

Research Centre for Ecosystem Resilience Publications

Foreword

The Research Centre for Ecosystem Resilience (ReCER) at Botanic Gardens of Sydney undertakes research that describes and interprets natural processes, and guides the conservation and restoration of resilient ecosystems. This common vision of undertaking research that is relevant to on-ground actions is especially apparent in our annual publication booklets.

In 2025, we highlighted the benefits of employing genetics early in the conservation process, shared a pathway to recovery for species devastated by myrtle rust, describe a workflow that simplifies using genetic information to develop seed sourcing strategies for restoration, and demonstrate how spatial, genetic and environmental data can be combined to prioritise areas for conservation. We also prepared 11 reports for the NSW Saving our Species Program providing applied guidance for the management of a dozen threatened species.

A highlight in 2025 was incorporation of the Restore and Renew webtool in the Adapt NSW website, making it more accessible and embedding genomic guidance into the NSW Government's program of action.

In this booklet we bring together abstracts of publications from the 2025 calendar year. ReCER staff, students or research associate authors are indicated in bold. Most are open access and can be downloaded from the links provided below, making it convenient for conservation and restoration practitioners and policymakers to access our latest guidance.



Maurizio Rossetto
Head of Research Centre
for Ecosystem Resilience

Peer-reviewed publications

The impact of taxonomic confusion on conservation resources – Why population genomics should inform threatened species determination.

Manuela Cascini, Chantelle Doyle, Aaron Mulcahy, Eilish McMaster, Richard Dimon, Patricia Hogbin, Marlien van der Merwe, Jia-Yee Samantha Yap, Maurizio Rossetto
Biological Conservation, Volume 306, 111113
<https://doi.org/10.1093/gbe/evae238>

Threat determinations are the primary legal tools guiding conservation decisions to protect threatened species. Therefore, accurate taxonomic delimitation of these taxa is crucial for effective actions. Advances in genomics now offer powerful and cost-effective tools for rigorous taxonomic assessment but current listing processes rarely use population genomics to inform taxonomic boundaries before finalising listings. Here we discuss two examples highlighting the consequences of inadequate taxonomic resolution on biodiversity conservation. To avoid misdirected efforts and resources, we advocate that genomics is incorporated into conservation policy and management as a key companion to taxonomic assessment.



IN BRIEF: Demonstrating value of genetics up front

These two publications highlight the benefits of employing genetics early in the conservation process.

Doyle et al. explore the cost and benefit of incorporating conservation genetics in the NSW Saving our Species program. Despite a reported sentiment that costs are prohibitive, the cost of genetic sampling, analysis and advice is less than 10% of the total Government investment and will continue decreasing proportionally throughout the years as other management occurs.

Cascini et al. highlight the value of population genetics when determining a species' conservation status. They explore the impact of taxonomic confusion on conservation resources using two case studies, *Pultenaea maritima* and *Astrotricha crassifolia*, and advocate that genomics be incorporated into conservation policy and management as a key companion to taxonomic assessment to avoid misdirected efforts and resources.



Conservation genomics within government led conservation planning: an Australian case study exploring cost and benefit for threatened flora.

Chantelle Doyle, Manuela Cascini, Jia-Yee Yap, Hannah Matthews, Patricia Hogbin, Trevor Wilson, Erica Mahon, Diane Brown, Aaron Mulcahy, Rachel Brown, Maurizio Rossetto
Annals of Botany, Volume 135, Issue 6
<https://doi.org/10.1093/aob/mcae222>

The importance of conserving plant genetic diversity has been recognized since the 1980s, but genetic research tools for improving conservation remain largely absent from standard planning. Using an Australian case study framework of the New South Wales government's Saving our Species (SoS) programme, we outline the costs and benefits associated with conducting genomic analysis within a conservation strategy to inform, for example, taxonomic resolution, targeted monitoring, translocations and ex situ collections. Despite a reported sentiment that costs are prohibitive, our study identified that where genetics reports have been provided (32 to date), the cost of genetic sampling, analysis and advice is <10 % of the total government investment (SoS programme) and will continue decreasing proportionally throughout the years as other management occurs. We identified that the largest government investment was for maintenance and monitoring actions. On-ground practitioner feedback from the reports identified that the main reason for requesting genetics was to inform translocation or ex situ collection. However, from the total of 269 plant species with translocation or ex situ conservation actions planned, 75.4 % still do not have provisions for genomics, suggesting that knowledge of the utility of this practice is low among practitioners. Responsive feedback also demonstrated that 90 % of respondents seek additional learning, and thus there is merit in providing future genomics-focused workshops.

Pathways to recovery: genomics and resistance assays for tree species devastated by the Myrtle Rust pathogen.

Stephanie Chen, Jia-Yee S. Yap, Veronica Viler, Craig Stehn, Karanjeet Sandhu, Julie Percival, Geoff Pegg, Tracey Menzies, Ashley Jones, **Karina Guo,** Fiona Giblin, **Joel Cohen,** Richard Edwards, **Maurizio Rossetto,** Jason G. Bragg

Molecular Ecology. 34.

<https://doi.org/10.1111/mec.70030>

Myrtle rust is a plant disease caused by the invasive fungal pathogen *Austropuccinia psidii* (G. Winter) Beenken, which has a global host list of 480 species. It was detected in Australia in 2010 and has caused the rapid decline of native Myrtaceae species, including rainforest trees *Rhodamnia rubescens* (Benth.) Miq. (scrub turpentine) and *Rhodomyrtus psidioides* (G. Don) Benth. (native guava). Ex situ collections of these species have been established, with the goal of preserving remaining genetic variation. Analysis of reduced representation sequencing (DArTseq; $n = 444$ for *R. psidioides*) was resequenced at genome scale, revealing large historical effective population sizes, and little variation among individuals in inferred levels of deleterious load. In *Rhodamnia rubescens*, experimental assays ($n = 297$) identified individuals that are putatively resistant to myrtle rust. This highlights two important points: there are tangible pathways to recovery for species that are highly susceptible to rust via a genetically informed breeding programme, and there is a critical need to act quickly before more standing diversity is lost.



Defining species-specific seed sourcing strategies for restoration: an example of how to use genetic data to inform seed collections for multiple co-occurring species.

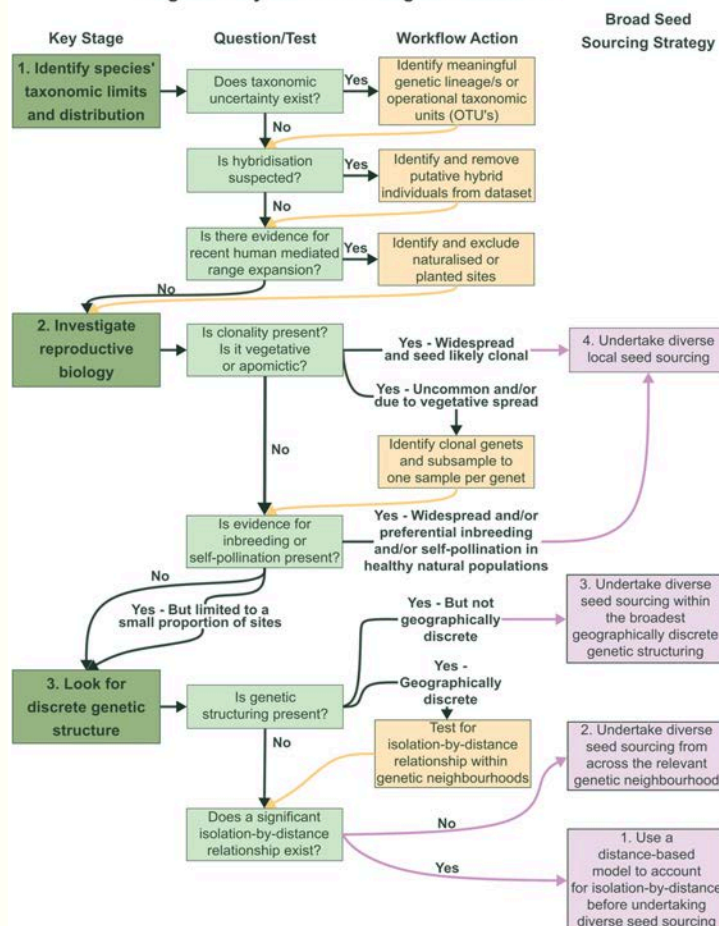
Patrick Fahey, Jason Bragg, Richard Dimon, Eilish McMaster, Jessica O'Hare, **Patricia Hogbin, Marlien van der Merwe, Maurizio Rossetto**

Restoration Ecology Volume 33, Issue 5

<https://doi.org/10.1111/rec.70063>

Generalized guidance such as “local is best” has prevailed regarding seed sourcing strategies for ecological restoration in the past. A shift is currently underway in this guidance, moving toward using pre-adapted material in the face of human induced climate change and species-specific strategies to maximize the success and self-sustainability of restoration plantings. Meanwhile, population-level genetic data is proving an increasingly valuable tool to achieve this, providing restoration biologists insights into evolutionary history and processes that impact restoration practices. Combining these factors is a major step toward the development and implementation of species-specific, evolutionarily informed seed sourcing strategies. We seek to establish a balanced approach that bridges the gap between broad generalizations, which lack the nuance needed for successful restoration of individual species, and the highly intensive and costly bespoke single-species studies sometimes undertaken. To this end, we present a workflow and decision-making process to develop species-specific seed sourcing strategies using Single Nucleotide Polymorphism (SNP) data and test its implementation on 10 common and abundant woodland species frequently used in ecological restoration in Australia. The workflow we have developed highlights factors that need to be considered when undertaking ecological restoration including taxonomic uncertainties, hybridization, and range extensions resulting from human activities. It also helps to develop insights into species' reproductive biology and biogeography to enable informed seed movement across the landscape. Thus, it establishes a framework for undertaking restoration genomics studies to facilitate the development of evolutionarily informed seed sourcing. This in turn will help ensure the successful establishment of self-sustaining restored populations.

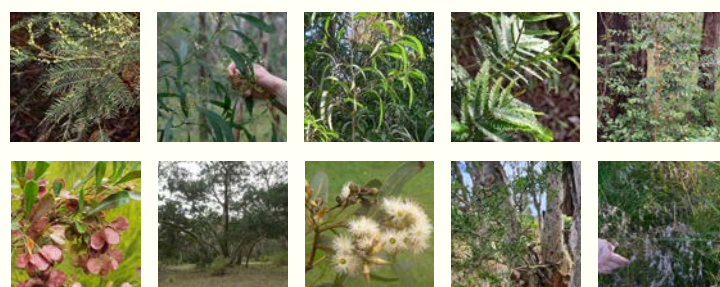
Workflow for developing species specific seed sourcing strategies for genetically informed ecological restoration



Flowchart showing the three-stage workflow developed by Fahey et al. as a standardized decision-making tool when developing species-specific seed sourcing strategies. Four broad seed sourcing strategies are the endpoint of the workflow and are detailed in the text of this study.

IMPLICATIONS FOR PRACTICE:

- Understanding species' individual evolutionary and reproductive biology is important in maximizing the success of restoration plantings.
- When developing guidance regarding ecological restoration, a balance needs to be struck between broad generalizations that do not factor in species-specific considerations and costly and time-consuming bespoke studies of individual species; a goal which can be assisted with standardized methodologies and decision-making processes.
- Population-level genetic data is a powerful tool to improve the success and sustainability of ecological restorations; however, it can be a daunting and apparently complex to utilize for practitioners. This can be ameliorated through clear and concise workflows, decision-making tools, and examples of its impacts.



Use of the workflow and decision-making process for developing species-specific seed sourcing strategies was tested for 10 common and abundant woodland species frequently used in ecological restoration in Australia: *Acacia decurrens*, *A. falcata*, *A. implexa*, *A. parramattensis*, *Breynia oblongifolia*, *Dodonaea viscosa*, *Eucalyptus baueriana*, *E. fibrosa*, *Melaleuca decora*, and *Themeda triandra*.

Combining spatial, genetic, and environmental risk data to define and prioritize *in situ* conservation units.

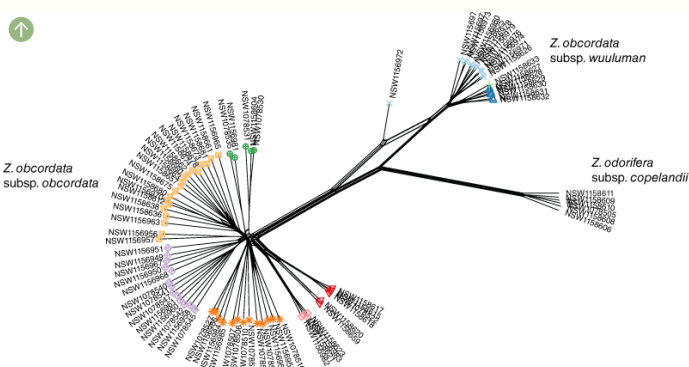
Eilish McMaster, Richard Dimon, Andrew Baker, Craig Harre, Justin Mallee, Aleks Maric, Peter Richards, Matthew Wiseman, Simon Ho, **Maurizio Rossetto**
Ecol Evol. 26;15(5):e71251
<https://doi.org/10.1002/ece3.71251>

In situ management aims to preserve species and their genetic integrity within their natural habitat. To achieve this, conservation strategies must strike a balance between safeguarding genetic diversity, mitigating environmental risks, and addressing practical management constraints. Here, we present a clear and reproducible framework that addresses these goals. We applied this framework to the Nightcap reserves in the Gondwanan Rainforests of Australia, a UNESCO World Heritage site impacted by the 2019/20 Black Summer fires. We analyzed the genetic diversity of 12 rainforest tree species, including three endangered species—*Eidothea hardeniana*, *Uromyrtus australis*, and *Elaeocarpus sedentarius*—and examined how fire risk, influenced by the presence of fire-dependent species such as eucalypts, impacts genetic diversity. To guide specific *in situ* management for the endangered species, we developed a flexible framework that uses clustering algorithms (DBSCAN and k-means) to define spatial management units while considering resource limitations (e.g., maximum perimeter or area). Our framework also incorporates a composite genetic value metric (combining Essential Biodiversity Variables heterozygosity, allelic richness, and genetic differentiation) and evaluates future fire risk based on vegetation flammability. This approach allowed us to identify priority management areas while adhering to resource constraints. We provide some reproducible examples of how the proposed framework can be applied, either partially or fully, to optimize *in situ* conservation efforts. Its flexibility allows for adjustments to fit different habitat types, species, and environmental threats, making it a valuable tool for enhancing conservation management across diverse conservation contexts.

Conservation genomics uncovers disjunct subspecies and critically low diversity in *Zieria obcordata* A.Cunn. (Rutaceae).

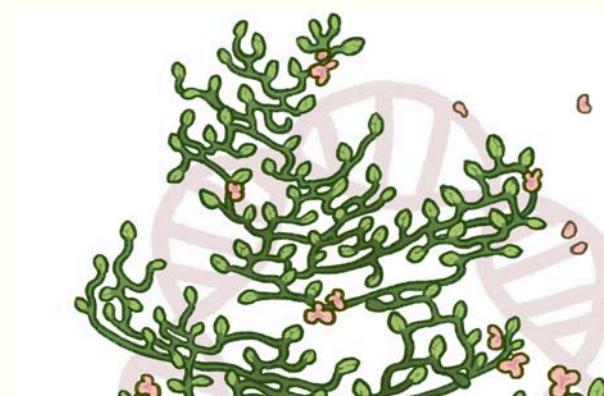
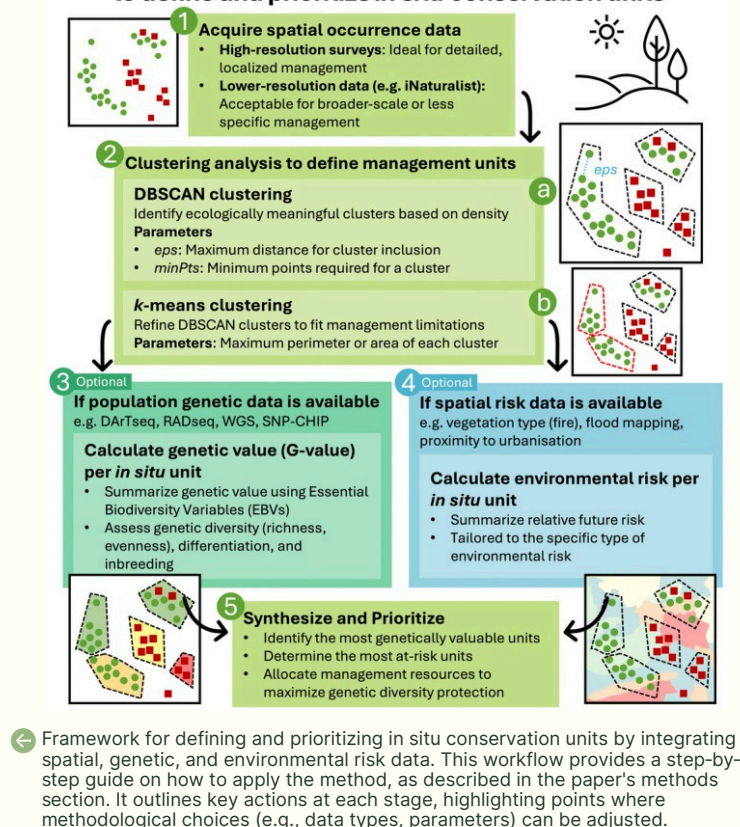
Eilish S. McMaster, Marco Duretto, **Jia-Yee Samantha Yap**, **Maurizio Rossetto**
Australian Systematic Botany, 38(1)
<https://doi.org/10.1071/SB24034>

Zieria obcordata A.Cunn. (Rutaceae), an endangered species endemic to central New South Wales, Australia, faces significant conservation challenges due to limited occurrence in two small, isolated populations. Using genome-wide SNPs (DARtseq), we examine genetic relationships and diversity within and between these populations, and make comparisons with other *Zieria* species. Our results confirm that *Z. obcordata* is a distinct species, with the Bathurst and Wellington populations showing sufficient genetic divergence to warrant recognition as two subspecies: *Z. obcordata* subsp. *obcordata* and *Z. obcordata* subsp. *wuuluman*. Minor morphological differences further support this classification. Genomic analyses reveal minimal gene flow between the subspecies, along with extremely low heterozygosity and high inbreeding coefficients within each. Compared to other *Zieria* species, including *Z. covenyi*, *Z. cytisoides*, *Z. laevigata*, *Z. odorifera* and *Z. smithii*, both subspecies exhibit exceptionally low genetic diversity, likely due to geographic isolation, genetic drift and inbreeding. We provide conservation assessments for both subspecies and conclude that each qualifies to be listed as Critically Endangered under the New South Wales Biodiversity Conservation Act 2016. We recommend strategies to facilitate gene flow between the subspecies to improve genetic diversity and enhance fitness.



Population genomic analyses of *Zieria obcordata* subspecies.

Combining spatial, genetic, and environmental risk data to define and prioritize *in situ* conservation units



Evaluating kinship estimation methods for reduced-representation SNP data in non-model species.

Eilish McMaster, Patricia Lu-Irving, Marlien van der Merwe, Simon Ho, **Maurizio Rossetto**
Mol Ecol Resources 25(8):e70038.
<https://doi.org/10.1111/1755-0998.70038>

Accurate kinship estimation between close relatives is crucial in conservation and restoration but remains challenging in wild populations due to structure and inbreeding. The efficacy of kinship inference using reduced-representation sequencing data (e.g., DARtseq, RADseq) is also uncertain. We evaluated the sensitivity and precision of six kinship methods (Goudet's beta dosage, KING Homo, KING Robust, PC-Relate, APLINK, RelateAdmix) at detecting parent-offspring and sibling relationships. Analyses were conducted on 3395 individuals and 363 families from six non-model Australian plant species: *Acacia terminalis*, *Acacia suaveolens*, *Banksia serrata*, *Banksia aemula*, *Hakea sericea* and *Hakea teretifolia*. Method performance varied across species and filtering parameters. Goudet's beta dosage and RelateAdmix performed well in low-structure, noninbred species but were less reliable in structured or inbred contexts. PLINK offered a balance of sensitivity and precision but was sensitive to filtering and often underestimated relatedness. KING Robust was highly precise but missed many true relatives. PC-Relate showed high false positives and is not recommended for similar applications. We recommend PLINK for general use, Goudet's beta dosage and RelateAdmix for low-structure species, and KING Robust for high-precision needs. Comparing multiple methods is advisable, as each has different assumptions and complementary strengths. Further theoretical development is needed for species with high inbreeding.

Geographically proximate rare species exhibit strong population divergence while maintaining intraspecific genetic diversity in *Homoranthus* (Myrtaceae).

Eilish McMaster, Peter Pemberton, Jeremy Bruhl, Adam Fawcett, John Hunter, Manu Saunders, Elizabeth Wandrag, **Jia-Yee Samantha Yap**, Ian Telford, **Maurizio Rossetto**, Rose Andrew

Annals of Botany, mcaf316

<https://doi.org/10.1093/aob/mcaf316>

Species with small geographic ranges provide insights into adaptation, speciation, and genetic drift, while also presenting clear conservation challenges. *Homoranthus* A.Cunn. ex Schauer (Myrtaceae), an Australian genus with many narrow endemics, offers a model for understanding how ecological and spatial factors drive diversification. We examined a regional hotspot with a high number of *Homoranthus* narrow endemics to assess patterns of genetic diversity and inform both evolutionary understanding and conservation planning. We generated genome-wide SNP data using DArTseq for 282 individuals across 13 *Homoranthus* species (40% of the genus), including ten narrow endemics, to assess population genetic structure and diversity. All species showed strong genetic isolation, even over a few kilometres, with populations diverging within hundreds of meters. *Homoranthus lunatus* includes two highly divergent, non-sister lineages, suggesting taxonomic revision. Inbreeding was common but unrelated to range size, and heterozygosity remained moderate, indicating intrinsic buffering of genetic diversity. Genome sizes were notably small relative to other angiosperms. Ecological isolation, life-history traits, and limited dispersal drive both speciation and extinction risk in *Homoranthus*. Diversification and endemism are linked to habitat fragmentation, highlighting the need for conservation strategies that address ecological connectivity as well as species protection.

Evidence of landscape-driven repeated adaptation among 13 *Eucalyptus* species.

Collin Ahrens, **Jason Bragg**, **Marlien van der Merwe**, **Maurizio Rossetto**

Evolution, Volume 79, Issue 6

<https://doi.org/10.1093/evolut/qpaf049>

Local adaptation is the biological process by which native populations become more fit. Intraspecific patterns of local adaptation occur through shifts in allele frequency within or near genes and may occur similarly across species. Identifying repeated adaptation across species increases statistical power to determine causal genes driving adaptation and reveals insights into the nature of evolution. These types of insights could have theoretical and applied applications, particularly as the climate continues to change. We interrogate repeated molecular adaptation across 13 eucalypt species. In total, we found 38 candidate genes with shared putatively adaptive signals in as many as 12 species. This suite of genes contains important functions, including myeloblastosis (MYB) proteins, acyl-CoA dehydrogenases, and Leucine-rich kinases. Species with restricted and widespread geographical distributions shared putative patterns of adaptation, and phylogenetic closeness did not increase patterns of repeated adaptation compared to geographic overlap. This work provides further evidence that repeated adaptation can occur among orthologs, which may play a consistent role in local adaptation.

Small but mitey: A gapless telomere-to-telomere assembly of an unidentified mite with a streamlined genome.

Richard Edwards, **Stephanie Chen**, Bruce Halliday, **Jason Bragg**

Genome Biology and Evolution, Volume 17, Issue 2

<https://doi.org/10.1093/gbe/evaf023>

A draft assembly of the rainforest tree *Rhodamnia argentea* Benth. (malletwood, Myrtaceae) revealed contaminating DNA sequences that most closely matched those from mites in the family Eriophyidae. Eriophyoid mites are plant parasites that often induce galls or other deformities on their host plants. They are notable for their small size (averaging 200 µm), distinctive four-legged body structure, and heavily streamlined genomes, which are among the smallest known of all arthropods. Contaminating mite sequences were assembled into a high-quality gapless telomere-to-telomere nuclear genome. The entire genome was assembled on two fully contiguous chromosomes, capped with a novel TTTGG or TTTGGTGTGG telomere sequence, and exhibited clear signs of genome reduction (34.5 Mbp total length, 68.6% arachnid Benchmarking Universal Single-Copy Ortholog completeness). Phylogenomic analysis confirmed that this genome is that of a previously unsequenced eriophyoid mite. Despite its unknown identity, this complete nuclear genome provides a valuable resource to investigate invertebrate genome reduction.

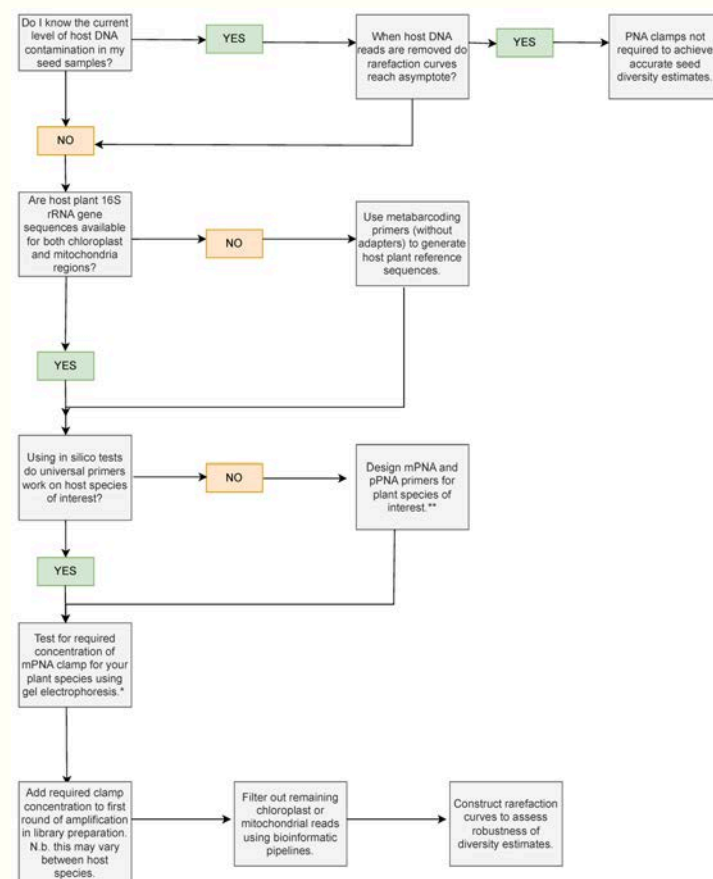
To clamp or not to clamp: enhancing seed endophyte metabarcoding success.

Allison Mertin, Linda Blackall, Douglas Brumley, **Edward Liew**, **Marlien van der Merwe**

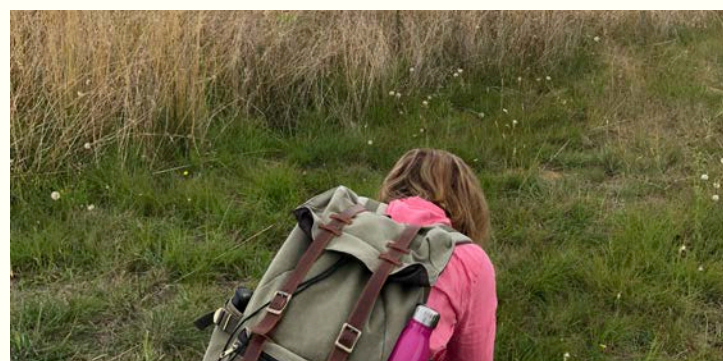
Seeds 2025, 4(3)

<https://doi.org/10.3390/seeds4030028>

Seed microbes play crucial roles in plant health, but studying their diversity is challenging due to host DNA contamination. This study aimed to optimise methodologies for investigating seed microbiomes across diverse plant species, focusing on the efficacy of peptide nucleic acid (PNA) clamps to reduce host DNA amplification. We tested PNA clamps on three plant species: *Melaleuca quinquenervia* (tree), *Microlaena stipoides*, and *Themeda triandra* (grasses). The effectiveness of PNA clamps was assessed through in silico analysis, axenic tissue culture, and metabarcoding techniques. In silico analysis confirmed the specificity of PNA clamps to the 16S rRNA gene V4 region of chloroplasts in the grass species. Axenic tissue culture experiments showed that applying PNA clamps at both 1 µM and 0.25 µM concentrations significantly reduced plant DNA amplification. Metabarcoding analyses further confirmed that PNA clamps effectively suppressed host DNA, enhancing microbial diversity estimates across all three species while preserving core microbial taxa. The efficacy of the clamps varied among host species, with *T. triandra* exhibiting the highest blocking efficacy, and chloroplast clamps outperforming mitochondrial ones. This study demonstrates that PNA clamps are a useful for improving seed endophyte metabarcoding datasets, although they require optimisation for some plant species. This knowledge will contribute to enhancing our understanding of seed microbiome diversity and its ecological implications.



① Decision flowchart showing key considerations and experiments that can be used to assess whether PNA clamps are needed for the study species of interest



Fossil insect-feeding traces indicate unrecognized evolutionary history and biodiversity on Australia's iconic *Eucalyptus*.

Alejandro Giraldo, Peter Wilf, Michael Donovan, **Robert Kooyman**, Maria Gandolfo
New Phytologist. Volume 245, Issue 4.

<https://doi.org/10.1111/nph.20316>

Fossilized plant-insect herbivore associations provide fundamental information about the assembly of terrestrial communities through geologic time. However, fossil evidence of associations originating in deep time and persisting to the modern day is scarce. We studied the insect herbivore damage found on 284 *Eucalyptus frenguelli* leaves from the early Eocene Laguna del Huncó rainforest locality in Argentinean Patagonia and compared damage patterns with those observed on extant, rainforest-associated *Eucalyptus* species from Australasia (> 10 000 herbarium sheets reviewed). In the fossil material, we identified 28 insect herbivory damage types, including 12 types of external feeding, one of piercing-and-sucking, five of galls, and 10 of mines. All 28 damage types were observed in the herbarium specimens. The finding of all the fossil damage types on extant *Eucalyptus* specimens suggests long-standing associations between multiple insect herbivore lineages and their host genus spanning 52 million years across the Southern Hemisphere. This long-term persistence, probably enabled through niche conservatism in wet eucalypt forests, demonstrates the imprint of fossil history on the composition of extant insect herbivore assemblages. Although the identities of most insect culprits remain unknown, we provide a list of *Eucalyptus* species and specific population locations to facilitate their discovery, highlighting the relevance of fossils in discovering extant biodiversity.

Global advances in phylogeny, taxonomy and biogeography of Lauraceae.

Lang Li, and other including **Marlien van der Merwe**.

Plant Diversity Volume 47, Issue 3

<https://doi.org/10.1016/j.pld.2025.04.001>

Over the past two decades, our understanding of Lauraceae, a large family of woody plants, has undergone significant advances in phylogeny, taxonomy, and biogeography. Molecular systematic studies have elucidated the basic relationships within the family with plastid phylogenomic analyses providing robust support for deep-level relationships between Lauraceae lineages, leading to the recognition of nine tribes: Hypodaphnideae, Cryptocaryeae, Cassytheae, Neocinnamomeae, Caryodaphnopsidae, Mezilaureae, Perseae, Laureae, and Cinnamomeae, with Mezilaureae validated here. Nuclear genomes and comparative genomics studies have also clarified aspects of the family's evolutionary history and metabolic diversity. Taxonomic studies have focused mainly on the most diverse regions, e.g., tropical Asia, tropical America, and Africa (Madagascar), with six new genera described and five reinstated since the last major overview of the family. The extensive fossil record suggests that Lauraceae diversified globally during the Late Cretaceous and Early Cenozoic. Biogeographic studies indicate that different lineages of the family are sorted into Gondwanan and Laurasian lineages, with patterns resulting from the disruption of boreotropical flora and multiple long-distance dispersal events. Phylogeographic studies, predominantly from East Asia, have shown patterns of in situ survival and demographic stability or expansion during the Quaternary. Nevertheless, many systematic relationships within the family remain unresolved and further research is needed into the complex biogeographic history and ecological roles of Lauraceae. A multifaceted approach integrating genomic studies, field work, morphological and ecological investigations is therefore needed to understand the evolution and diversity of this ecologically and economically significant plant family.

Local adaptation drives leaf thermoregulation in tropical rainforest trees.

Kali Middleby, Rebecca Jordan, Alexander Cheesman, **Maurizio Rossetto**, Martin Breed, Darren Crayn, Lucas Cernusak
Global Change Biology 31 (9) e704612

<https://doi.org/10.1111/gcb.70461>

Tropical forests play a critical role in biodiversity, carbon sequestration, and climate regulation, but are increasingly affected by heatwaves and droughts. Vulnerability to warming may vary within and between species because of phenotypic divergence. Leaf trait variation can affect leaf operating temperatures—a phenomenon termed 'limited homeothermy' when it helps avoid heat damage in warmer conditions. However, evidence for this capacity and the relative roles of acclimation or adaptation remain mited. We measured photosynthetic heat tolerance and leaf thermal traits of three co-occurring rainforest tree species across a thermal gradient in parameterised with field-measured traits, we predicted variation in leaf-to-air temperature differences

(ΔT_{trait}) and resulting thermal safety margins. We combined this with individual-based genome-wide data to detect signals of adaptive divergence and validated findings in a glasshouse trial with provenances grown under contrasting temperature and humidity conditions. Intraspecific trait variation reduced ΔT_{trait} and increased heat tolerance in warmer sites for *Darlingia darlingiana* and *Elaeocarpus grandis*, but not *Cardwellia sublimis*. As a result, thermal safety margins declined less steeply with increasing growth temperature in species capable of increased heat tolerance and avoidance, indicating these strategies can effectively buffer warming. All species showed genomic signals of selection, with associations to temperature and moisture variables. In *E. grandis*, glasshouse results confirmed a negative cline in ΔT_{trait} with temperature of origin. Although contrasting growth temperature and humidity lead to acclimation of individual traits, their coordination maintained ΔT_{trait} across the conditions imposed. Our findings provide evidence of limited homeothermy and suggest climate gradients have selected for trait combinations that reduce leaf temperatures at warmer sites in some but not all species. Given the rapid pace of climate change, those species with limited capacity to adjust their thermal safety margins through acclimation or adaptation may be at greater risk of local extinction.

Restoring a critically endangered grassland orchid by co-planting to improve pollination and selecting sites based on pollinator availability

Noushka Reiter, **Richard Dimon**, Björn Bohman, Michael Batley, Alex McLachlan, John Woodward, Ryan Phillips
Front. Plant Sci. Volume 16

<https://doi.org/10.3389/fpls.2025.1566543>

In many geographic regions grasslands have been heavily cleared and degraded, which represents a challenge for translocating threatened flora back into these landscapes. As most plant species require animals for pollination, pollinators are potentially a key limitation for re-establishing populations. For the Critically Endangered orchid *Diuris fragrantissima*, we identify the pollinator(s), survey for pollinators at candidate translocation sites, test if remnant size affects bee species richness, and test if pollination rates can be enhanced through co-planting with rewarding plant species. We found that *D. fragrantissima* is visited by ten species of bee but is only effectively pollinated by two native species, *Lipotriches* (Austronomia) sp. (Halictidae) and *Lasioglossum* (Chilalictus) *orbatus* (Halictidae), and the introduced honeybee *Apis mellifera* (Apidae). Interestingly, *A. mellifera* was responsible for the greatest number of pollinia removals and depositions. Pollinators of *D. fragrantissima* were not detected at some candidate translocation sites, with bee species richness and overall abundance significantly increasing with grassland remnant size. The pollination of *D. fragrantissima* was significantly enhanced through the presence of *Wahlenbergia stricta* (Campanulaceae) within 30 cm of plants, but not *Arthropodium strictum* (Asparagaceae) or *Dianella reflexa* (Asphodelaceae). We recommend that prior to conservation translocations of *Diuris* that pollinator surveys are undertaken, with preference given to larger grassland remnants. *Apis mellifera* may serve to buffer *D. fragrantissima* against loss of native pollinators from remnant grassland but could have adverse effects on other native species. We show that co-planting with rewarding species may be an effective approach for improving pollination success of threatened orchids.

Seed banking impacts native *Acacia ulicifolia* seed microbiome composition and function

Dylan Russell, Vaheesan Rajabal, Matthew Alfonzetti, **Marlien van der Merwe**, Rachael Gallagher, Sasha Tetu
Environmental Microbiome, Volume 20, article number 4

<http://doi.org/10.1186/s40793-024-00657-3>

Seed banks are a vital resource for preserving plant species diversity globally. However, seedling establishment and survival rates from banked seeds can be poor. Despite a growing appreciation for the role of seed-associated microbiota in supporting seed quality and plant health, our understanding of the effects of conventional seed banking processes on seed microbiomes remains limited. In this study we investigated the composition and functional potential of seed-associated bacterial epiphytes associated with stored and freshly collected seeds of a native plant, *Acacia ulicifolia*, using both 16S rRNA gene sequencing and culture-based approaches. Seeds obtained from seed banking facilities were found to host significantly less diverse bacterial populations, with substantial reductions in both low-abundance taxa and in community members commonly identified in freshly collected *A. ulicifolia* seeds. Bacteria with key plant growth promoting traits including IAA production, ACC deaminase activity, phosphate solubilisation, siderophore activity, and nitrogen fixation were identified in seed epiphytic communities, but these beneficial traits were less prevalent in stored seed compared to fresh seeds. Overall, these results suggest that epiphytic seed microbiomes may undergo significant changes during the storage process, selecting for bacteria tolerant to storage conditions, and potentially reducing the population of plant-growth promoting bacteria on seeds.

The Genomics for Australian Plants (GAP) framework initiative – developing genomic resources for understanding the evolution and conservation of the Australian flora

Lalita Simpson et al. including **Jason Bragg**, Trevor Wilson
Aust Syst Bot (2025) 38 (3): SB24022.
<https://doi.org/10.1071/SB24022>

The generation and analysis of genome-scale data – genomics – is driving a rapid increase in plant biodiversity knowledge. However, the speed and complexity of technological advance in genomics presents challenges for the widescale use of genomics in evolutionary and conservation biology. We introduce and describe a national-scale collaboration conceived to build genomic resources and capability for understanding the Australian flora: the Genomics for Australian Plants (GAP) Framework Initiative. We outline (a) the history of the project including the collaborative framework, partners and funding; (b) GAP principles such as rigour in design, sample verification and documentation, data management and data accessibility; and (c) the structure of the consortium and the four associated activity streams (reference genomes, phylogenomics, conservation genomics and training), with the rationale and aims for each of these. We show, through discussion of successes and challenges, the value of this multi-institutional consortium approach and the enablers, such as well-curated collections and national collaborative research infrastructure, all of which have led to a substantial increase in capacity and delivery of biodiversity knowledge outcomes.

Paleobotany reframes the fiery debate on Australia's rainforest edges.

Peter Wilf, **Robert Kooyman**
New Phytologist. Volume 245, Issue 4.
<https://doi.org/10.1111/nph.20301>

The tall eucalypt forests (TEFs) of the Australian tropics are often portrayed as threatened by 'invasive' neighboring rainforests, requiring 'protective' burning. This framing overlooks that Australian rainforests have suffered twice the historical losses of TEFs and ignores the ecological and paleobiological significance of rainforest margins. Early Eocene fossils from Argentina show that biodiverse rainforests with abundant *Eucalyptus* existed > 50 million years ago (Ma) in West Gondwana, shaped by nonfire disturbance factors such as landslides and volcanic flows. Humid volcanic environments with eucalypts were also present in eastern Australia over much of the Cenozoic. The dominance of fire-adapted eucalypts appears to be geologically recent and is linked to Neogene C4 grassland expansion, Pleistocene climate cycles, and human activity. We suggest that characterizing TEFs and rainforests as adversarial results from misinterpreting the evolutionary history and expansion-contraction dynamics of a single humid forest system, whose features are now heavily modified by human activities. The resulting management practices damage the outstanding World Heritage values and carbon storage of affected areas and thus have impacts far beyond Australia. The fossil evidence shows that rainforest margins preserve ancient, still evolving, and globally significant forest interactions that should be prioritized for restoration and research.

Unpublished reports prepared for the NSW Saving our Species program

Conservation genomics of *Allocasuarina portuensis* in support of ex-situ management.

Monica Fahey, J Ryan, Jia-Yee Samantha Yap, Marlien van der Merwe, Maurizio Rossetto

Allocasuarina portuensis (Nielsen Park she-oak) is an endangered species originally discovered at Nielsen Park within the Sydney Harbour National Park. Prior to its extinction in the wild, an ex-situ conservation collection was secured. The species is now primarily represented by the ex-situ collection at the Australian Botanic Garden nursery, with ongoing efforts to reintroduce it to its former habitat through translocation. This genomic study, funded by NSW Government's Saving our Species (SoS) program, was undertaken to assess the genetic composition of the ex-situ collection to inform its management.

This study confirms that plants labelled as *A. portuensis*, primarily sampled from the ex-situ collection and including one planted individual collected at Nielsen Park, represent a genetically distinct lineage. No evidence of hybridisation with other species was detected. The lineage comprises 21 genotypes, mostly in the ex-situ collection and one at Nielsen Park, and all of which forms a unique evolutionary lineage. We confirmed that the lineage is diploid and found comparable levels of heterozygous loci amongst the genets. However, we found that amongst the screened individuals there are duplications with individual plants being genetically identical to others in the collection. The genetic data also indicated that most of the individuals show high relatedness to at least one other individual amongst the screened plants. This information is important to apply to translocation where breeding amongst kin (siblings or cousins) should be minimised to decrease the effects of inbreeding.

We recommend implementing robust labelling systems for both the ex-situ collection and translocation sites to enable effective long-term monitoring and management, ensuring that the information provided in this study can be applied to future translocation projects. To gain a more comprehensive understanding of available genetic diversity, we recommend screening the earlier seed collections held at PlantBank, as well as individuals from previous translocations not included in this study. This screening should also include seedlings grown from seed collected from translocated site/s to determine whether hybridisation has occurred, as this may help explain the observed lack of recruitment at translocation sites. We also provide guidance on selecting individuals to implement genetically diverse plantings, to minimise inbreeding and improve translocation outcomes.

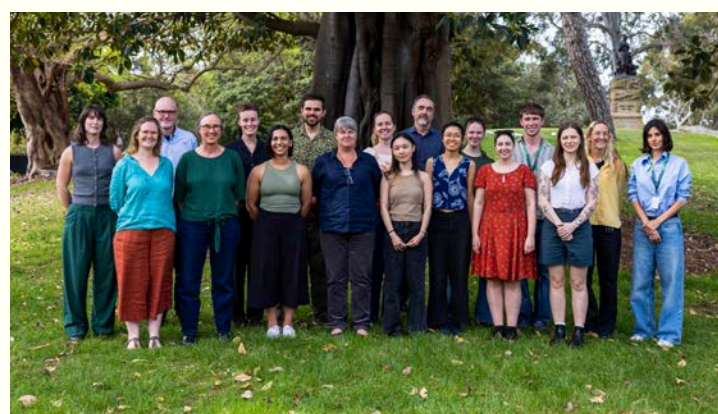
botanicgardens.org.au/receer



Conservation genomics of *Astrotricha* sp. Wallagaraugh (R.O.Makinson 1228) in support of management.

Elish McMaster, Alyssa Martino, Richard Dimon, Jia-Yee Samantha Yap, Maurizio Rossetto

This genomic study was undertaken to support the conservation and management of *Astrotricha* sp. Wallagaraugh (Merimbula Star-hair), listed as Endangered in NSW where it only exists in two localities, and as Critically Endangered in parts of Victoria. Using high-resolution genomic data mostly for the NSW distribution, we assessed genetic diversity, population structure, and connectivity within the species to provide support for the species' management in NSW. Our genomic analyses indicate two populations in NSW, with the herbarium specimens representing the species' Victorian distribution forming a third population. Gene flow between populations is highly restricted despite being separated by 20–70 km. In NSW, genetic diversity was higher in the Tura Beach–Merimbula population compared to the Yambulla population, both showed inbreeding, with high kinship detected among individuals within sites. Notably, we identified areas of concern, namely the Yambulla population and a site (Middle Beach) within the Tura Beach–Merimbula population which displayed low diversity and inbreeding, requiring genetic rescue to ensure long-term survival. We provide recommendations for establishing ex-situ collections for each population that can be applied as sources for translocation.



The ReCER team 2025.

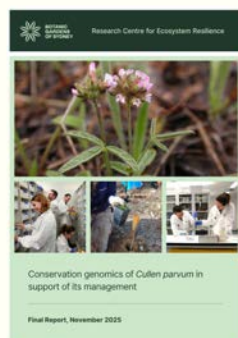
Conservation genomics of *Cullen parvum*: in support of management.

Caroline Cristofolini, Jia-Yee Samantha Yap, Maurizio Rossetto

Cullen parvum is a threatened perennial herb with a broad but highly localised distribution across New South Wales (NSW), Victoria (VIC) and South Australia (SA). In NSW, the species found at six sites across the Riverina, South Western Slopes and South Eastern Highlands, and active management occurs under the Saving Our Species (SoS) program. This study, funded by SoS, aimed to assess genetic health of NSW populations and inform management, and examine genetic patterns across species' broader distribution from opportunistic sampling from SA and VIC.

The results indicate that *C. parvum* has three geographically and genetically isolated populations in NSW, with differentiation following an isolation-by-distance pattern. Genetic diversity is present within each population; however, some sites are spatially isolated and exhibit elevated levels of inbreeding. The Biin Birri site forms part of one of these populations, and the site includes translocated individuals that are highly related, whereas the wild individuals are unrelated. The Old Junee site represents a unique and unmanaged population with very low plant numbers, making it particularly vulnerable to local extinction.

We provide population-specific recommendations for management and emphasise the need to minimise inbreeding by carefully selecting and sourcing material for any future supplementation or translocation, particularly where populations are small. We also found that the VIC samples were genetically similar to those from NSW relative to those in SA. Therefore, if genetic rescue is required in VIC, requesting to source material from NSW would be appropriate, rather from SA, which is highly genetically divergent from both NSW and VIC populations and may represent a distinct species.



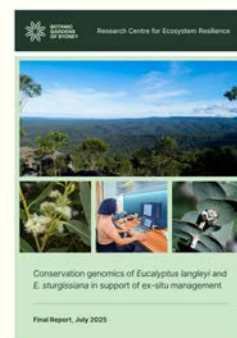
Conservation genomics of *Eucalyptus langleyi* and *Eucalyptus sturgissiana* in support of ex-situ management.

Alyssa Martino, Samantha Yap, Maurizio Rossetto

Eucalyptus langleyi and *E. sturgissiana* are two mallee species endemic to the Shoalhaven region of New South Wales. Both species are listed as Vulnerable under the Biodiversity Conservation Act 2016 (NSW) and managed by the same threatened species officer. This conservation genomics study on both *Eucalyptus* species, funded by the New South Wales government's Saving Our Species (SoS) program, was conducted to examine the species' relationship with related species, and if distinct, assess the species' genetic health and potential for hybridisation.

This study supports that *E. langleyi* is part of a species complex with other green ashes as per previous finding; *E. sturgissiana* is distinct from other members of Maidenaria section, including *E. bridgesiana*, *E. cinerea*, *E. dalrympleana*, *E. deanei*, and *E. viminalis*. Both *E. langleyi* and *E. sturgissiana* are each characterised as having a single, interbreeding genetic population. Signs of inbreeding were detected in both species, with Bomaderry Creek site identified as a conservation priority for *E. langleyi* and a site south of the Yarramunmun Trail identified for *E. sturgissiana*. Two hybrids were also detected among sampled *E. sturgissiana*. The Australian National Botanic Gardens (ANBG) ex-situ collection contains material with source information consistent with the genetic information from this study.

To support effective on-ground management such as translocation for both species, further genomic analyses are recommended to identify genetically pure individuals and assess the extent of inbreeding and hybridisation across each population. For *E. sturgissiana*, we further recommend conducting germination trials from seed collected across subpopulations and genetically screening the resultant seedlings to seek to understand the observed lack of natural recruitment in the wild.



Conservation genomics of *Davidsonia johnsonii* in support of assisted migration and ex-situ management.

Monica Fahey, Jia-Yee Samantha Yap, Maurizio Rossetto

The Smooth Davidson's Plum (*Davidsonia johnsonii*) is an endangered rainforest tree only known from approximately 30 locations Ballina district in northeast New South Wales to Currumbin Valley in southeast Queensland. Reproduction is primarily through root suckers (asexual) and there are only two confirmed cases where plants have produced fertile seed. This study utilised high throughput genomic data to provide insights about the species' genetic health and support genetically representative translocation and ex-situ programs.

We found *D. johnsonii* is genetically distinct from *D. jerseyana* and *D. pruriens* with no evidence of interspecies hybridisation. The kinship analysis indicated that *D. johnsonii* utilises a mixed reproductive strategy, with extensive clonality and high relatedness detected among individuals. Low genetic variation in *D. johnsonii* indicates the species can be managed as a single population and while historically connected, each site sustained prolonged inbreeding and now comprises a separate deme/family unit. We did not find any evidence of human-assisted dispersal as genets were not shared between sites and kinship followed a general pattern of isolation-by-distance.

We provide genomically guided recommendations that include: (1) The implementation of a translocation program that mixes individuals from isolated demes to facilitate genetic rescue. We provide an optimised selection of individuals that maximises genetic diversity for translocation efforts in consultation with the threatened species officer. We recommend implementing a robust tagging system of individual plants to track the surviving genets and facilitate monitoring of sexual success. (2) Frequent monitoring and conducting targeted crosses to assess the capacity of *D. johnsonii* to sexually reproduce. We can provide further recommendations if additional adjustments are made to the translocation.



Conservation genomics of *Eucalyptus recurva* in support of management.

Elish McMaster, Alyssa Martino, Jia-Yee Samantha Yap, Maurizio Rossetto

Eucalyptus recurva (Mongarlowe mallee) is one of Australia's rarest plants, with only six adult individuals remaining. The species faces severe reproductive failure, isolation among adults, and hybridisation with nearby eucalypts, and its occurrence on private land adds further management challenges. To support recovery planning, the Research Centre for Ecosystem Resilience (ReCER) undertook this conservation genomics study to determine the parentage of the ex situ individuals and to assess the relatedness and genetic health of the wild adults.

ReCER analysed 65 *E. recurva* plants, including all wild adults, historical ex situ individuals, and recent seedlings produced by hand crosses in 2023, as well as nearby eucalypt species to detect potential hybridisation. All wild adults were genetically unique, with individuals more genetically similar to others at the same site (Mongarlowe or Windellama) than to those at the other site. Some adults are closely related, increasing the risk of inbreeding. Most 2023 seedlings represent the intended A × C cross, while several others were identified as hybrids with *E. rubida* or *E. mannifera*, or as selfed progeny. *E. recurva* was also found to be most closely related to *E. sturgissiana* of the species analysed.

ReCER recommends maintaining detailed pedigree records, delaying large-scale planting of closely related A × C seedlings, and prioritising genetically diverse crosses particularly between sites. Additional guidance includes sampling multiple stems when collecting cuttings to capture within-tree variation and exploring controlled hybridisation under monitored ex situ conditions to help increase genetic diversity.



Conservation genomics of *Grevillea beadleana* in support of management.

Caroline Cristofolini, Elish McMaster, Chantelle Doyle, Jia-Yee Samantha Yapp, Maurizio Rossetto

This genomic study was conducted to support conservation planning for the endangered *Grevillea beadleana* (Beadle's Grevillea), a rare shrub with six known wild populations in New South Wales. Using high-resolution genomic data, we assessed genetic diversity, population structure, and connectivity within the species, and compared it to closely related *Grevillea* species from the *Aspleniifolia/Hookeriana* subgroup. Our analyses indicate that *Grevillea beadleana* is genetically distinct from other species within the subgroup, with no evidence of hybridisation. Within each of the four sites, individuals are highly genetically similar and exhibit extremely limited heterozygosity, consistent with the species having a strong propensity toward self-fertilisation and inbreeding. The genetic differences detected between sites reflect pronounced drift-mediated differentiation, caused by extensive within-site inbreeding. This suggests that unsampled sites are likely to harbour additional genetic variation, though this variation is likely to be homogenous within each site. Extreme drift and inbreeding suggest deleterious alleles are likely to have been purged from these remaining 'populations'. However, to enhance the species' long-term adaptability and resilience, increasing genetic diversity through genotype mixing at a new site is recommended. Given the species' unique genetic context, this intervention should be preceded by controlled crossing trials and offspring monitoring to assess the fitness of the mixed-source planting. The crossing trials can be undertaken at ABGMA which maintains a living collection representing all four sites.



Conservation genomics of *Grevillea shiressii* in support of management..

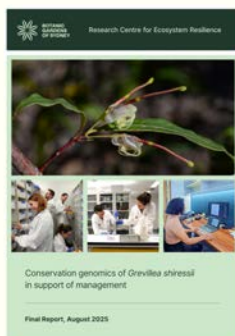
Alyssa Martino, Caroline Cristofolini, Jia-Yee Samantha Yapp, Maurizio Rossetto

This genomic study was conducted to support the conservation and management of *Grevillea shiressii* (Mullet Creek Grevillea), a Vulnerable shrub endemic to the Central Coast of New South Wales. Using high-resolution genomic data, we assessed genetic diversity, population structure, and connectivity within the species, and compared it to the related Queensland endemic, *G. singuliflora*, as well as other *Grevillea*s from New South Wales previously analysed by ReCER.

Our analyses indicate that *Grevillea shiressii* is genetically distinct and exhibits extremely low genetic diversity within its two populations. The observed very low heterozygosity in each population, suggests sustained inbreeding occurring within each population, resulting in each population being only represented by a single genet. One genet comprises individuals from subpopulations near Mooney Mooney Creek and its surrounds. The other genet includes individuals from Myron Brook. The naturalised Merewether population belongs to the Myron Brook genet, indicating the site is the likely provenance of these individuals. The planted individuals sampled from Mangrove Creek Dam Picnic Area and Hunter Regional Botanic Gardens belong to the Mooney Mooney genet.

We confirm hybridisation has occurred between *G. shiressii* and *G. speciosa*, as well as between *G. shiressii* and an unknown species. According to nursery records, these hybridisation events occurred naturally. Ongoing vigilance is needed to detect potential hybrids in wild populations and to manage the risk of genetic swamping. Given the extremely small population size and low genetic diversity detected, the species has limited adaptive capacity. Although translocation may help to increase plant numbers and support species survival, it is important to weigh the costs and benefits – particularly when resources might be better directed towards species with greater need or chances of recovery.

If conservation action is undertaken, we recommend maintaining the two genets ex-situ as insurance to safeguard the species' survival. Controlled crossing trials in ex-situ conditions may help to introduce limited new diversity; however, it is essential to verify that the progeny are viable, genetically pure, and the result of cross-pollination rather than selfing. Introducing individuals from the Mooney Mooney genet into the naturalised Merewether population could serve as a test case for cross-pollination success.



Conservation genomics of *Leionema lamprophyllum* subsp. *fractum* in support of management. .

Manuela Cascini, Jia-Yee Samantha Yapp, Maurizio Rossetto

Leionema lamprophyllum subsp. *fractum* S.A.J.Bell (Rutaceae) is a critically endangered shrub with an extremely restricted and disjunct distribution. Its two known populations are 200 km apart, with a population at the Broken Back Range of Pokolbin State Forest, and another at the Munghorn Gap Nature Reserve near near Mudgee. This study used genome-wide SNP data to investigate *L. lamprophyllum* subsp. *fractum*, testing its distinction from other taxa and assessing genetic diversity and gene flow patterns to inform its conservation management. Our findings indicate that *Leionema lamprophyllum* subsp. *fractum* is genetically distinct from other subspecies (subsp. *orbiculare*, subsp. *lamprophyllum*, subsp. *obovatum*). There is evidence to suggest that subsp. *fractum* is polyploid, with a genome size that is approximately three times larger than that of the geographically most proximate subspecies, subsp. *orbiculare*, located approximately 100 km away. The two disjunct populations of subsp. *fractum* exhibited low genetic diversity and slight differentiation from each other. Based on these results, we recommend conducting further surveys in unsurveyed areas with suitable habitat, as the identification of additional populations may yield further insights about the subspecies' ploidy and contribute to a broader understanding of ploidy variation across the species. We also recommend testing the viability and evolutionary representativeness of existing seeds stored at the Australian PlantBank to assess their potential for future propagation and conservation efforts.

Conservation genomics of *Leionema westonii* in support of ex-situ management.

Manuela Cascini, Jia-Yee Samantha Yapp, Elish McMaster, Maurizio Rossetto

Leionema westonii is a critically endangered shrub, known from a single, extremely small population within Oxley Wild Rivers National Park on the Northern Tablelands of New South Wales. This conservation genomics study, funded by the NSW Government's Saving Our Species (SoS) program, aimed to assess the species' genetic distinctiveness and genetic health, and to provide genomic based recommendations for its conservation. The results confirm that *L. westonii* is genetically distinct from the other *Leionema* species included in this study. Within *L. westonii*, very low genetic diversity remains, with individuals forming closely related family units. These patterns are consistent with a population bottleneck in a disturbance-prone landscape, leading to inbreeding among close relatives. A few instances of near identical individuals were also detected, although it is unclear whether this is due to the species persisting vegetatively or sexual reproduction between highly related individuals. During the study, ReCER became aware of an ex-situ collection of *L. westonii*. The genetic diversity represented by this collection is unknown and genetic screening is required to determine its composition. Controlled crossing trials under ex-situ conditions will help to understand the species' reproductive biology. If no viable progeny is produced, it will be important to weigh the costs and benefits of further intervention, particularly if resources could be better directed towards species with greater need or chances of recovery.



Updated report on the conservation genomics of *Lenwebbia* sp. Main Range.

Alyssa Martino, Jia-Yee Samantha Yapp, Maurizio Rossetto

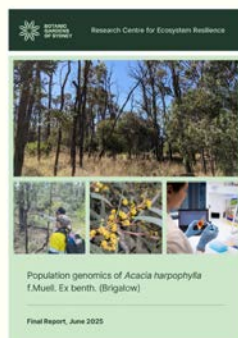
In 2022, The Royal Botanic Gardens was contracted by the DPE to conduct a conservation genomics study on *Lenwebbia* sp. Main Range to guide the development of ex-situ collections that can subsequently be used in research and restoration programs. The results of the 2022 study indicated more sampling was needed to understand the complex relationship between *L. sp. Main Range*, *L. sp. Blackall Range*, *L. prominens*, and *L. lasioclada*. Here, our updated findings from 177 individuals of *Lenwebbia* largely correspond with those of the 2022 report. We identified genetically intermediate individuals of all three species, indicating these lineages form part of a species complex that are openly hybridising. Further, genetic diversity was comparable between all species. Assessment of the newly acquired material within the ex-situ collection determined the collection of *L. sp. Main Range* contained duplications which can be reduced to improve nursery resource efficiency. Given the evidence for a species complex, we recommend managing *Lenwebbia* spp. as a complex for effective long-term conservation. We recommend implementing controlled inoculation trials and field assessments to evaluate myrtle rust susceptibility across taxa, and pursuing controlled hybridisation experiments, particularly focusing on introgression resistance traits into susceptible *L. sp. Main Range* individuals. Given the observed admixture, there is potential to harness existing genetic diversity for resistance breeding.

Other unpublished reports

Population genomics of *Acacia harpophylla*

Eilish McMaster, Maurizio Rossetto

This study examines the genetic diversity, population structure, and conservation considerations for *Acacia harpophylla* (Brigalow), a tree species native to eastern Australia. A total of 225 individuals were sampled from 39 sites across Queensland and New South Wales. Results showed low population structure and strong gene flow among sites, even those hundreds of kilometres apart, indicating that genetic material (seeds or pollen) is moving effectively across the landscape. Differences between trees mostly followed an isolation-by-distance pattern, meaning trees that are closer together tend to be more genetically similar. The species overall exhibits high genetic diversity and low levels of inbreeding, both indicators of good genetic health. However, around 14% of individuals showed unusually high genetic variation within themselves, consistent with polyploidy (having extra sets of chromosomes), a condition often linked to clonality. These potentially clonal individuals were mainly found at a few sites, where a lack of seedlings suggests limited or no sexual reproduction. These findings have direct implications for conservation and restoration. While Brigalow shows broad genetic connectivity and resilience, areas with high levels of clonality may face long-term reproductive challenges. Restoration efforts should prioritise the use of genetically diverse, sexually reproducing individuals from multiple populations, avoid sourcing from highly clonal sites, and aim to maintain or enhance gene flow across the landscape.



Conservation genomics of *Bertya opposens* in support of management

Saphira Bloom-Quinn, Marlien van der Merwe
A report to Fields Environmental Solutions

Bertya opposens (F.Muell. ex. Benth.) Guymer is a shrub or small tree from Queensland and New South Wales. It has a scattered distribution and is only known from two sites in New South Wales: a small population in Nurrungal and a large population at Jacks Creek State Forest. One or two other populations may exist on private property near Coolabah and Cobar. It is considered at high risk of extinction in New South Wales and is listed as vulnerable. Halford and Henderson (2002) recognised 28 species of *Bertya*. They examined 48 specimens of *B. opposens* and noted morphological variation in habit, indumentum colour and leaf shape across its range, however, they did not consider this variation merited formal recognition. Fatemi et al. tested the revision of Halford and Henderson (2002). For their analysis of *B. opposens*, they examined 12 vouchers, of which three originated from New South Wales. Using phenetic analyses, they determined that *Bertya* sp. (Clouds Creek SF, M. Fatemi 4) warrants species recognition separate to *B. opposens*.

This conservation genomics study aims to provide genetically informed recommendations for the management of the species. Primarily, the genetic suitability and health of the proposed seed source site, Jacks Creek State Forest. Additionally, this study aims to assess genetic diversity across the range of *B. opposens* by examining representative samples from Queensland and comprehensive samples from New South Wales. This report also investigates the relationship of *Bertya* sp. (Clouds Creek SF) with *B. opposens* so as to consider it in relation to conservation management of the focus species. Lastly, it investigates the genetic representativeness of ex-situnursery samples held by BioBank.

The data reveals that Jacks Creek State Forest has moderately high genetic diversity and low inbreeding suggesting it is suitable from a genetic perspective as a seed source for augmentation in conservation projects.

Samples can be distinguished at just 5km distance, suggesting that more genetic variants will be captured with additional site sampling at Jacks Creek State Forest. The seedlings that were sequenced are representative of the diversity at Jacks Creek State Forest. Our analyses also show that *Bertya opposens* has low levels of inbreeding and clonality in wild populations, suggesting that the preferred mating system is outcrossing



(mating with unrelated individuals). Therefore, effective restoration work should minimise inbreeding by avoiding planting cuttings or seedlings from the same mother together.

We also find that populations from Fordsdale and Clouds Creek are highly differentiated from each other and from Jacks Creek State Forest, and probably represent a different species. This highlights the need for further taxonomic attention on the genus *Bertya* to resolve these issues, which is outside the scope of this study. The closest relatives to Jacks Creek State Forest were found in south-west Queensland: Teelba, Devine State Forest, Chesterton Range National Park and Orkadilla State Forest. These fall in the regions of Darling Downs, Maranoa and Warrego.

Conservation genomics of *Microtis angusii* in support of translocation.

Jia-Yee Samantha Yap, Maurizio Rossetto
A report to Transport for New South Wales

Microtis species are morphologically similar, requiring genetic analysis for accurate species identification. The endangered *Microtis angusii* closely resembles the more common *M. parviflora* and *M. unifolia*, and they may occur sympatrically. As *Microtis angusii* is suspected at the proposed Wakehurst Parkway (WHPW) improvements project site, we conducted a genomic study to verify species identity, assess genetic diversity and inform translocation.

Our analyses identified two distinct genetic groups at WHPW. One group includes individuals morphologically identified as *M. angusii* from the Type location and other sites in Ingleside. The second comprises individuals identified as *M. parviflora* sampled from multiple locations. Additionally, we detected a small number of putative hybrids. Since orchids readily hybridise, it is important to prevent the introduction of other *Microtis* species into the translocation of *M. angusii*. Morphological misidentifications were also observed, reinforcing the necessity of genetic data for accurate classification.

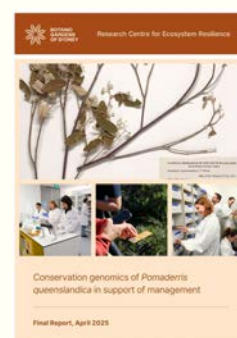
Our findings indicate *M. angusii* at WHPW exhibit high levels of kinship, consistent with clonality or self-pollination. Genetically distinct individuals (genets) were however detected, and they were genetically unique compared to *M. angusii* populations from elsewhere, emphasizing the importance of conserving genetic diversity at WHPW. Given that the proposed translocation site south of WHPW contains *M. parviflora*, we recommend selecting an alternative site devoid of *Microtis* species to prevent hybridisation. Only two genets of *M. angusii* were salvaged, and we advised that the translocation include *M. angusii* from other locations, following our recommendations. We emphasise that all individuals targeted for planting should be genetically tested to maintain genetic purity and diversity to support long-term sustainability of the planted population.

Conservation genomics of *Pomaderris queenslandica*

Saphira Bloom-Quinn, Marlien van der Merwe
A report to Fields Environmental Solutions

Pomaderris queenslandica (C. T. White), known commonly as 'Scant Pomaderris', is a shrub with a scattered distribution across Queensland and New South Wales. In NSW, it is listed as endangered under the BC Act 2016, threatened by habitat loss and other factors. The two focus populations of this report are Jacks Creek State Forest, a wild population, and Velyama Offsets, a restored population. They are located approx. 40km apart, south of Narrabri in northern NSW. Plants at Velyama Offsets were germinated from seed from a now-cleared wild site, Leard State Forest, and it has since also been augmented with additional material including from Jacks Creek State Forest. This conservation genomics study aims to provide insight into the genetic diversity and relatedness of the two sites, as well as placing them in context of the species more broadly. Based on the genetic findings we provide advice for the management of the species.

We find that the two sites of interest, Jacks Creek State Forest and Velyama Offsets are clearly differentiated from each other, but that there is almost no variation within a site. All tested material at each site was respectively recovered as a single genet (clone), except for a single individual at Jacks Creek State Forest that was recovered as a unique genet. All tested nursery samples were recovered as the same dominant genet at Jacks Creek State Forest. The same genet found at Velyama Offsets can also be found nearby at wild sites Gunnedah and Deriah Aboriginal Area. We did not find any evidence that reproduction is occurring between the genets at Velyama



We did not find any evidence that reproduction is occurring between the genets at Velyama Offsets and Jacks Creek State Forest. In terms of individual variability (heterozygosity), all individuals were highly heterozygous. This is often found in asexually reproducing or polyploid species. Other wild sites included in the study show similar patterns, suggesting that such 'single genet sites' are 'typical' for the species. The data indicate that reproduction, at both study sites as well as the other sampled sites, is likely asexual, in line with other research that found asexual reproduction was very common in the genus *Pomaderris* (Chen et al. 2019). In the case of *Pomaderris queenslandica* it is also most likely that seeds are produced via apomixis – a mechanism of seed production in the absence of fertilisation and recombination.

Although the absence of sexual reproduction raises concerns about the long-term adaptive potential of the species and the accumulation of harmful mutations, apomixis can also be viewed as a legitimate evolutionary pathway that ensures genotypes 'proven' to work at a particular site persist without being 'mixed up' by sexual reproduction. In fact, asexual reproduction can be a winning strategy especially in harsh and isolated environments or where there is mate scarcity.

For management, we recommend a focus on collecting small amounts of seed per individual, instead focussing on collecting from multiple individuals. While material from Velyama Offsets and Jacks Creek State Forest can be mixed in translocation these may not reproduce with each other and should be monitored so that Jacks Creek State Forest does not swamp the material from Leard State Forest. We also recommend seed is sampled from known Velyama Offsets (Leards origin) mothers, clearly labelled, and germinated for further restoration work.

Foredune restoration at the Worimi Conservation Lands: Genetic differentiation and diversity in a translocated population of coastal spinifex.

Jason Bragg

This report describes a genetic study of a beach grass (*Spinifex sericeus*) population at the Worimi Conservation Lands, NSW, Australia. At this location, a foredune became eroded, leading to the exposure of a site with significant cultural value. A project was initiated to stabilize the foredune, which included the planting of coastal spinifex. Spinifex plants were obtained from a nursery for planting at the site. This report examines the genetic variation in Spinifex plants near the planting site (hereafter, the 'local population'), and in the plants that were translocated to the site (the 'translocated population').

The local population and translocated population of Spinifex were weakly genetically differentiated from each other ($F_{ST} = 0.21$). This level of differentiation is appropriate, especially as it appears to reflect a gradual increase in differentiation between sites as a function of their distance apart. Individual plants in the translocated population showed a slightly elevated tendency to be clonal, or to be closely related, relative to individual plants collected from natural populations. This is likely to slightly reduce the genetic diversity in the translocated population. However, the number of plants for translocation was quite large (hundreds), so that a substantial number of genetically unique individuals were available for planting. The translocation population was obtained from a region that currently experiences temperature conditions similar to those that are predicted for the local population site in 2070.

The *Spinifex sericeus* population that was translocated to the beach at Worimi Conservation Lands is likely to bring a suite of novel alleles to the site, and promote adaptive capacity. The observed level of differentiation between the local population and the translocated population is unlikely to result in incompatibility. The source population is also likely suited to changes in climate that are predicted for the region of the Worimi Conservation Lands.



Articles

Hedging our bets: partnering horticulture and conservation

Chantelle Doyle

For the team at the Research Centre for Ecosystem Resilience (ReCER), a request from the Blue Mountains Botanic Garden to design a hedge of the towering *Nothofagus moorei*, or Antarctic beech, sparked a unique collaboration between science and horticulture. What began as a practical garden upgrade has grown into a pioneering conservation project, blending genetics, ecology, and design to safeguard one of Australia's most ancient and vulnerable trees. [Read more](#)



Persoonia conservation and the power of community

Chantelle Doyle

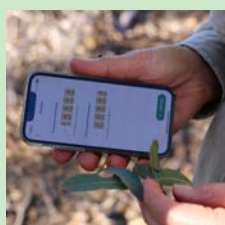
In the lower Hunter Valley, a new nature reserve has become a sanctuary for one of Australia's rarest plants, with scientists, First Nations leaders and the local community collaborating. The collaborative efforts include translocation, with a planting layout designed using genetic information to minimise inbreeding and maximise genetic diversity in the next generation. [Read more](#)



Cascading questions for leafless Bossiaea

Chantelle Doyle

Working with stakeholders from different Australian states, geneticists have helped to clarify taxonomy and conservation planning for seven leafless Bossiaea species, five of which are threatened with extinction. [Read more](#)



New Update

ReCER Field Collection app

In 2025, the ReCER Field Collection app was updated to incorporate additional fields related to seed collection. Our Field Collection app is a mobile app that enables plant field collectors to accurately record field data associated with samples using a digital device (smart phones and tablets). The app is freely available for other field collectors and can be downloaded from the [Apple App Store](#) or [Google Play Store](#).

Seed production areas for climate-resilient restoration

Marlien van der Merwe, Tricia Hogbin

A new collaborative research project will help increase the availability of genetically diverse native seed for climate-resilient restoration. Seed production areas can produce vast quantities of quality, genetically diverse seed to support climate-resilient restoration, if designed and managed correctly. Ongoing monitoring and evaluation are vital to ensure seed quality.

The genetic health and representativeness of a network of seed production areas established by Murray Local Land Services is being assessed by the Research Centre for Ecosystem Resilience (ReCER) at the Botanic Gardens of Sydney in a new project supported by the NSW Environmental Trust. Results will guide the development of protocols to assess, monitor and improve seed production areas. [Read more](#)



Saving the Eastern Suburbs Banksia Scrub.

Chantelle Doyle

A group of passionate golfers and volunteer Bushcarers, are working with geneticists to determine why Wallum Banksia, *Banksia aemula*, is not recruiting in the critically endangered Eastern Suburbs Banksia Scrub. [Read more](#) (page 18).



Application of genomic guidance

Climate-ready: Planting seeds of resilience in Yass Valley

Yass Area Network share how the Restore and Renew webtool is helping to guide seed selection for their climate-ready revegetation project.

[Read more](#)



Growing stronger: How new science is restoring the River Red Gum in the Hunter Valley

Rather than sourcing seed from small, remnant stands of River Red Gum and risking low genetic diversity, the NSW Saving our Species program used the Restore and Renew webtool's genomic guidelines to identify multiple sources, including 'future climate matched' sites further north.

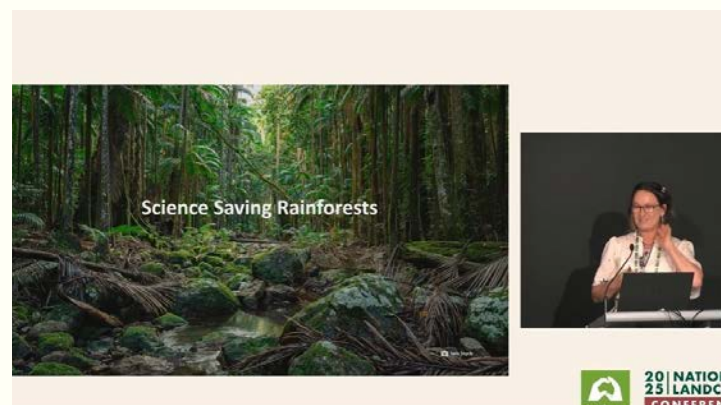
[Read and watch more](#)



Genetic Rescue of the Big Scrub Rainforest

Renee Borrow from the Big Scrub Rainforest Conservancy spoke at the 2025 National Landcare conference on the genetic rescue of the Big Scrub Rainforest, demonstrating how they are using an understanding of genetic neighbourhoods to design of their living seedbank plantation. Her presentation includes helpful practical information, including an overview of how they are using the freely available [ReCER Field Collection App](#) to collect metadata for the plants they collect propagule material from, and a smart planting layout that encourages cross pollination and maximises genetic diversity of seed.

[Watch here.](#)



ReCER e-newsletter

Research updates for restoration and conservation practitioners and policymakers

Sign up to the occasional ReCER e-newsletter for practitioner and policymaker updates, new publications, news, events and opportunities.

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Selected media features

[Restore and Renew featured on Network 10 Planet Shapers](#)

'Seeds of restoration' was an apt name for a feature on the Restore and Renew project on Network 10's TV show Planet Shapers. Watch it for a nice overview of what the Restore and Renew webtool is, the science behind it, and how it can help guide restoration of resilient, climate-ready native vegetation. [Watch](#)



[Genomics guiding Big Scrub restoration on ABC Landline](#)

Restoration genomic research by ReCER is guiding the establishment of seed production areas that will provide plants for restoration of Big Scrub rainforest. Less than 1 per cent of the original big scrub forest remains. Mark Dunphy, from the Big Scrub Rainforest Conservancy, describes the value of our genomic guidance in the feature. *"The problem...It's always been about local provenance. You must get the seed from the local area and plant it back. Well, that is all very fine if you have a big enough population, but if you've got bugger all left, then you've got to actually get material from outside and stop inbreeding."* [Watch](#)



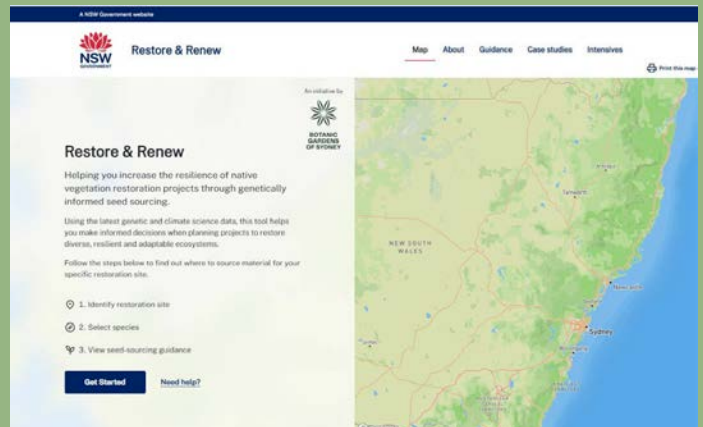
Restore and Renew moves to a new home

The Restore and Renew webtool moved to a new home on the AdaptNSW website December 2025.

The webtool first launched 8 years ago and has been sharing genetically informed seed sourcing guidance ever since. We're excited that this move, facilitated by a partnership with the NSW Department of Climate Change, Energy, the Environment and Water (DCCEEW), embeds genomic guidance into the NSW Government's program of action to inform and empower all sectors of society to adapt to climate change.

The move has been accompanied by the development of new resources, including:

- resources page full of helpful information about why it is important to consider genetics when sourcing plants for ecological restoration.
- FAQ and genomics glossary.
- Case studies highlighting how the webtool is guiding resilient restoration.
- Intensive reports (see below).



Explore the new webtool at

climatechange.environment.nsw.gov.au/resources/restore-and-renew-webtool

Visit Restore and Renew intensives projects page to download restoration genomics reports

Intensive projects are collaborations between ReCER and other organisations to obtain more detailed information beyond that provided in the Restore and Renew webtool. They are written up as publicly available reports that can serve as resources to inform restoration initiatives.

[Download intensives](#)

