Conservation genetics of high elevation endemic plant species of the Gondwana Rainforests of Australia World Heritage Area (Queensland section)

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Cover Image: The view from Lamington NP towards Springbrook NP, the two major parks that protect high elevation cloud forest in South-East Queensland. Image credit: Patrick Fahey

Executive Summary

This report provides the findings and management recommendations arising from the conservation genetics of high elevation endemic plant species of the Gondwana Rainforests of Australia World Heritage Area (Queensland section) project, a collaboration between Queensland Herbarium and Biodiversity Science, and the Office of the Great Barrier Reef and World Heritage, Department of the Environment, Tourism, Science and Innovation.

Climate change is recognised as a major threatening process for many of the flora species that contribute to the Outstanding Universal Value (OUV) of the Gondwana Rainforests of Australia World Heritage property. High elevation endemic species are considered to be amongst the most at risk due to their specialised habitats and limited ability to track changing climate conditions up slope. Given our growing understanding of the unique diversity present in the high elevation, cool temperate rainforests of the Wollumbin Caldera at the north of the world heritage property, building knowledge of the ecology, evolutionary history and threats the endemic flora species face is a pressing conservation issue.

Conservation genetics is a powerful tool in the modern conservationist's toolbox, allowing for a deep understanding of species' evolutionary relationships and distinctiveness, natural genetic patterns and adaptive potential in the face of threatening processes. Management recommendations can increasingly be targeted based upon species' individual genetic and reproductive processes to ensure that cost-benefits are maximised.

For this study, a full inventory of the flowering plants of the Gondwana Rainforests of Australia World Heritage Area (Queensland section) was built, including an assessment of how these species align with key values related to the Outstanding Universal Values of the property. Four target species were then identified for a conservation genetics study based upon their alignment with the OUV attributes and practical considerations: *Eucryphia jinksii*, *Pittosporum oreillyanum*, *Pomaderris notata* and *Syzygium nebulosum*. Fieldwork was then undertaken in Lamington, Springbrook and Border Ranges National Parks to locate wild populations of these four target species and to collect tissue samples for genotyping. In total, 174 field collected samples, 10 pre-existing herbarium specimens and 4 cultivated specimens were genotyped across the four target species, and these samples were analysed alongside significant outgroup samples of closely related congeners to investigate evolutionary patterns.

The study found strong evidence that all four of the target species represent highly distinct evolutionary lineages, supporting the hypothesis that the high elevation forests of the GRWHA have acted as important refuges for unique and significant biodiversity over evolutionary time periods. However, climate suitability modelling undertaken in this study and recent research suggests that ecosystem collapse may be a major risk to their continued persistence. This demonstrates that, along with the species that comprise them, these high elevation ecosystems are of high conservation value and additional management and protections may be warranted.

Species-level threats and genetic patterns differ significantly between the four target species, from *Eucryphia jinksii* which persists as a single genetic population with low genetic diversity facing acute risk of extinction, to *Pittosporum oreillyanum* that shows high genetic diversity and gene flow around the Wollumbin Caldera and faces no identifiable acute extinction risks. Putative adaptive potential in the face of climate change varied between the target species also, but none can be assumed to be able to survive a potential collapse of the cloud forest ecosystems in the face of lifting cloud levels. For

this reason, it is recommended that insurance collections be established for all species in case of stochastic (eg. wildfire, extreme drought, disease etc.) or gradual loss of wild populations.

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Key terms

Adaptability/Adaptive potential: The ability of a population to survive and reproduce under changing environmental conditions.

Allele: Alternate versions of DNA sequence at a given location within the genome.

Anthropocene: The current time period during which human activity is a major driver of planetary change.

Australasia: A geographic region consisting of Australia, New Guinea, New Zealand, New Caledonia and adjacent Pacific Islands.

Congener: Species belonging to the same taxonomic genus.

Conspecific: Individuals or populations belonging to the same taxonomic species.

DNA: Deoxyribonucleic acid; the molecule that carries genetic information and is the basis of inheritable traits.

Effective Population Size: The size of an idealised population which would give rise to the rate of inbreeding and genetic diversity loss observed in an actual population under consideration. This provides a representation of how many genetically unrelated individuals are taking part in reproduction within an actual population and is generally smaller than the census population size.

Gene flow: The movement of genetic material such as differing alleles (see above) between individuals or a group of individuals by processes such as dispersal of seed and pollen.

Genet: A set of genetically identical individuals that result from clonal reproduction such as vegetative spread or the production of clonal seed.

Genetic bottleneck: A sharp reduction in genetic diversity caused by a reduction in population size or by sampling of seed from too few individuals.

Genetic distinctiveness: How different the genetic diversity of a population is compared to the genetic diversity in other populations of the same species.

Genetic diversity: The totality of genetic variation present in a population and a determinant of adaptability and adaptive potential.

Genetic structure: The amount and distribution of genetic variation within and between populations across the landscape.

Genome: The full set of genetic information of an organism, consisting primarily of cellular DNA and/or RNA.

Graminoid: Plants with a grass-like habit, i.e. long, blade-like leaves and greatly reduced flowers.

Heterozygosity: The average proportion of DNA sites in the genome where the two copies (or alleles) are different across a sample of individuals. Heterozygous refers to having two different copies of DNA at a particular location within the genome, as opposed to homozygous (see below) where the two copies at a location are the same.

Homozygous: Having two identical copies of DNA at a particular location within the genome, as opposed to heterozygous where the two copies at a location are different. See above.

Hybridization: The successful interbreeding of two distinct populations or species.

Inbreeding: The mating of individuals that are genetically closely related within a population leading to the production of progeny.

Inbreeding depression: A reduction of fitness of offspring resulting from the interbreeding of parents that are genetically close relatives.

Isolation by distance: The term used to describe the change of shared genetic material across geographic space due to dispersal ability limiting the mating between individuals. Importantly this often does not lead to discrete population structure and local adaptation if populations are continuous across the landscape.

Maternal line: All offspring from the same mother plant.

Maintenance of maternal lines: The practice of keeping seed or other material collected from a particular mother plant identifiable and separate from that of other mother plants through the process of collection through to propagation and planting. Upon planting, maternal lines should be traceable to individuals but should be interplanted to maximise interbreeding and mixing of genetic diversity in progeny.

McPherson Range: The eastward spur of the Great Dividing Range running from approximately along the NSW-QLD border between approximately Wallangara in the west and Tweed Heads in the east. This includes the ranges contained in the Mount Barney NP, Border Ranges NP, Lamington NP and Springbrook NP.

Mother plant: An individual plant from which seed has been collected.

Outbreeding: The mating of individuals that are not genetically closely related leading to the production of progeny.

Outbreeding depression: A reduction of fitness of offspring resulting from the interbreeding of parents that are highly genetically distinct.

Plasticity: The capacity of a single genotype to produce different phenotypes (morphological, physiological, or behavioural traits) in response to varying environmental conditions.

Polyploidy: The possession of more than two complete paired sets of chromosomes, a condition common in plants and often associated with inter-specific hybridization.

Population: A group of individual plants growing in the same place at the same time and interbreeding freely.

Private alleles: Alleles observed only in a single population, thus being private to that population.

Progeny: Offspring of a plant, typically seed.

Putative: Generally thought to be or to exist or have existed.

Ramet: An individual organism which arises from clonal reproduction as a part of a clonal genet.

Regional Ecosystem (RE): Vegetation communities in a bioregion that are consistently associated with a particular combination of geology, landform and soil.

Relictual: Organisms, populations, or ecosystems that are surviving remnants of a formerly widespread species or group, now restricted to isolated, often specialized, habitats.

Self-Pollination/Selfing: The effective pollination of the flowers of an individual plant by pollen from that same individual.

Single Nucleotide Polymorphism (SNP): A position in a genome where a different nucleotide is present between individuals. For example, individuals from one population may be homozygous for a G nucleotide in a particular position in their genome, while those from a different population may be homozygous for an A nucleotide at the same position in their genome.

Site: A specific locality where genetic samples or seeds have been collected.

Stochastic: An event with a random probability of occurring that can be analysed statistically but predicted with low confidence.

Sustainability/Self-sustaining: The ability of a planting to survive and reproduce in the long-term with minimal further active investment.

Wollumbin Caldera: The large bowl-shaped geological feature resulting from previous volcanic activity of Wollumbin-Mt Warning. Here predominately referring to the rim of this geological feature which includes the southern and eastern erosional faces of the McPherson range in Border Ranges NP, Lamington NP and Springbrook NP.

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Introduction

Context

The Gondwana Rainforests of Australia World Heritage Area (hereafter GRWHA) is a World Heritage listed property consisting of many individual reserves across southeast Queensland and northeast New South Wales that contain most of the remnant warm temperate and subtropical rainforest found in the region. Within Queensland, five national parks form the northern extent of both the World Heritage property and warm temperate rainforests in Australia, namely Springbrook NP, Lamington NP, Mount Chinghee NP, Mount Barney NP and Main Range NP (UNESCO World Heritage Centre 2025). Springbrook and Lamington NPs sit on the northern and northwestern edge of the Wollumbin Caldera (part of the wider Mcpherson Range) and reaching elevations of over 1100m in places (Manley *et al.* 2020). These national parks abut the NSW-QLD border and other interstate reserves; some also part of the GRWHA property. Of particular interest amongst these NSW reserves for this study is Border Ranges NP, which captures the western edge of the Wollumbin Caldera with areas of similar high elevation as seen in Lamington and Springbrook NPs.

Two of the three criteria for the property's Outstanding Universal Value relate to the high biological value and diversity of these reserves (UNESCO World Heritage Centre 2025):

- Criterion ix: be outstanding examples representing significant on-going ecological and biological processes in the evolution and development of terrestrial, fresh water, coastal and marine ecosystems and communities of plants and animals.
- Criterion x: contain the most important and significant natural habitats for in-situ conservation of biological diversity, including those containing threatened species of outstanding universal value from the point of view of science or conservation.

These criteria are strongly linked to the flora species of the property, including species that represent the following OUV attributes:

- ix(a) Outstanding record of the 'Age of the Pteridophytes' from the Carboniferous Period with some of the oldest elements of the world's ferns represented
    - This value is not addressed in this study.
- ix(b) Outstanding record of the 'Age of Conifers' in the Jurassic Period with one of the most significant centres of survival for Araucarians
    - This value is not addressed in this study.
- ix(c) Primitive angiosperms
    - This is somewhat outdated terminology but is here taken to mean early-diverging Angiosperm lineages i.e. the ANA Grade, Ceratophyllaceae, Chloranthaceae and Magnolids.
- ix(d) Relict angiosperms
    - This is here taken to mean angiosperm species that have persisted in the rainforests of the property as their close relatives (i.e. congeners) have gone extinct or only survived in other temperate rainforests in southern Australia, New Zealand or South America. Examples include *Nothofagus moorei*, *Eucryphia jinksii* and *Akania bidwillii.*
- ix(e) Golden age of rainforests
    - Here taken to reference the abundance of Gondwanan plant families in the rainforest flora, including, but not limited to, Araucariaceae, Cunoniaceae, Myrtaceae and Proteaceae.

- ix(f) a unique record of vegetation development in the Miocene, particularly the origins and rise to dominance of ix(f)1 cold adapted (temperate) flora
    - An unclear value as the much of the GRWHA represent areas where temperate rainforest has declined and been invaded by subtropical rainforest species during the Miocene rather than developed and risen to dominance
- ix(f) a unique record of vegetation development in the Miocene, particularly the origins and rise to dominance of ix(f)2 dry adapted floras
    - Here taken to reference the transitional sclerophyll forest and heathlands that occur on rainforest margins from which much of the current dry flora of Australia is believed to originate.
- ix(l) Outstanding examples of ongoing evolutionary processes for flora and fauna
    - Here taken to reference both ongoing speciation within the property and between the Gondwanan Rainforests, Tropical Forests of northeast Queensland and temperate rainforest of southern Australia as well as the continued integration of lineages of Sunda origin into rainforest communities and the decline of cool temperate adapted Gondwanan lineages on geological timescales.
- x(a) Rare and threatened plants
    - Here taken to include narrow range endemics and taxa of conservation significance including those listed under State and Commonwealth conservation legislation.
- x(f) Relict and primitive plants
    - See values ix(c) and ix(d) above.
- x(i) Rare and threatened flora and fauna species that are rainforest specialists
    - With regards to flora species, this is here taken to reference the subset of species representing value x(a) that are restricted to rainforest habitat.
- x(j) Other vegetation including a diverse range of heaths, rocky outcrop communities, forests and woodlands with a high diversity of plants and animals that add to habitat for rare, threatened and endemic species
    - This value is of relevance for rare and threatened flora of high elevation heaths which hold a significant amount of unique diversity.

An increasingly pressing threat to many of the flora species that represent the OUV of the GRWHA property is climate change, which threatens to have both direct impacts such as increased temperatures and changes to rainfall regimes, but also indirect impacts such as increased wildfire and disease risks. High elevation flora communities are at increased threat from climate change as they are often both dependant on specific climatic conditions for persistence and, unlike communities of lower slope positions which can potentially track conditions upslope, generally have nowhere to move to track their climatic niche.

In the GRWHA (QLD section), two dominant Regional Ecosystems (RE's) are restricted to high elevations, and both are largely restricted to the World Heritage property (Figure 1; Department of the Environment, Tourism, Science and Innovation 2025a; b). Both RE's include Gondwanan and early diverging angiosperm species amongst their dominant tree taxa and there are several flora species limited to only these communities (Table 1; Department of the Environment, Tourism, Science and Innovation 2025a; b). The taxa endemic to these two RE's are subject of this report, which explores the

potential impacts of climate change and management actions needed to mitigate these impacts at a species-specific level.

Table 1: An overview of the two high-elevation regional ecosystems that are habitat for the high elevation endemic plant species that are the topic of this report.

High elevation Regional Ecosystem	Community type	Characteristic species
12.8.5	Complex notophyll vine forest (≥600m elevation)	*Argyrodendron actinophyllum*, *Sloanea australis*, *S. woollsii*, *Cryptocarya erythroxylon*, *Ficus watkinsiana*, *Dysoxylum fraserianum*, *Ackama paniculosa*, *Karrabina benthamiana*, *Orites excelsus*, *Acmena ingens*, *Syzygium corynanthum*, *S. crebrinerve* and *Citronella moorei*
12.8.6	Simple microphyll fern forest	*Nothofagus moorei* and/or *Doryphora sassafras*, *Ackama paniculosa*, *Orites excelsus*

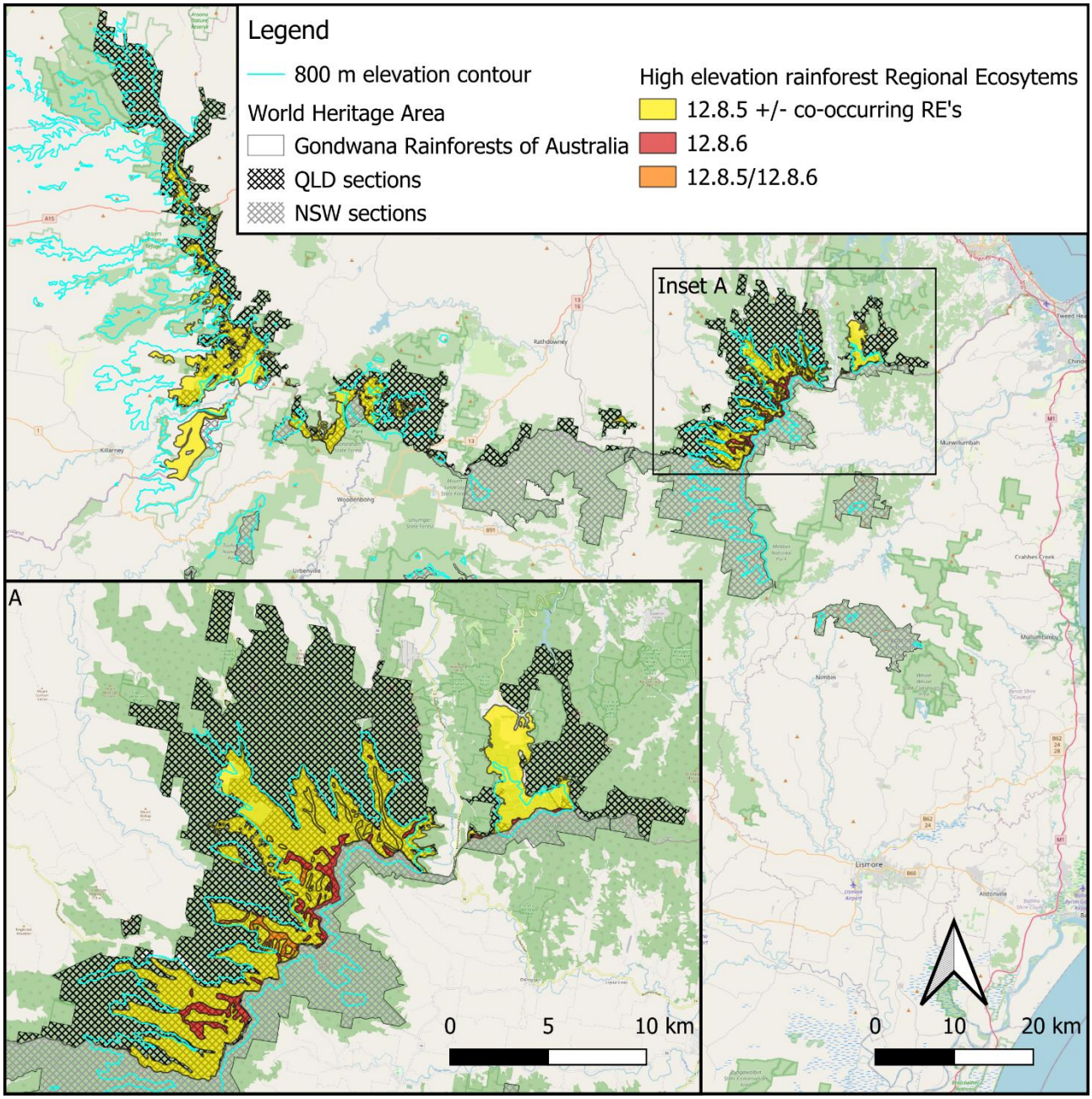

Figure 1: Map of the high elevation areas (800 m+, teal contour) in the Queensland section of the Gondwana Rainforests od Australia World Heritage Area (dark hashing). Overlaid is the distribution of the two high elevation Regional Ecosystems (12.8.5 and 12.8.6) which support the species that form the topic of this report. Orange areas represent the occurrence of both RE's in proximity below the scale that could be mapped independently. Inset A shows Springbrook NP and Lamington NP, where the highest concentration of narrow range, high elevation rainforest taxa occur.

High elevation cloud forests

Australian high elevation ecosystems take varying forms dictated by the local abiotic conditions, from the alpine meadows of the Australian Alps and Tasmania where cold temperatures are the driving factor (Kirkpatrick and Bridle 1998), to the tropical cloud forests of Mount Bartle Frere and Mount Bellenden Ker that experience some of the wettest conditions on the continent (Hoyle *et al.* 2023) due to persistent cloud cover. The floral community assembly patterns of the cloud forests of the GRWHA property, particularly those along the NSW-QLD border, are heavily influenced by both the wet conditions and cool temperatures of the high elevations where they occur. To further this point, the species make up of RE 12.8.6, particularly the dominance of *Nothofagus moorei* and *Doryphora sassafras,* marks it as the most northerly extension of cool temperate forests in Australia, growing at a latitude otherwise characterised by warmer subtropical conditions. Likewise, one hypothesis regarding the environmental restriction of several high elevation endemic species to these areas is the consistently high air and soil moisture availability (Kooyman *et al.* 2014), potentially supporting species that cannot survive at lower elevations where moisture levels vary more significantly temporally.

Floristically, these cloud forests contain a mixture of common rainforest taxa and narrow-range high elevation endemics. They include a higher proportion of Gondwanan-lineage taxa than lowland subtropical rainforests that have seen greater influence by the arrival of Sunda lineages, most of which have evolved in more tropical climates (Yap *et al.* 2018). The endemic elements of the high elevation flora are a mix of species from genera that are widespread and common in rainforests (e.g. *Pittosporum oreillyanum* and *Syzygium nebulosum*), genera that are associated with high elevation and/or exposed habitats (e.g. *Coronidium telfordii*, *Lenwebbia* spp., *Pomaderris notata* and *Uromyrtus lamingtonensis*) and genera associated with cool temperate rainforests that are largely absent from surrounding subtropical and tropical rainforests (e.g. *Eucryphia jinksii* and *Nothofagus moorei*).

The threat posed by climate change

These cloud forests and the endemic species they support are at high risk from imminent impacts of climate change. Particularly concerning is the lifting of cloud cover and an associated decrease in air and soil moisture levels (Narsey *et al.* 2020). Recent modelling by the Australian Bureau of Meteorology has suggested a ~1 m per year lifting of average cloud levels is possible (Narsey *et al.* 2020). In addition, as temperatures rise, there is an increasing risk of the cool temperate forests being exposed to prolonged heat stress-inducing conditions to which they are not adapted (Narsey *et al.* 2020). Furthermore, decreased moisture and rainfall levels is coupled with increased fire risk, a disturbance event that rainforest taxa are generally poorly adapted to.

Layered on top of this is the building evidence that these remnant cool temperate rainforests represent climatically buffered areas that have experienced far less change to their local climate than the broader landscape, allowing species that have limited plasticity and adaptive potential to persist in place (Kooyman *et al.* 2014). This leaves these species poorly equipped to survive the rapid environmental changes of the Anthropocene. Coupled with this is the fact that the realised niche of these high elevation endemics occurs as scattered ‘sky islands’ in a sea of conditions outside this realised niche. This suggests it is unlikely these species will be able to move along with their preferred climate envelope, meaning the ability of these species to persist without human intervention is uncertain and potentially very limited.

Conservation genetics of rare plants

Population genetics provides a tool to understand many aspects of the reproductive and evolutionary biology of threatened species that are otherwise difficult to study. In addition to testing species boundaries to ensure real and sensible evolutionary units are the basis of conservation listings (Cascini *et al.* 2025), conservation genetics can (Rossetto *et al.* 2021):

- Explore the breeding system, level of inbreeding and clonality of natural and disturbed populations.
- Investigate patterns of gene flow and genetic divergence between populations.
- Estimate levels of genetic diversity and adaptive potential of rare and threated species in the face human induce threatening processes such as climate change and novel diseases.

While the level of confidence in the patterns observed across most of these areas is slightly lower than if experimentation was to be conducted, the time and resources needed are far less, meaning undertaking study of multiple species concurrently is feasible. This allows for understanding of entire vegetation communities to be estimated based upon the individual species that they consist of. Despite not directly investigating the adaptive pathways responsible for environmental tolerances and their plasticity under different conditions, significant literature shows that neutral markers show patterns in line with adaptive markers (Lind and Lotterhos 2025; Dimon *et al.* 2026). Therefore, adaptive potential can be measured indirectly using neutral markers to test levels of diversity and gene flow across the landscape

Once a strong understanding of a species biology is established, population genetic data can then be used to guide and optimise conservation management activities to help achieve maximal benefits for the resources invested (Rossetto *et al.* 2021, 2023; Cascini *et al.* 2025). Guidance for managers can take the form of data driven prioritisation, risk assessments and recovery action planning, and the optimisation of translocations and ex-situ collections to ensure genetic diversity is conserved as insurance against systematic and stochastic threats to wild populations.

Identifying Target species

Inventory of flowering plants from the Gondwana Rainforests of Australia World Heritage Area (QLD section)

To identify suitable target species for conservation genetic study during this project, an inventory and classification of all flowering plant species native to the GRWHA (QLD section) was built using a quantitative approach of defining a species distribution as all areas within 500m of a high-quality occurrence record. This proved somewhat imprecise for measuring high elevation endemism given the complex topography of the study region and so a qualitative final step was used to identify species that met these criteria.

Initial species lists were downloaded from WildNet for the five individual national parks that constitute the GRWHA (QLD section): Main range NP, Mount Barney NP, Mount Chinghee NP, Lamington NP and Springbrook NP. These were then combined to form a single species list for the entire GRWHA (QLD section), however as parts of the constituent parks are not included in the GRWHA, a small proportion of species on the final list are not known to occur the GRWHA (QLD section) but were included in further analyses as they may still be of interest regarding management of the individual national parks.

A name check was then conducted for this species list against the Australian Plant Census (APC) (Council of Heads of Australasian Herbaria 2025), which is utilised by the Atlas of Living Australia (Atlas of Living Australia 2025), the data source from which species records were later sourced. Where a species' scientific name differed between the two data sources, (largely due to differences in generic classification and species/subspecies delimitations) the APC taxonomy was adopted to allow the use of ALA records. Where a species recognised by the Queensland Flora and Fungi Census (Queensland Herbarium 2025) was considered conspecific with a related species in the APC, the broader taxonomic definition employed by the APC was adopted. Finally, there were a small number of recently described species that are recognised as valid but that have no records available on ALA yet, and thus information was drawn from the literature where appropriate, however, no quantitative analysis could be undertaken for these species.

Another group which had to be excluded from quantitative analysis was species with a sensitive status in QLD, which for this study was all members of the orchid family, Orchidaceae. Record locations for these species are obscured on ALA, and non-obscured records could not be sourced within the time frame of the first phase of this project. Thus, only factors sourced from literature (namely the conservation status, growth form and status as a rainforest species or not) of Orchid species is provided in the inventory associated with this report.

In total, 1229 flowering plant species from 138 taxonomic families are included in our species list for the national parks that constitute the GRWHA (QLD section). Overall, the species level representation of taxonomic families is consistent with the broader Australian flora, with the five most represented families being: Leguminosae (Fabaceae) with 103 species, Orchidaceae with 99 species, Myrtaceae with 98 species, Poaceae with 70 species and Asteraceae with 59 species. The bulk of families (91 families) are represented by fewer than 5 species in the GRWHA (QLD section). At the genus level 570 genera are represented on the GRWHA species list. A total of 331 genera are represented by a single species, with the five most diverse genera being: *Eucalyptus* (36 species), *Acacia* (29 species), *Solanum* (18 species), *Pterosylis* (16 species) and *Cyperus* (14 species). The full list of species can be found in the inventory spreadsheet accompanying this report.

Of the 1229 flowering plants on the assembled species list, 440 were confirmed as rainforest taxa from the literature, with a further 182 being classed as marginal rainforest species, meaning they occur both in the margins of rainforests and in wet sclerophyll forest. Table 2 summarises the growth form of the 1229 species, with the vast majority of species being terrestrial woody trees and shrubs (658 species) or non-woody herbs and graminoids (402 species). Other lifeforms including aquatic plants, epiphytes, mistletoes and climbers together make up a much smaller proportion of the species list, with 168 species in total. As shown in Table 3, 100 species on the species list had a conservation status across state and federal legislation, representing ~8% of the total number of flowering plant species.

Table 2: A summary of the growth forms of flowering plant species that occur within the national parks that constitute the GRWHA (QLD section), as determined from the literature.

Growth form	Number of species
Aquatic plants	2
Climber	113
Epiphyte	40
Graminoid	148
Herb	254
Mistletoe	13
Shrub	246
Shrub or small tree	180
Tree	233

Table 3: Summary of the number of species with a current conservation status under the Nature Conservation Act 1992 (NCA) and Environment Protection and Biodiversity Conservation Act 1999 (EPBC Act) that occur in the national parks that constitute the GHWA. Numbers in brackets show species listed at any level only under that act. Note at time of writing, some species have different listing levels between the two acts.

Act	Number of Critically Endangered taxa	Number of Endangered taxa	Number of Vulnerable taxa	Number of Near Threatened taxa
NCA – State level	10 (5)	13 (6)	54 (27)	21 (20)
EPBC Act – Federal level	4	6 (1)	32 (1)	-

Quantitative analysis of species list

All records for all species other than those discussed above were downloaded from the Atlas of Living Australia using the *Galah* package in R (Westgate *et al.* 2023) and filtered using the *processALA* package (Wilson 2025). The filtering process entailed splitting the records into type (observational records vs herbarium specimen backed records), and using the *FilterALAdata* function to remove duplicate records, records with missing coordinates and those identified as cultivated within the ALA data framework (note not all records from cultivation are identified as such within ALA and thus cannot be filtered out using automated processes). Initial testing showed the inclusion of observational records sometimes resulted in larger species distributions that were of questionable validity, and as it was not feasible to manually check the records and distributions for all taxa being investigated, the decision was reached to only utilise specimen-backed records for the quantitative analysis. This was on the basis that the identifications of specimen-backed records are significantly more reliable and therefore more confidence can be placed in the resulting species distributions.

Further filtering was then undertaken on the herbarium specimen-backed records to ensure only those with reliable locational information were employed in qualitative analyses. This secondary filter involved removing all records with no coordinate accuracy value or one above 5 km and those with a minimum distance to another record more than 5% of the maximum distance between any two records. The latter filter removed any outlying records that may have erroneous coordinates. This set of records was then used for each species to undertake the quantitative analyses outlined below.

Next, the *red: IUCN Redlisting tool* package for R (Cardoso and Branco 2025) was used to calculate each species area of occupancy (AOO) and extent of occurrence (EOO) using 2 km^2 resolution to provide range size estimates. In line with thresholds employed by the IUCN red list criteria and the Common Assessment Method (CAM) employed within Australia (IUCN 2012), species with AOO estimates of <500 km2 and/or EOO estimates of <5000 km2 (criteria for the *Endangered* status) are considered to have a restricted range, and species with an AOO estimate of <10 km2 and/or EOO estimate of <100 km2 (criteria for the *Critically Endangered* status) to be narrow ranged endemics.

To identify species endemic to the GRWHA (QLD section) a 500 m buffer around all records in the filtered dataset was established as a polygon map layer, and a 2km buffer added to the boundaries of the GRWHA (QLD section) in a separate polygon map layer. This approach was undertaken both to account for spatial uncertainty in the datasets and to capture records in habitat that may strictly lie outside the GRWHA (QLD section) but be part of contiguous ecosystems. These two polygon layers were then overlaid and the proportion of the species distribution that fell within the buffered GRWHA (QLD section) was calculated. A 70% threshold was used to identify species highly dependent on the GRWHA (QLD section) as habitat and a 90% threshold was used to identify GRWHA (QLD section) endemic species.

To identify high elevation endemic species, the proportion of the 500 m buffer around records that was above an elevation above 800 m was calculated. In this case a 90% threshold for the proportion above 800 m was used to identify high elevation endemic species and a 70% threshold used for species which primarily occur at high elevations. As much of the New England Tablelands bioregion lies above 800 m of elevation, several of the species identified as being either primarily of, or endemic to, high elevations were not narrow range endemics strictly associated with the high elevation rainforests of the GRWHA (QLD section), which were the species that this analysis sought to identify. Additionally, for a small number of species a lack of reliably georeferenced herbarium backed records

lead to a suspected overestimation of the proportion of the species distribution that sits above 800 m of elevation, as indicated in the findings of the report.

GRWHA (QLD section) endemic taxa

Nine flowering plant species met the implemented threshold to be considered GRWHA (QLD section) endemic species (Table 4), with a further seven species meeting the looser threshold to be considered highly dependent on the GRWHA (QLD section) as habitat (Table 5). Issues in the methodology used were identified as a species (*Solanum serpens*) was identified as a GRWHA (QLD section) endemic due to a lack of reliably georeferenced herbarium specimen backed records across much of its distribution. The majority of GRWHA (QLD section) endemic and dependant species are closely associated with volcanic geology that is exposed in many locations in and around the GRWHA (QLD section), with very few taxa of closed forest or woodlands included.

Table 4: Flowering plant species identified as endemic to the GRWHA (QLD section) by quantitative analysis and the habitat they occupy. Note that these findings are dependent on the availability and accuracy of georeferenced herbarium specimen backed records for the individual species.

Species identified as GRWHA (QLD section) endemics	Habitat
Coronidium telfordii	Rocky outcrops and ledges on the margin of *Nothofagus* forest on the McPherson Range
Eucryphia jinksii	Rainforest tree known only from a small number of stands in Springbrook NP
***Lenwebbia* sp. (Main Range P.R.Sharpe+ 4877)**	Shrub to small tree of rainforests on steep slopes of the Main and McPherson ranges
Parsonsia tenuis	Rainforest climber of high elevation areas of the McPherson Range
Senecio scabrellus	Rocky (Rhyolite) outcrops and ledges of the Main and McPherson ranges
Solanum serpens	Rare rainforest shrub of northern New South Wales and South-East Queensland
Uromyrtus lamingtonensis	Rocky outcrops and ledges at high elevations of the McPherson Range
Wahlenbergia scopulicola	Rock (Rhyolite) outcrops of the McPherson Range
Zieria montana	Rocky heath on the summit of Mt Barney

Table 5: Flowering plant species identified as dependant on habitat within the GRWHA (QLD section) by quantitative analysis (i.e. >70% of distribution with 2km of GRWHA (QLD section)) and the habitat they occupy. Note that these findings are dependent on the availability and accuracy of georeferenced herbarium specimen backed records for the individual species

Species identified as GRWHA (QLD section) habitat dependent	Habitat
Acronychia suberosa	Rainforest tree of restricted distribution on the McPherson, Border and Nightcap ranges.
Doryanthes palmeri	Rocky outcrops of the Main, McPherson, and Nightcap ranges and Wollumbin/Mt Warning
Philotheca obovatifolia	Rare heathland shrub with a disjunct distribution between the McPherson Range and Werrikimbe NP
Pittosporum oreillyanum	High elevation rainforests of the McPherson and Border ranges
Podolepis monticola	High elevation exposed slopes of the Border and McPherson ranges
Westringia rupicola	Rhyolite cliffs of McPherson Range and adjacent areas
Wahlenbergia glabra	Rocky (Basalt) outcrops and ledges of the Main and McPherson ranges

Narrow Range Endemics

The amount of variation in range size as measured by AOO and EOO was significant across the species for which it was calculated (1130 species excluding orchids), which is to be expected. Over 20% of species tested (236/1130 species) met both the AOO (<500 km2) and EOO (<5000 km2) thresholds from the IUCN red list and CAM *Endangered* criteria. This may in part be the result of our strict filtering of the distributional records resulting in under sampling of species ranges. This could be addressed in future by adjusting filtering to allow for observational records to be included in analyses without falsely overestimating species distributions. It also appears that this is not a strict enough criterion for defining narrow-range endemic species in isolation.

The thresholds from the *Critically Endangered* criteria (AOO < 10 km^2, EOO <100 km^2) proved more useful when identifying narrow range endemic flowering plants with the identified species presented in Table 6. Many of these species proved to be those restricted to the heathlands near the summits of Mt Barney and Mt Maroon. As Mt Maroon sits outside the GRWHA, this meant that a significant proportion of the identified narrow range endemics did not also meet our criteria for being GRWHA (QLD section) endemic or dependant (Table 6). Many of these narrow-range endemics have conservation listings already, but we identified a small number of species that may warrant a conservation assessment, which are discussed further later in this report.

Table 6 (overleaf): Flowering plant species identified as being narrow range endemics by meeting the range size thresholds adapted from the IUCN redlist and CAM Critically Endangered criteria.

Narrow range endemic species	Met AOO threshold	Met EOO threshold	GRWHA (QLD section) endemic or dependant	Current conservation status under NCA and EPBC Act
Acacia saxicola	Yes	Yes		Vulnerable / None
Astrotricha pauciflora	Yes	Yes		None / None
Bertya ernestiana	Yes	Yes		Vulnerable / Vulnerable
Eucryphia jinksii	Yes	Yes	Endemic	Critically endangered / None
Schoenus rupicola	Yes	Yes		None / None
Zieria montana	Yes	Yes	Endemic	Critically endangered / None
Arundinella grevillensis		Yes		Vulnerable / None
Coronidium lindsayanum		Yes		None / None
Coronidium telfordii		Yes	Endemic	None / None
Cupaniopsis tomentella		Yes		Vulnerable / Vulnerable
Gossia gonoclada		Yes		Critically endangered / Endangered
***Lenwebbia* sp. (Main Range P.R.Sharpe+ 4877)**		Yes	Endemic	Critically endangered / Critically endangered
Leptospermum barneyense		Yes		Endangered / None
Muellerina flexialabastra		Yes		None / None
Parsonsia tenuis		Yes	Endemic	Vulnerable / None
Podolepis monticola		Yes	Dependant	Vulnerable / None
Solanum serpens		Yes	Endemic	None / None
Tetramolopium vagans		Yes		Vulnerable / None
Uromyrtus lamingtonensis		Yes	Endemic	Vulnerable / None
Westringia rupicola		Yes	Dependant	Vulnerable / Vulnerable
Zieria adenodonta		Yes		Near threatened / None

High elevation endemics

This proved the most challenging characteristic to quantitatively evaluate. This is partly due to McPherson and Main ranges not reaching higher elevations than large areas of similar elevation in the New England Tablelands meaning several widespread species are classed as high elevation endemics under our criteria (Table 7). Underestimation of select species distributions, namely *Parsonsia fulva* and *Pentaceras australe,* due to a lack of reliably georeferenced herbarium backed records resulted in them incorrectly being recognised as being high elevation endemics. Finally, the steep, complex topography of the study area led to species known to only occur at high elevations (800+ m) not being identified in the analysis due to the 500 m buffer around records extending across steep slopes that drop below the elevational threshold over very short distances. Future work to broaden the pool of species records employed and high-resolution elevation maps may help address these issues with the methodology.

Table 7: Flowering Plant species of the national parks that constitute the GRWHA (QLD section) that met the distributional proportion thresholds to be classed as high elevation endemics. Note that some species do not meet the typical definition of being high elevation endemics due to the elevation of the New England Tablelands, and others may be affected by the availability of reliably georeferenced herbarium specimen backed records.

Species	High elevation endemism threshold met
Gaultheria viridicarpa	90%
****Parsonsia fulva***	90%
Trisetum spicatum	90%
Zieria montana	90%
Acacia adunca	70%
Agiortia cicatricata	70%
Berberidopsis beckleri	70%
Carex lobolepis	70%
Coronidium telfordii	70%
Eucalyptus banksii	70%
Eucalyptus codonocarpa	70%
Kunzea obovata	70%
Lenwebbia lasioclada	70%
***Lenwebbia* sp. (Main Range P.R.Sharpe+ 4877)**	70%
Olearia oppositifolia	70%
****Pentaceras australe***	70%
Thelionema grande	70%
Veronica grosseserrata	70%

*Proportion of species distribution above 800m (i.e. at high elevation) likely overestimated due to a lack of reliable records to use in analysis.

Species that may benefit from conservation assessment based upon findings of this report

One species stood out as potentially in need of a conservation assessment, *Coronidum telfordii*, as it met the criteria for being a GRWHA (QLD section) endemic, a narrow range endemic and a high elevation endemic. This species grows in small section of the McPherson Range on the edge of high elevation *Nothofagus* forests, with a potential second small population in the Main Range. It is noted that other species of flowering plants with similarly limited distributions within the same habitat (e.g. *Uromyrtus lamingtonensis, Pomaderris notata*) are already listed under the NCA in Queensland. Being limited to high elevation wet forests, this species may experience population decline due to climate change, making it eligible for listing under criteria B of the CAM.

The five further species listed below met our criteria for being narrow range endemics but lacked a current conservation status under both the NCA and EPBC Act. This suggests they at least partially meet the criteria for being listed under the CAM process, and if any population decline is observed, projected or inferred they would be meet the full criteria for listing. Therefore, more robust estimates of their distribution size and further investigation of these species' population trajectories may be warranted. The five species are:

- *Astrotricha pauciflora*
- *Coronidium lindsayanum*
- *Muellerina flexialabastra*
- *Schoenus rupicola*
- *Solanum serpens*

Gondwanan plant families

The existing literature was consulted to identify flowering plant lineages of Gondwanan origin that occur in the GRWHA (QLD section). This was primarily done at the family level, but there are also some known lineages within plant families believed to be of Gondwana origin, and these were also identified. The primary sources consulted included Yap *et al.* (2018) and Kooyman *et al.* (2014). The distribution of lineages was also checked using Kew's Plants of the World Online (POWO 2025a) to check for Gondwanan distribution patterns. In addition to lineages that show a traditional Gondwanan distributional pattern (i.e. occurring across South America, Africa and Australasia), lineages that are endemic to, or believe to recently originate from, Australia and/or Australasia were also identified. These lineages also represent ancient and unique diversity that contribute to the GRWHA's Outstanding Universal Value.

Table 8 below lists the plant families putatively identified as being of Gondwanan origin. Also identified are family's endemic to Australia, broader Australasia (Australia, New Guinea, New Zealand, New Caledonia and adjacent Pacific Islands) and significant putatively Gondwanan lineages within select families. Overall, Myrtaceae was the most specious Gondwanan lineage within the GRWHA (QLD section), representing on quarter of all species from Gondwanan lineages (98 species of 399 total Gondwanan lineage species). Three other putatively Gondwanan lineages were represented by more than 20 species in the GRWHA (QLD section): the Zanthoxyloideae subfamily of Rutaceae (41 species), Sapindaceae (36 species), and Proteaceae (30 species). The remaining 194 Gondwanan species belonged to the 37 other putatively Gondwanan lineages.

Table 8: Families putatively identified as either being of Gondwanan origin or containing significant lineages of Gondwanan origin. Also shown is the number of species belonging to each lineage of Gondwanan origin that occur within the GRWHA (QLD section) constituent National Parks, some of which may not occur in the GRWHA (QLD section) itself.

Family	Gondwanan Lineage	Number of species occurring in GRWHA (QLD section) constituent National Parks
Alstroemeriaceae	Yes	1
Atherospermataceae	Yes	3
Berberidopsidaceae	Yes	2
Casuarinaceae	Yes	4
Cunoniaceae	Yes	9
Elaeocarpaceae	Yes	7
Escalloniaceae	Yes	2
Haemodoraceae	Yes	1
Loranthaceae	Yes	9
Monimiaceae	Yes	7
Myrtaceae	Yes	98
Nothofagaceae	Yes	1
Pennantiaceae	Yes	1

Petermanniaceae	Yes	1
Picrodendraceae	Yes	5
Proteaceae	Yes	30
Restionaceae	Yes	1
Sapindaceae	Yes	36
Winteraceae	Yes	1
Hemerocallidaceae	Yes, when recognised as distinct family	9
Argophyllaceae	Australasian endemic family	1
Corynocarpaceae	Australasian endemic family	1
Eupomatiaceae	Australasian endemic family	2
Paracryphiaceae	Australasian endemic family	2
Ripogonaceae	Australasian endemic family	4
Rousseaceae	Australasian endemic family	2
Stylidiaceae	Australasian endemic family	2
Aphanopetalaceae	Australian endemic family	1
Doryanthaceae	Australian endemic family	1
Gyrostemonaceae	Australian endemic family	1
Macarthuriaceae	Australian endemic family	1
Xanthorrhoeaceae	Australian endemic family when recognised as distinct family	3
Goodeniaceae	Family suspected to be of Australian origin	8
Haloragaceae	Family suspected to be of Australian origin	6
Laxmanniaceae	Family suspected to be of Australian origin	18
Philydraceae	Family suspected to be of Australian origin	2
Pittosporaceae	Family suspected to be of Australian origin	12
Ericaceae (Epacridoideae)	Putatively ancient Gondwanan lineage within family	16
Lauraceae (lineage including *Cryptocarya*, *Endiandra and Beilschmedia*)	Putatively ancient Gondwanan lineage within family	18
Rhamnaceae (Ziziphoids)	Putatively ancient Gondwanan lineage within family	14
Rutaceae (Zanthoxyloideae)	Putatively ancient Gondwanan lineage within family	41

Selection of target species

Only three species met our criteria for being both a narrow range endemic and a high elevation endemic: *Zieria montana*, *Lenwebbia* sp. (Main Range P.R.Sharpe+ 4877) and *Coronidium telfordii*. Of these *Zieria montana* occurs in high elevation heathland in Mt Barney NP rather than being one of the high elevation rainforest species we were targeting, and thus it was ruled out as a target species. Conversely, *Lenwebbia* sp. (Main Range P.R.Sharpe+ 4877) met all our criteria but is already the subject of an ongoing conservation genetics study through the Botanic Gardens of Sydney (M. Rossetto, personal communications) and was thus ruled out for this project. Being a member of Asteraceae, *Coronidium telfordii* is not a member of a Gondwanan lineage, but due to the identified need for a conservation assessment, we decided it was a suitable potential target species despite not meeting this criterion.

The narrow range endemism criterium was weighted as the most important for species selection for practical reasons around the time and effort needed to collect tissue material from the full set of the target species populations within the project timeline. On this basis, a further two rainforest associated species from Gondwanan lineages that are narrow range endemics, but not high elevation endemics, were identified as target species for genetic study: *Eucryphia jinksii* (Critically Endangered under NCA) and *Uromyrtus lamingtonensis* (Vulnerable under NCA).

Finally, to complete the list of potential target species we identified the species that were identified as high elevation endemics and of conservation significance. This added five further species to the list. Three of these belonged to lineages of putatively Gondwanan origin: *Pomaderris notata* (Ziziphoid Rhamnaceae), *Pittosporum oreillyanum* (Pittosporaceae) and *Syzygium nebulosum* (Myrtaceae). *Syzygium nebulosum* was only formally described in 2025 and thus does not have a current NCA listing, however the authors of the description suggests it may meet the criteria for a vulnerable status (Weber and Forster 2025). The remaining two species, *Euphrasia bella* and *Gaultheira viridicarpa*, are both listed as endangered under the NCA, but do not belong to a Gondwanan lineage. This left the potential target species list for conservation genetic study as the follow eight species:

- *Coronidium telfordii* – GRWHA (QLD section) endemic, high elevation endemic (quantitative), narrow range endemic, marginal rainforest habitat
- *Eucryphia jinksii* – Gondwanan family, GRWHA (QLD section) endemic, high elevation endemic (qualitative), narrow range endemic, rainforest habitat, listed species – critically endangered (NCA)
- *Euphrasia bella* – GRWHA (QLD section) endemic, high elevation endemic (qualitative), marginal rainforest habitat, listed species – endangered (NCA)
- *Gaultheria viridicarpa* - High elevation endemic (quantitative), marginal rainforest habitat, listed species – endangered (NCA)
- *Pomaderris notata* - Putative Gondwanan lineage, GRWHA (QLD section) endemic, high elevation endemic (qualitative), marginal rainforest habitat, listed species – vulnerable (NCA)
- *Pittosporum oreillyanum* - Putative Gondwanan family, GRWHA (QLD section) endemic, high elevation endemic (qualitative), rainforest habitat, listed species – near threatened (NCA)
- *Uromyrtus lamingtonensis* - Gondwanan family, GRWHA (QLD section) endemic, high elevation endemic (qualitative), narrow range endemic, marginal rainforest habitat, listed species – vulnerable (NCA)

- *Syzygium nebulosum* – Species only described during projects timeline, thus not included in inventory and classification, but is a high elevation endemic of rainforest habitat, and has the potential to meet criteria for listing under CAM process. Likely also meets the GRWHA (QLD section) dependant endemism criteria (70%-90% of distribution in GRWHA (QLD section)).

Collecting trips in Springbrook NP, Lamington NP and Border Ranges NP were then planned with the intention of sampling all potential target species that could be practically and safely located and accessed, as concerns existed around sample collecting difficulty (i.e. cliff dwelling species). This practical approach to final target species choice resulted in sufficient sampling of four taxa for conservation genetics study:

- *Eucryphia jinksi*
- *Pomaderris notata*
- *Pittosporum oreillyanum*
- *Syzygium nebulosum*

Eucryphia jinksii

Eucryphia is a member of the Cunoniaceae, a typical Gondwanan family, but also shows a Gondwanan distribution at the genus level. Two species are native to southern South America and five to rainforest of eastern Australia (POWO 2025b). Of the Australian species, three are common to dominant elements of the temperate rainforests of Tasmania (*Eucryphia lucida* and *E. milliganii*) and southeast NSW and far eastern Victoria (*E. moorei*). The remaining two Australian taxa are highly restricted species of mountain top cloud forests of QLD, *E. wilkiei* on Mount Bartle Frere in north Queensland and *E. jinksii* in Springbrook NP in the GRWHA (QLD section) (Figure 2).

Eucryphia jinksii meets more OUV attributes than any other plant species from the GRWHA (QLD section), being a threatened, relictual species from a Gondwanan family that was likely a major component of the temperate rainforests of Gondwana. The species' rarity is not the result of human impacts in the last 500 years, rather reflecting the population's long-term survival in a climatically buffered microsite. It has been hypothesised that the species is highly dependent on permanently moist soils and potentially groundwater for survival (City of Gold Coast 2025). Thus, it is also a good example of ongoing evolutionary processes within the world heritage property in that its fate reflects the retreat of cool temperate rainforests in the face of ongoing aridification, and it represents a species that is on a possible path to extinct on a geological time scale independent of anthropogenic impacts.

This species is listed as Critically Endangered under the NCA; with the main threats it faces including climate change leading to decreased moisture levels, changes to fire regimes and ground water depletion. Two populations are known within Springbrook NP; a larger one on the clifftops along the NSW-QLD border southwest of Best of All Lookout and a smaller one in a drainage gully that feeds Cave Creek on west facing slopes ~900 m to the north (Figure 2; D. Jinks, personal communications, 12th January 2026). A potential extinction level disturbance was almost experienced in 2019 during the Black Summer fires, which reached within 7 km of the species' distribution (Department of the Environment, Tourism, Science and Innovation 2023). With the fire resilience of the species untested, had these fires reached the populations, the species may have been rendered extinct in the wild in a single event. Overall, *Eucryphia jinksii* presents as a textbook case for the need for ex situ conservation activities to ensure the species survival against stochastic and systematic impacts to the limited wild populations. While other species within the genus are well known in cultivation, past observations have suggested *E. jinksii* may be harder to propagate from both seed and cutting than congeners and is no more robust to water stress in cultivation than in in situ conditions (D. Jinks, personal communications, 12th January 2026).

The main questions we aim to address for *Eucryphia jinksii* are:

- How much genetic diversity remains in the relictual populations of *E. jinksii* that may foster adaptation to climatic changes?
- Are the two known populations genetically divergent from one another?
- Is there evidence of clonality and/or sexual reproduction in the species?
- How are populations of the species expected to be impacted by predicted climate change?
- How many individuals would need to be included in an ex-situ collection to conserve 90% of the species genetic diversity?

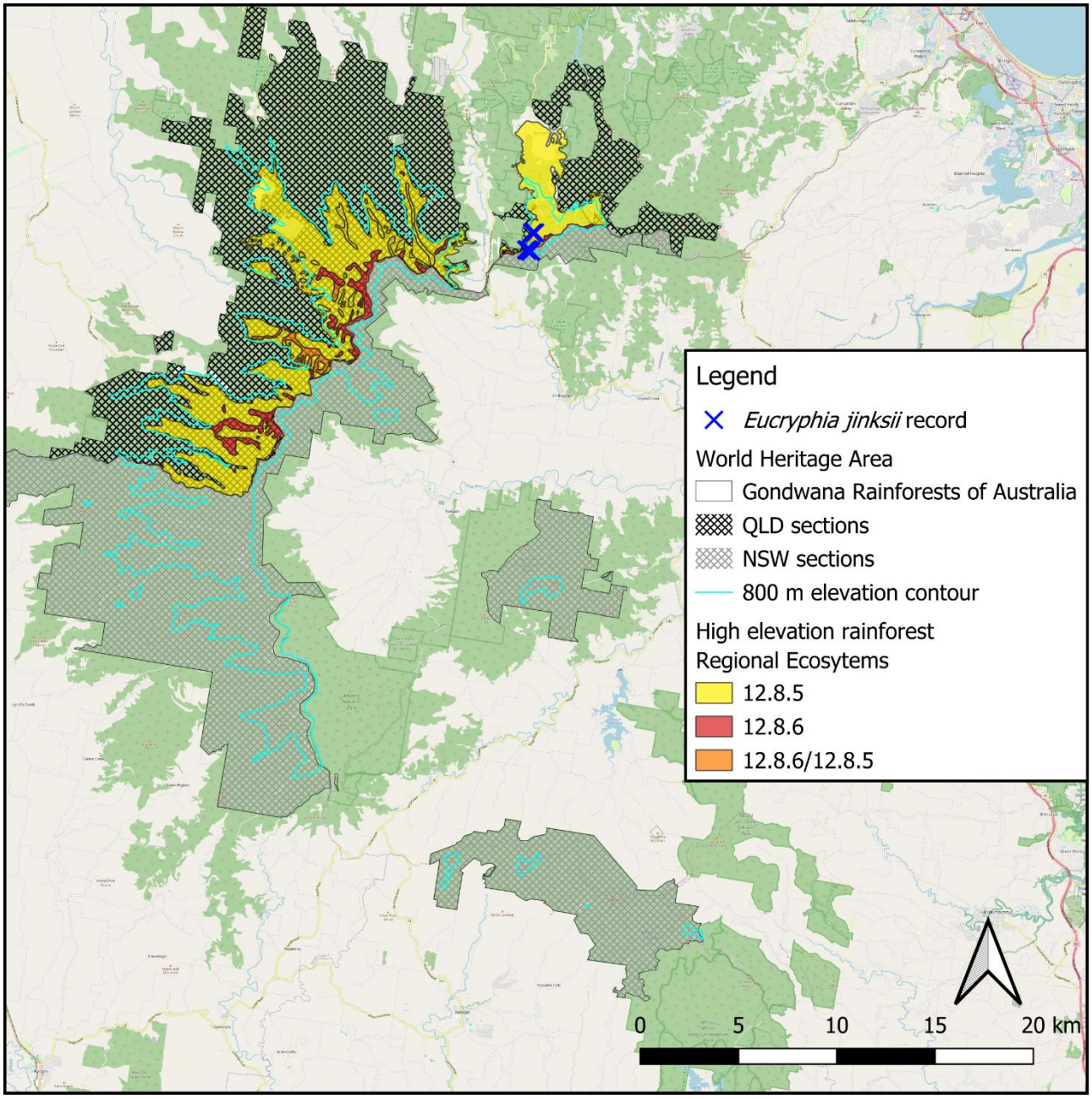

Figure 2: Map showing the distribution of Eucryphia jinksii *around the Wollumbin Caldera, showing the species is restricted to two sites above 800 m elevation within 1km of each other in Springbrook NP. The southernmost cliff site straddles the QLD-NSW border making the species native to both states, despite access being limited to the QLD side of the border.*

Pittosporum oreillyanum

Pittosporum is a relatively large genus of ~250 species primarily distributed across the southern hemisphere of the Old World (Australia, New Zealand, the Pacific and south and south-east Asia and sub-Saharan Africa) (POWO 2025c). It is a member of the family Pittosporaceae, which contains eight other genera all endemic to Australia and New Guinea, suggesting all extant members of the family may share an origin in Australia and *Pittosporum* has subsequently dispersed out of the continent to its current wider range. The APC currently recognises 21 species native to the Australian mainland and Tasmania, with three further species natives of Australian offshore islands, although the latter show closer affinities to extra-Australian species than to the mainland species (Council of Heads of Australasian Herbaria 2025). Morphological and molecular phylogenies have shown *P. oreillyanum* forms a clade with four eastern Australian species historically placed in the separate genus *Citriobatus* (Cayzer *et al.* 2000; Chandler *et al.* 2007): *P. lancifolium*, *P. multiflorum*, *P. spinescens* and *P. viscidium*.

Pittosporum oreillyanum is primarily associated with RE 12.8.6, the more geographically restricted and higher elevation of the two high elevation rainforest RE's, occurring in Springbrook, Lamington and Border Ranges NPs (Figure 3). In places such as Best of All Lookout (Mount Mumdjin) within Springbrook NP, it co-occurs with its close relative *P. multiflorum* without morphological evidence of hybridisation. While seemingly filling a similar ecological niche as *P. oreillyanum* (dense, spiney understorey shrub), *P multiflorum* is common in rainforests from near sea level to 1100+ m elevation from approximately Bega in southern NSW to Gympie in southeast Queensland. Previous population genetic study has shown *P. multiflorum* is potentially polyploid and frequently self-pollinates, leading to complex genetic patterns (M. Rossetto, personal communications, 18th November 2025).

Pittosporum oreillyanum is currently listed as Near Threatened under the NCA, with limited population or habitat loss to date due to human activity. However, as a strict endemic of high elevation cloud forest, climate change is a key threatening factor for the species moving forward.

The main questions we aim to address for *Pittosporum oreillyanum* are:

- Does *P. oreillyanum* show evidence for ploidy variation and high levels of inbreeding as seen in the related *P. multiflorum*?
- How much gene-flow has occurred around the Wollumbin Caldera, and what population structure has this given rise to?
- How are populations of the species expected to be impacted by predicted climate change?
- How many individuals would need to be included in an ex-situ collection to conserve 90% of the species observed genetic diversity?

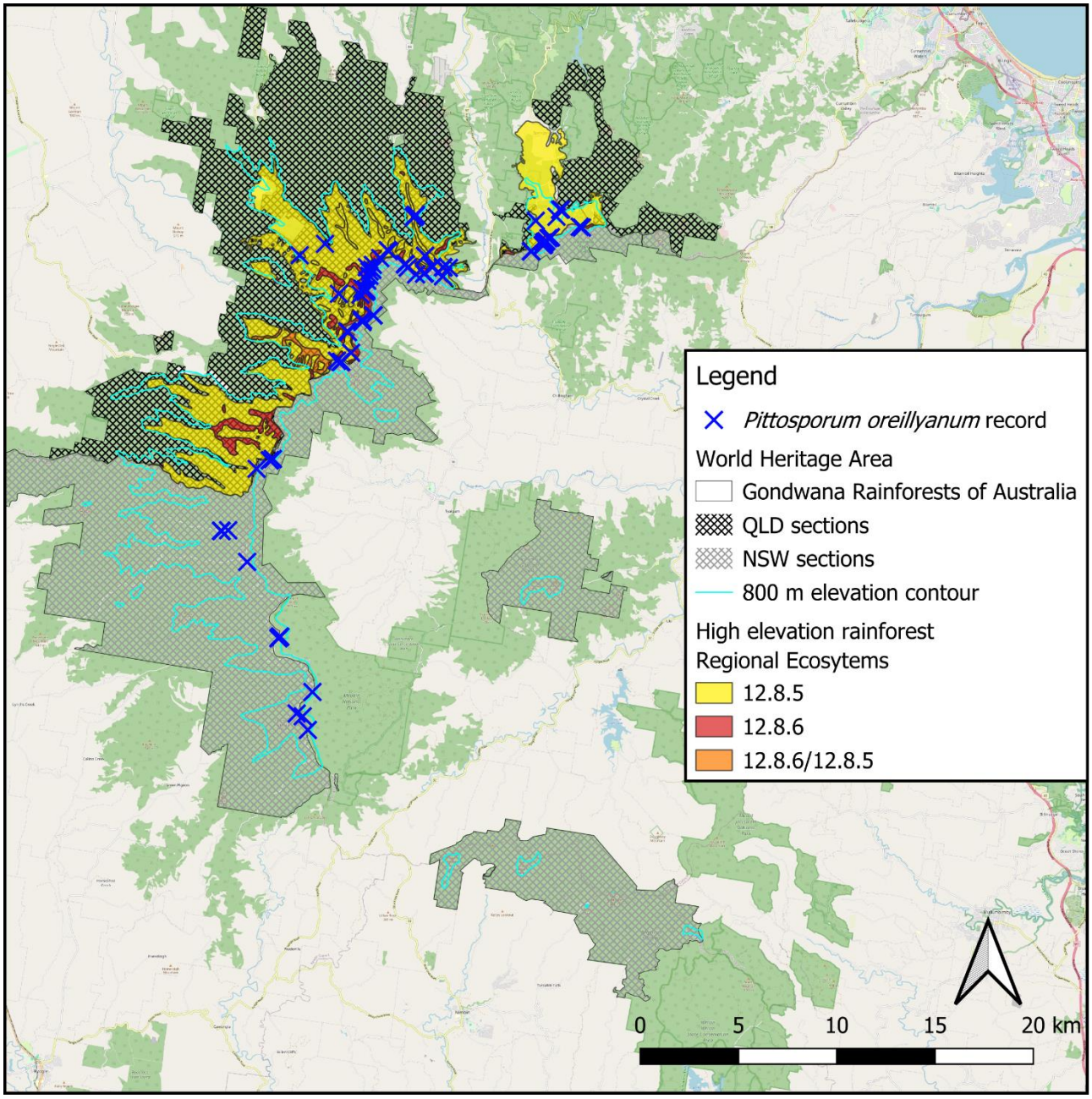

Figure 3: Map showing the distribution of Pittosporum oreillyanum *around the Wollumbin Caldera. The species occurs in three reserves (Springbrook NP, Lamington NP and Border Ranges NP) at elevations above 800 m. The species is closely associated with* Nothofagus moorei *forest, suggesting there is possibly unrecorded populations in under-surveyed areas of RE 12.8.6 in Lamington NP between Mount Throakban and Cockscomb Point.*

Pomaderris notata

Pomaderris is a genus of ~70 species belonging to the putatively Gondwanan Ziziphoid lineage within the broader Rhamnaceae family. Most species in the genus are endemic to Australia, primarily the south-eastern states, with eight species, three shared with Australia, native to New Zealand. Six sections have been recognised within *Pomaderris* based upon morphology, with *P. notata* belonging to the largest, sect. *Pomaderris*. However, a recent phylogenetic study has shown these sections to not be monophyletic, with most members of sect. *Pomaderris* belonging to what was termed clade D in the study (Nge *et al.* 2021). While the sample of *P. notata* used in that study failed in the lab and the species was therefore not included in the phylogeny, based upon the placement of its presumed closest relatives, it is expected to also be a member of clade D (F. Nge, personal communication, 23rd January 2025). Despite this, its precise relationship to other species has never been explored, with previous authors hypothesising *P. cinerea* from the south coast of NSW to be the most similar based upon morphology (Blake 1945).

Previous work has shown significant ploidy variation within the genus, with assumed consistently diploid, triploid and tetraploid species reported by a previous study looking at 37 taxa (Chen *et al.* 2019). *Pomaderris notata* was not included in this investigation and as its relationship to congeners is unresolved, its ploidy level is unexplored. Ploidy has been shown to have important ecological and conservation impacts in *Pomaderris* (Chan *et al.* 2022). Of note is the relationship between ploidy levels and fire response, with polyploid species producing larger seed that germinate and grow faster than diploid species, which is likely adaptive in high fire frequency areas (Chan *et al.* 2022).

Most *P. notata* populations likely never experience fire as the species primarily occurs in small patches of high elevation heaths in exposed rocky locations amongst cloud forest. This very specific habitat has led to the species having a very scattered distribution, being recorded from four locations in Queensland, all within Lamington NP: Moonlight Crag, Araucaria lookout, Mount Wagawn and Garagoolba Lookout (Figure 4). Surveys by ecologist Lui Weber suggest the species is also present on Cockscomb, representing a fifth (unsampled) population within Lamington NP. In NSW, five high elevation populations are known, three within Border Ranges NP, one atop Wollumbin/Mt Warning in Wollumbin NP and one atop Sphinx Rock in Nightcap NP. In addition, one unusual lowland population is known in NSW from an elevation of ~130m in roadside vegetation above Kunghur Creek (Figure 4). Due to its small, isolated populations, *P. notata* is listed as Vulnerable under the NCA in QLD and Vulnerable in NSW under the BCA (2016).

The main questions we aim to address for *Pomaderris notata* are:

- Which other species of *Pomaderris* is *P. notata* closely related to?
- What is the putative ploidy of *P. notata*?
- Has the lowland population on Kunghur Creek been correctly identified as *P. notata*? And if so, is the population evolutionarily distinct from the high elevation populations?
- Does the geographic isolation of the populations of *P. notata* result in limited geneflow and high genetic divergence between populations?
- Is there evidence for clonality or elevated inbreeding within these small, isolated populations?
- How are populations of the species expected to be impacted by predicted climate change?
- How many individuals would need to be included in an ex-situ collection to conserve 90% of the species observed genetic diversity?

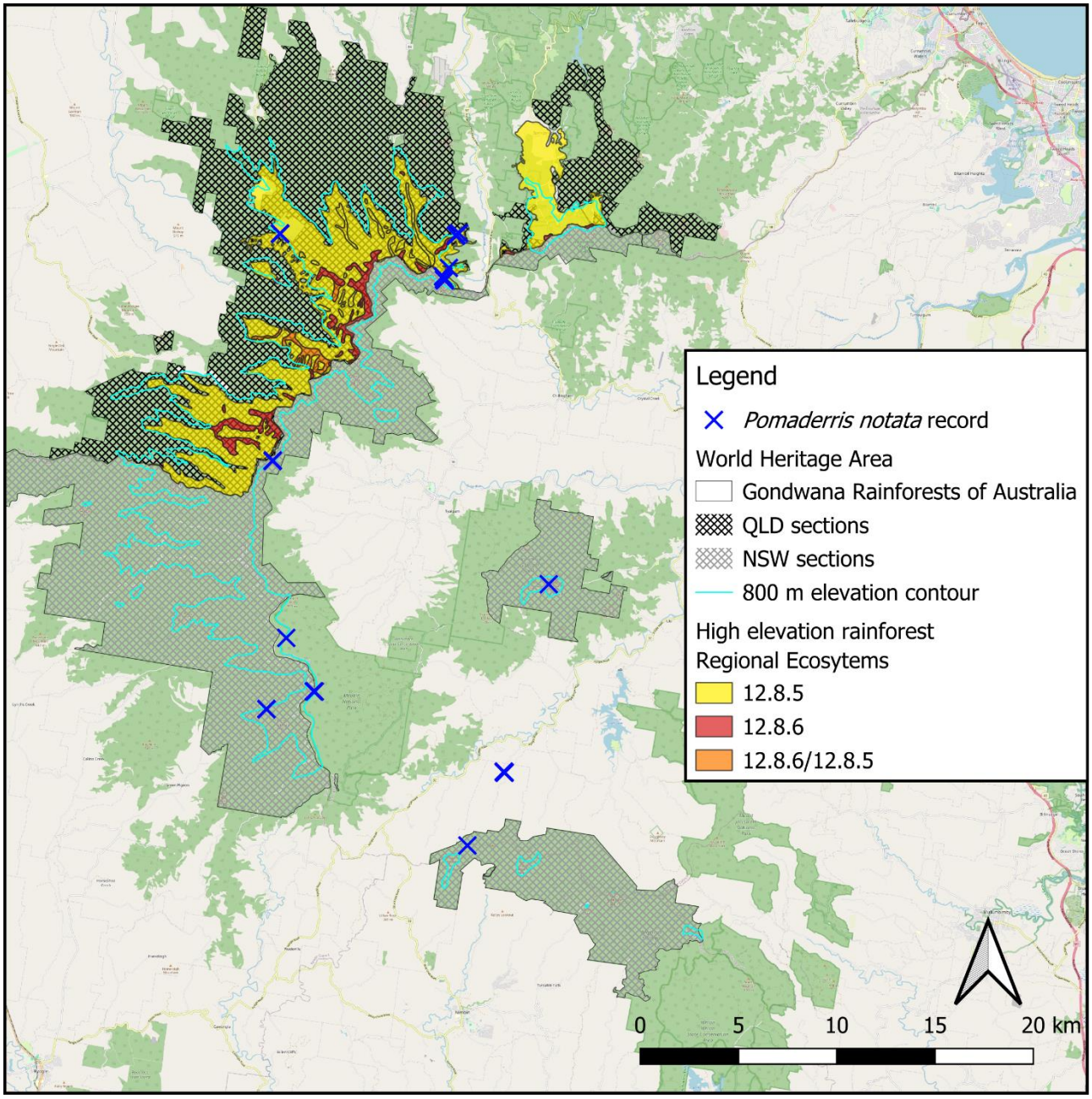

Figure 4: Map showing the distribution of Pomaderris notata *around the Wollumbin Caldera. The species occurs in four reserves (Lamington NP, Border Ranges NP, Wollumbin NP and Nightcap NP) primarily at elevations above 800 m. The species mostly occurs on exposed basalt amongst high elevation rainforest, often in more-or-less monospecific stands. A single lowland population is known from Khungur Creek downstream of the Nightcap NP population (Sphinx Rock), occurring in roadside vegetation at ~130m elevation.*

Syzygium nebulosum

Syzygium is sometimes cited as the largest tree genus by number of species globally, with Plants of the World Online (POWO 2025d) currently recognising >1200 species, including those currently placed in *Acmena*, *Acmenosperma* and *Waterhousea* on the QLD Flora and Fungi Census (Bean and Guymer 2025). Interestingly, recent phylogenetic studies have placed the genus as a possible close relative of another ecologically important and specious tree genus within the Myrtaceae, with *Syzygium* being resolved as one of the possible sister lineages to Tribe Eucalypteae (Baker *et al.* 2022). Not among the species currently recognised by the most recent version of both of these authorities is *Syzygium nebulosum*, due to the publication describing it as a distinct taxon only being published in 2025 (Weber and Forster 2025). Previously populations now included within this taxon were identified as *S. crebrinerve*, and the new species is presumed to be closely related to both *S. crebrinerve* and *S. oleosum*, common elements of subtropical rainforests at varying altitudes (Weber and Forster 2025).

The description of *S. nebulosum* records it occurring in wet microsites above ~900m elevation around the Wollumbin Caldera in Springbrook, Lamington and Border Ranges NPs, and potentially on Wollumbin/Mt Warning itself (Weber and Forster 2025). The species has not yet been assessed under the CAM framework for conservation listing, with the original publication suggesting a vulnerable status may be appropriate (Weber and Forster 2025).

The main questions we aim to address for *Syzygium nebulosum* are:

- Does molecular data support *S. nebulosum* as a distinct species with regard to *S. crebrinerve*?
- How much gene-flow has occurred around the Wollumbin Caldera, and what population structure has this given rise to?
- How are populations of the species expected to be impacted by predicted climate change?
- What do these finding tell us about the need for a CAM assessment for conservation listing of the species?
- How many individuals would need to be included in an ex-situ collection to conserve 90% of the species observed genetic diversity?

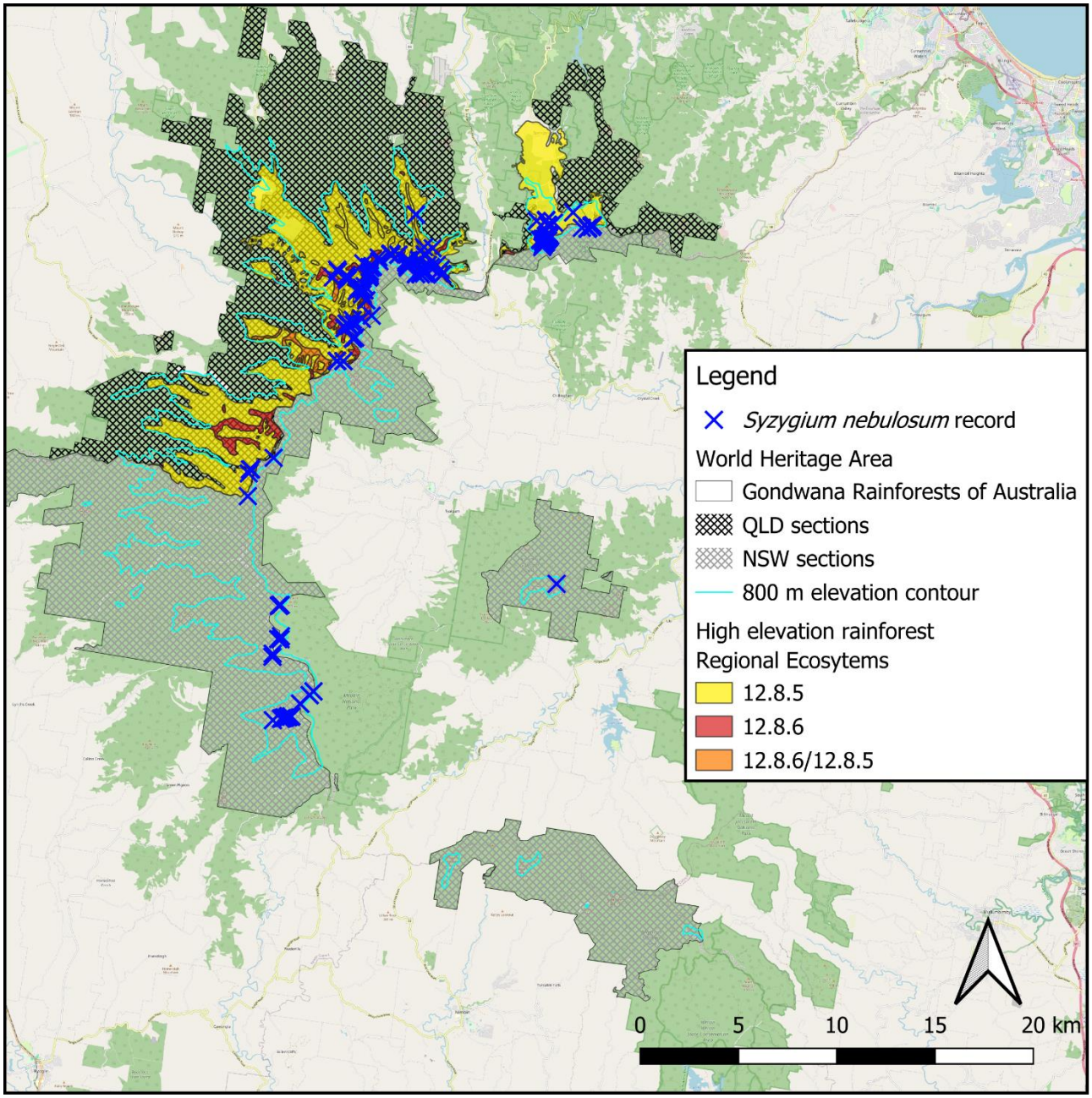

Figure 5: Map showing the distribution of Syzygium nebulosum *around the Wollumbin Caldera. The species occurs in four reserves (Springbrook NP, Lamington NP, Border Ranges NP and Wollumbin NP) at elevations above 800 m. The species is closely associated with* Nothofagus moorei *forest, suggesting there is possibly unrecorded populations in under surveyed areas of RE 12.8.6 in Lamington NP between Mount Throakban and Cockscomb Point.*

Summary of Methodology

Field sampling

Field sampling for the four target species was undertaken across three national parks in 2025: sampling in Springbrook and Lamington NP's was undertaken under the QHBS exemption under the Nature Conservation (Plants) Regulation 2020 and Nature Conservation (Protected Areas Management) Regulation 2024, while sampling in Border Ranges NP was undertaken in collaboration with the Botanic Gardens of Sydney under NSW scientific permit SL100569. Due to the inaccessible nature of the high elevation vegetation in these parks, sampling was limited to only locations that were practical and safe to access within the project timeline. This meant that the total number of samples collected for all four species was below the original target of 94 samples, however good geographic representation was achieved for all species.

In addition to the collection of tissue for genetic study, this fieldwork also served as informal surveys of the target species' populations. This was particularly true for *Eucryphia jinksii,* as all individuals that could be located at both populations were sampled and GPS coordinates captured. For the three other species leaf tissue was collected from up to 12 individuals at each sampling location and dried on silica gel.

Outgroup samples of related taxa of *Pittosporum*, *Pomaderris* and *Syzygium* were also collected from locations in Southeast Queensland where possible. Dried tissue samples along with accompanying voucher specimen are to be accessioned into the QHBS collection for long term preservation. Where field sampling of all relevant taxa could not be completed or there were extra wells available on the sequencing plate, specimens held in the Queensland Herbariums collection were destructively sampled and added to sequencing runs. In addition to newly sequenced samples, all species were co-analysed with existing DArTseq datasets held by the Research Centre for Ecosystem Resilience, Botanic Gardens of Sydney (*Pittosporum*, *Pomaderris* and *Syzygium*) and Australian Tropical Herbarium (*Eucryphia*). Overall, comprehensive sampling of all relevant outgroup species was achieved for all four target species.

Genetic data generation and analysis

DArTseq data generation

Leaf material from all samples was sent to Diversity Array Technologies Pty Ltd (Canberra) for DNA extraction, sequencing, and dataset assembly. DArTseq is a reduced representation sequencing technique resulting in tens of thousands of single nucleotide polymorphisms (SNPs) that can be used for population genetic analyses (Sansaloni *et al.* 2011). Genotyping was highly successful for all target species, and where possible two reports were requested for each species, one containing the outgroup samples and used for testing species boundaries and hybridisation, and a second containing only the target species used for infra-specific genetic analyses.

Confirmation of species limits

The first step taken in the employed analytical workflow was to test taxonomic boundaries and ensure the target species represented distinct evolutionary linages. To do this the larger genetic datasets containing all outgroup samples were analysed using phylogeny estimation in IQ-TREE V2.3.6 (Minh *et al.* 2020), phylogenetic networks in *Splitstree* V6.4.13 (Huson and Bryant 2024), principal components analysis (PCoA) and admixture analysis in Structure V2.3.4 (Pritchard *et al.* 2000). Any individual samples or sites of the target species which clustered with an outgroup would have been taken to

represent either misidentifications or evidence for taxonomic incongruencies, however no samples showed such issues across all species. Clustering intermediate between the target species and an outgroup would have been taken to represent hybridisation but again, no samples showed such issues across all species. Finally, the relationship of the target species to congeners was established by examining placement in phylogenetic trees and networks. Our findings regarding the taxonomic relationships of all target species are provided in species-specific findings and implications sections. Note that all phylogenies included are midpoint rooted for visual simplicity, and thus basal nodes cannot be considered true relationships.

Population genetic analyses

Using the smaller, ingroup dataset for each species infraspecific genetic analyses were undertaken in R (R Development Core Team 2024). First pairwise kinship values were calculated between all samples to check for clonality (defined as kinship values above 0.4) and sampling of first- and second-generation relatives. Where clonality was observed, genets were subsampled to only one ramet (individual plant) in all subsequent analyses.

To investigate genetic structure and geneflow across the target species distributions a further PCoA was undertaken, along with an admixture analysis (utilising *sNMF*); and pairwise F_{st} values and private alleles per population were calculated. Levels of genetic diversity and inbreeding were estimated using standard population genetic parameters for all sites with 5 non-clonal samples of the target species.

Species distribution modelling and climate change threat assessments

To help assess the potential impacts of climate change on the long-term survival of wild populations of the four target species, species distribution modelling was employed. This allows an estimation of how habitat suitability for individual species may change across the landscape as environmental factors, in this case bioclimatic factors, change through time. Management can then be undertaken considering predicted changes in areas and suitability of habitat at the species level to minimise the risks of species decline nor extinction.

Study area and species records

Study area

The modelling region was defined as southeast Queensland and the central east coast of New South Wales, including the South Eastern Queensland (SEQ), New England Tablelands (NET), NSW North Coast (NNC), and Sydney Basin (SB) bioregions (Department of Climate Change, Energy, the Environment and Water 2023), which encompass the biogeographical distribution of subtropical rainforest in Australia. We referenced the Queensland Herbarium's Potential Habitat Modelling methodology to model the study species (Laidlaw and Butler 2021); however, given their currently known distributions and the inclusion of future climate projections, we applied a modified approach and sourced alternative datasets to cover the study area.

Species records

Species occurrence records were downloaded from the Atlas of Living Australia (Atlas of Living Australia 2025) for *Eucryphia jinksii*, *Pittosporum oreillyanum* and *Pomaderris notata*. These were then

filtered to remove duplicate records, records with high coordinate uncertainty and those from cultivation in R using the Galah (Westgate *et al.* 2023) and processALA (Wilson 2025) packages. To these records, field collected tissue sample records from this study were add to these records to complete the final record sets. As *Syzygium nebulosum* was only described during this study, occurrence records were not available on ALA, and therefore the *iNaturalist* (https://www.inaturalist.org. Accessed 25/09/2025) records that could be confidently identified as this species, primarily uploaded by one of the species authors, were used along with field collected tissue records. To address autocorrelation and sampling bias resulting from limited sample size and restricted, clustered spatial patterns in species records, data were filtered and duplicate entries removed (Kramer-Schadt *et al.* 2013; Boria *et al.* 2014; Soley-Guardia *et al.* 2024).

Bioclimatic variables

We selected four bioclimatic variables as candidate predictors for our models, based on ecological priors and expert input (Table 9; Laidlaw and Butler 2021). These included annual (mean annual temperature and precipitation), seasonal (temperature seasonality), and limiting environmental factors such as precipitation of the driest quarter. These variables are known to reflect the biological and eco-physiological tolerance range of plant species (Fitzpatrick *et al.* 2008).
Bioclimatic datasets were sourced from the Queensland Future Climate – climate projection data and services for Queensland, which also provide coverage for the entire Australasian region (Trancoso *et al.* 2024). The dataset provides temperature and precipitation anomalies derived from up to 15 Global Climate Models (GCMs), aligning with the Coupled Model Intercomparison Project Phase 6 (CMIP6; Eyring *et al.* 2016), developed to support the IPCC Sixth Assessment Report (AR6; IPCC 2023). Climate projections are available for three Shared Socioeconomic Pathways (SSPs: SSP1-2.6, SSP2-4.5 and SSP3-7.0) at yearly intervals up to 2100. All datasets are bias-corrected using SILO data from 1975 – 2000. These projections are provided at a 10 km spatial resolution, statistically downscaled using the Conformal Cubic Atmospheric Model (CCAM) under the Coordinated Regional Climate Downscaling Experiment (CORDEX) framework (Thatcher *et al.* 2015; Meinshausen *et al.* 2020; Chapman *et al.* 2023), and were resampled using the 9 second Digital Elevation Model (DEM; Hutchinson *et al.* 2008). The baseline is derived from the averaged SSP3-7.0 simulation data for the period 1995 - 2014.

Table 9: A list of predictor variables explored for the SDMs and their percentage contribution to the final models. The minimum and maximum values of each predictor variable to the currently known location of the species are given.

Predictor variable	*E. jinksii*			*P. orellyanum*			*P. notata*			*S. nebulosum*		
	min	max	%	min	max	%	min	max	%	min	max	%
Annual mean temperature (˚c)	18.4	18.5	-	16.0	18.6	18.3	16.9	19.2	8.7	16.0	19.0	20.6
Temperature seasonality (SD*100) (˚c)	365.9	367.5	0.1	364.0	379.2	18.8	364.8	380.4	10.5	363.9	380.6	11.5
Annual precipitation (mm)	1829.3	1855.8	99.9	1406.1	1890.6	60.0	1644.4	1744.7	79.1	1400.1	1898.8	66.9
Precipitation of driest quarter (mm)	138.4	141.5	-	115.4	143.5	2.9	107.6	135.9	1.6	107.8	144.0	1.0
Total % model contribution			100			100			99.9			100

Modelling species distributions with Maxent

Maxent

We chose Maxent v3.4.3 (Phillips *et al.* 2006, 2017; Hijmans *et al.* 2024) to model the potential habitat distribution of the study species. Maxent is a program for modelling species distributions which statistically correlates presence-only records to predictor variables based on the principle of the maximum entropy algorithm (Phillips *et al.* 2017). It has been widely applied for modelling habitat distributions of species under both current and future environments and can be applied with small numbers of occurrence records (Merow *et al.* 2013; van Proosdij *et al.* 2016).

Model selection, fitting and validation

Prior to model development, we tested all variables for multicollinearity using Spearman's rank correlation. To account for limitations in species occurrence data, we employed jackknife cross-validation for species with fewer than 20 records (*E. jinksii* and *P. notata*) and spatial block cross-validation for species with larger sample sizes (*P. oreillyanum* and *S. nebulosum*). Additionally, we tuned the feature classes and regularisation multiplier to optimise model performance (Dudík *et al.* 2007; Muscarella *et al.* 2014; Kass *et al.* 2025). Clustered spatial patterns in species occurrences rendered the Area Under the Curve (AUC) metric ineffective as a measure of model performance in this study. Alternatively, we used the Akaike Information Criterion corrected for small sample sizes (AICc) for selection of the optimal model settings and for model validation. AICc is a statistical measure for model comparisons considering both prediction error and model complexity, making it widely used in machine learning model selection (Symonds and Moussalli 2011). As AICc decreases with decreasing residual error, the lower the AICc score indicates better model fit (Portet 2020).

The final baseline models were run with ten thousand background points, with 500 iterations and the default cloglog format, which represents habitat probability values ranging from 0 to 1 for each grid cell in the model (Phillips *et al.* 2017).

Future projections

Future projections were explored for the three futures (2050, 2070 and 2090) and one SSP (SSP3-7.0) using an ensemble of five GCMs (ACCESS-ESM1.5, CMCC-ESM2, EC-Earth3, GFDL-ESM4, MPI-ESM1-2-LR, Trancoso *et al.* 2024). Initial sensitivity analysis was conducted for the four bioclimatic variables across all three SSPs and 15 GCMs at four-time steps: baseline and projections centred around 2050, 2070 and 2090. For each combination, we compared maximum, average, minimum, 10th, 50th, and 90th percentile values, as well as ranges, to assess the variability of future projections. Temperature-related variables consistently showed an increasing trend across all combinations, whilst rainfall was highly variable both within and between SSPs and GCMs, with no clear relationship between temperature and rainfall fluctuations.

SSP3-7.0 is a high-emissions scenario from the IPCC AR6 framework, broadly aligned with current global emission trajectories and commonly used for policy planning in Queensland (Rohan Eccles, personal communication, April 15, 2025). It represents the regional rivalry storyline, which describes a geopolitical context characterised by heightened nationalism, regional conflict, and declining international cooperation (Meinshausen *et al.* 2020). Under this pathway, global emissions continue to rise, roughly doubling by 2100 and corresponding to an estimated 2.8 - 4.6 °C of warming above pre-industrial levels (IPCC 2021). SSP3-7.0 is often treated as a high-emissions scenario since SSP5-8.5 is widely considered to have unrealistically high emissions.

We employed multi-dimensional analysis to identify an optimal set of GCMs that are both representative of the ensemble's central trends and sufficiently diverse to capture the range of climate projections for the study areas, while excluding outliers that could bias models due to extreme projections (Esser *et al.* 2025). Four bioclimatic variables from each GCM projection were mapped into a multivariate space and reduced in dimensionality using Principal Component Analysis (PCA). Pairwise Euclidean distances between centroids were calculated, and hierarchical clustering was applied to identify representative GCMs based on their proximity to either cluster centroids or the global centroid across all GCMs, representing the study region. This analysis identified five GCMs, which were averaged to provide future climate inputs for the models.

Uncertainties and limitations

While modelling species habitat distribution in response to climate change is an active field of research, SDMs are subject to uncertainties and limitations. For example, spatial bias in presence data can occur when sampling effort across a study extent is not uniform, potentially resulting in the exclusion of areas where the species could have been identified if present (Gutierrez-Velez and Wiese 2020). In this study, the precision of the species location data was relatively high; however, obtaining additional presence locations through further field surveys could improve model validity, although using natural occurrence data in SDMs might under-predict potential distribution range, as plant species in particular do not necessarily fully encompass their fundamental niche (Jiménez and Soberón 2022).

Variable selection and dataset accuracy are also a potential source of uncertainty in SDMs (Soley-Guardia *et al.* 2024). In this study, only climatic variables were explored to model the broad climatic domain. However, exclusion of other environmental variables can be predicted to have resulted in models with increased modelled impact of climate variables on species distributions. Climate projections are also subject to uncertainty, as different combinations of downscaling methods, GCMs, and emission scenarios may yield different outcomes (Beaumont *et al.* 2008; Shimizu-Kimura *et al.* 2017). In this study, an ensemble of five GCMs was used, and therefore these uncertainties were averaged at the time of the modelling.

Lastly, we employed clamping to prevent future projections beyond known bioclimatic ranges. A preliminary test conducted prior to running the models confirmed that clamping did not substantially alter the potential distribution of suitable habitat under future projections. However, caution should be exercised when interpreting model outputs - SDMs do not directly predict extinction risk, as they do not incorporate key ecological factors such as genetic and evolutionary factors, reproductive and life-history traits, demographic factors, dispersal and metapopulation dynamics, and biotic interactions (Keith *et al.* 2008; Zurell *et al.* 2023; Shimizu *et al.* 2024). Despite these limitations, the results of this study demonstrate that SDMs are useful to evaluate general trends in the primarily climatic habitat distribution of the study species at both continental and regional scales under climate change.

Development of management guidance

Based upon the learnings of the field sampling, genetic study and climate modelling, consideration was first given to whether the current conservation status of the four target species under the NCA and CAM was supported or if a reassessment may be justified. We then infer adaptive potential based upon inferred effective population size and observed genetic diversity at the level of categorical classes (very low, low, moderate or high adaptive potential). Combined with the results of climate suitability modelling, the impact risk of climate change on each target species is then summarised, and management recommendations to ensure the species genetic diversity is maintained provided.

While optimisation of propagule collection schemes for translocations or ex-situ insurance populations was initially planned for all species, the incomplete and geographically uneven sampling of *Pomaderris notata* and *Syzygium nebulosum* means that these approaches can only be successfully applied to *Eucryphia jinksii* and *Pittosporum oreillyanum* at this time. The goal of capturing 90% of common alleles in insurance population is a standard target based upon the United Nations' Convention on Biological Diversity target (United Nations Convention on Biological Diversity 2021). Therefore, the goal of optimisation approaches employed was to determine the minimal sampling effort, using the number of individuals as a proxy of for the number of propagule lines collected, that always captured 90% of common alleles in the genetic dataset for a species.

For *Eucryphia jinksii*, given its highly restricted distribution and highly representative sampling (>5% of all wild individuals), individual level optimisation was undertaken, disregarding the assignment of genets to populations. Ten thousand random sets of genotyped samples were selected for each total sample number. The proportion of common alleles captured in each iteration was then quantified. We took the optimal scheme to be the one with the lowest number of samples that always resulted in the capture of >90% of common alleles present in genetic dataset, thus allowing for flexibility in choice of samples to collect propagules from.

Given its large population and representative rather than census level genetic sampling, for *Pittosporum oreillyanum* the optimisation approach used was a random site sampling technique. Ten thousand random sets of genotyped samples were selected for each possible number of sites, sampling five genets per site. The proportion of common alleles captured in each iteration was then quantified. We took the optimal scheme to be the one with the lowest number of sites that always resulted in the capture of >90% of common alleles present in genetic dataset, thus allowing for flexibility in site choice.

Findings and Implications

Overview of data and findings

In light of this study and the description of three new high elevation endemic flowering plant species during the timeframe of the study (*Syzygium nebulosum*; Weber and Forster 2025; novel *Daphnandra* sp. (Weber, Forster, *et al.* preprint) and *Ripogonum* sp. (Weber, Mallee, *et al.* preprint), a better understanding of the uniqueness and biodiversity value of the high elevation ecosystems of the GRWHA is being built. It is becoming clear that the high elevation rainforest RE's (12.8.5 and 12.8.6) of the property supports much unique biodiversity, with many of the species' endemic to these habitats being evolutionarily distinct and reproductively isolated from their closest relatives.

Interestingly, there is significant observable variation in the distributions, population sizes and genetics of these high elevation species, even amongst the subset of four species covered in this report. *Eucryphia jinksii* is an example of a true relictual species, a member of a cool climate lineage isolated to ever shrinking habitat as the climate has warmed and temperate rainforest has been replaced by subtropical forests. This has led to low genetic diversity, moderate clonality and inbreeding, and putatively low adaptive potential. Both *P. oreillyanum* and *S. nebulosum* belong to genera common in subtropical and tropical forests of Australasia and south-east Asia but are evolutionarily distinct high-elevation specialist species. Both these species are relatively common in their high elevation habitat, with large populations and moderate to high geneflow across there distributions; all factors suggesting good genetic health and moderate adaptive potential. Finally, *P. notata* shows a third pattern, occurring in discrete patches of suitable habitat (exposed rhyolite amongst high elevation rainforest) and exhibiting greater population structuring and more limited gene flow between populations, while still showing high genetic health (moderate diversity levels and low inbreeding rates).

These patterns lead to differing assessments of vulnerability to the impacts of climate change between these species. *Eucryphia jinksii* is putatively under acute and direct threat of extinction, due to decreased soil moisture availability, increased fire risks and ongoing climate change. For both *P. oreillyanum* and *S. nebulosum*, no direct or acute environmental threats can be identified, however both past research (Narsey *et al.* 2020) and our climate suitability models suggest that collapse of the high elevation RE's in which they grow may be the greatest threat they face (Bergstrom *et al.* 2021; Rowland *et al.* 2025). Disease (myrtle rust) is another notable threat particular to *S. nebulosum* amongst the four target species, and Myrtaceae species in the GRWHA more broadly. Given *P. notata* is proven to be able to survive and reproduce in low elevation climates by the existence of the Kunghur Creek population, it would appear climatic changes pose limited direct threat to the species. This is reinforced by its habitat being best defined by non-climatic factors (i.e. exposed rhyolite amongst rainforest). However, a hypothesised factor limiting the species distribution, fire sensitivity, suggests indirect impacts of climate change (i.e. increased frequency and intensity of fire events) may pose significant risk to the species long-term survival.

Management implications to arise from these finding include: the need for ongoing and increased fire management within the GRWHA to limit any increase in intensity and frequency of fire events, the need for ongoing population monitoring, in particularly for the acutely threatened *E. jinksii* and to understand the impacts of myrtle rust on *S. nebulosum*, and the need for insurance populations of threatened high elevation endemic species in case of ecosystem collapse due to climate change. Insurance populations may take the form of translocations, seed bank collections, or ex-situ cultivated populations, but it is clear a multi-jurisdictional approach between at least Queensland and New South Wales managers will be needed to achieve representative populations of the species with cross-border distributions.

Species specific genetic patterns & conservation management guidance

Eucryphia jinksii

Population size, distribution and status

Eucryphia jinksii has an extremely restricted distribution, occurring only at two locations between 700 m and 800 m elevation within Springbrook NP: a ~250 m strip along the top of the south facing cliffs in the south-west corner of the park and in a drainage gully ~900 m to the north (Figure 6). In total, less than 40 stems could be located during the collecting trip targeting this species. The gully population is the smaller of the two, with fewer than 10 individuals observed and 6 field samples collected during the collecting trip for this project, with an estimated population size of 40 to 50 individuals based on past, more extensive site visits (D. jinks, personal communications 14th January 2026). While an underestimate of the true population size due to the steep terrain limiting safe access, 29 individuals were recorded and sampled from the cliff population, with a total estimate size for this population being <500 individuals. Precise locations of all recorded individuals were provided to QPWS-P's Springbrook Rangers to help inform park management.

Table 10 summarises the sampling scheme for *E. jinksii*. Of note is that all individuals observed in both populations were mature and most were reproducing vegetatively via coppice growth, with no *E. jinksii* seedlings or saplings observed during this study. Furthermore, field observations of the spread of individuals at the cliff site led to a hypothesis that at least some spatially proximate stems arose from vegetative resprouting after trunk falls. Overall, these observations suggest recruitment from seed is possibly rare in the wild. While the cliff populations showed minimal signs of disturbance impacts, several large trunks at the gully population were recently broken and toppled, likely during Cyclone Alfred in March 2025, or the subsequent large storms experienced in the months preceding the site visit. Despite this, the extensive coppicing observed across the two populations suggests this kind of disturbance event may not lead to mortality of ramets.

Table 10: Summary of the sampling scheme employed for Eucryphia jinksii *in this study. All located wild individuals of the species were collected for genotyping, representing a census population size well below 1000 known individuals.*

Genotyped population code	Location	Coordinates	Number of samples successfully genotyped
Cliff	Along cliff tops at QLD-NSW border on south-east edge of Springbrook NP	Confidential	30 (1 herbarium sheet)
Gully	In drainage gully on south-east edge of Springbrook NP, ~900 m north of cliff population	Confidential	8 (2 herbarium sheets)
Cultivated	Cultivated individuals at Springbrook and Blue Mountains Botanic Gardens	-	4

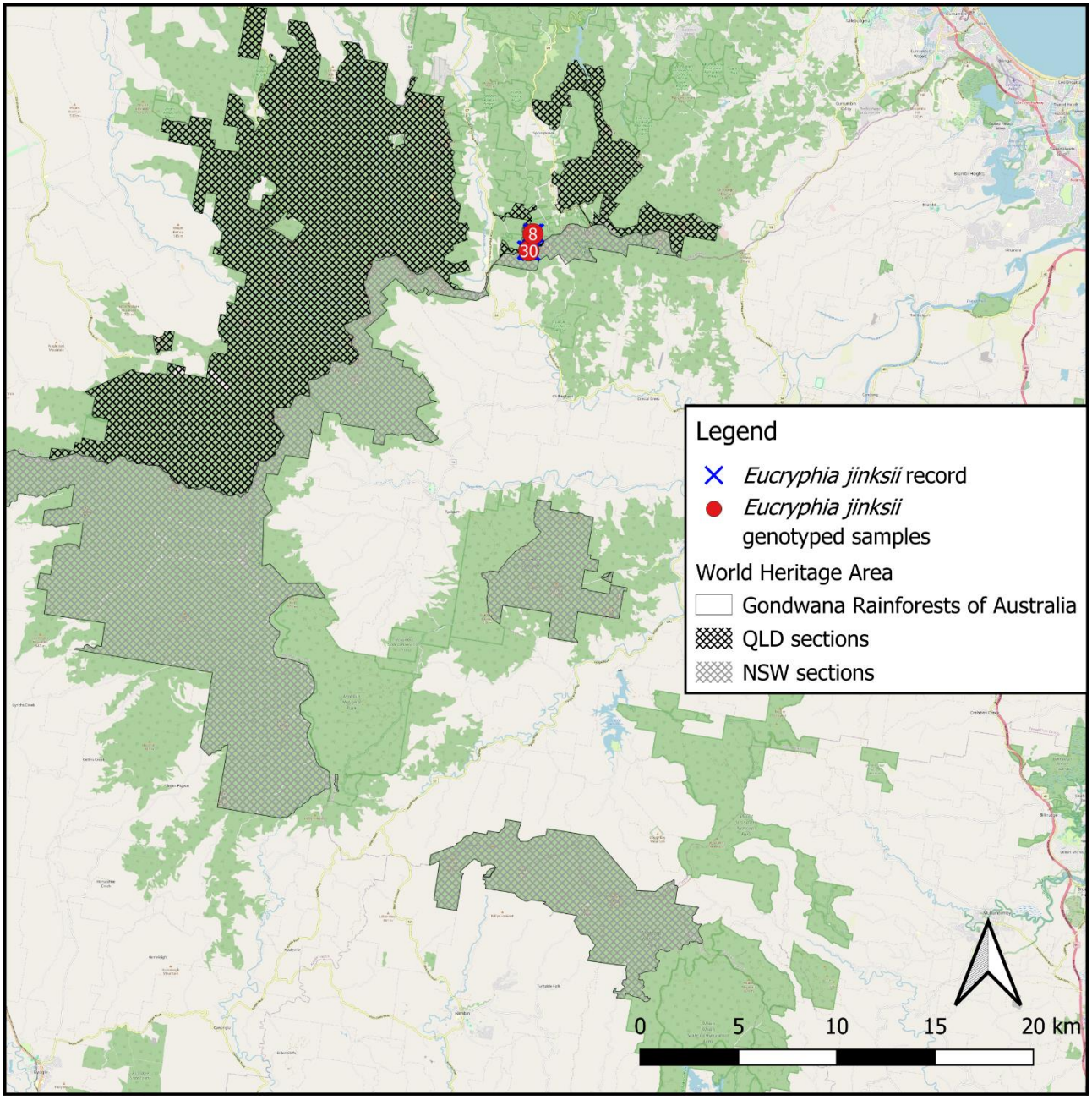

Figure 6: Map showing the sampling scheme for wild Eucryphia jinksii *used for this project. All individuals that could be located at both known populations of the species were sampled, totalling 38 sampled individuals.*

Evolutionary relationships and hybridisation

As illustrated in Figure 7, Figure 8 and Figure 9, genetic evidence strongly supports *E. jinksii* as a distinct species as currently circumscribed. Figure 7 and Figure 8 support the North Queensland narrow range, high elevation endemic *E. wilkiei* as being most closely related to *E. jinksii* in agreement with the conclusions of studies investigating morphology (Forster and Hyland 1997) and wood anatomy (Poole and Barnes 2004). This suggests both species are relicts of a time when cooler temperate rainforests were more widespread in eastern Australia and have survived in-situ by retreating up slope into favourable microhabitats as climates have warmed.

Due to the highly uneven sampling effort between the two Queensland taxa and those from south-eastern Australia and South America leading to biases in the DArTseq dataset, it is not possible to draw robust conclusions regarding the relationship of the Queensland lineage to the rest of the genus. However, there is good support for the two Tasmanian endemic species (*E. milligani* and *E. lucida*) being each other's closest relatives, and *E. moorei* from the south-east corner of mainland Australia being related to the Tasmanian species (Figure 7 and Figure 8). Given the geographic isolation of the two Queensland species, the lack of any hybrids in the dataset is as expected. However, hybridisation between geographically isolated species is known to be possible in cultivation the genus, with the commonly cultivated *E.* x *intermedia* being a hybrid between the Tasmanian *E. lucida* and Chilean *E. glutinosa.*

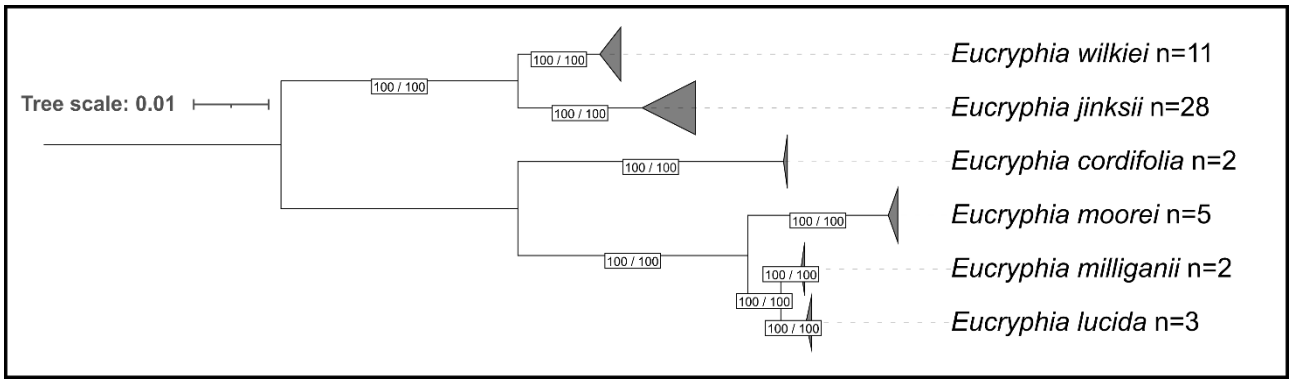

Figure 7: The IQTree phylogeny estimated using DArTseq data for Eucryphia*, including all species except the South American native* E. glutinosa *which his presumed to be closely related to* E. cordifolia *based upon geographic and morphological evidence. Hybrid samples are also excluded from the analyses as they violate the assumption of bifurcating relationships. Clades representing species level grouping of samples are collapsed with sample numbers per species shown. Note the tree is midpoint rooted meaning that while the close relationship between the two range restricted Queensland species (*E. jinksii *and* E. wilkiei*) is supported, the sister relationship between these species and the rest of the genus is not.* Eucryphia moorei*, a native of southeast NSW is suggested to be more closely related to the Tasmanian endemic taxa than the Queensland species.*

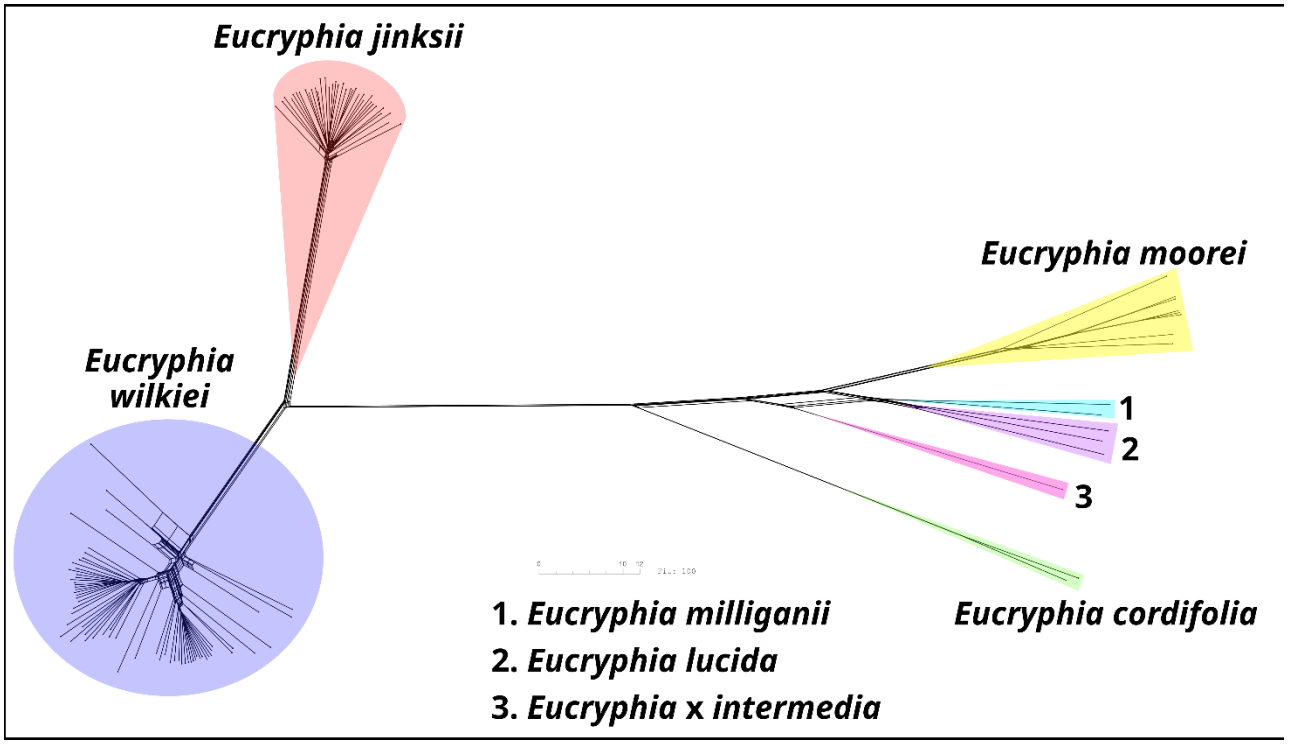

Figure 8: The SplitsTree phylogenetic network estimated using DArTseq data for Eucryphia, including all species except the South American native E. glutinosa *which his presumed to be closely related to* E. cordifolia *based upon geographic and morphological evidence. The phylogenetic network supports a close relationship between the two narrow range species native to Queensland (*E. jinksii *and* E. wilkiei*) and between the two Tasmanian endemic taxa (*E. milliganii *and* E. lucida*).* Eucryphia moorei*, a native of southeast NSW is suggested to be more closely related to the Tasmanian than the Queensland species.*

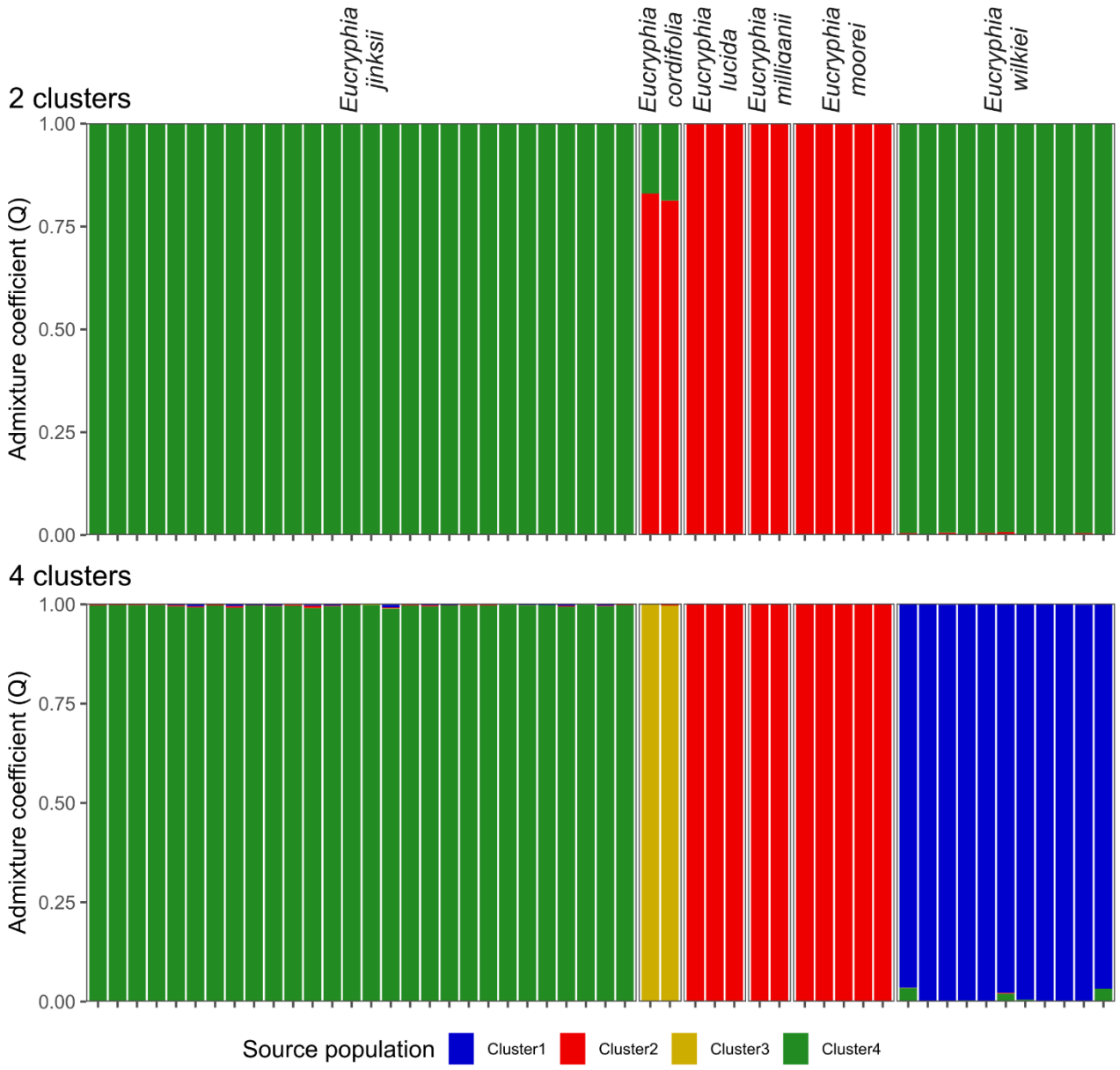

Figure 9: Admixture plot showing the results of 2 and 4 cluster STRUCTURE analyses of Eucryphia *DArTseq data. In the 2-cluster analysis* E. jinksii *and* E. wilkiei *form one cluster and the remaining four species the second cluster, with minimal genetic admixture. In the 4 -cluster analysis*, E. jinksii, E. wilkiei *and E.* cordifolia *each form distinct genetic clusters, with the three remaining southeast Australian species forming the final cluster. While these results support current the current taxonomy of the genus and suggest a close relationship between the Queensland taxa, further interpretation is avoided due to the bias in sampling across species which likely bias genetic clustering results.*

Key Genetic Findings

Ploidy

DArTseq read count analysis suggests *E. jinksii* is a putative diploid.

Reproductive biology

In line with field observations, there was some clonal genets observed in the Cliff population. Of note is three clonal ramets that were observed to be growing in a more or less linear arrangement within 5 metres of one another supporting the hypothesis these individual stems are the result of resprouting of a historical fallen trunk. A further two pairs of clonal ramets were each collected within 20 m of one another in the Cliff population. One set of clonal samples was observed between a field collected and existing herbarium sheet from the Gully population, however this likely reflects unintentional resampling of the same stem rather than true clonality.

Despite this, most sampled individuals are suggested to arise from out-crossed seed. Moderate inbreeding coefficients were observed at both populations (Table 11), which is likely due to the small population size of the species rather than self-pollination given the pattern of kinship values shown in Figure 10. Overall, the data suggest a mixed to outcrossing mating system in ideal circumstances which are not achieved due to the small population size.

Genetic structuring, diversity and gene flow

As can be seen in Figure 11 and Figure 12, the *E. jinksii* Gully samples contain a subset of the genetic diversity of the Cliff samples, suggesting the former may have arisen via seed dispersal from the latter population. The cultivated samples originate from seed collected at the Gully population, with the maternal tree being included in the sampled Gully population individuals.

Given the small population size and very low genetic diversity, it is possible to examine genetic diversity of *E. jinksii* at the individual allele level. Per Figure 12, 183 SNPs (366 total alleles) were observed across the two wild populations and cultivated individuals. Of the 366 alleles, the vast majority (319, 87.2%) were present in both wild populations, with most of the remainder only present in the Cliff population (45, 12.3%). Only two alleles (0.5%) were unique to the Gully population, which may reflect either post-dispersal mutations or alleles not detected in the Cliff population due to incomplete population sampling.

No unique alleles were detected in the Cultivated individuals, which is to be expected. A single allele was shared between only the Gully population and cultivated individuals, which is unsurprising as this is where seed was collected for cultivation (D. Jinks, personal communications, 12th January 2026). Less expected are the 5 alleles shared between only the Cliff population and cultivated individuals, which may suggest the genetic diversity of the Gully population was undersampled or that pollen flow is ongoing between populations. Given *Eucryphia* species are pollinated by a wide range of flying insects, particularly large dipterans (flies) and bees (Mallick and Driessen 2009), insect mediated pollen movement across the 900 m between populations is reasonable. However, the kinship analysis shows this pollen donor was not included in our sampling for either population.

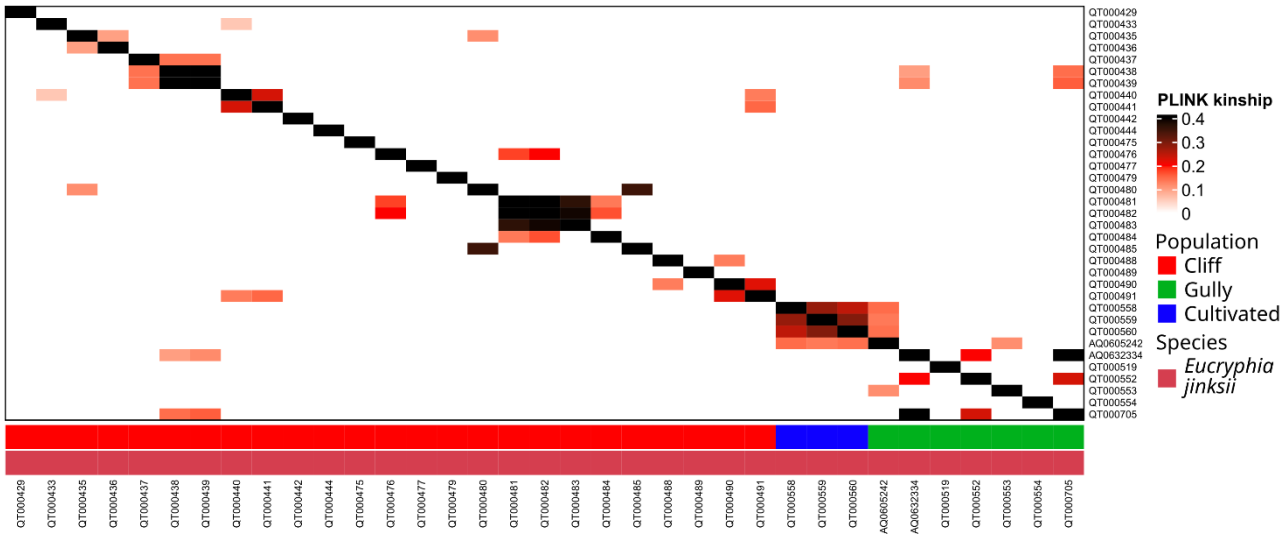

Figure 10: Heatmap of pairwise kinship values between genotyped Eucryphia jinksii *individuals. Values at or above 0.4 represent genetically identical samples mostly arising through clonality, while values between 0 and 0.4 represent individuals with familial relationships up to ~2 generations removed. Three groups of clonal individuals are present amongst the Cliff population samples, matching field observations that some stems appear to arise from fallen trunks at this site. One pair of clonal samples was observed amongst the Gully population samples, however this was between a field sample and a sampled Herbarium sheet, so it is likely these samples represent accidental duplicate sampling of the same individual rather than clonality. Familial relationships are also observed between individuals growing at the two wild sites, suggesting ongoing geneflow between these two populations. All cultivated individuals share first generation familial relationships (i.e. siblings and/or parent offspring) along with a familial relationship to an individual from the Gully population which is possibly the mother tree from which seed was originally sourced.*

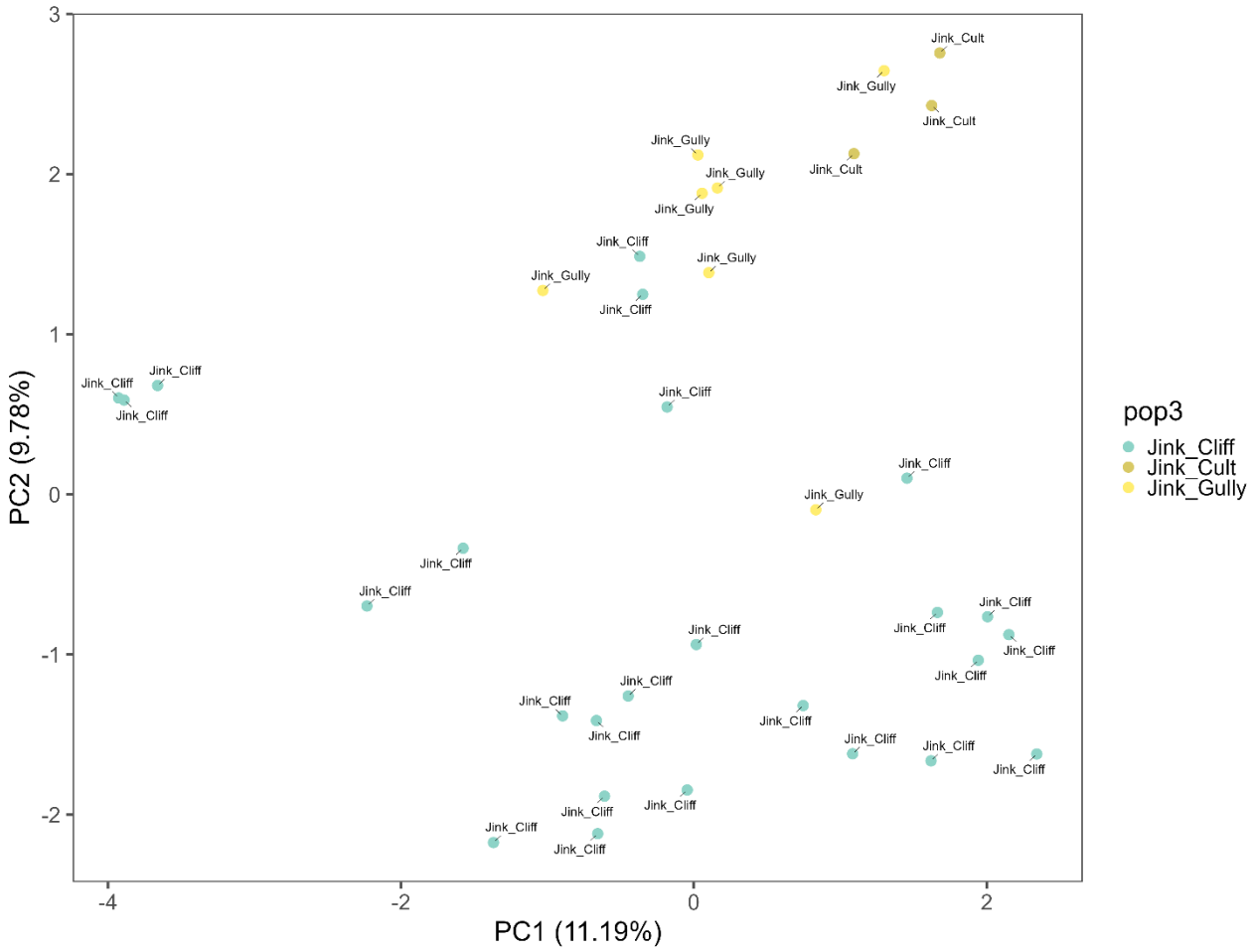

Figure 11: PCA plot of all genotyped Eucryphia jinksii *samples showing the lack of genetic structuring in the species, with the Cliff and Gully populations not plotting separately. The analysis also supports the cultivated samples as coming from one of the sampled individuals from the Gully population.*

Table 11: Key population genetic parameters of E. jinksii populations represented by 5 or more genets in the DArTseq dataset (H_o = observed heterozygosity, H_e = expected heterozygosity, uH_e = unbiased expected heterozygosity). A total of 197 high quality, variable loci were used for calculations.

Population	Allelic richness	H_o	H_e	uH_e	Inbreeding coefficient	Unbiased inbreeding coefficient
Cliff population	1.2024	0.2011	0.2875	0.3179	0.3005	0.3674
Gully population	1.2284	0.2309	0.275	0.3014	0.1604	0.2339

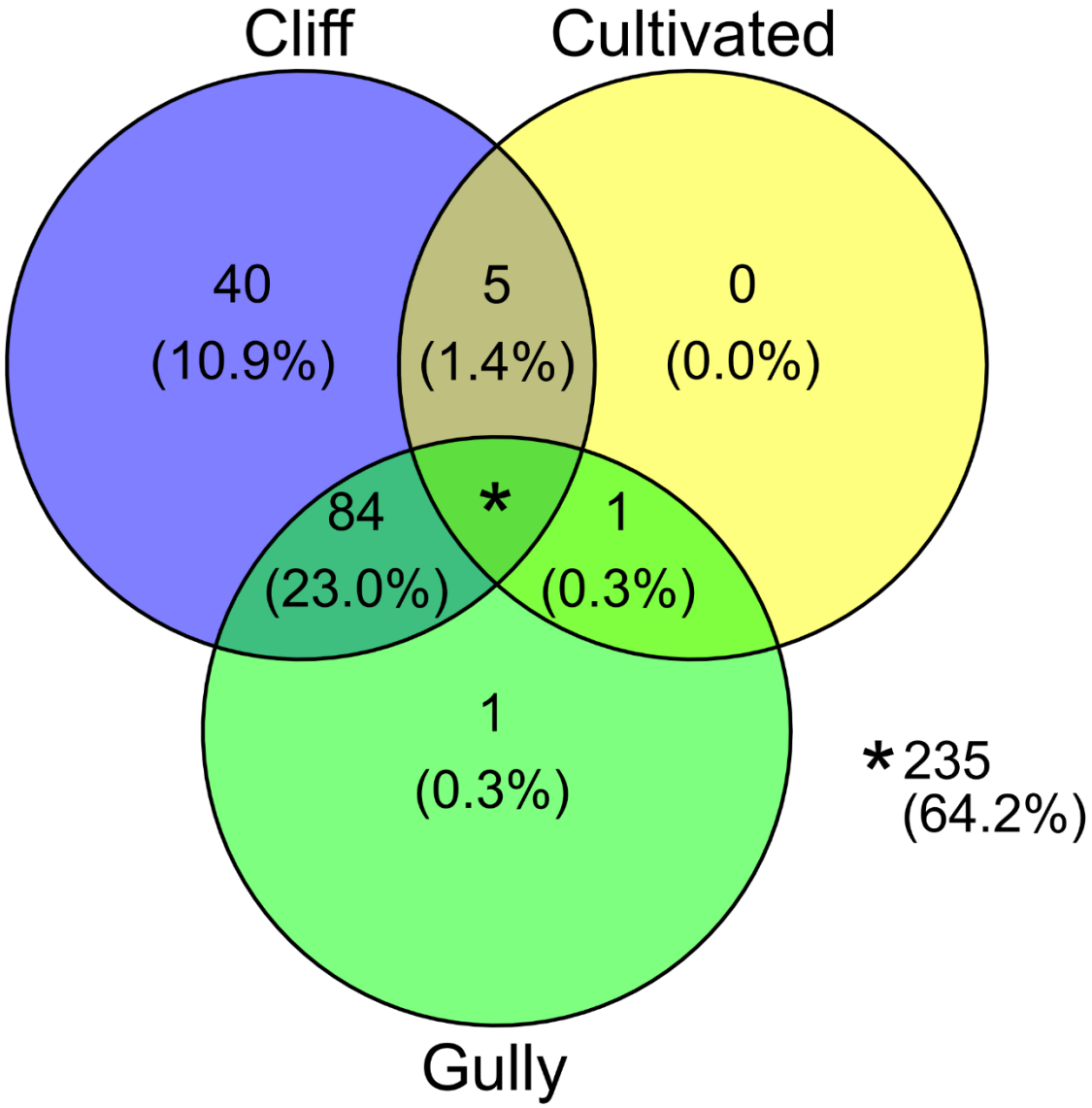

Figure 12: Venn diagram of individual alleles present across the Cliff, Gully and cultivated populations of Eucryphia jinksii. *Numbers represent how many alleles are shared by only those groups, with percentages are the proportion of the total alleles present only in the relevant subset of the sampling. Most alleles (65%) are common and shared between all three sets of individuals, with a further 23% shared between the two wild populations. A moderate proportion (~11%) of alleles are unique to the Cliff population, with very few (0.5%) unique to the Gully population. Overall, this plot is indicative of the Gully population and cultivated individuals representing a subset of the genetic diversity present in the larger Cliff population rather than being distinct populations. As the complete sampling was undertaken of the Cliff population, it is not possible to determine if the 2 (0.5%) alleles not recorded from this population may be present in unsampled individuals.*

Modelled impacts of climate change

Figure 13 shows the projected areas of climate suitability for *E. jinksii* under climate change in the years 2050, 2070 and 2090, along with the present climate suitability model. Under current conditions the model shows suitable climates occurring in the Wollumbin Caldera, where the species is known from, along with Dorrigo NP and an area slightly to the north of Goonengerry NP in the Far North Coast of NSW. This area of suitable climate is far larger than the area in which *E. jinksii* naturally occurs, which combined with the very limited records of the species leading to difficulties with fitting a model, suggests it is unlikely to reflect the true climatic tolerances of the species, and thus any finding must be cautiously interpreted. By 2050, we see a drastic decline in areas that match the species modelled climatic niche, with small areas of higher modelled suitability remaining only in Dorrigo NP, well to the south of the species extant distribution. A modest increase in modelled climate suitability is projected for 2070 and 2090, particularly in Dorrigo NP.

Management recommendations

Based upon literature evidence and the findings of this study, the current threat status of *Critically Endangered* is considered appropriate for *E. jinksii* under the CAM. There is strong evidence for the species total wild population to be fewer than 500 ramets, representing even fewer genets due to clonality. Furthermore, the two wild populations represent a single gene pool, with the smaller Gully population holding effectively no unique genetic diversity compared to the larger Cliff population. Given the small population size, moderate observed inbreeding and low genetic diversity observed, inferred adaptive potential is very low for this species. Therefore, we conclude there is a high risk of the species going extinct in the wild in the face of climate change and novel disturbance regimes (i.e. increased fire risk), and thus a genetically representative translocated or insurance population is needed to ensure the species' long term persistence.

Due to the species' small population and limited genetic diversity, only a small number of maternal lines would be needed to capture the full diversity of the species, with optimisation analysis suggesting any 15 randomly selected (non-clonal) propagule lines would capture 90% of the common alleles present across the species distribution. These propagule lines could take the form of either cuttings (a technique successfully used for other *Eucryphia* species; Barnes *et al.* 2000; Vidal *et al.* 2019; Tiscornia *et al.* 2023) or seed. However, previous attempts to grow *E. jinksii* from cuttings have shown low success and, despite good seed germination rates, the species has been challenging to maintain in cultivation (D. Jinks, personal communications, 12th January 2026). A future avenue to explore for this species given its low genetic diversity and elevated inbreeding rates may be to increase diversity in cultivated populations using controlled crosses with congeners, particularly the most closely related *E. wilkiei,* as a form of genetic rescue.

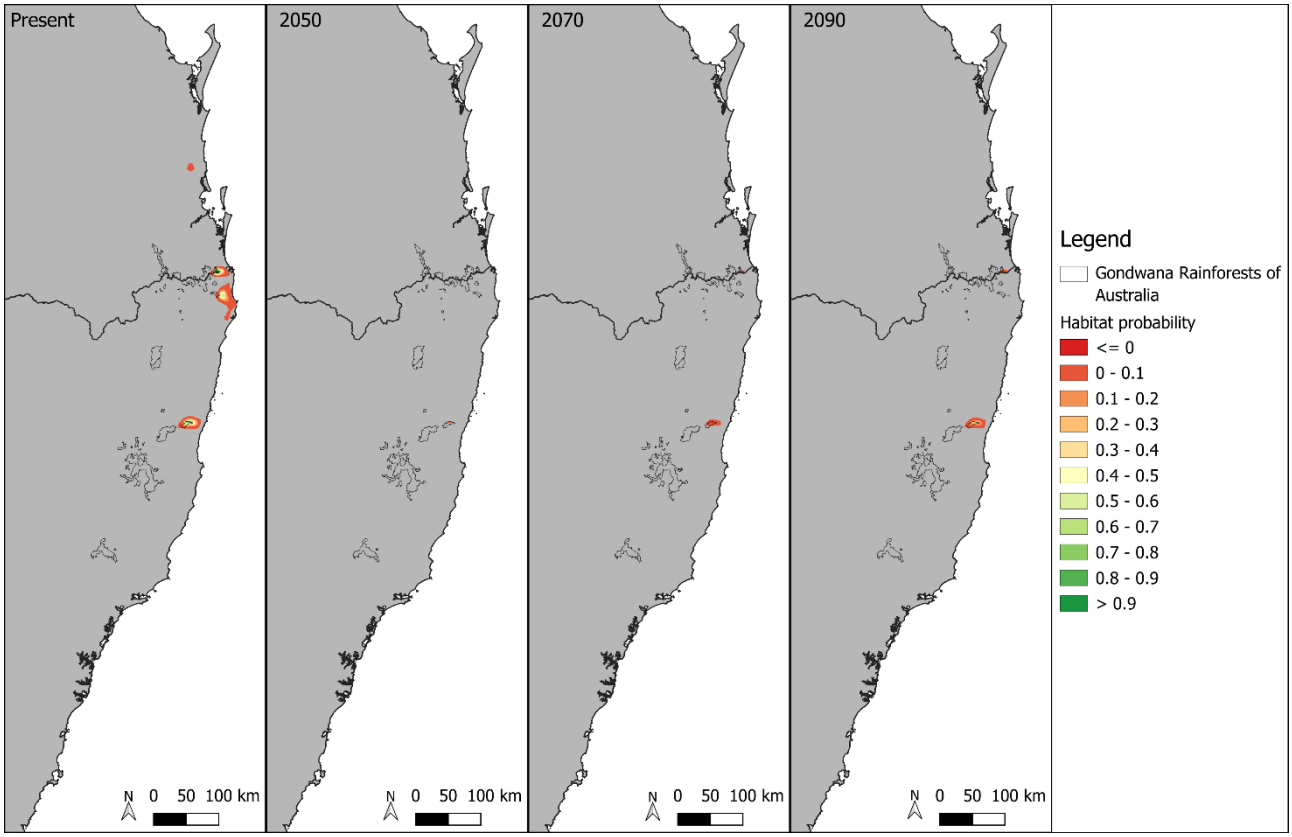

Figure 13: Results of climate habitat modelling for Eucryphia jinksii *for present conditions and then projected onto predict conditions in the years 2050, 2070 and 2090. Predicted habitat suitability in each map cell is a value between zero and one, with one being high confidence suitable climate. In line with the species being rare and potentially range limited by a factor not included in the model (i.e. soil water availability), the model of suitable climate under present conditions is not a good match to the species realised distribution. When projected to 2050, we see a near complete loss in modelled suitable climate apart from a small area of Dorrigo NP. A small increase in area is seen in 2070 and again in 2090, primarily in Dorrigo NP, but also at Springbrook NP where the species currently occurs.*

Pittosporum oreillyanum

Population size, distribution and status

Pittosporum oreillyanum is restricted to areas of the Wollumbin Caldera above 800m (primarily above 900m), predominately in *Nothofagus* forest (RE 12.8.6; Figure 14). Its distribution is dispersed across several discrete areas: within the highest elevation parts of Springbrook NP - primarily Mt Thillinmam and Mount Mumdjin, within Lamington NP both between Mt Wagawn and Mt Throakban (including at Joalah Lookout) and at Cockscomb Point, and within Border Ranges NP at Antarctic Beech Picnic Area, the Pseudo-Pinnacle and Bar Mountain (Figure 14). However, it is likely there are unrecorded populations at unsurveyed high points along the top of the Wollumbin Caldera, particularly between Lamington NP and Border Ranges NP. During field sampling for this project, a previously unrecorded population of *P. oreillyanum* was located and sampled growing under the *Eucryphia jinksii* Cliff population on the southern edge of Springbrook NP.

Table 12 summarises the sampling scheme for *P. oreillyanum*, but of note is that the species was not located for sampling from Bar Mountain and Mt Thillinmam, and the remote populations at Mt Throakban and Cockscomb were not accessed for sampling. Field observations suggest the species is long-lived and slow growing, with a low turnover rate. As no evidence for population decline was recorded (e.g. minimal sick or dead individuals) at any site, the species population appears stable. Overall, the only observable threats to the species' persistence are climate change and the associated changes to local moisture and disturbance regimes

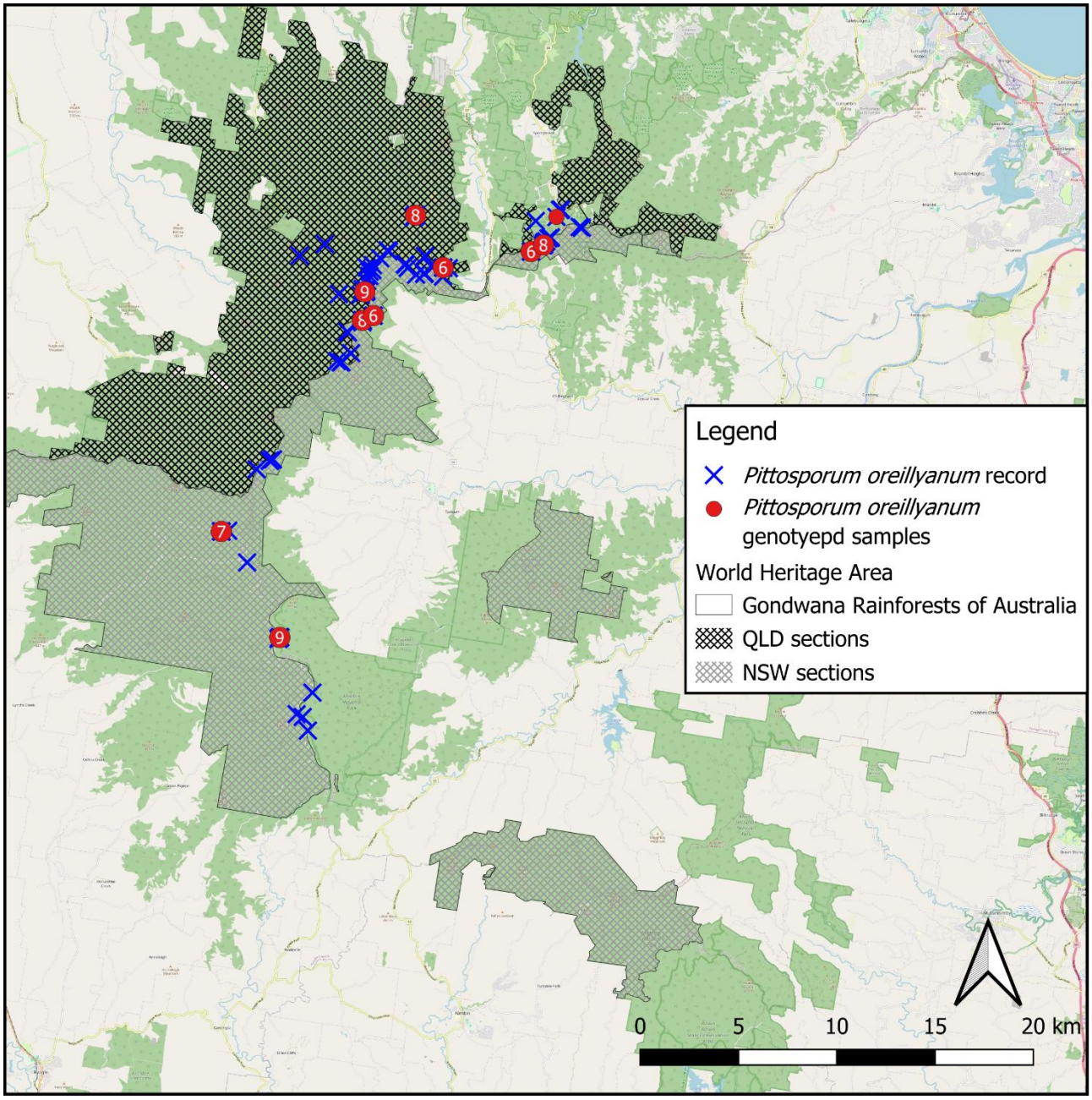

Figure 14: Map showing the sampling scheme for wild Pittosporum oreillyanum *used for this project. While both Bar Mountain and Mount Thillinmam were visited for collecting, the populations of this species at both sites were not located in the time available. Due to limited access options, no populations between the Antarctic Beech Picnic Area and Echo point sites could not be sampled within the scope of this project.*

Table 12: Summary of the sampling scheme employed for Pittosporum oreillyanum *in this study. Population codes match those used in subsequent analysis and figures. While a minimum of 6 samples per site was the aim of sampling, at two sites, O5 and O11, only lone individuals were located.*

Genotyped population code	Location	Coordinates	Number of samples successfully genotyped
O1	Psuedo Pinnacle, Border Ranges NP	-28.4225, 153.1278	9
O2	Antarctic Beech Picnic Area, Border Ranges NP	-28.3741, 153.0974	7
O3	Echo Point, Lamington NP	-28.2775, 153.1709	8
O4	Cominan Lookout, Lamington NP	-28.2753, 153.1766	6
O5	Albert River Circuit, Lamington NP	-28.2658, 153.1698	1
O6	Mt Bithongabel, Lamington NP	-28.2642, 153.1724	8
O7	Wagawn Track, Lamington NP	-28.2533, 153.2129	6
O8	Joalah Lookout, Lamington NP	-28.2294, 153.1985	8
O9	Eucryphia cliff site, Springbrook NP	Confidential	6
O10	Best of All, Springbrook NP	-28.2430, 153.2651	8
O11	Springbrook Maze, Springbrook NP	-28.2302, 153.2718	1

Evolutionary relationships and hybridisation

As illustrated in Figure 15, Figure 16 and Figure 17 genetic evidence strongly supports *P. oreillyanum* as a distinct species as currently circumscribed. In agreement with previous studies (Cayzer *et al.* 2000; Chandler *et al.* 2007), it is supported as a member of the *Citriobatus* lineage alongside *P. multiflorum, P. viscidium, P. spinescens* and *P. lancifolium*. The genetic data places *P. oreillyanum* as possibly sister to a clade consisting of *P. multiflorum* and *P. spinescens*, with these three species sharing smaller, more ovate leaves and denser, more robust spines than *P. viscidium* and *P. lancifolium*.

Despite co-occurring samples of *P. multiflorum* and *P. oreillyanum* from Best of All Lookout in Springbrook NP being genotyped, no evidence for hybridisation or geneflow between these species was recorded from any site (Figure 16 and Figure 17). This suggests complete reproductive isolation has evolved between these species despite their geographically close relationship.

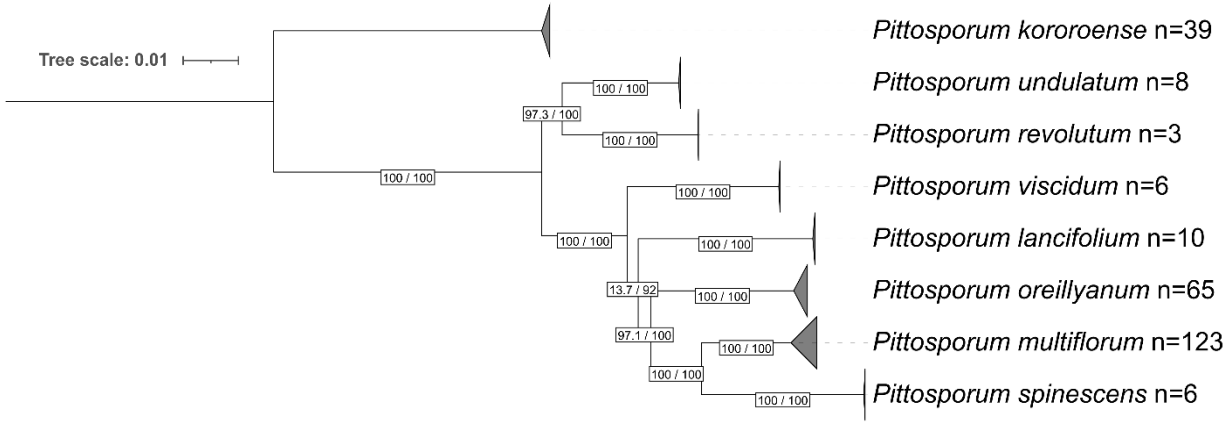

Figure 15: The IQTree phylogeny estimated using DArTseq data for sampled Pittosporum *species. Clades representing species level grouping of samples are collapsed with sample numbers per species shown. Note the tree is midpoint rooted meaning that the sister relationship between* P. kororoense *and remaining species is not supported. Pittosporum oreillyanum is confirmed as belonging to clade with the four species previously placed in* Citriobatus *(*P. multiflorum, P. spinescens, P. viscidium *and* P. lancifolium*). The analysis suggests* P. oreillyanum *is more closely related to* P. multiflorum *and* P. spinescens *than these three species are to* P. viscidium *and* P. lancifolium*.*

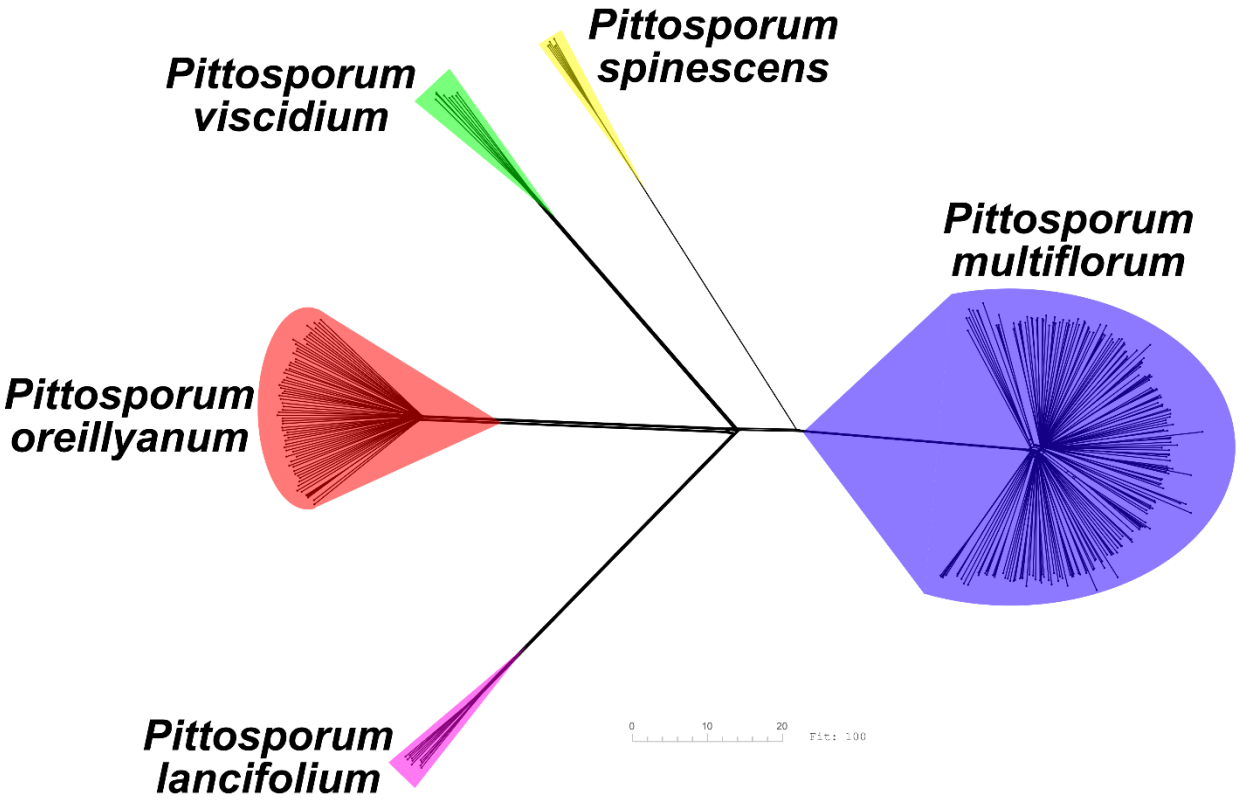

Figure 16: The SplitsTree phylogenetic network estimated using DArTseq data for Pittosporum*, including all species in the* Citriobatus *lineage. The phylogenetic network supports all species as currently circumscribed and shows not evidence for hybridisation or introgression in the wild despite sympatric distributions.*

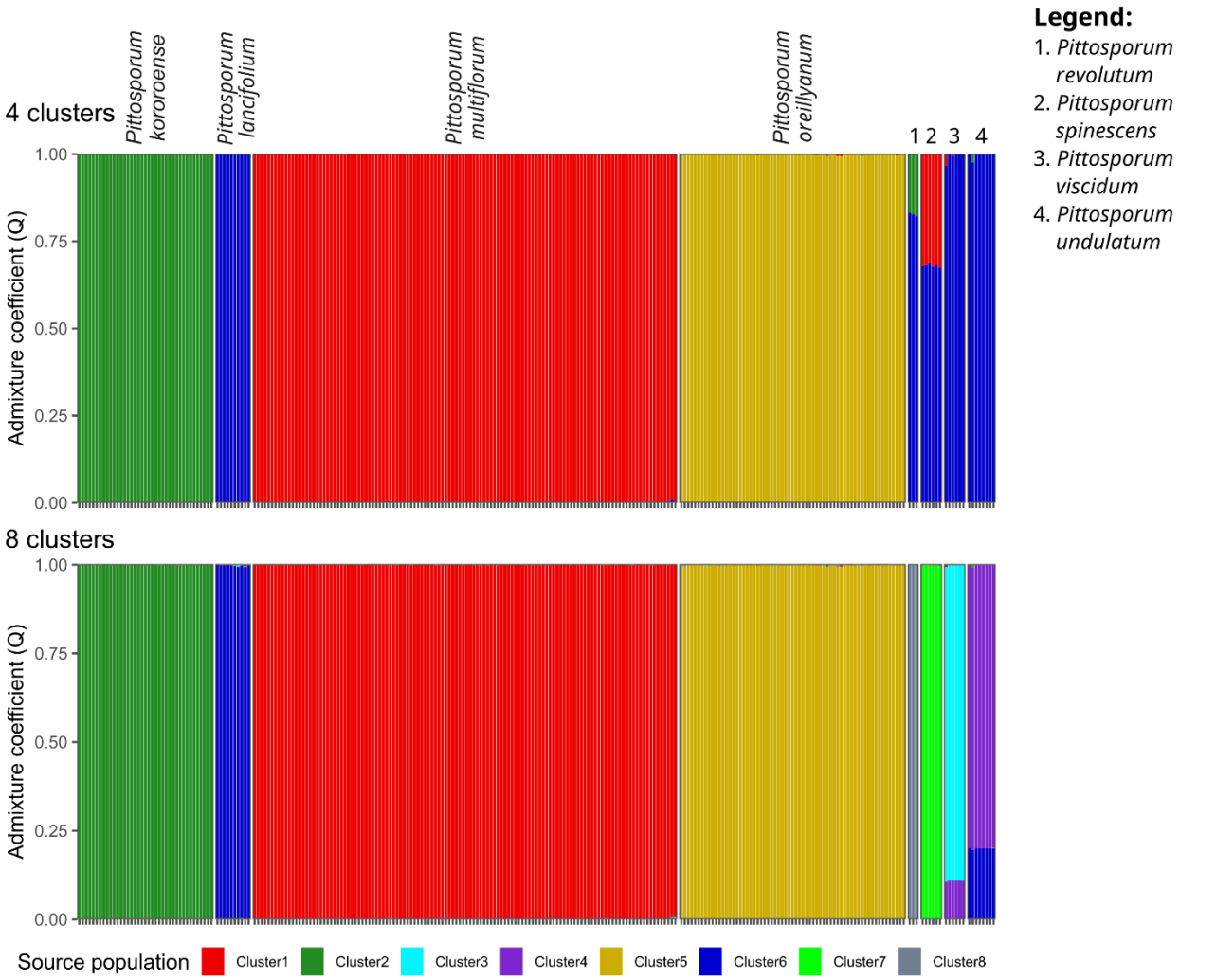

Figure 17: Admixture plot showing the results of 4 and 8 cluster STRUCTURE analyses of Pittosporum *DArTseq data. In the 4-cluster analysis* the well sampled P. kororoense, P. multiflorum and P. oreillyanum each form distinct genetic clusters *with minimal genetic admixture, with the five remaining poorly sampled species all being predominately assigned to a fourth cluster. In the 8-cluster analysis, each sampled species is primarily assigned to a unique genetic cluster, with some minor admixture between* P. lancifolium, P. viscidium *and* P. undulatum. *While these results support current the current taxonomy of the sampled species, further interpretation is avoided due to the bias in sampling across species which likely bias genetic clustering results.*

Key Genetic Findings

Ploidy

DArTseq read count analysis suggests *P. oreillyanum* is a putative diploid.

Genetic diversity and reproductive biology

Within site genetic diversity of *P. oreillyanum* was in line with, if not higher than, outgroup species (excluding the possibly polyploid *P. multiflorum*) and was even across all sampled sites (Table 13). This suggests reasonable evolutionary potential exists in all populations that may assist with adaptation to gradual environmental changes.

Potential clonality was observed for *P. oreillyanum* at one site (Joalah Lookout; Figure 18), but this is hypothesised to be due to sampling mistakes due to difficulty accessing individuals. The four samples concerned were collected within 2 metres of one another and may represent different parts of the same individual rather than true clonality. No evidence for high levels of selfing or inbreeding was observed for *P. oreillyanum* (Table 13), unlike for the more common *P. multiflorum* which shows extensive evidence for high rates of selfing and/or inbreeding. Overall, a mating system with high levels of outcrossing pollination, low self-pollination, and very little if any apomixis or vegetative spread is hypothesised.

Genetic structuring and gene flow

The Border Ranges NP *P. oreillyanum* populations showed shallow divergence from the sampled Springbrook NP and Lamington NP populations (Figure 19). This is likely driven by reduced geneflow due to distributional breaks in Lamington NP southwest of Mt Throakban, although sampling of the Cockscomb Point population may close this divergence. Divergence between sampled sites within Springbrook NP and Lamington NP matched geography well and reflects an isolation-by-distance (IBD) pattern (Figure 20).

Very few private alleles were observed from any site, suggesting relatively significant and recent geneflow between all populations. Given the species dehiscent fruit with a colourful, sticky seed mass (Cayzer *et al.* 2000), gene flow may be facilitated by dispersal of seed by birds around the Wollumbin Caldera.

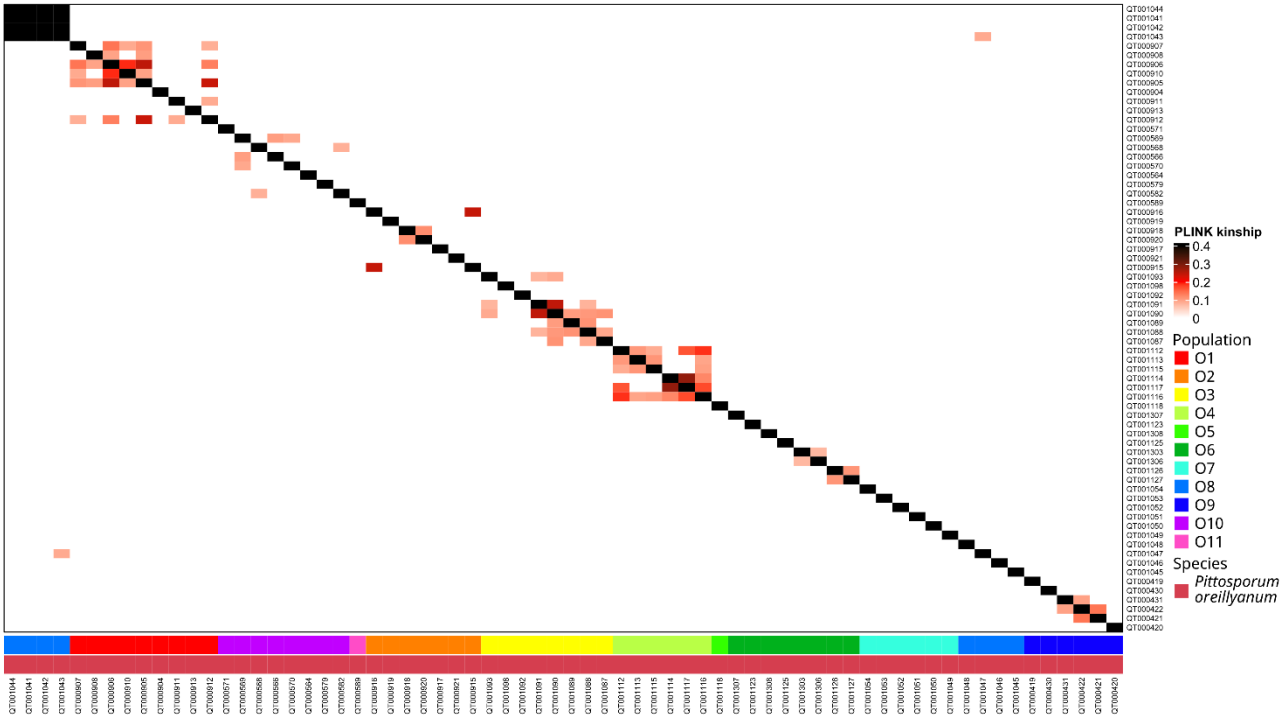

Figure 18: Heatmap of pairwise kinship values between genotyped Pittosporum oreillyanum *individuals. Values at or above 0.4 represent genetically identical samples mostly arising through clonality, while values between 0 and 0.4 represent individuals with familial relationships up to ~2 generations removed. One clonal genet of four individual ramets are recorded at the Joalah Lookout. While this may represent true clonality due to vegetative spread, it is possibly due to sampling mistakes due to difficulty accessing individuals. The four samples concerned were collected within two metres of one another and may represent incidental collection of different parts of the same individual rather than true clonal ramets. Familial relationships are also observed between individuals growing at most sites, reflecting ongoing out-crossing sexual reproduction.*

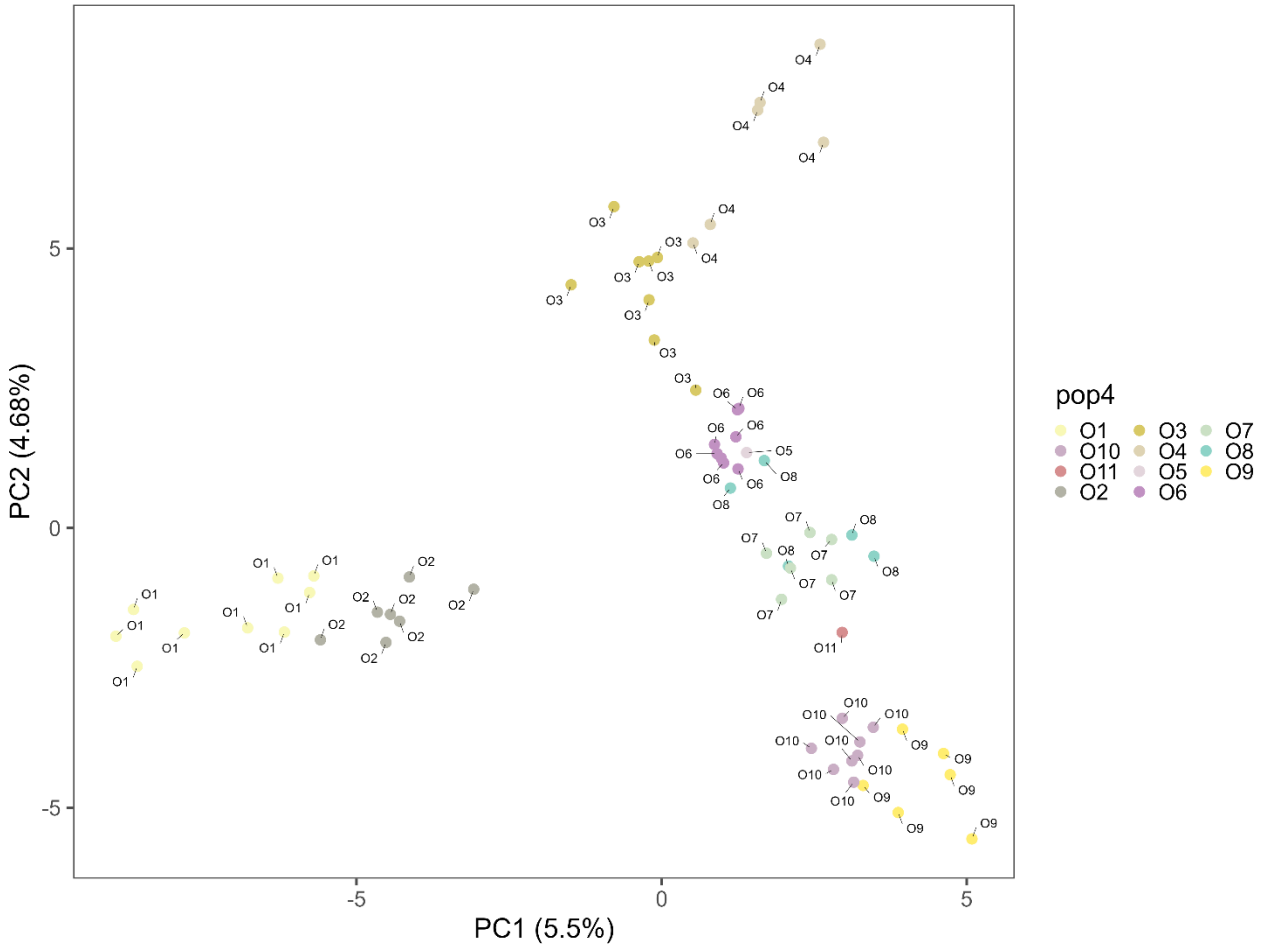

Figure 19: PCA plot of all genotyped Pittosporum oreillyanum *samples showing the shallow divergence of Border Ranges populations (O1 and O2) from those in Lamington NP and Springbrook NP. Clustering of Lamington NP and Springbrook NP populations suggests an east to west genetic gradient, with a very minor divergence across the Numinbah Gap between the two national parks. Overall, this plot suggests there is limited discrete genetic structure across the distribution of P. oreillyanum and that some gene flow is maintained between all populations as a factor of geographic distance.*

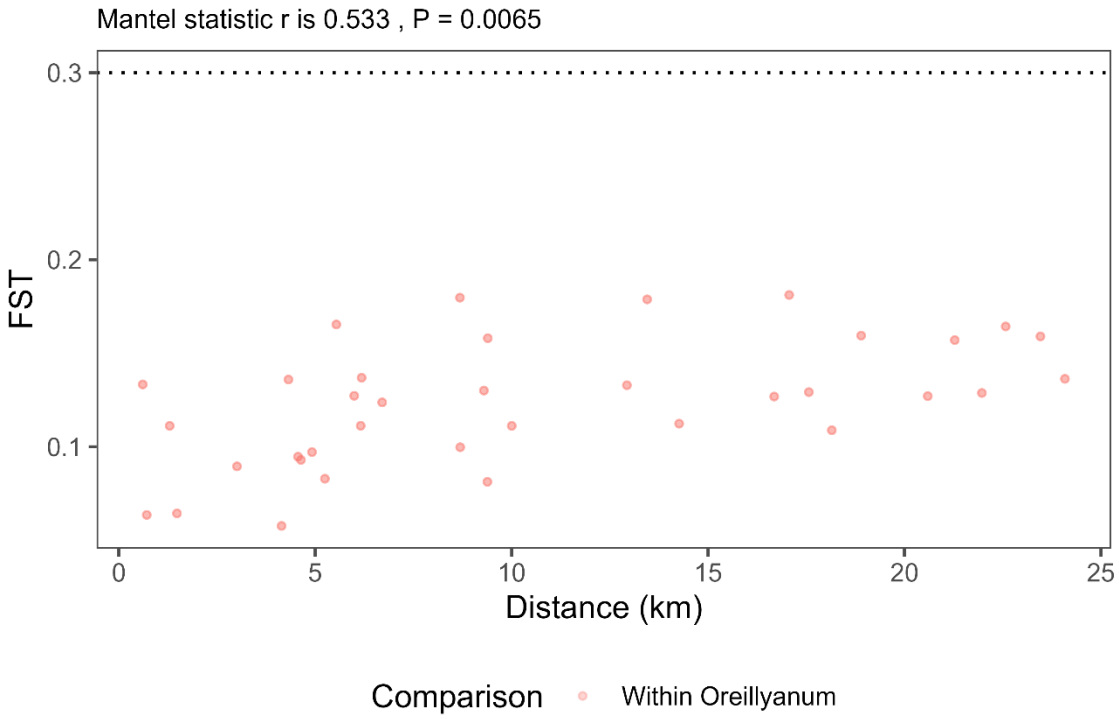

Figure 20: The isolation-by-distance plot for all P. oreillyanum *sites where 5 or more samples were successfully genotyped. The x-axis shows pairwise geographic distance and y-axis pairwise genetic distance (F_{st}), with results of the mantel test showing a statistically significant relationship between the two with geographic distance explaining ~50% of genetic differentiation between sites.*

Table 13: Key population genetic parameters of P. oreillyanum *populations represented by 5 or more genets in the DArTseq dataset (H_o = observed heterozygosity, H_e = expected heterozygosity, uH_e = unbiased expected heterozygosity). A total of 2217 high quality, variable loci were used for calculations.*

Population	Private alleles	Allelic richness	H_o	H_e	uH_e	Inbreeding coefficient	Unbiased inbreeding coefficient
O1	0	1.2739	0.2773	0.278	0.3044	0.0025	0.089
O10	0	1.2839	0.2878	0.2972	0.3254	0.0316	0.1156
O2	0	1.278	0.2815	0.2843	0.3112	0.0098	0.0954
O3	3	1.293	0.2961	0.2959	0.3237	-7e-04	0.0853
O4	2	1.2854	0.2895	0.2644	0.2891	-0.0949	-0.0014
O6	0	1.2895	0.2918	0.3087	0.3377	0.0547	0.1359
O7	1	1.3	0.3032	0.3066	0.3355	0.0111	0.0963
O8	2	1.2742	0.2782	0.2796	0.312	0.005	0.1083
O9	2	1.2812	0.2845	0.2877	0.3149	0.0111	0.0965

Modelled impacts of climate change

Figure 21 shows the projected areas of climate suitability for *P. oreillyanum* under climate change in the years 2050, 2070 and 2090, along with the present climate suitability model. The model shows high suitability around the Wollumbin Caldera where the species occurs, but also in Nightcap NP and Mount Jerusalem NP to the immediate south, from which the species has never been recorded. Further south, an area of putatively suitable climate located in and around Dorrigo NP and in the Illawarra region south of Sydney. By 2050, we see a drastic decline in areas that match the species modelled climatic niche, with small areas of higher modelled suitability remaining only in Lamington NP and Dorrigo NP. A modest increase in modelled climate suitability is projected for 2070, particularly in Dorrigo NP, before further contraction in 2090, leaving no areas of high modelled similarity to the species current climatic niche.

Management recommendations

Based upon available literature and the findings of this study, the current threat status of *Near Threatened* is considered appropriate for *P. oreillyanum* under the CAM. There is no evidence the species has experienced decline in population size, distribution or genetic diversity in the past 500 years, with the only observable threat to the species being climatic change. Given the high genetic diversity observed and large effective population size, and thus moderate inferred adaptive potential, the climatic habitat modelling showing a severe and immediate decline in suitable habitat should be taken with caution.

These results suggest *P. oreillyanum* would be most vulnerable to ecosystem scale perturbations or widescale displacement of the high elevation forests rather than a direct threat to the species. As such, no specific in-situ management recommendations are made. However, a precautionary approach is recommended for this species such as undertaking collection of propagule material (seed, cuttings or live plants) to form an insurance collection (either a translocation, seed bank or ex-situ live population) should wild populations experience sudden and rapid decline. Genetic optimisations suggest that collecting five seed lines from three sites (fifteen total seed lines) would reliably capture 90% of common alleles present across the species distribution. This is in line with the observation of ongoing gene flow between populations leading to low genetic structuring. When considering the distribution of *P. oreillyanum*, it seems prudent to collect seed from one site in each of the three national parks in which the species occurs as a secondary method of ensuring good genetic representation.

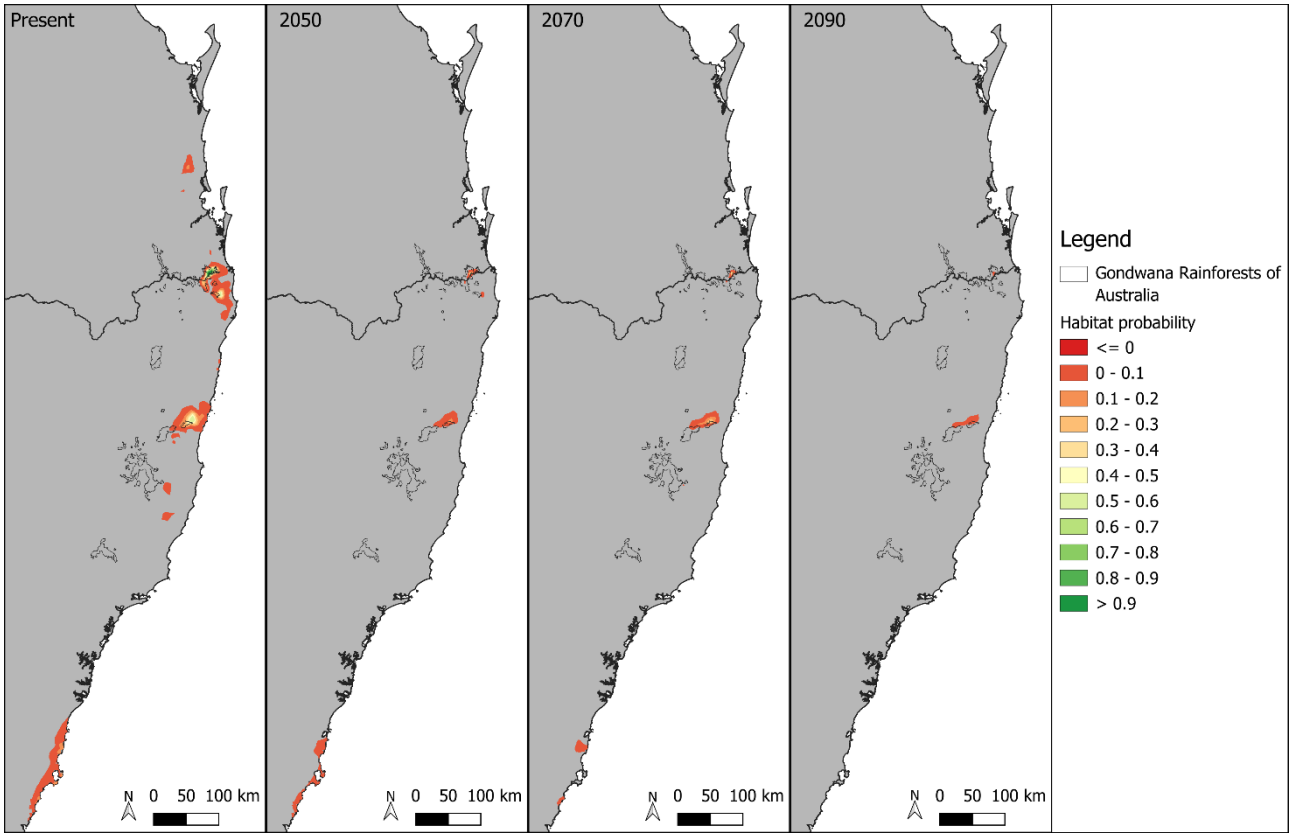

Figure 21: Results of climate habitat modelling for Pittosporum oreillyanum *for present conditions and then project onto predict conditions in the years 2050, 2070 and 2090. Predicted habitat suitability in each map cell is a value between zero and one, with one being high confidence suitable climate. Under present climate conditions, modelled areas of potentially suitable climate are more widespread than the species realised distribution, particularly in the Nightcap Range and around Dorrigo NP, with low confidence suitable climate also present in the Illawarra region, potentially suggesting the species distribution is dispersal limited. By 2050, we see a stark decrease in areas of predicted suitable climate, leaving just small areas of low probability suitable climate in Lamington NP, Dorrigo NP and the Illawarra region. The former two show increased predicted suitability in 2070, before declining even further in 2090.*

Pomaderris notata

Population size, distribution and status

Pomaderris notata is primarily known from ten exposed rhyolite outcrops amongst rainforest above 700 m elevation on the Wollumbin Caldera and Wollumbin (Mt Warning) itself, where they frequently grow as a dominant shrub species (Figure 22). While often not mapped as such due to small patch sizes, these populations primarily occur in communities corresponding to high elevation montane heath (RE 12.8.19) rather than either of the high elevation rainforest RE's. A single, small, low elevation (~130 m) population is known from along Khungur Creek below the Sphinx Rock (Nightcap NP) population (Figure 22). Despite initial scepticism that this population truly represented *P. notata* given it's taller, more slender growth form, genetic data confirms the identity of this population as *P. notata*. Kunghur Creek originates near the top of the northern slope of Mount Burrell, atop which *P. notata* grows on Sphinx Rock. It is therefore hypothesised that this lowland population is the result of seed dispersal down the creek giving rise to a highly localised lowland stand. Unfortunately, this hypothesis could not be tested using the genetic data in this study, as Sphinx Rocks was not accessible for field collections.

Table 14 summarises the sampling scheme for *P. notata*, with all known populations in Queensland sampled. However, the remote NSW populations on Cockscomb Point (Border Ranges NP), Sphinx Rock (Nightcap NP), Wollumbin (Wollumbin NP) were not accessed for sampling. Furthermore, the Psuedo-Pinnacle population within Border Ranges NP was not relocated for sampling, and only a single individual at Bar Mountain could be safely reached for sampling as the species primarily grows on the top of a cliff side at this location. Field observations suggest the species is long-lived, with a low turnover rate and minimal seedling recruitment was observed. As no evidence for population decline was recorded (e.g. minimal sick or dead individuals) at any site, the species population appears stable. Overall, the only observable threats to the species' persistence are climate change and the associated changes to local moisture and disturbance regimes.

Table 14: Summary of the sampling scheme employed for Pomaderris notata *in this study. Population codes match those used in subsequent analysis and figures. While a minimum of 6 samples per site was the aim of sampling, at the Bar Mountain site, the population grows on a cliff side and so was largely inaccessible for sampling leading to only a single individual being genotyped. In addition, Garragoolba Lookout was not visited during field visits so is only represented by a single preexisting herbarium specimen.*

Genotyped population code	Location	Coordinates	Number of samples successfully genotyped
Notata1	Roadside vegetation along Kunghur Creek Road, above Kunghur Creek	-28.4844, 153.2447	6
Notata2	Bar Mountain Lookout, Border Ranges NP	-28.4556, 153.1210	1
Notata3	Moonlight Crag, Lamington NP	-28.2379, 153.1280	8
Notata4	Mt Wagawn, Lamington NP	-28.2591, 153.2135	10
Notata5	Garragoolba Lookout, Lamington NP	-28.2536, 153.2158	1 (herbarium specimen)
Notata6	Araucaria Lookout, Lamington NP	-28.2386, 153.2197	6

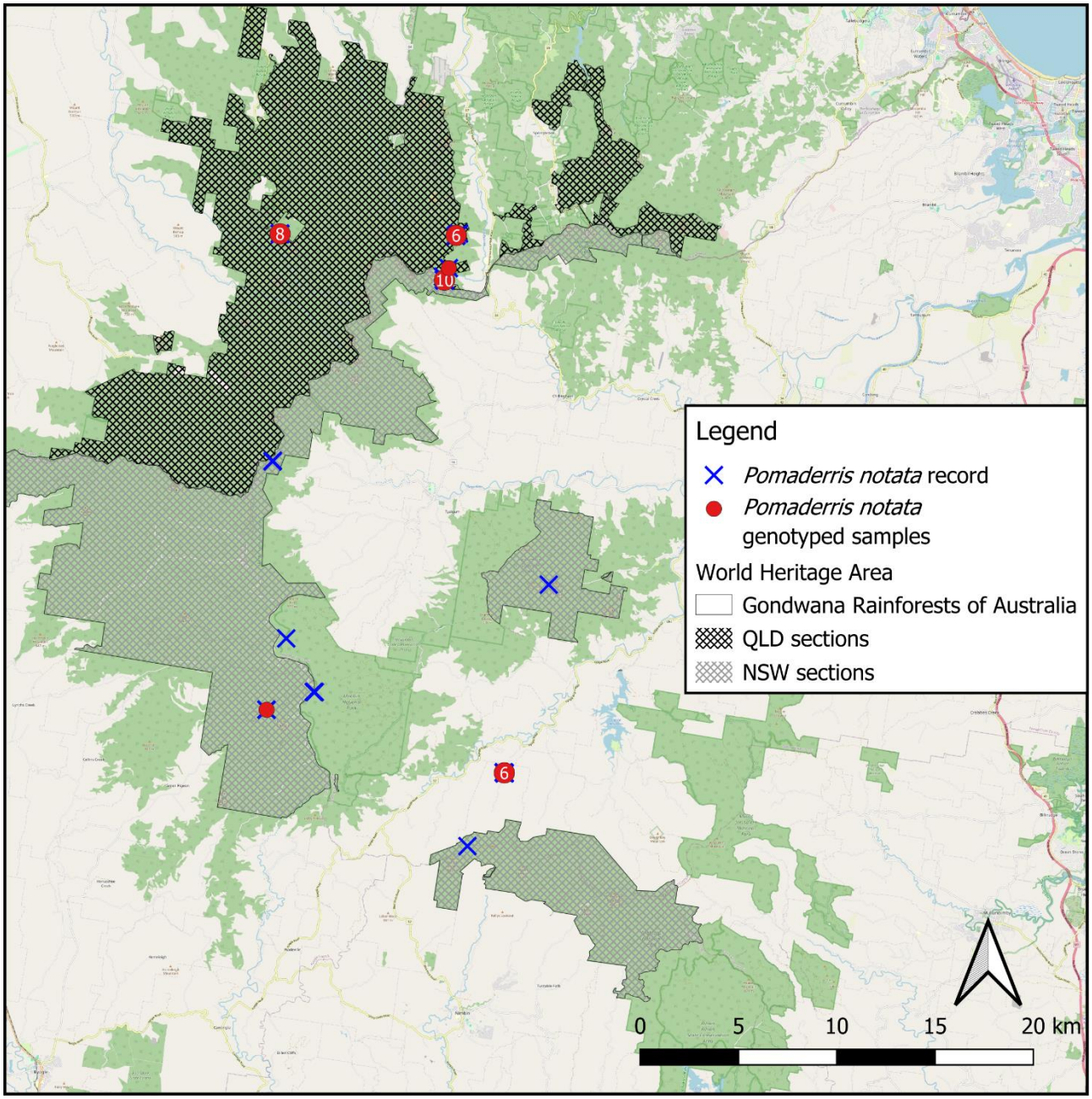

Figure 22: Map showing the sampling scheme for wild Pomaderris notata *used for this project. While the Bar Mountain site was visited and observed, the rugged terrain of the site prevented the collection of more than a single sample. Due to limited access options, the populations at Cockscomb Point, the Psuedo Pinnacle in Border Ranges NP, Wollumbin and Sphinx Rock could not be sampled within the scope of this project.*

Evolutionary relationships and hybridisation

As illustrated in Figure 23, Figure 24 and Figure 25, genetic evidence strongly supports *P. notata* as a distinct species as currently circumscribed, including the lowland Kunghur Creek population. There are significant discrepancies between the DArTseq phylogeny used here and that of Nge *et al.* (2021), which did not include *P. notata*. The discrepancies between these two phylogenies may be due to the taxonomic uncertainties, the different markers showing different relationships and the impacts of polyploid samples on the datasets. The DArTseq data used here supports *P. notata* as a distinctive species within subgenus *Pomaderris. Pomaderris clivicola*, a highly range restricted species that occurs in the vicinity of Gayndah, ~320 km north-northeast of *P. notata*'s range, is suggested to be a close relative of *P. notata* (Figure 23). Both species are genetically quite distinct within the subgenus, however.

No evidence for hybridisation between *P. notata* and any other species was observed in the genetic data, however this likely due to the species lack of occurrence overlap with congeners. This means hybridisation may be biologically possible and only opportunity limited.

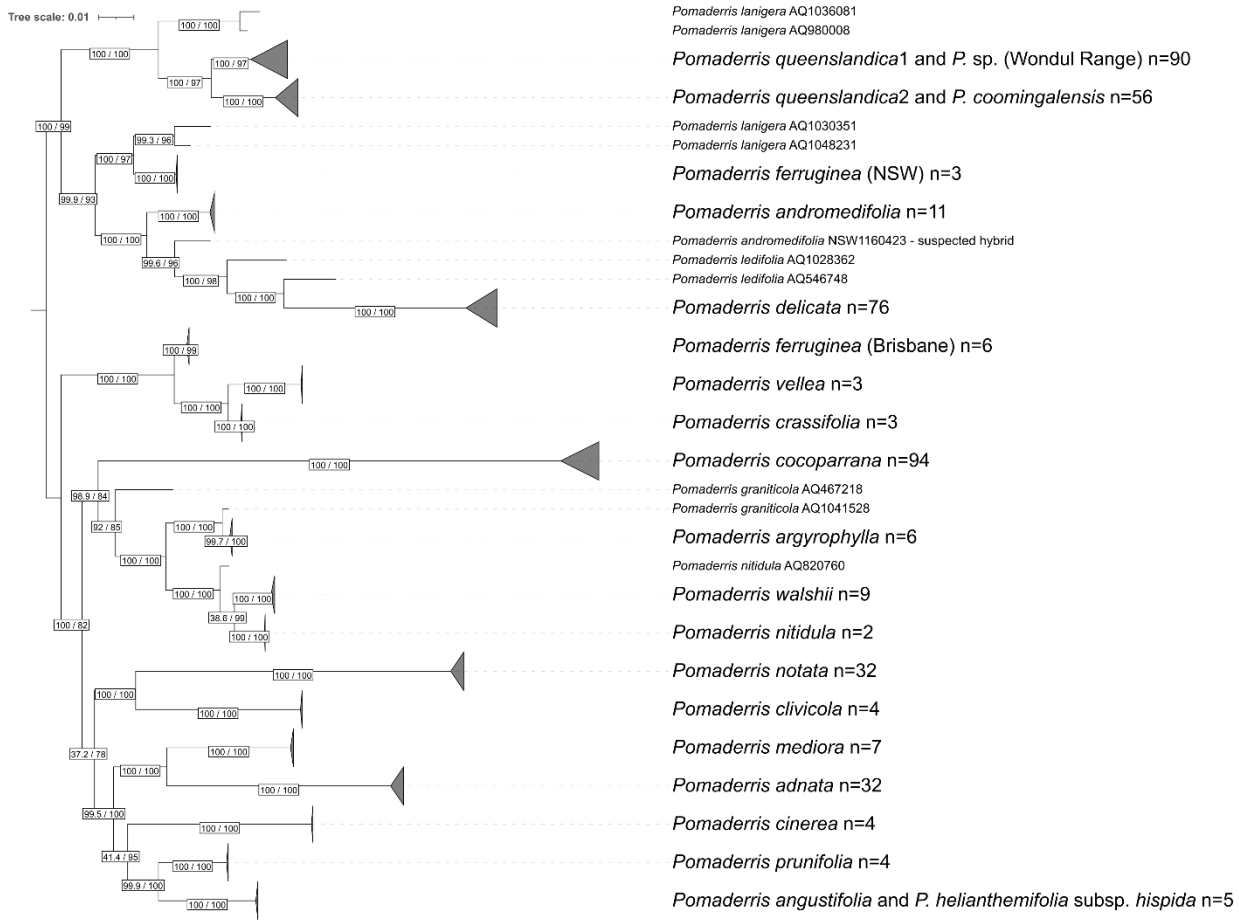

Figure 23: The IQTree phylogeny estimated using DArTseq data for sampled Pomaderris *taxa. Hybrid samples are excluded from the analysis as they violate the assumption of bifurcating relationships. Clades representing species level grouping of samples are collapsed with sample numbers per species shown. Note the tree is midpoint rooted. While several species are not supported as monophyletic clades, suggesting further taxonomic study is needed in the genus, all* P. notata *samples (including the lowland Kunghur Creek site) form a well-supported clade. The* P. notata *clade is supported as most closely related to* P. clivicola*, another rare species from central Queensland, an evolutionary relationship not previous suggested in the literature.*

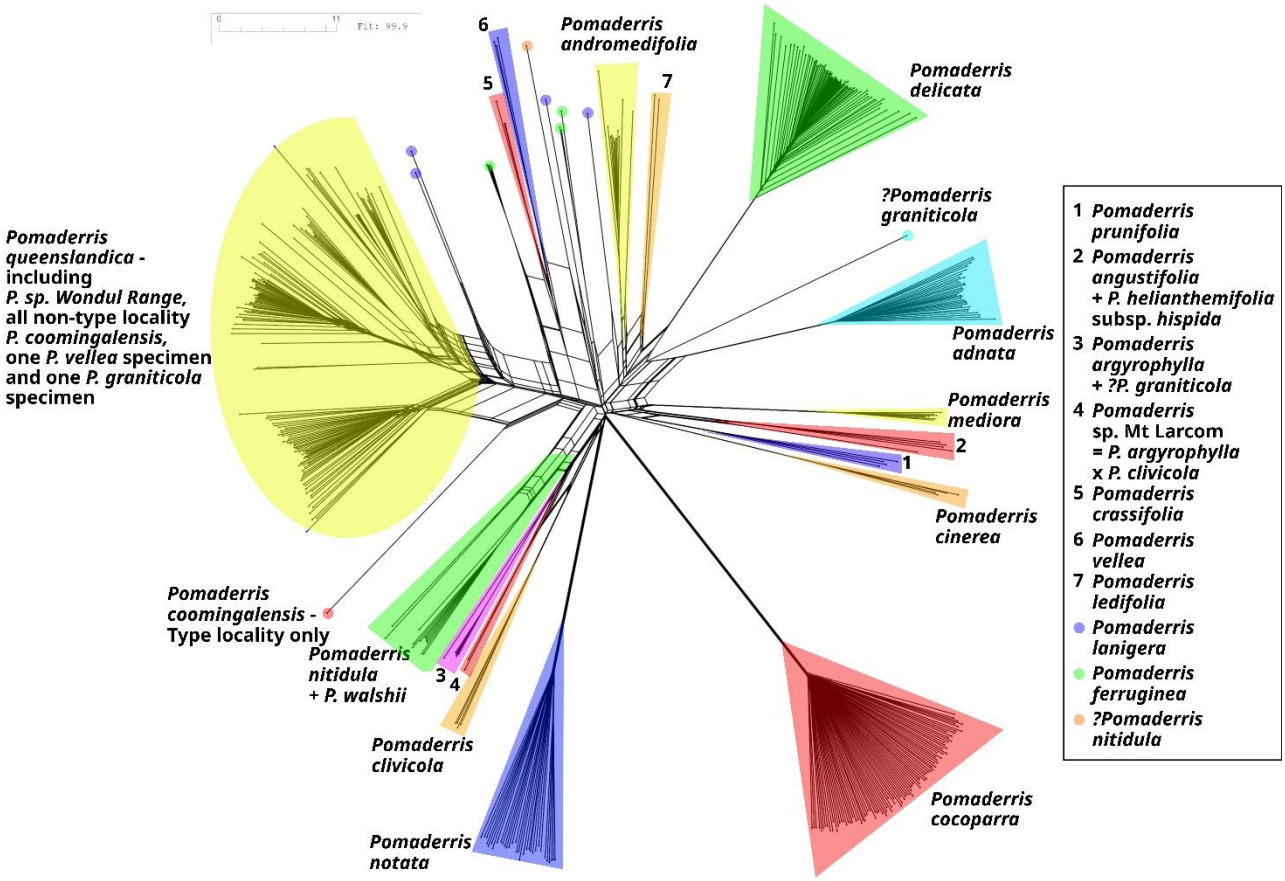

Figure 24: The SplitsTree phylogenetic network estimated using DArTseq data for Pomaderris *subgenus* Pomaderris*, including all species sampled in this study. The phylogenetic network supports* P. notata *as currently circumscribed and shows not evidence for hybridisation or introgression between this species and any other species. Hybridisation is suggested for several other samples included in the dataset, including all samples of the phrase name taxon* Pomaderris *sp. (Mt Larcom J.Brushe JB259). Another notable finding is the lack of support for* P. coomingalensis *as currently circumscribed as distinct from* P. queenslandica*, as* P. coomingalensis *is currently listed as Endangered under the NCA.*

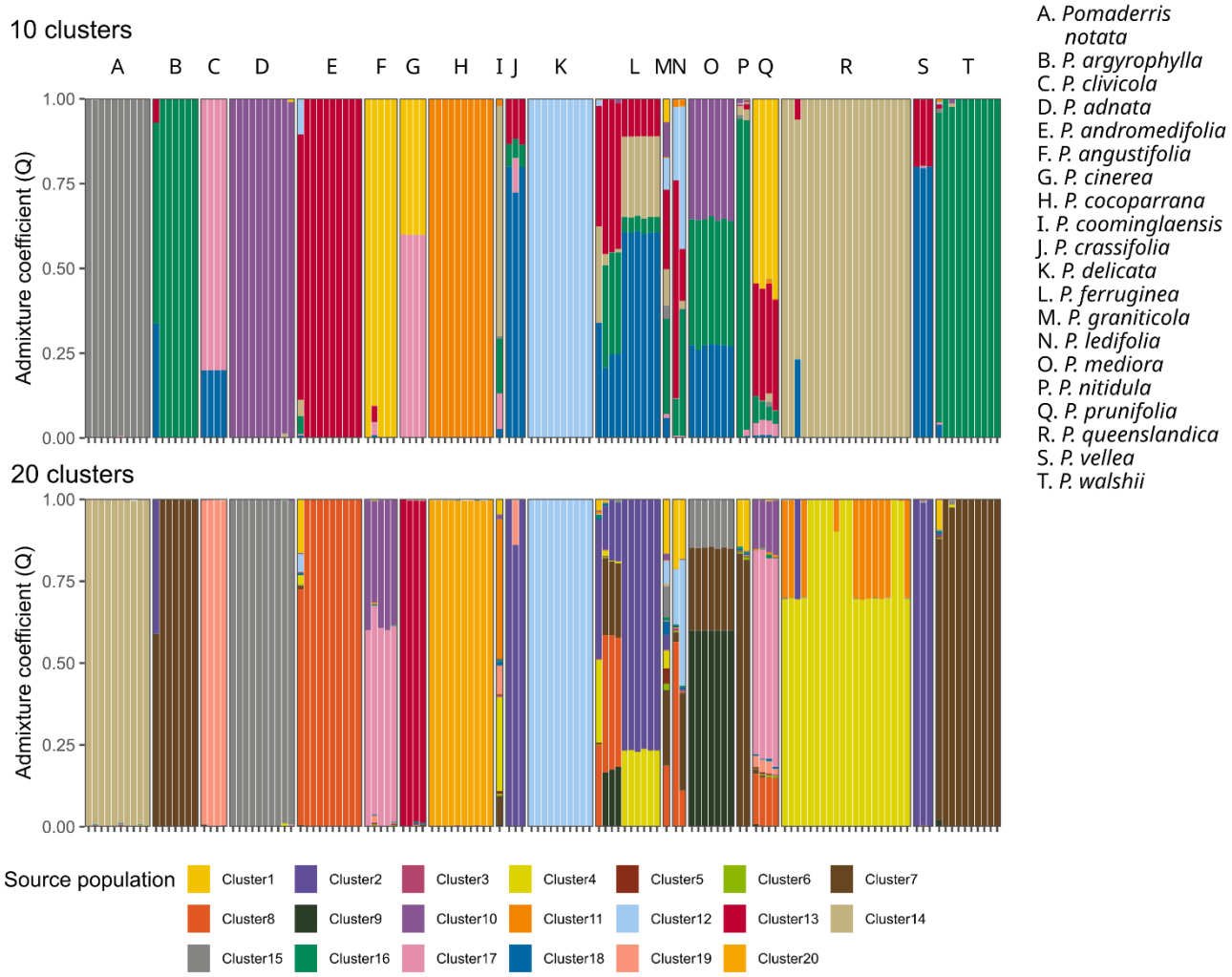

Figure 25: Admixture plot showing the results of 10 and 20 cluster STRUCTURE analyses of Pomaderris *DArTseq data. Samples are grouped by genetic identification. Overall, across both plots, the range restricted, diploid species (including* P. notata*) tend to form distinct genetic clusters, while the more widespread, polyploid taxa show various patterns of partial assignment to multiple clusters. This possibly reflects a hybrid origin of the polyploid lineages. These results support the taxonomic circumscription of the diploid species including* P. notata *but suggest further taxonomic investigation is needed primarily in the more widespread polyploid lineages.*

Key Genetic Findings

Ploidy

DArTseq read count analysis suggests *P. notata* is a putative diploid.

Genetic diversity and reproductive biology

Genetic diversity was high in most *P. notata* populations, with the Kunghur Creek population showing slightly lower diversity than the Wollumbin Caldera populations (Table 15). It is not possible to compare the diversity of *P. notata* to most other species of *Pomaderris*, as many of the other sampled species are polyploid, however *P. cocoparrana*, another range restricted, diploid species had genetic diversity in line with that observed for *P. notata*. No evidence for elevated inbreeding was observed in any *P. notata* population represented by at least 5 samples (Table 15).

No clonality was observed at any site for *P. notata*, although kinship groupings (first- and second-degree relatives) were observed at most sites (Figure 26). In the larger high elevation populations (Moonlight Crag, Araucaria Lookout and Mt Wagawn) this may reflect an inability to spatially separate sampled individuals within sites due to the steep terrain in which the species occurs rather than the underlying biology of the species. However, the familial relationships between all samples from the Khungur Creek site support the hypothesis that this population results from a single dispersal event from Sphinx Rock. Overall, the lack of evidence for inbreeding and clonality suggests reproduction and dispersal of *P. notata* is primarily via out-crossed seed.

Genetic structuring and gene flow

The lowland Kunghur Creek population was shown to be moderately genetically divergent from populations on the Wollumbin Caldera (Figure 27 and Figure 28). As the Sphinx Rock population was not sampled, we cannot say whether the lowland population is unique within the species genetically as well as ecologically, or if the isolation is between Sphinx Rock (Nightcap NP) and the Wollumbin Caldera populations. Each population in the Wollumbin Caldera was shown to be genetically distinct from one another (Figure 27), suggesting limited gene flow between populations. In addition, *P. notata* showed the significant private alleles per population (40 – 110 alleles each; Table 15), furthering evidence for restricted gene-flow between sites. Overall, it appears likely that seed and pollen dispersal between sites is low after initial colonisation events. Insects are the assumed pollinators of *Pomaderris* generally (Patykowski *et al.* 2014; Simmons *et al.* 2025) and most *P. notata* populations are >3 km apart, a distance pollinating insects rarely travel (de Jong *et al.* 2005). Likewise, passive seed dispersal, primarily via gravity or water, is the suggested dispersal method for *Pomaderris* species, with ant's known to be responsible for some local dispersal of seed (Patykowski *et al.* 2016; Simmons *et al.* 2025). Neither gravity nor water are likely to be able to transport seed between the exposed locations *P. notata* grows, further supporting the hypothesis of rare, stochastic long-distance dispersal events giving rise to the isolated populations of the species.

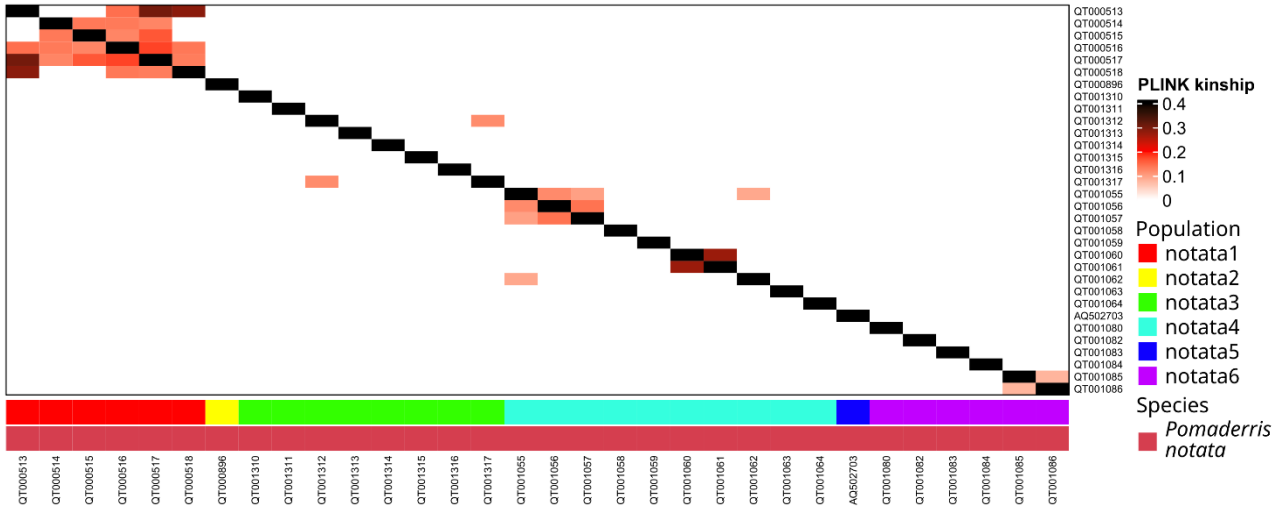

Figure 26: Heatmap of pairwise kinship values between genotyped Pomaderris notata *individuals. Values at or above 0.4 represent genetically identical samples mostly arising through clonality, while values between 0 and 0.4 represent individuals with familial relationships up to ~2 generations removed. No clonal genets are observed in the dataset, reflecting all reproduction occurring through pollination and seed production with no evidence for vegetative spread or apomixis (production of clonal seed). Familial relationships are also observed between individuals growing at most sites, reflecting ongoing out-crossing sexual reproduction. All samples from the Kunghur Creek population show shared familial relationships, suggesting the small population has only bred amongst itself and most individuals likely come from a small number of parental plants.*

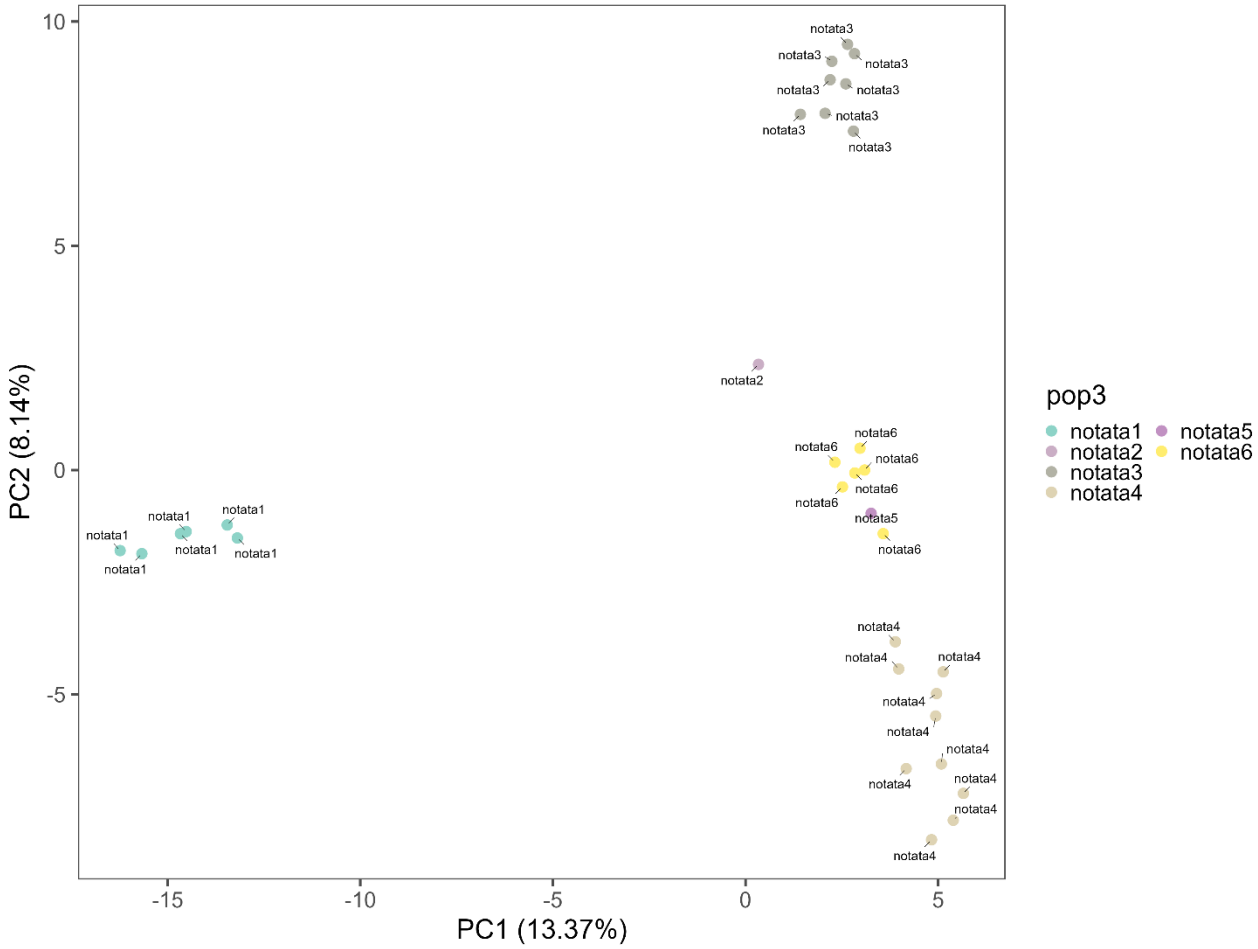

Figure 27: PCA plot of all genotyped Pomaderris notata *samples showing the genetic distinctiveness of the Kunghur Creek population (notata1) from the sampled Wollumbin Caldera populations. Clustering of Lamington NP and Springbrook NP populations reflected isolation of the geographically distinct populations, with the single Garragoolba Lookout (notata5) sample not separating from the Araucaria Lookout population (notata6), possibly due to a lack of samples from the former site. Overall, this plot suggests each population of P. notata is genetically discrete, and hints at a possible increased divergence between populations on the Wollumbin Caldera and those elsewhere (represented by the Kunghur Creek population).*

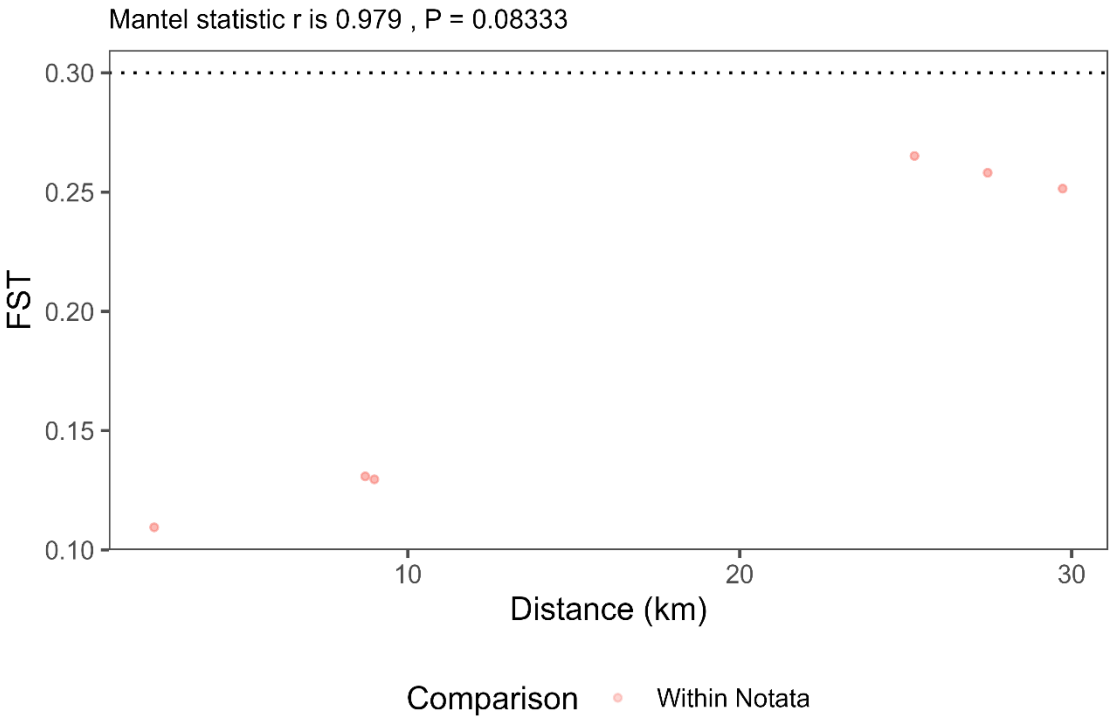

Figure 28: The isolation-by-distance plot for all P. notata *sites where 5 or more samples were successfully genotyped. The x-axis shows pairwise geographic distance and y-axis pairwise genetic distance (F_{st}). As only four sites were available for inclusion in mantel test, the result is not statistically significant despite a high r value.*

Table 15: Key population genetic parameters of P. notata *populations represented by 5 or more genets in the DArTseq dataset (H_o = observed heterozygosity, H_e = expected heterozygosity, uH_e = unbiased expected heterozygosity). A total of 3333 high quality, variable loci were used for calculations.*

Population	Private alleles	Allelic richness	H_o	H_e	uH_e	Inbreeding coefficient	Unbiased inbreeding coefficient
notata1	110	1.2471	0.2517	0.2377	0.2603	-0.0589	0.033
notata3	67	1.2766	0.2799	0.29	0.3172	0.0348	0.1176
notata4	45	1.2842	0.2875	0.2858	0.3125	-0.0059	0.08
notata6	50	1.2781	0.2816	0.2873	0.3143	0.0198	0.104

Modelled impacts of climate change

Figure 29 shows the projected areas of climate suitability for *P. notata* under climate change in the years 2050, 2070 and 2090, along with the present climate suitability model. When examining the current climate model, it was concluded that this modelling technique is not useful for this species given the widespread areas of suitable climate in which the species does not occur. There are two likely contributors to this issue: the small number of populations leading to model fitting issues, and the fact the species' ecological niche is defined by environmental factors not captured by the set of bioclimatic variables used. *Pomaderris notata* occurs only (excluding the aberrant Kunghur Creek population) on exposed rhyolite outcrops at high elevation, a realised habitat niche not defined by climate. While it appears likely the species requires high rainfall to survive given it grows amongst rainforest vegetation, this requirement operates at a broader scale than the species specialised niche. Overall, we refrain from interpreting the forward projections of the climate model here.

Management recommendations

Based upon literature evidence and the findings of this study, the current threat status of *Vulnerable* is considered appropriate for *P. notata* under the CAM criteria (IUCN 2012). There is indirect evidence the species has experienced decline in population size at both Moonlight Crag (due to construction) and Kunghur Creek (road construction and paddock clearing). There is no evidence for a reduction in distribution area or genetic diversity in the past 500 years. The only observable threat to the species is climatic change and associated changes to disturbance regimes, particularly fire.

The climate models for this species and its non-climatically defined microhabitat mean the potential impacts of direct climatic change is unknown, and potentially less important than for the three other species studied here. However, as previous work has shown diploid *Pomaderris* species, as *P. notata* is putatively identified as, are less adapted to fire than polyploid species (Chan *et al.* 2022) and as *P. notata* predominately grows amongst rainforest that infrequently, if ever, burns, we hypothesis it may be fire sensitive and have few adaptations to regenerate after a burn. Combined with the fact the species occurs as spatially restricted populations, increased fire impacts may pose a significant threat to the survival of individual populations.

A precautionary approach is recommended for this species, including the undertaking collection of propagule material (seed, cuttings or live plants) to form an insurance collection (either a translocation, seed bank or ex-situ live population) should wild populations experience sudden and rapid decline due to climate change or high impact fire events. As only four geographically biased sites were represented by five or more genets in our dataset, propagule collection optimisation analysis was not feasible for *Pomaderris notata.* However, given the species' small number of geographically discrete populations, and the evidence for restricted gene flow between them observed here, collecting multiple propagule lines from all known populations would be recommended to ensure the capture of representative genetic diversity from across the species distribution.

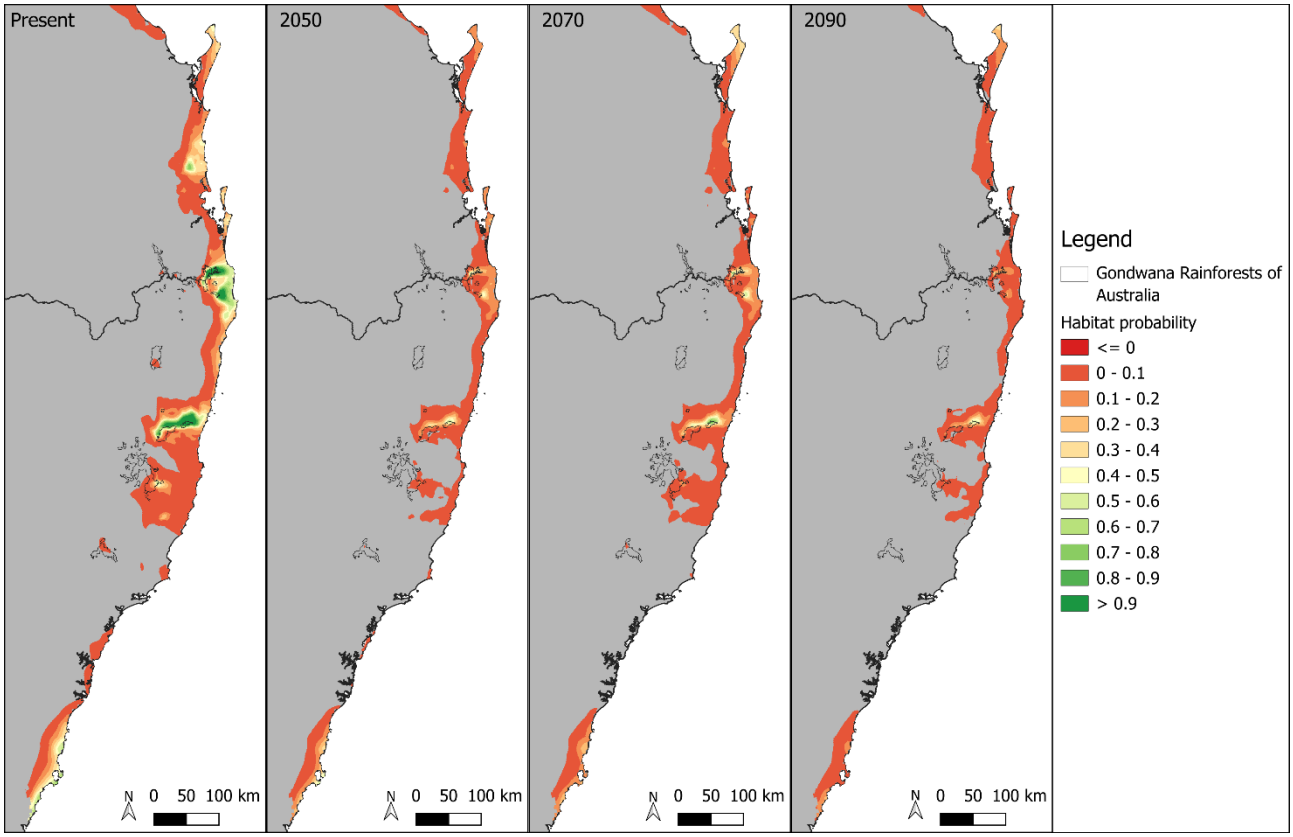

Figure 29: Results of climate habitat modelling for Pomaderris notata *for present conditions and then project onto predict conditions in the years 2050, 2070 and 2090. Predicted habitat suitability in each map cell is a value between zero and one, with one being high probability suitable climate. In line with the species being a specialist of a particular edaphic habitat (exposed rhyolite outcrops) and the presence of a population in dramatically different climatic conditions to the remaining population (i.e. the lowland Kunghur Creek population), we see the climate suitability model suggest climate plays a marginal role in defining the species distribution. For this reason, we refrain from further interpreting the results of the climate suitability analysis.*

Syzygium nebulosum

Population size, distribution and status

Syzygium nebulosum is restricted to areas above 800m (primarily above 900m) in the Wollumbin Caldera (and putatively also Wollumbin itself), predominately in areas with very high soil moisture at the head of drainage systems (Figure 30). With the reidentification of all *Syzygium crebrinerve* records at high elevation, *S. nebulosum* is the only species in *Syzygium* subgenus *Syzygium* (per Craven and Biffin 2010 and Low *et al.* 2022) to occur in the high elevation rainforests of the GRWHA (QLD section). Monospecific stands were observed growing in drainage lines on Mt Wagawn, suggesting the species may be a dominant canopy species in this microhabitat at high elevation and that it may require access to permanently wet soils.

Syzygium nebulosum has a known distribution consisting of several discrete areas: within the highest elevation parts of Springbrook NP, primarily on Mt Thillinmam and Mount Mumdjin, within Lamington NP both between Mt Wagawn and Mt Throakban (including at Joalah Lookout) and between Cockscomb Point and the NSW border, and within Border Ranges NP between Pinnacle Hill and Bar Mountain. We conclude this species is more common than outlined in the taxonomic treatment (Weber and Forster 2025), given minor survey effort recorded new stands on Mt Wagawn and the western slope of Mt Mumdjin.

Table 16 summarises the sampling scheme for *S. nebulosum.* Field collections were supplemented with destructive samples from existing specimens in the BRI collection to expand geographic coverage but of note is that the species was not sampled from the remote populations at Cockscomb Point and Wollumbin. Population level sampling (>5 genets) was only achieved at three sites (Bar Mountain, Mt Wagawn and Mt Mumdjin/Best of All), due to difficulties locating individuals with foliage within reach from ground level within closed forest.

Significant coppice growth and individuals of varying age classes (including some seedlings) were observed in the field, suggesting the species has a high capacity for regeneration. As no observable evidence for population decline was recorded (e.g. minimal sick or dead individuals) at any site, the species populations appear stable. The only observable threats to species persistence were disease, climate change and the associated changes to local disturbance regimes. Potential myrtle rust impact was observed in some populations, although there was no evidence for disease induced tree death. However, as myrtle rust can have severe impacts on recruitment even in the absence of plant death (Carnegie and Pegg 2018), further research is needed to understand the impacts of this disease on the species' long term persistence.

Table 16: Summary of the sampling scheme employed for Syzygium nebulosum *in this study. Population codes match those used in subsequent analysis and figures. While a minimum of 6 samples per site was the aim of sampling, at several sites, fewer individuals were located meaning this aim was only reached at three sites. Furthermore, four sites are represented only by preexisting herbarium specimen. This sampling represents the first formal records of the species at populations N4, N8, N9 and N10, suggesting the species is more common in Lamington NP than indicated by existing records.*

Genotyped population code	Location	Coordinates	Number of samples successfully genotyped
N1	Bar Mountain Picnic Area, Border Ranges NP	-28.4587, 153.1321	6
N2	Psuedo Pinnacle, Border Ranges NP	-28.4224, 153.1283	1 (herbarium specimen)
N3	Cocks Comb, Lamington NP	-28.2963, 153.1576	1 (herbarium specimen)
N4	Cominan Lookout, Lamington NP	-28.2755, 153.1757	1
N5	Mt Bithongabel, Lamington NP	-28.2635, 153.1714	3
N6	Border Track, Before Albert River Circuit, Laimington NP	-28.2544, 153.1577	1
N7	Mount Merino, Lamington NP	-28.2476, 153.1895	1 (herbarium specimen)
N8	Wagawn Track, Lamington NP	-28.2559, 153.2119	13
N9	Araucaria Track, Lamington NP	-28.2446, 153.2074	1
N10	Joalah Lookout, Lamington NP	-28.2291, 153.1987	2
N11	Best of All, Springbrook NP	-28.2410, 153.2660	9
N12	Type Locality, Along Repeater Station Rd, Springbrook NP	-28.2340, 153.2672	3 (3 herbarium specimen)
N13	Mt Thillinmam, Springbrook NP	-28.2354, 153.2883	1

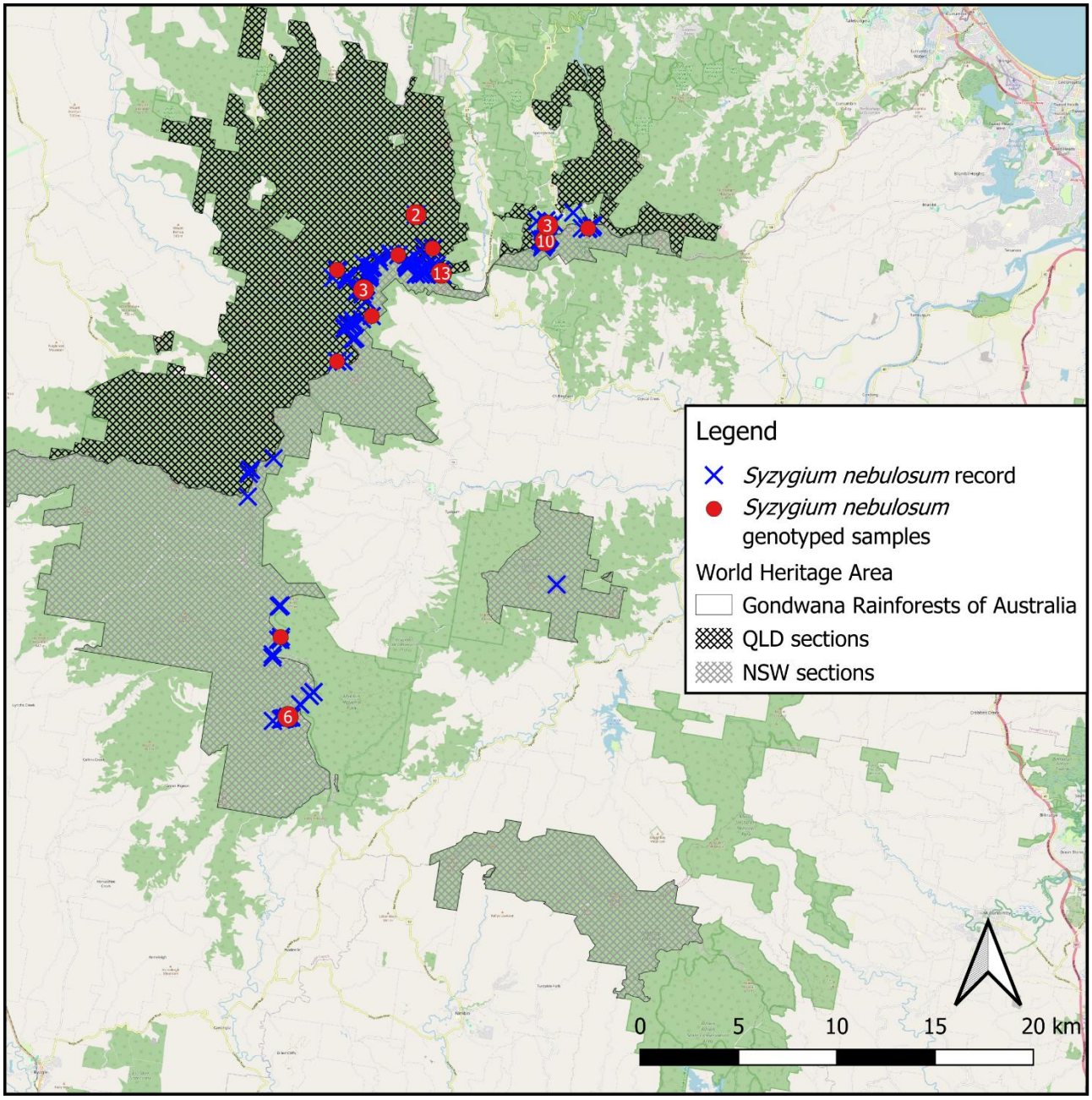

Figure 30: Map showing the sampling scheme for wild Syzygium nebulosum *used for this project. Due to limited access options, no populations between the Bar Mountain and Echo point sites and on Wollumbin could be sampled within the scope of this project.*

Evolutionary relationships and hybridisation

As illustrated in Figure 31, Figure 32 and Figure 33, genetic evidence strongly supports *S. nebulosum* as a distinct species as circumscribed by Weber and Forster (2025). Of note is that the species is not supported as a close relative of *S. crebrinerve*, from which it was segregated (Figure 31). Rather evidence points to a basal relationship to all other *Syzygium* subgenus *Syzygium* species, excluding *S. corynanthum,* present in subtropical Queensland and New South Wales and given the diversity of the genus in tropical rainforests of North Queensland and New Guinea, it is not possible to hypothesis what its closest relatives are. However, the genetic data support the idea it represents a relictual species that is isolated from its closest relatives by its high elevation habitat.

Despite several other *Syzygium* species occurring in the McPherson Range, there is no evidence for any hybridisation between *S. nebulosum* and these species in the genetic data (Figure 32 and Figure 33). This suggests *S. nebulosum* may be completely reproductively isolated in contrast to the hybridisation known to occur between *S. australe, S. oleosum* and *S. paniculatum* (Lu-Irving and Rossetto 2021).

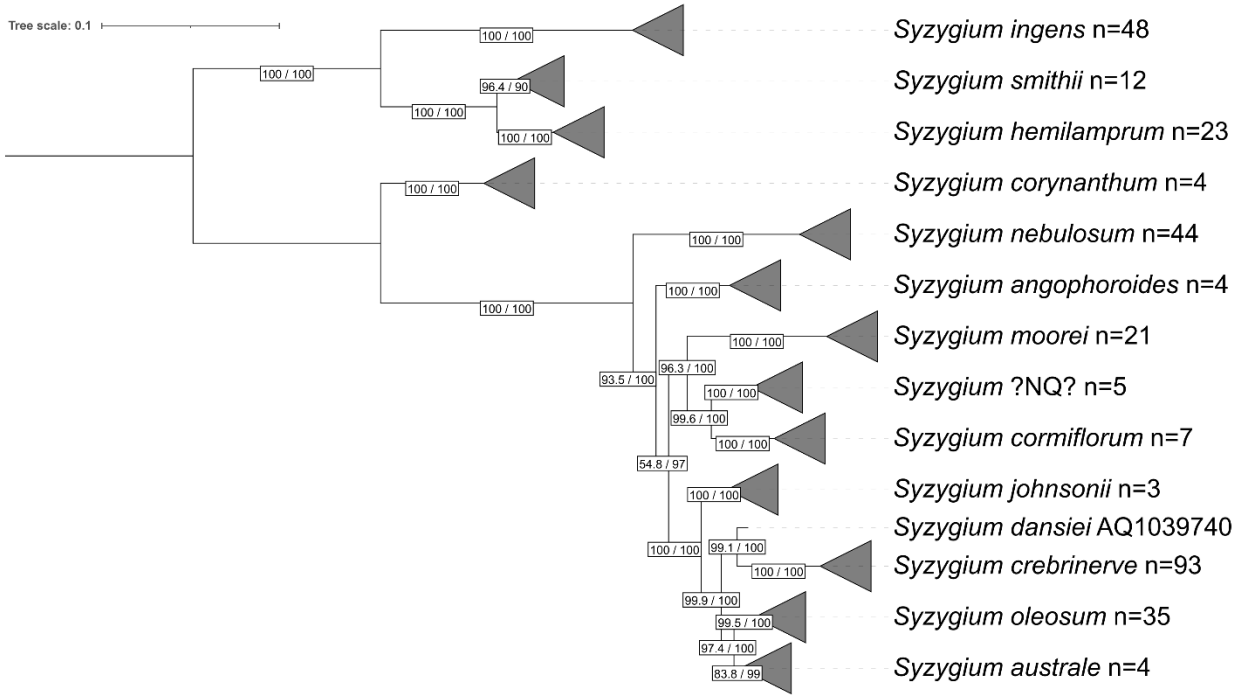

Figure 31: The IQTree phylogeny estimated using DArTseq data for sampled Syzygium *species. Hybrid samples (including all* S. paniculatum *samples) are excluded from the analyses as they violate the assumption of bifurcating relationships. Clades representing species level grouping of samples are collapsed with sample numbers per species shown. Note the tree is midpoint rooted meaning the basal relationship is a statistical hypothesis only, although it aligns with wider genus level phylogenies of* Syzygium*.* Syzygium nebulosum *is supported as a distinct lineage, not closely related to other* SEQ Syzygium *species including* S. crebrinerve *from which it was split. Note samples from one site in north Queensland identified as* S. crebrinerve *in the field have been misidentified and the voucher material could not be accessed to redetermination during this study. Therefore, these samples are labelled* as Syzygium ?NQ?.

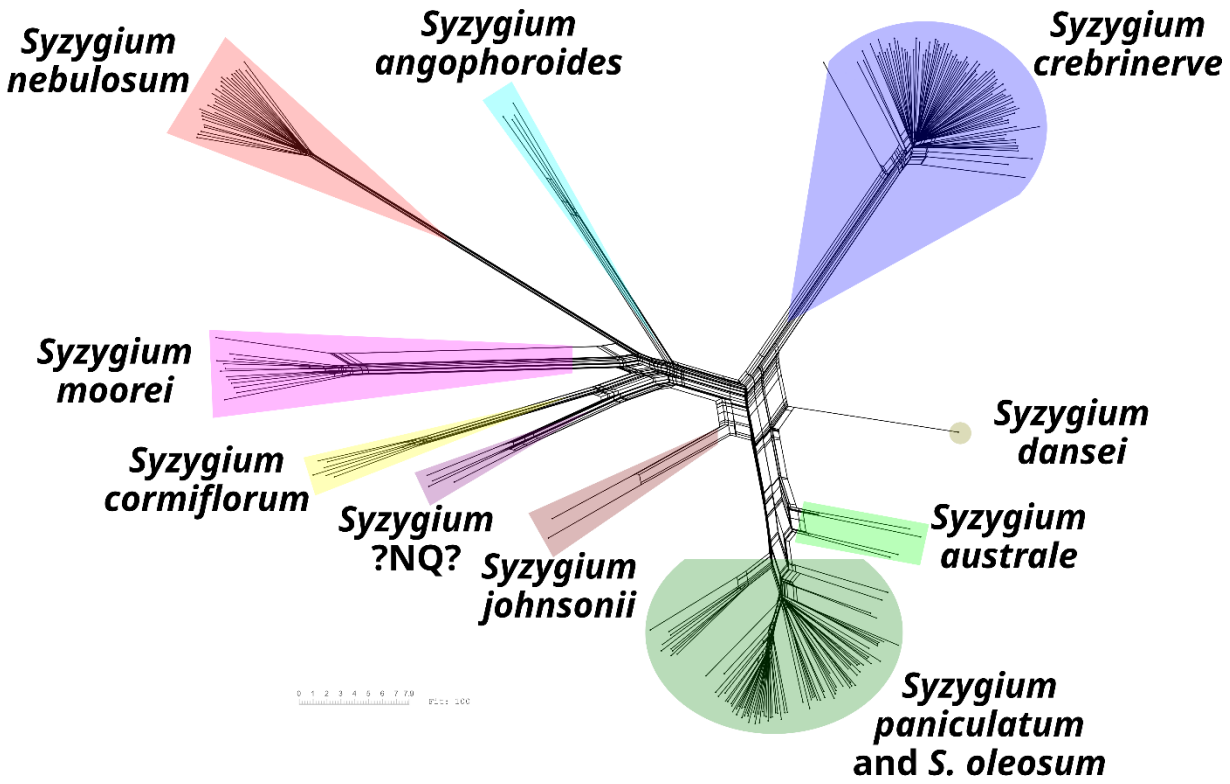

Figure 32: The SplitsTree phylogenetic network estimated using DArTseq data for Syzygium *subgenus* Syzygium *ingroup clade (i.e. excluding the highly distinct* S. corynanthum*), including species sampled in this study. The phylogenetic network supports* S. nebulosum *as currently circumscribed and shows no evidence for hybridisation or introgression between this species and any other species. Note samples from one site in north Queensland identified as* S. crebrinerve *in the field have been misidentified and the voucher material could not be accessed to redetermination during this study. Therefore, these samples are labelled* as Syzygium ?NQ?.

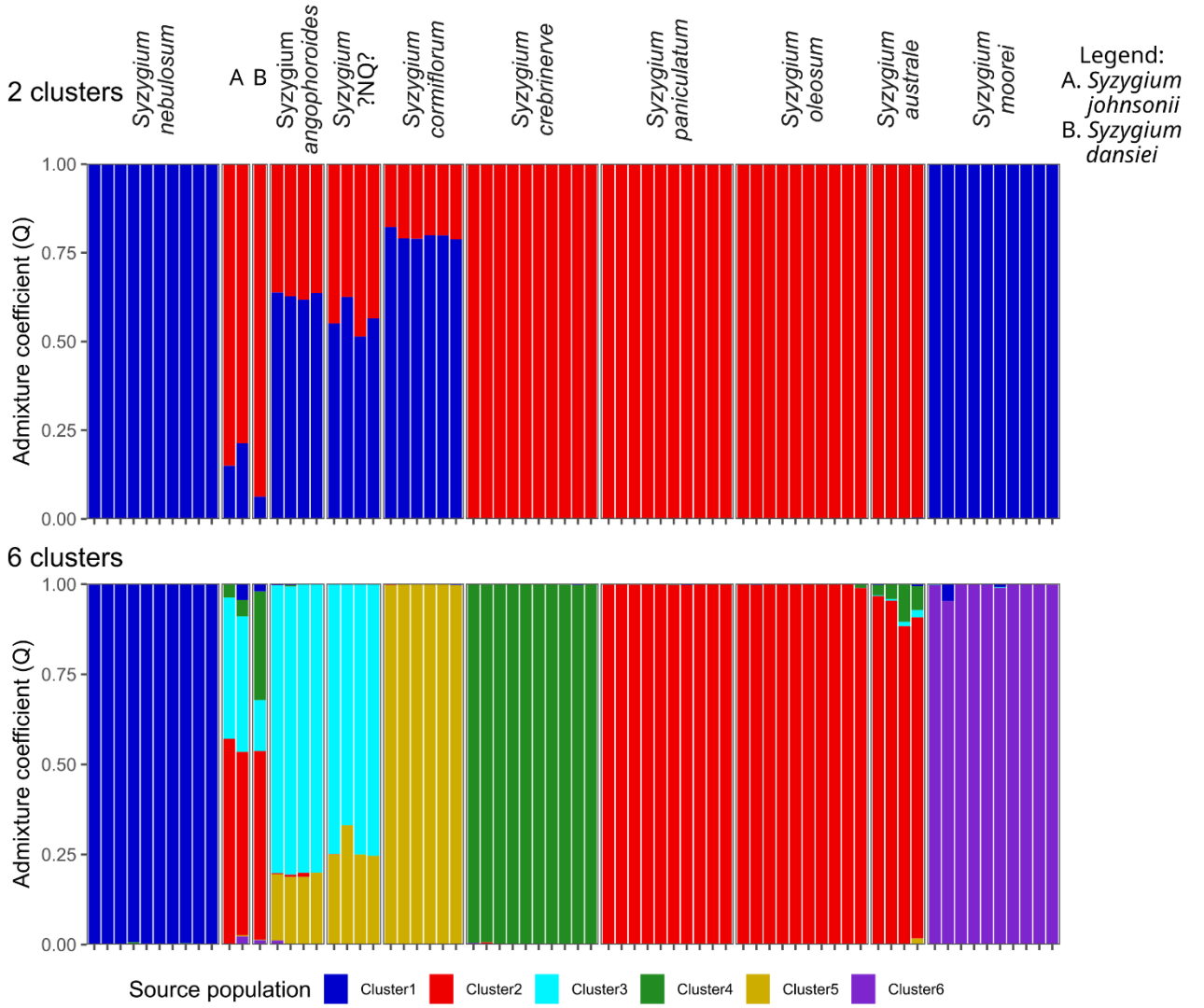

Figure 33: Admixture plot showing the results of 2 and 6 cluster STRUCTURE analyses of Syzygium *subgenus* Syzygium *ingroup taxa (excluding the highly distinct* S. corynanthum*) DArTseq data. In the 2-cluster plot,* S. nebulosum *and* S. moorei *are exclusively assigned to a cluster that is also partially present in species outside the* S. crebrinerve-australe-oleosum *complex. A bias toward 2-cluster analysis is a known issue in admixture analyses, and given the results of other analyses, we believe that issue is occurring here and thus do not treat this plot as informative. In the putatively more meaningful 6-cluster analysis,* S. nebulosum *is assigned to a unique genetic cluster, as are the well sampled* S. crebrinerve *and* S. moorei. Syzygium oleosum, S. paniculatum *and* S. australe *form a single cluster, in line with previous studies on these species showing a close evolutionary relatedness.*

Key Genetic Findings

Ploidy

DArTseq read count analysis suggests *S. nebulosum* is a putative diploid.

Genetic diversity and reproductive biology

Within-site genetic diversity of *S. nebulosum* was in line with, if not higher than, well sampled diploid outgroup species (i.e. *S. crebrinerve* and *S. oleosum*) and was even across the three well-sampled sites (Table 17). This suggests reasonable evolutionary potential exists in all populations that may assist with adaptation to gradual environmental changes.

Potential clonality was observed for *S. nebulosum* at several sites (Figure 34), likely due to some combination of vegetative spread (as evidenced by the extensive coppicing observed in the field and previous observations of suckering; Weber and Forster 2025) and apomixis, i.e. the production of clonal seed which is known in other *Syzygium* species, primarily in association with polyembryonic (multiple embryos per seed) seed production (Chantaranothai and Parnell 1994; Thurlby *et al.* 2012). One clonal genet was observed amongst the three herbarium sheets from the type locality on Repeater Station Rd in Springbrook, possibly representing either repeat collection of the same ramet or vegetative reproduction. At Mt Wagawn, two clonal genets were recorded, one consisting of four ramets within 20m of one another, the other of two within 20 m, suggesting vegetative reproduction. The final two clonal genets were collected in Border Ranges NP, one consisting of two samples at Bar Mountain (possibly collection error due to collection from recently fallen trunks) and the second a field sample from Bar Mountain and an herbarium sheet from the Psuedo-Pinnacle 4 km to the north, suggesting apomixis rather than vegetative reproduction.

Furthermore, several first-degree relatives were collected (Figure 34), likely due to the collection of material from a mother tree and offspring growing in proximity. More than reflecting any biologically significant patterns, this putatively reflects difficulties in locating and collecting material from well-spaced individuals in the steep terrain. Overall, the evidence presented here suggests a complex reproductive system including both vegetative and apomictic clonality, and out-crossed seed production.

Genetic structuring and gene flow

The Bar Mountain *S. nebulosum* population (N1) showed shallow divergence from the sampled Springbrook NP and Lamington NP populations (Figure 35). This is likely due to reduced geneflow across a distributional break from Lamington NP southwest of Mt Throakban, although further sampling of the Cockscomb Point population may close this divergence. Similarly shallow divergence exists between sampled sites within Springbrook NP (N3 to N10) and Lamington NP (N11 to N13; Figure 35) suggesting reduced gene flow across the Numinbah Gap. With only three populations represented by at least 5 samples, a test for an isolation-by-distance (IBD) pattern could not be reliable undertaken (Figure 36).

At least 120 private alleles were observed between the three sites with at least three samples (one per national park), suggesting some restriction to gene flow between the species' three main areas of occurrence. Overall, however, genetic divergence between all populations is minor suggesting some geneflow across the entire Wollumbin Caldera, in line with the hypothesis that the species' fleshy, edible fruit is dispersed by frugivorous animals (Weber and Forster 2025). This contrasts somewhat with the findings of less interrupted and more continuous gene flow across the Wollumbin Caldera for *Pittosporum oreillyanum.*

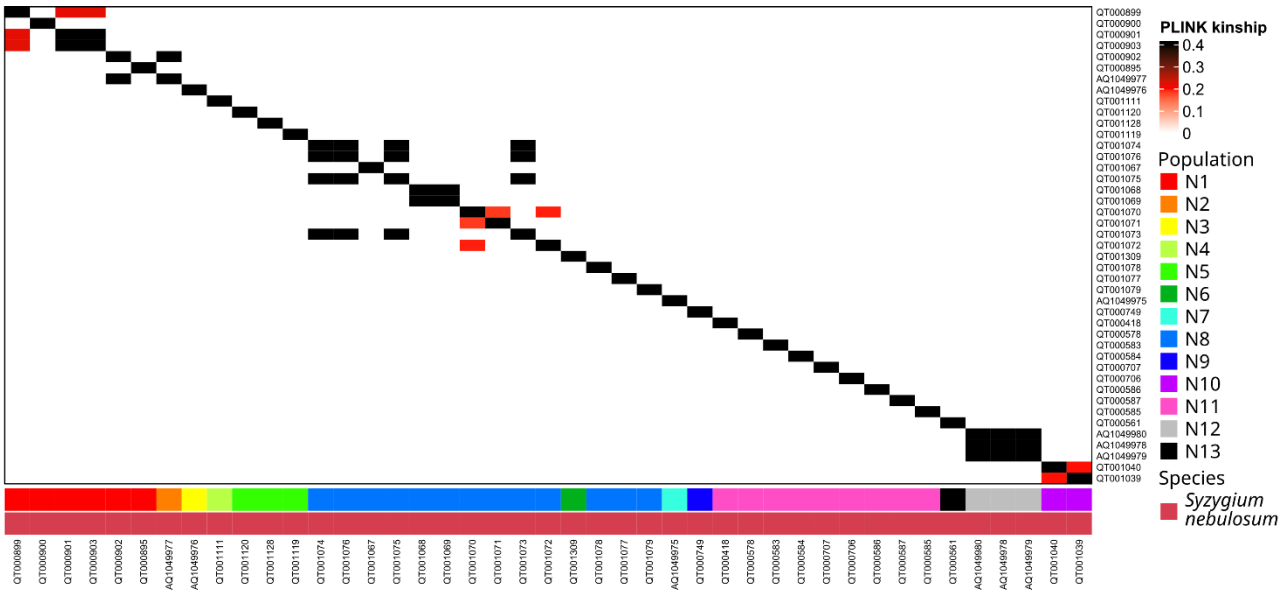

Figure 34: Heatmap of pairwise kinship values between genotyped Syzygium nebulosum *individuals. Values at or above 0.4 represent genetically identical samples mostly arising through clonality, while values between 0 and 0.4 represent individuals with familial relationships up to ~2 generations removed. Clonal genets were recorded from three sites, likely reflecting a combination of vegetative spread (suckering) and apomixis (production of clonal seed). Most clonal ramets were collected within 20 m of one another, suggesting suckering, however the presence of the same genet at both the Bar Mountain (N1) population and at the Pseudo-pinnacle (herbarium sheet), is more suggestive of apomixis. Familial relationships are also observed between individuals growing at some sites, reflecting ongoing out-crossing sexual reproduction.*

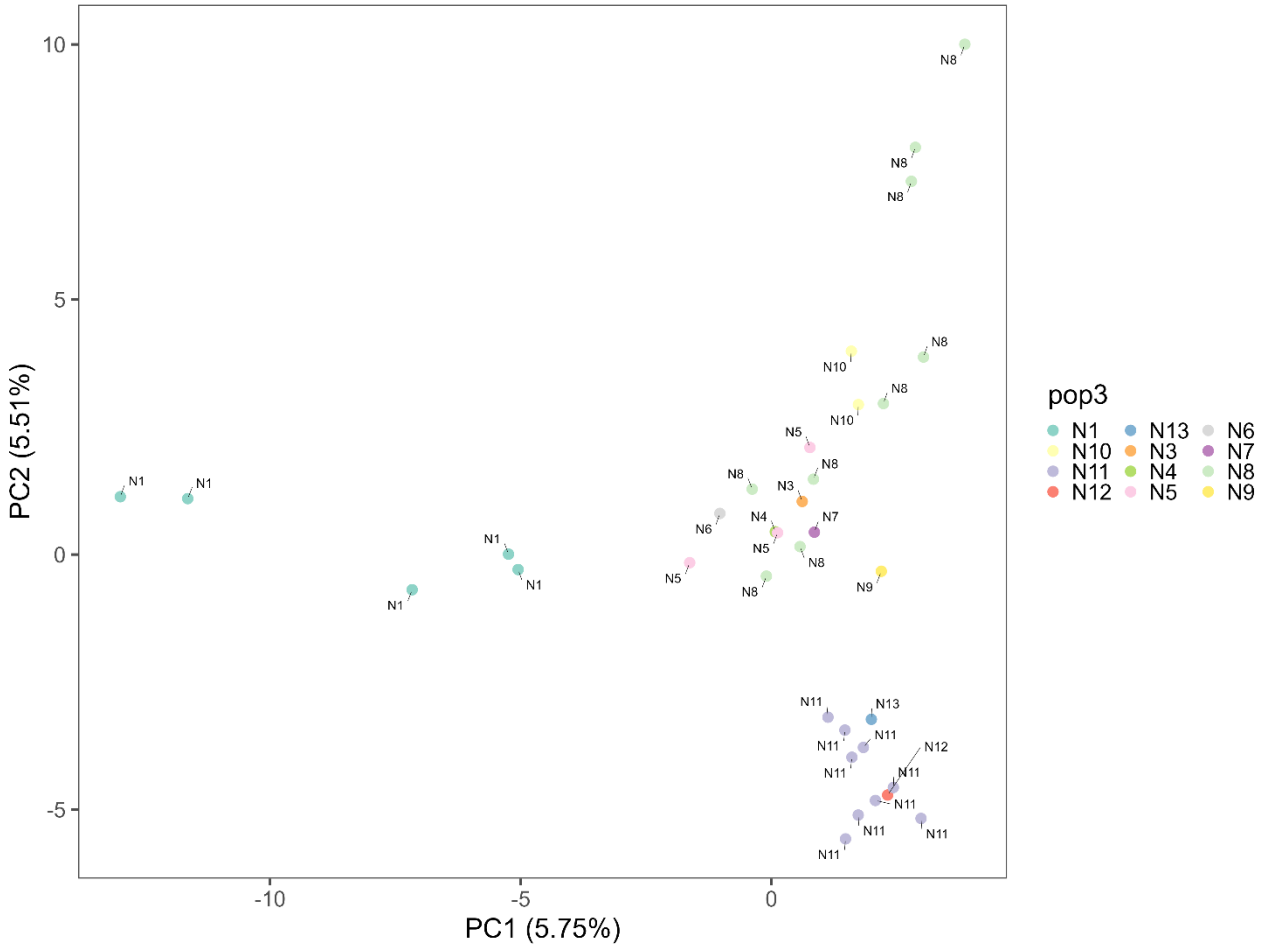

Figure 35: PCA plot of all genotyped Syzygium nebulosum *samples showing that the Bar Mountain population is somewhat genetically divergent from the remaining sampled populations. This may be the result of the large sampling gap between this site and the Lamington NP sampling sites rather than showing true discrete genetic structuring. A minor genetic distinction is also present between sites in Springbrook NP (N11, N12 and N13) and those in Lamington NP (N3 to N10), with sites within each national park not separating from one another in the plot. Overall, this plot suggests moderate geneflow between populations of* S. nebulosum*, particularly within Lamington NP.*

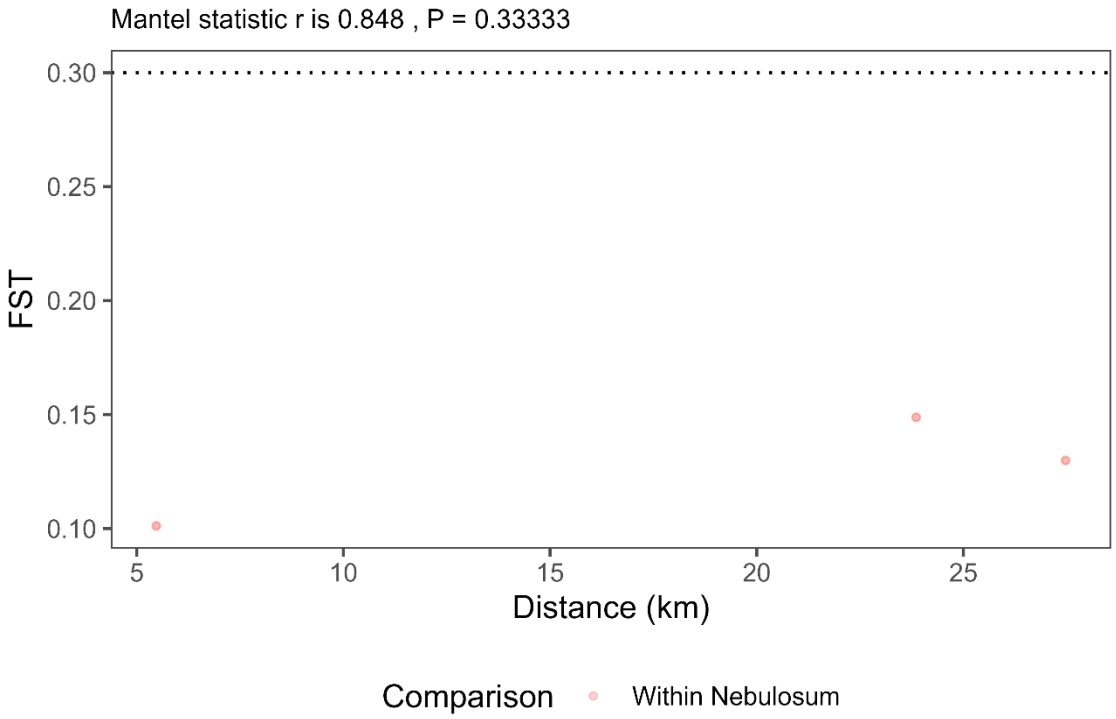

Figure 36: The isolation-by-distance plot for all S. nebulosum *sites where 5 or more samples were successfully genotyped. The x-axis shows pairwise geographic distance and y-axis pairwise genetic distance (F_{st}). As only three sites were available for inclusion in mantel test, the result is not statistically significant despite a high r value.*

Table 17: Key population genetic parameters of P. notata populations represented by 5 or more genets in the DArTseq dataset (H_o = observed heterozygosity, H_e = expected heterozygosity, uH_e = unbiased expected heterozygosity). A total of 2162 high quality, variable loci were used for calculations.

Population	Private allele	Allelic richness	H_o	H_e	uH_e	Inbreeding coefficient	Unbiased inbreeding coefficient
N1	127	1.2017	0.2053	0.268	0.299	0.234	0.3134
N8	132	1.2322	0.2363	0.2883	0.3157	0.1804	0.2515
N11	163	1.2243	0.2283	0.2963	0.3247	0.2295	0.2969

Modelled impacts of climate change

Figure 37 shows the projected areas of climate suitability for *S. nebulosum* under climate change in the years 2050, 2070 and 2090, along with the present climate suitability model. The current model shows high suitability around the Wollumbin Caldera where the species occurs, but also in Nightcap NP and Mount Jerusalem NP to the immediate south, from which the species has not been recorded. Further south, areas of putatively suitable climate are located in and around Dorrigo NP, in the NSW mid-North Coast region south-west of Port Macquarie and in the Illawarra region south of Sydney. By 2050, we see a drastic decline in areas that match the species' modelled climatic niche, with small areas of higher modelled suitability remaining in Lamington NP and Dorrigo NP, although an increase in habitat suitability is observed in the Illawarra region. A modest increase in modelled climate suitability is projected for 2070, particularly in Dorrigo NP, before further contraction in 2090, leaving no areas of high modelled similarity to the species current climatic niche.

Management recommendations

Based upon literature evidence and the findings of this study, the threat status of *Near Threatened* is considered putatively appropriate for *S. nebulosum* under the CAM criteria (IUCN 2012), although a formal assessment is yet to be completed. There is no evidence the species has experienced decline in population size, distribution or genetic diversity in the past 500 years, with the only observable threats to the species being climatic change and potentially disease (i.e. myrtle rust). Given the moderate genetic diversity and geneflow observed, and thus moderate inferred adaptive potential, the climatic habitat modelling showing a severe and immediate decline in suitable habitat should be taken with caution. These results suggest there's more risk from ecosystem-scale collapse or widescale displacement of the high elevation forests than from a direct threat to *S. nebulosum*.

Given the putative observations of myrtle rust in wild populations, and the known impacts of this disease on reproductive success (Carnegie and Pegg 2018) further research to better understand the resilience of both individuals and populations of *S. nebulosum* is strongly recommended. In addition, a precautionary approach is recommended for this species, undertaking collection of propagule material (seed, cuttings or live plants) to form an insurance collection (either a translocation, seed bank or ex-situ live population) should wild populations experience sudden and rapid decline. As only three populations were represented by five or more genets in the genetic dataset, and collection of five individuals from each of these three sites was insufficient to meet the goal of capturing 90% of common alleles, a full optimisation was not possible using the dataset for *S. nebulosum*. However, given this result, it is clear than propagule collections from at least two locations within each national park is needed to meet this target.

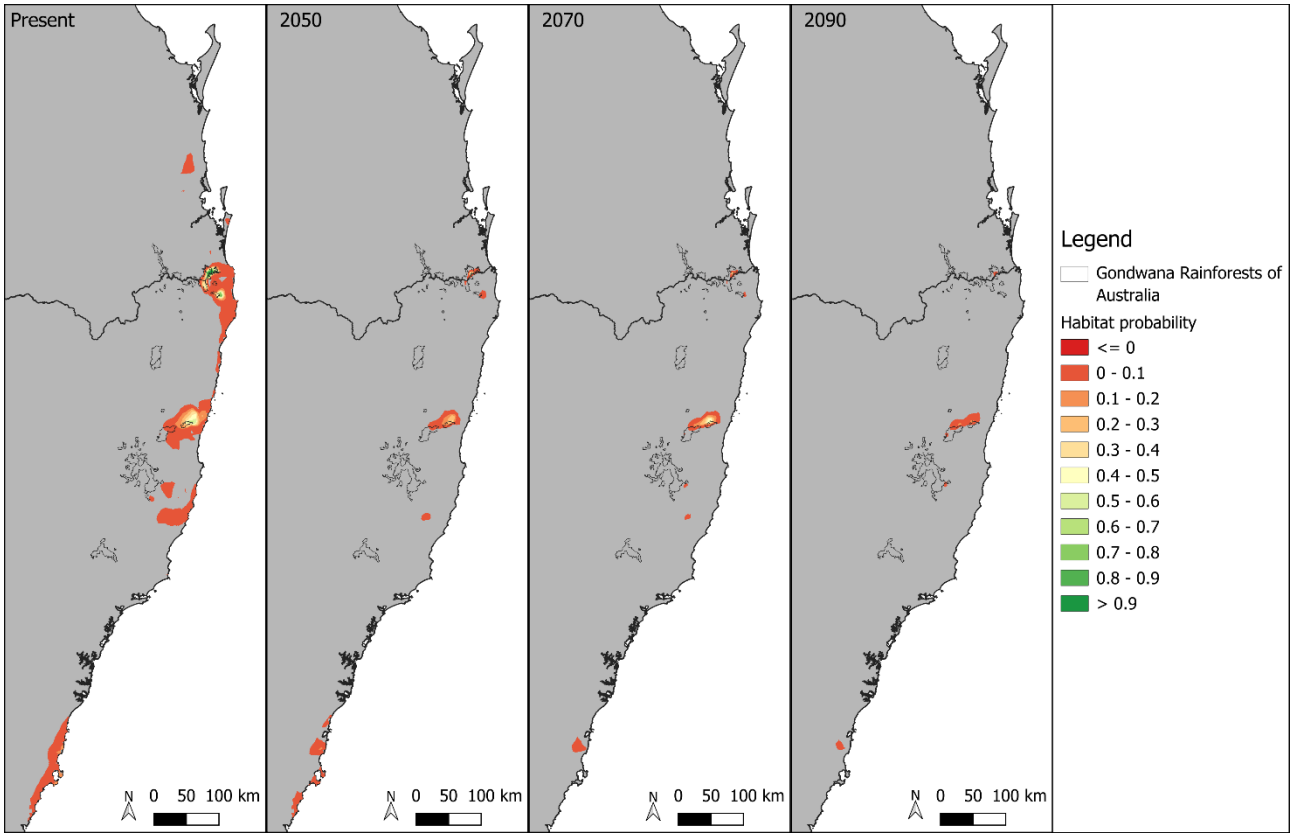

Figure 37: Results of climate habitat modelling for Syzygium nebulosum *for present conditions and then project onto predict conditions in the years 2050, 2070 and 2090. Predicted habitat suitability in each map cell is a value between zero and one, with one being high probability suitable climate. Under present climate conditions, modelled areas of potentially suitable climate are more widespread than the species realised distribution, particularly in the Nightcap Range and around Dorrigo NP, with low confidence suitable climate also present in the NSW Mid-North Coast and Illawarra region, potentially suggesting the species distribution is dispersal limited. By 2050, we see a stark decrease in areas of predicted suitable climate, leaving just small areas of low probability suitable climate in Lamington NP, Dorrigo NP and the Illawarra region. The former two show increased predicted suitability in 2070, before declining even further in 2090.*

Conclusions and Future Directions

Conclusions and future directions

A key conclusion from this study is that the high elevation rainforest of the GRWHA holds significant unique and divergent biological diversity that is substantially distinct from the diversity of lowland subtropical rainforests. All four study species are highly diverged genetic lineages within their respective genera. This suggests these high elevation ecological communities have been isolated for a significant evolutionary period and the species within them have developed distinct habitat preferences and strong reproductive barriers from related species. Despite three of the target species belonging to common and species rich genera, with congeners growing either in the same habitat (*Pittosporum oreillyanum*), in adjacent lower elevation habitat (*Syzygium nebulosum*) or in elevated habitat elsewhere in the GRWHA (*Pomaderris notata*), no evidence for hybridisation was observed for any species, further supporting this conclusion. Therefore, the two high elevation RE's (12.8.5 and 12.8.6) in the GRWHA (QLD section) where these species occur should be considered to have high conservation value and additional opportunities to support their protection should be explored.

Despite the consistent pattern of evolutionary distinctiveness identified in this study, the studied species showed individualised patterns of genetic diversity and geneflow around the Wollumbin Caldera depending on their population size, realised niche, and pollen and seed dispersal capabilities. These ranged from the highly restricted *Eucryphia jinksii* only occurring as a single genetic population with low genetic diversity and inflated inbreeding rates, to *Pittosporum oreillyanum* showing no discrete structure and a strong IBD pattern suggesting continuous and ongoing geneflow around the Wollumbin Caldera. This shows the value of undertaking species-specific population genetic studies to understand the threats individual species face and how best to target management actions.

Evidence suggests the four studied species have experienced only marginal population declines in the last five hundred years due largely to the remoteness of their habitat. For three of the studied species, there was also minimal evidence for immediate species-level extinction threats, with only *Eucryphia jinksii* considered under immediate direct threat of extinction due to its very restricted distribution, projected reduction in cloud water inputs, declining soil moisture levels and increasing wildfire risks (*Narsey* et al. 2020). While some other high elevation species do face additional specific threats such as changes to fire regimes in the exposed heaths where *Pomaderris notata* grows, and the impacts of myrtle rust on *Syzygium nebulosum,* ecosystem collapse in the face of climate change may threaten all high elevation endemic species (Narsey *et al.* 2020; Bergstrom *et al.* 2021). This is a risk that can only be marginally mitigated by on-ground management actions such as managing invasive species and wildfire risks, meaning establishing insurance populations of the rarest and most range restricted species may be needed to insure these species against extinction. Establishing these insurance populations will require resource investment to understand the best form of insurance population (i.e. translocated population, seed bank or ex situ cultivated population) for individual species and to ensure appropriate ongoing management.

Upcoming publications describing two newly recognised high elevation endemic plant species from the GRWHA (QLD section) (Weber, Forster, *et al* preprint.; Weber, Mallee, *et al.* preprint), highlights the importance of undertaking further survey work to understand the diversity and distribution of all high elevation endemic taxa in the GRWHA (QLD section). Of particular focus should be the remote and under-surveyed south-west areas of Lamington NP around Cockscomb Point and Point Lookout. This is a hotspot for high elevation endemics, but due to access difficulties, is unrepresented in physical collections including that of the Queensland Herbarium. Surveys should include the collection of plant

tissue material to allow for conservation genetics study of threatened and priority plant species of the GRWHA (QLD section), with field collection continuing to be the most complex and problematic component of such studies (including this one). Further studies aimed at understanding the true diversity and threats to the high elevation forests should widen the range of taxa to include groups not covered in this study such as ferns and non-vascular plants. Vitally, any survey work within the GRWHA should be conducted under appropriate research permits, in accordance with biosecurity hygiene protocols, and in close collaboration with the Queensland Parks and Wildlife Service.

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