploid characteristics but they retain sexual reproductive capacity. To enhance connectivity and diversity among *P. moorei* subpopulations, we propose spore collections and translocations as effective strategies. These findings provide essential insights for the conservation of *P. moorei* and contribute to informed conservation management decisions

Continued insights into the conservation genomics of *Pultenaea maritima* and *Pultenaea parviflora*: A follow-up report.

Eilish McMaster, Jia-Yee Samantha Yap, Maurizio Rossetto, Patrick Fahey

This study delved deeper into the genetic relationships and diversity of the vulnerable *Pultenaea maritima* and the more widely distributed *P. villosa*. To achieve this, we expanded the sample size significantly. Additionally, we conducted a follow-up investigation on the endangered *P. parviflora*, building upon the report previously generated by ReCER in 2022.



Conservation genomics of *Rhodamnia maideniana* in support of management.

Manuela Cascini, Jia-Yee Samantha Yap, Jason Bragg, Maurizio Rossetto

Rhodamnia maideniana, commonly referred to as smooth scrub turpentine, is a critically endangered species, threatened with extinction by the fungal disease Myrtle rust. Knowledge of the level and distribution of genetic diversity is pivotal for deciding on management actions for its survival and long-term conservation. Here, for the first time, the genetic characteristics of *R. maideniana* were analysed using high quality genome scans. *Rhodamnia maideniana* is a genetically distinct species, in agreement with current morphology-based taxonomic status. Genetic diversity is present, however there is minimal genetic structuring, thus it is recommended that the species is managed as a whole across its entire distribution. Furthermore, we found overall high level of inbreeding and low genetic diversity. Current ex situ collection at the Australian Botanic Garden Mount Annan represents only a portion of the species' genetic diversity, hence we recommend its expansion to incorporate as much in situ diversity as possible. Myrtle rust persists throughout the species' entire range and very few instances of resistance have been noted thus far. Only an exiguous number of *R. maideniana* individuals in poor health are persisting. Therefore, imminent extinction in the wild of *R. maideniana* is highly likely if not inexorable. In agreement with the Myrtle rust National Action Plan (Makinson et al. 2020) we urge for emergency-level action, and provide genome-based recommendations for its conservation and recovery.

Conservation genomics of *Syzygium paniculatum* Part II: evolutionary history and taxonomic implications.

Pat Lu-Irving, Stephanie Chen, Maurizio Rossetto

The evolutionary origin and affiliations of the endangered NSW endemic Magenta Lilly Pilly (*Syzygium paniculatum*) were investigated using whole-genome shotgun sequencing as well as genome-wide scans comparing *S. paniculatum* with expanded sampling of related species *S. oleosum* and *S. australe*. Sampling spanned the geographic ranges of all three species in New South Wales, as well as geographically distant populations of *S. oleosum* in Queensland. Analyses of these data confirmed that *S. paniculatum* forms a species complex with its common and widespread congeners. Interspecific introgression has played an important role in the evolutionary history of these species: the diverse sub-lineages of *S. paniculatum* identified in Part I of this study were likely formed by hybridisation among various parental lineages through time and space. We hypothesize that the widespread and genetically uniform *S. paniculatum* southern group arose via ancient introgression between *S. oleosum* and *S. australe*, undergoing a genetic bottleneck followed by a relatively rapid expansion into its present-day distribution. These findings demonstrate the need for taxonomic revisions and deliver the requisite evidence to inform them. We discuss likely taxonomic outcomes, but recommend that management decisions be guided directly by insights into evolutionary ecology such as those described here.

Conservation genomics of *Zieria obcordata* in support of management.

Eilish McMaster, Jia-Yee Samantha Yap, Maurizio Rossetto

Zieria obcordata is an endangered plant species with only two known populations near Bathurst and Wellington in New South Wales totaling approximately 12,000 individuals. This study was conducted to determine population structure and health of this species and provide the relevant recommendations for its conservation management. Genetic analyses found the *Z. obcordata* populations at Wellington and Bathurst are highly genetically distinct suggesting separate management is required for the differentiated entities. Both populations displayed critically low diversity and extreme levels of inbreeding, likely a result of an extended period of isolation, that make these populations increasingly vulnerable to disturbance and collapse. We provided the relevant recommendations including a review of the species' listing, prioritisation of the preservation of existing diversity in ex-situ collections and implementation of an experimental mixing if resources are available.

Other unpublished reports

Cumberland Plain Woodland Knowledge Infrastructure.

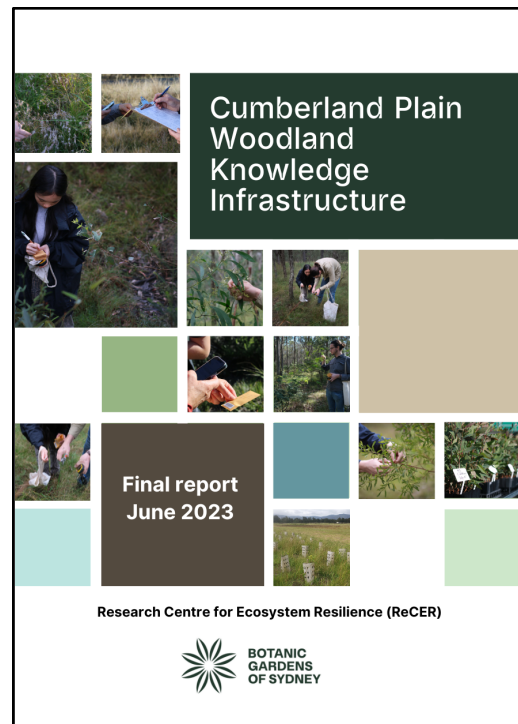
Patrick Fahey, Patricia Hogbin, Marlien van der Merwe, and Maurizio Rossetto

Ecological restoration is an essential tool in ensuring the persistence of native vegetation on the Cumberland Plain Woodland, especially in the face of a rapidly changing climate. Genetic information can help ensure material used in restoration is of appropriate provenance and sufficiently genetically diverse. Fail to adequately consider genetic diversity and we may end up with populations that exhibit low or no recruitment and are unable to adapt to change. These guidelines provide advice on how to source genetically diverse climate-ready seed for woodland species of the Cumberland Plain. While initially planned as a targeted study on the Cumberland Plain Woodland threatened ecological community, as data came to light, the scope of the project expanded to be applicable to all woodland communities of the Cumberland plain. Fifteen common woodland species, suitable for restoration of the Cumberland Plain, were sampled from across their distribution in New South Wales and population genetic analyses undertaken. Detailed guidelines for optimised seed collections and establishment of seed production areas are provided for eleven of these species, with the four remaining species proving unsuitable for such guidelines based upon the data gathered for this report. Eight species for which we present specific guidelines here have been added to the publicly available Restore and Renew webtool, allowing restoration practitioners to identify appropriate seed sourcing regions for specific restoration projects not only within the Cumberland Plain, but across NSW. However, the genetic patterns observed for the other three species violated the assumptions of the model employed by the webtool and so they could not be deployed there at this time (but will be in an upgrade of the webtool that is currently being developed). To show the practicalities of implementing the guidelines, a case study establishing a seed production area is presented.

Key findings of the restoration genetic study include showing that for all species investigated, gene flow is continuous between plant community types on the Cumberland Plain and that the 'local' genetic neighbourhood that includes the Cumberland Plain is geographically much larger than the Cumberland Plain. Therefore, targeted mixing of seed from differing communities from both within and outside the Cumberland Plain will have no negative consequences and increase the accessibility and genetic diversity of seed. Furthermore, we observed no evidence of a relationship between patch size and genetic diversity, suggesting that even small patches of remnant vegetation on the Cumberland Plain may hold important diversity and should not be dismissed because of their small size when collecting seed.

The objective of this pilot project was to demonstrate the utility of Restore and Renew style investigations and resulting knowledge infrastructure for guiding evolutionarily informed restoration for 10 keystone Cumberland Plain Woodland species. Restoration genomics has stepped into a new phase whereby we can now gather relevant genomic information quickly and cost-effectively, making it feasible for us to go beyond the initial scope of the project (namely to include 10 new CPW species into the Restore and Renew webtool) but to also generate additional species-specific information on restoration strategies and ex-situ collection developments.

Similar analysis could be undertaken for most species commonly used in restoration across the Cumberland Plain. Furthermore, the outcomes of this project have application far beyond the Cumberland Plain. The data and guidelines generated for at least eight species will be made freely accessible on the Restore & Renew webtool, thus providing valuable information that can guide genetically informed restoration of these species across NSW.



Blog posts

[Creating an optimised population of Sydney's newest Eucalypt](#)

Chantelle Doyle

To conserve populations of *Eucalyptus cryptica*, geneticists identified least related plants and designed a new population which maximised genetic diversity.

Key findings:

- After decades of puzzling taxonomists, genetics was used to support morphological studies and confirm a new species of Eucalypt. The new species received the name *Eucalyptus cryptica*.
- *Eucalyptus cryptica* is critically endangered and occurs only in northern Sydney in a cluster of fragmented populations, on private land at risk of development. The populations are threatened by genetic isolation and hybridisation, as well as weeds and changing fire regimes.
- To conserve the populations, geneticists identified least related plants and designed a new population which maximised genetic diversity.
- This new population was planted in southern Sydney in 2020 and 2022. The site is further south of the species' natural range, as part of a managing climate risk.
- Monitoring has shown excellent establishment but curious differences in growth between plants of the same age. These differences can be investigated with genetics and future population augmentation undertaken to help create a self-sustaining population.



[Genetics is helping save plant species decimated by myrtle rust](#)

Chantelle Doyle

Genetic information is helping to guide collection of myrtle rust impacted species for safe storage in botanic gardens. One day, these living collections may help restore wild populations.

Key points

- Myrtle rust is a devastating fungal disease that arrived in Australia in 2010 and has since spread to all states except Western Australia.
- It impacts at least 350 of Australia's native plant species in the Myrtaceae family, including eucalypt, paperbark, bottlebrush, tea tree and lilly pilli.
- Once common plants, such as Native Guava and Scrub Turpentine, have become critically endangered in the wild because of myrtle rust.
- The only option to save some species is to create living collections in botanic gardens.
- Genetic information is helping design living collections and breeding programs for rust resistance, to ensure they are genetically diverse and representative of wild populations.
- Long term, it is hoped that resistant plants can be returned to the wild to help restore decimated populations

[Ensuring research informs conservation and restoration](#)

Tricia Hogbin

The Research Centre for Ecosystem Resilience team (ReCER) team gathered at the Crommelin Field Station at Pearl Beach in May to ponder how to ensure our research continues to best inform the restoration and conservation of resilient ecosystems.



[Genomic research guiding the recovery of threatened flora](#)

Tricia Hogbin and Chantelle Doyle

Conservation genomic research by the Research Centre for Ecosystem Resilience (ReCER) at the Botanic Gardens of Sydney has helped guide the recovery of over 30 threatened plant species. To commemorate National Threatened Species Day 2023, we kick off a new regular feature where we highlight how conservation genomics is informing the on-ground management of threatened plants. In this post, we highlight how genomic information is helping to: overcome habitat fragmentation for the critically endangered Julian's Hibbertia, create a living insurance collection of Native Guava before it becomes extinct in the wild, and restore an endangered population of River Red Gum.

Selected Media Features

[WANDERING SEEDS: Millennia before Europeans arrived in Australia, humans helped shape the distribution of the continent's plants](#)

Elizabeth Pennisi
Science. 381 (6658)

[ABC Landline: Saving Gums: Protecting the Hunter's river red gums](#)

Romy Stephens
Landline. Series 2023 Sunday 29/10

