Science Saving Rainforests Project: A genomic workflow for sourcing restoration material

BOTANIC GARDENS OF SYDNEY

THE UNIVERSITY OF QUEENSLAND AUSTRALIA

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We acknowledge the traditional custodians of the lands this project takes place. We pay our respects to all Aboriginal & Torres Strait Islander cultures and recognise the example First Nations Peoples have set in protecting & nurturing the environment for future generations.

Science Saving Rainforests Project
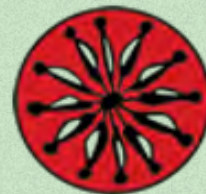

photo: Iain Stych

- Genetically informed restoration practices for 30 threatened and 30 common species

- Help guide ongoing restoration by BSRC to develop Seed Production Areas and re-establish connectivity corridors

Part 1: Where to Source Material From?

Build upon current Restore and Renew workflow (Rossetto et al. 2021) using SNP datasets

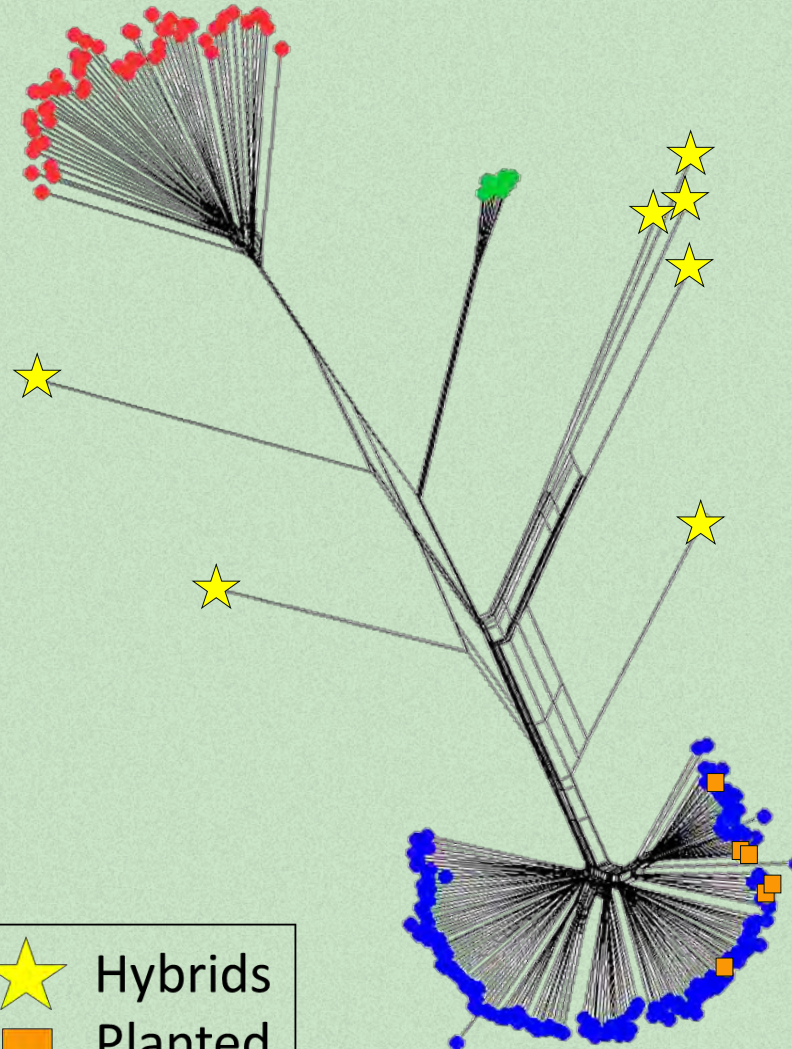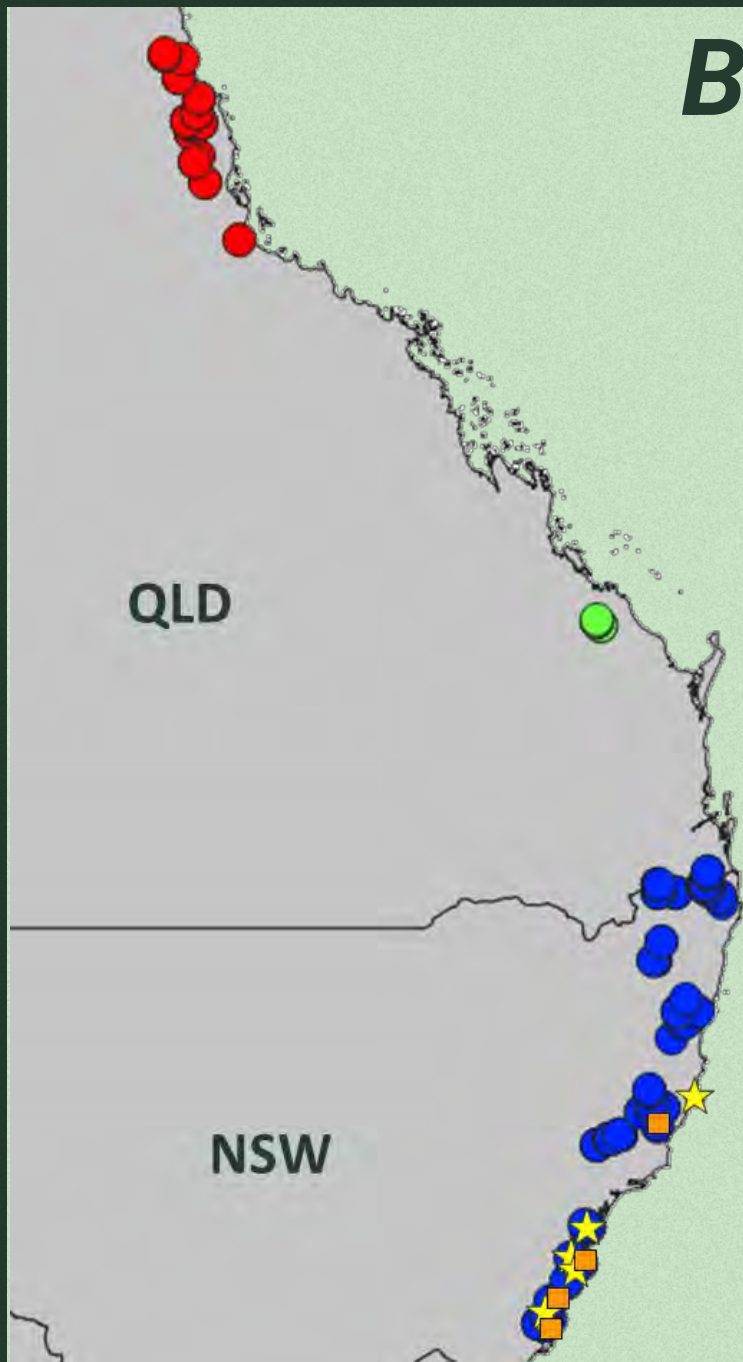**Step 1**: **Identify species boundaries and reproductive strategies**

- Taxonomic resolution

- Hybridisation

- Planted/naturalised sites
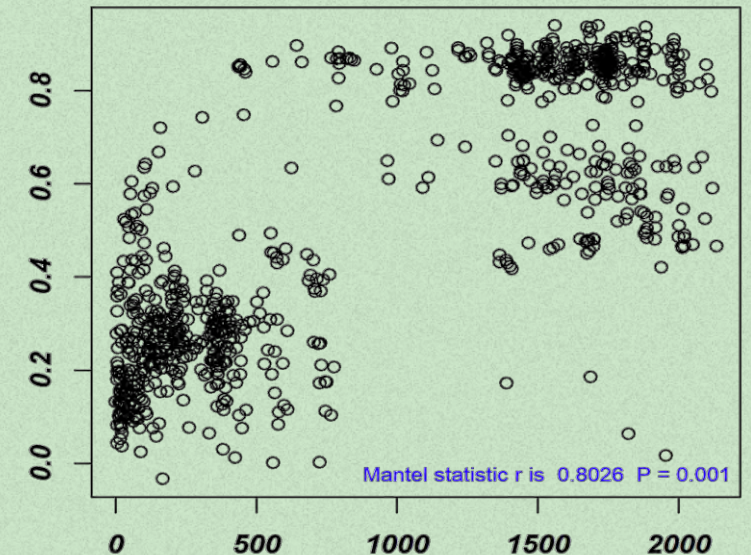
- Clonality

Step 2: Identify Genetic Neighbourhoods

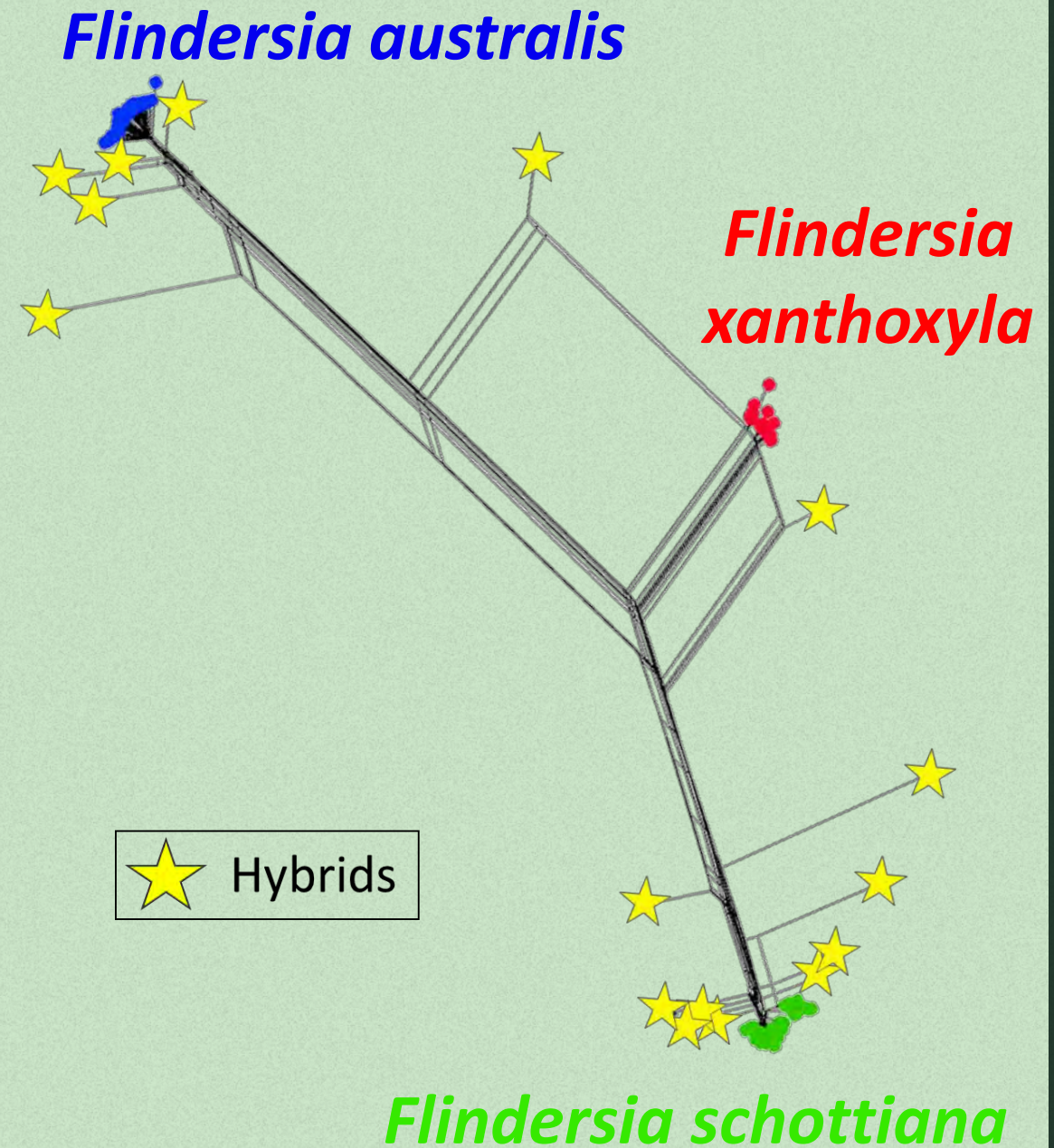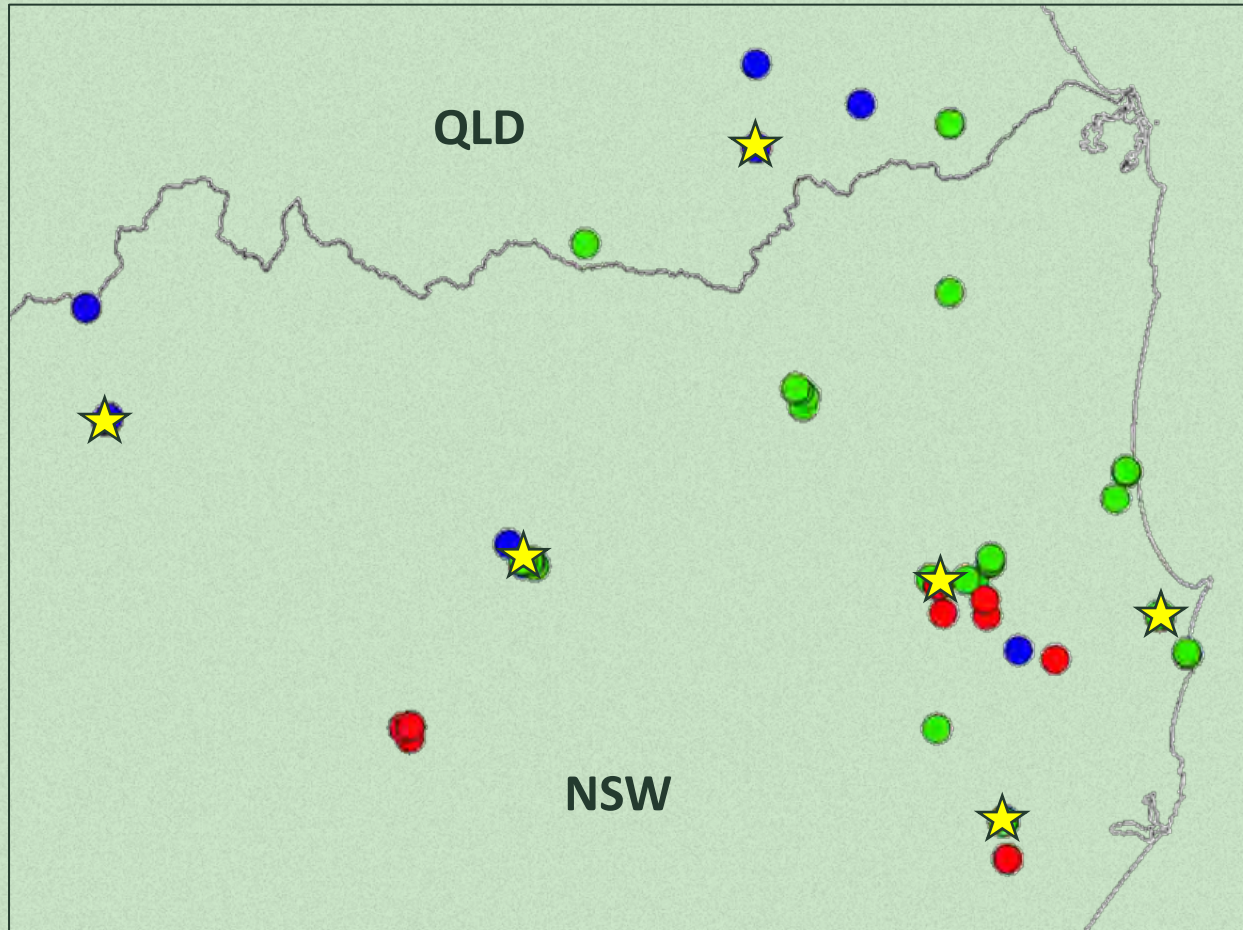- identify patterns of structure and isolation by distance

Brachychiton acerifolius

- **Highly divergent clades**
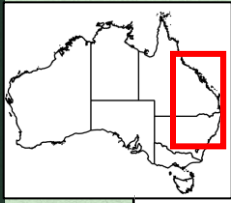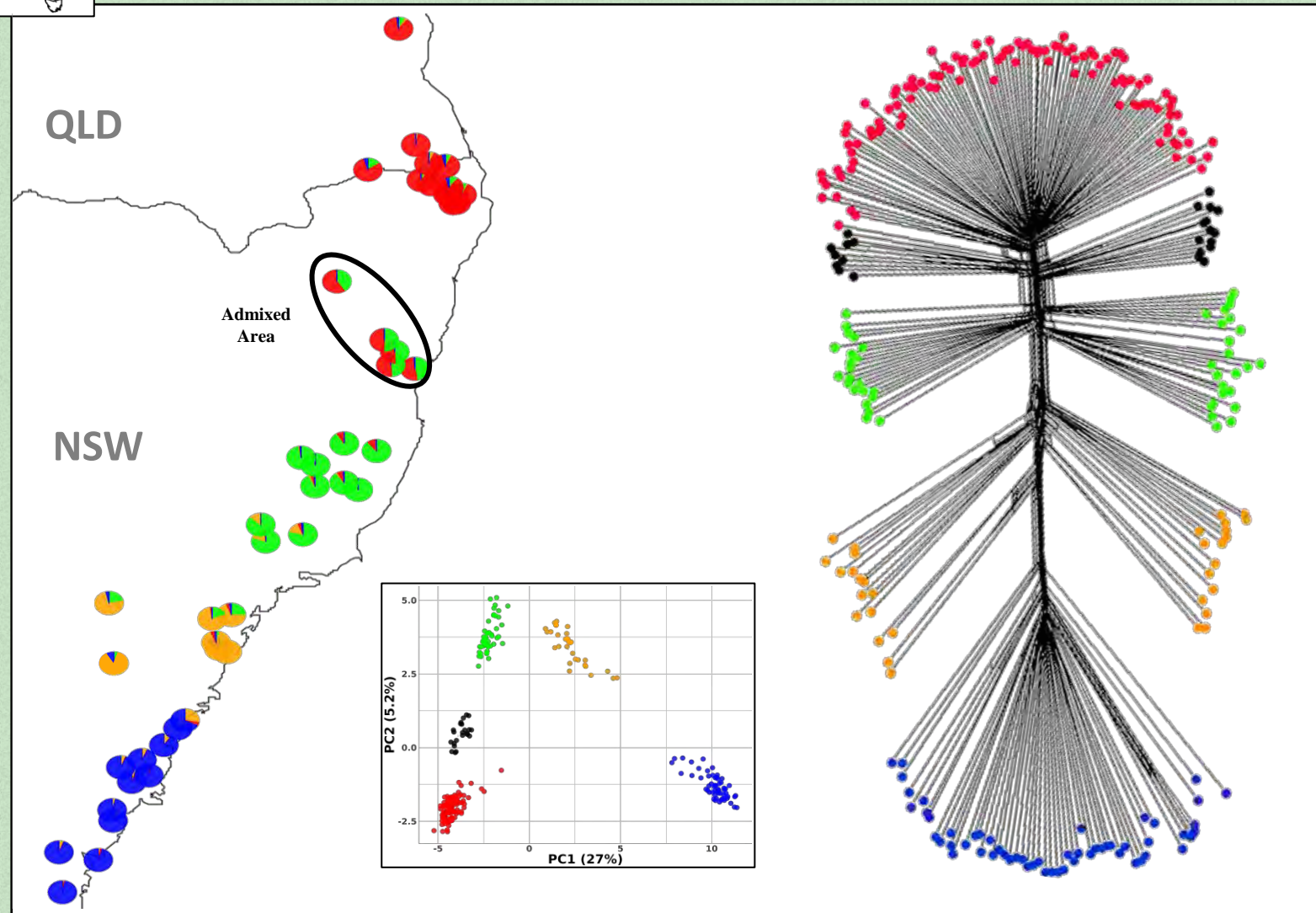- **Hybridisation**
- **Planted Individuals**

QLD

NSW

★ Hybrids

■ Planted

Mantel statistic r is 0.8026 P = 0.001

Hybridisation in Flindersia

Flindersia australis

Flindersia xanthoxyla

QLD

NSW
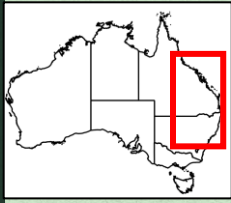
⭐ Hybrids

Flindersia schottiana
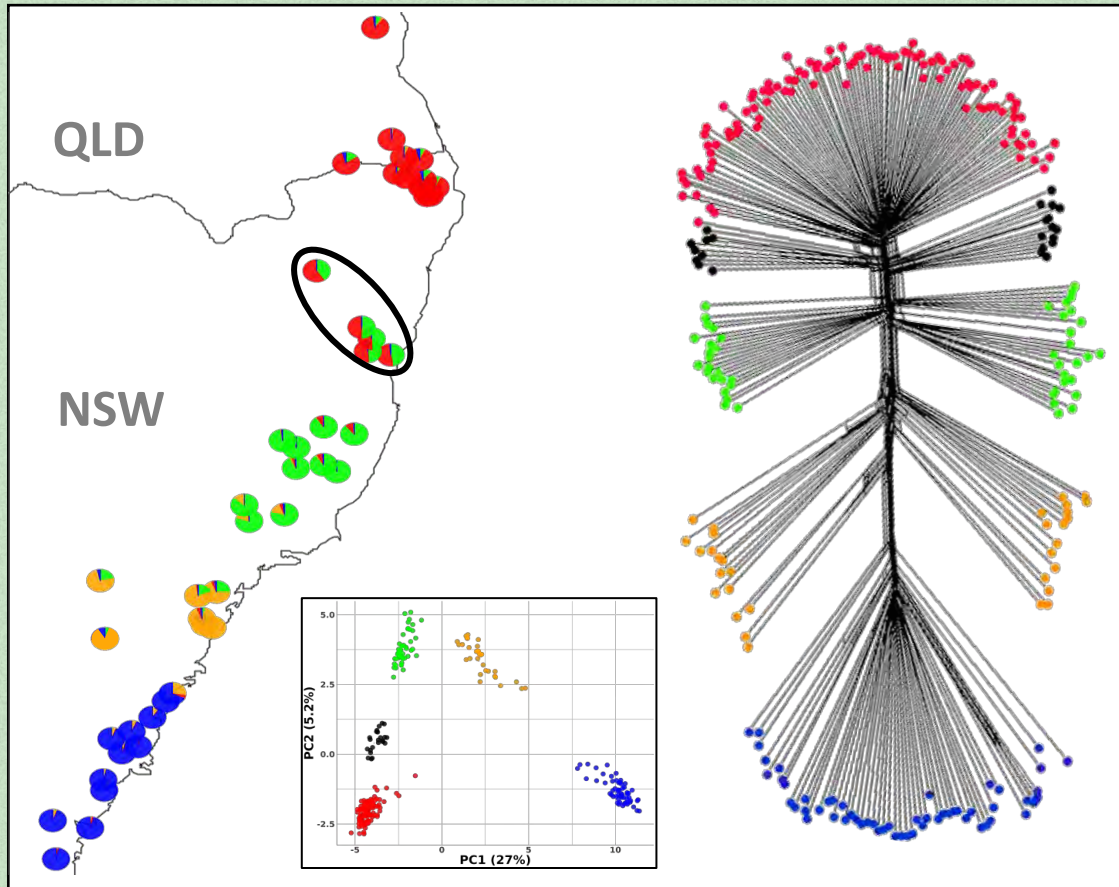
Identifying Local Genetic Neighbourhoods

- *Clonality detected*

- *Regions of admixture*
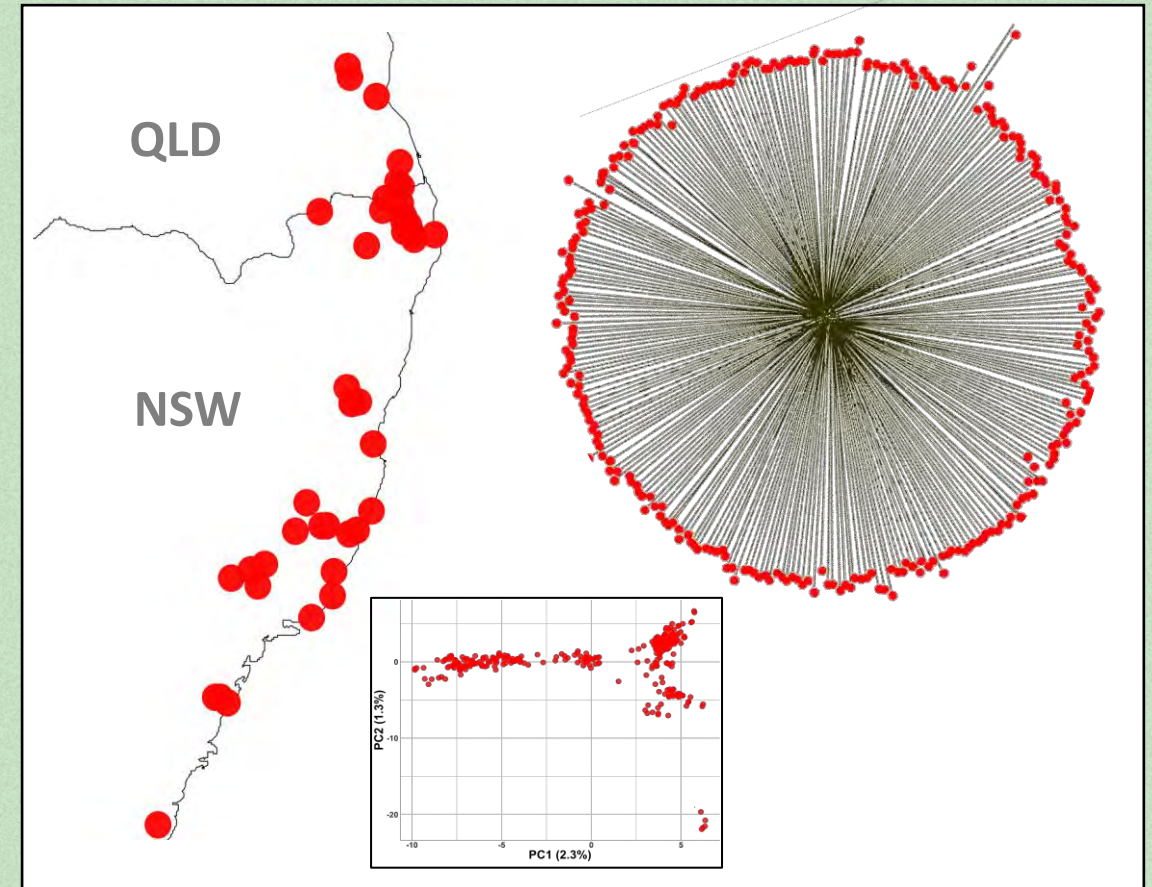
Doryphora sassafras
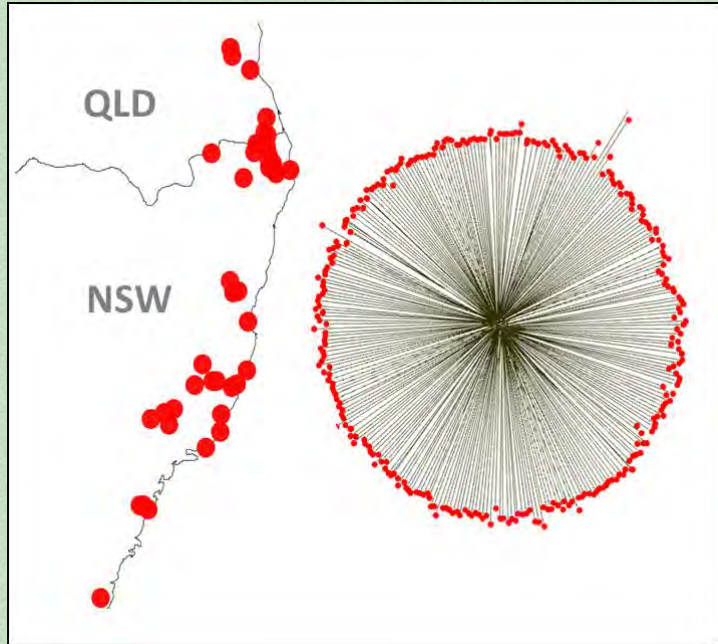
Identifying Local Genetic Neighbourhoods

Doryphora sassafras

Planchonella australis

Redefining what is local

- Gene flow is occurring at a broad geographic scale

- 100's of kilometres not 100's of metres

- Extends the range of available sites practitioners can use in restoration projects

- Not constrained to limited supply of remnant populations

Part 2: Optimising genetic diversity for restoration of the Big Scrub

- Develop sourcing strategies which capture at least 90% genetic diversity for the local genetic neighbourhood

- Incorporate climate-resilient material

- Replicate across multiple species – minimise logistics for sampling material for multiple rainforest species
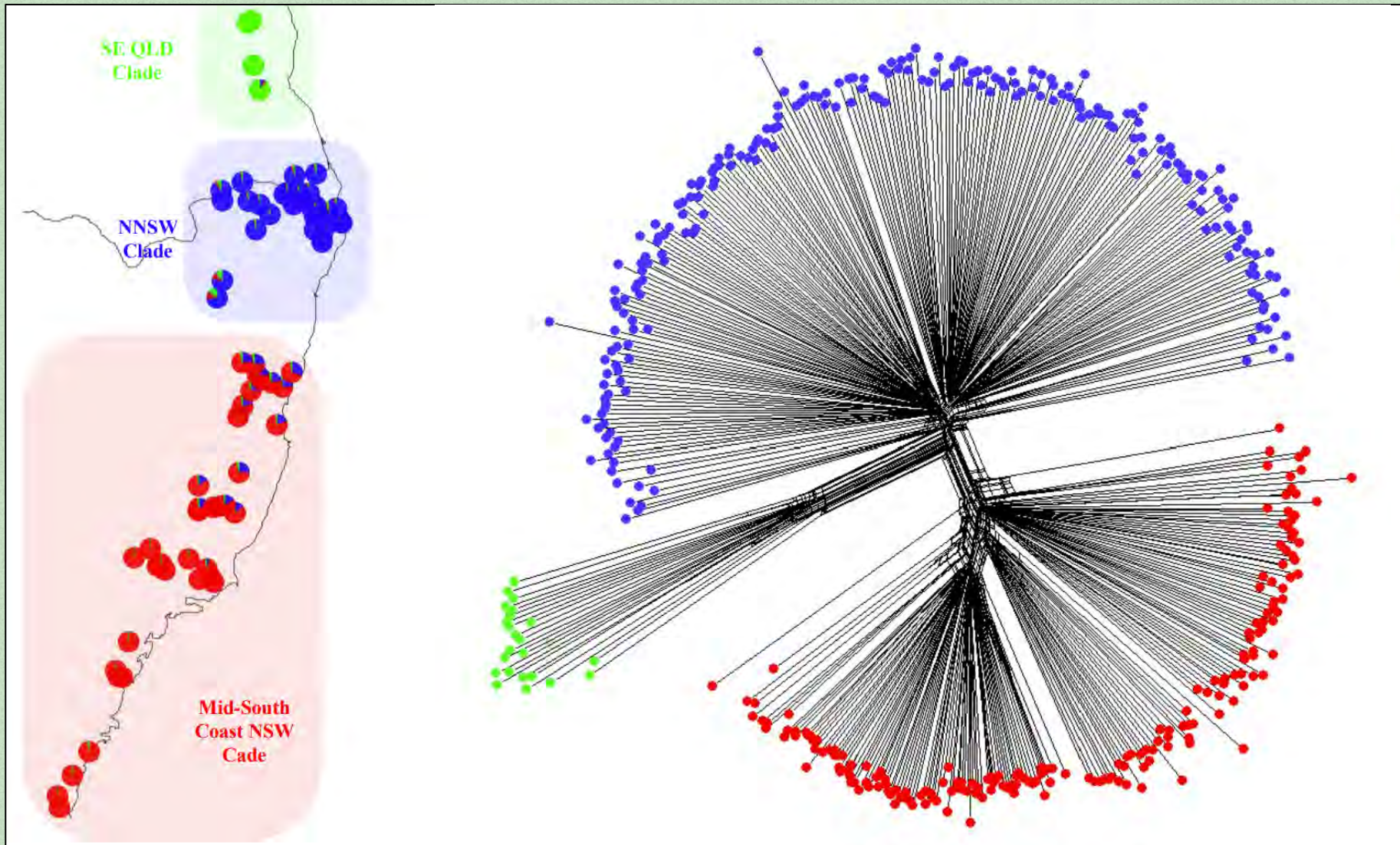
OptGenMix – Analytical tool for optimising genetic diversity of restoration material

- Simulated annealing optimisation algorithm (Bragg et al. 2020)

- Method 1: Individual-Based OptGenMix

- Method 2: Site-Based OptGenMix (Dimon et al. in prep)

- Identify the number of sites and samples needed to capture 90% of common alleles
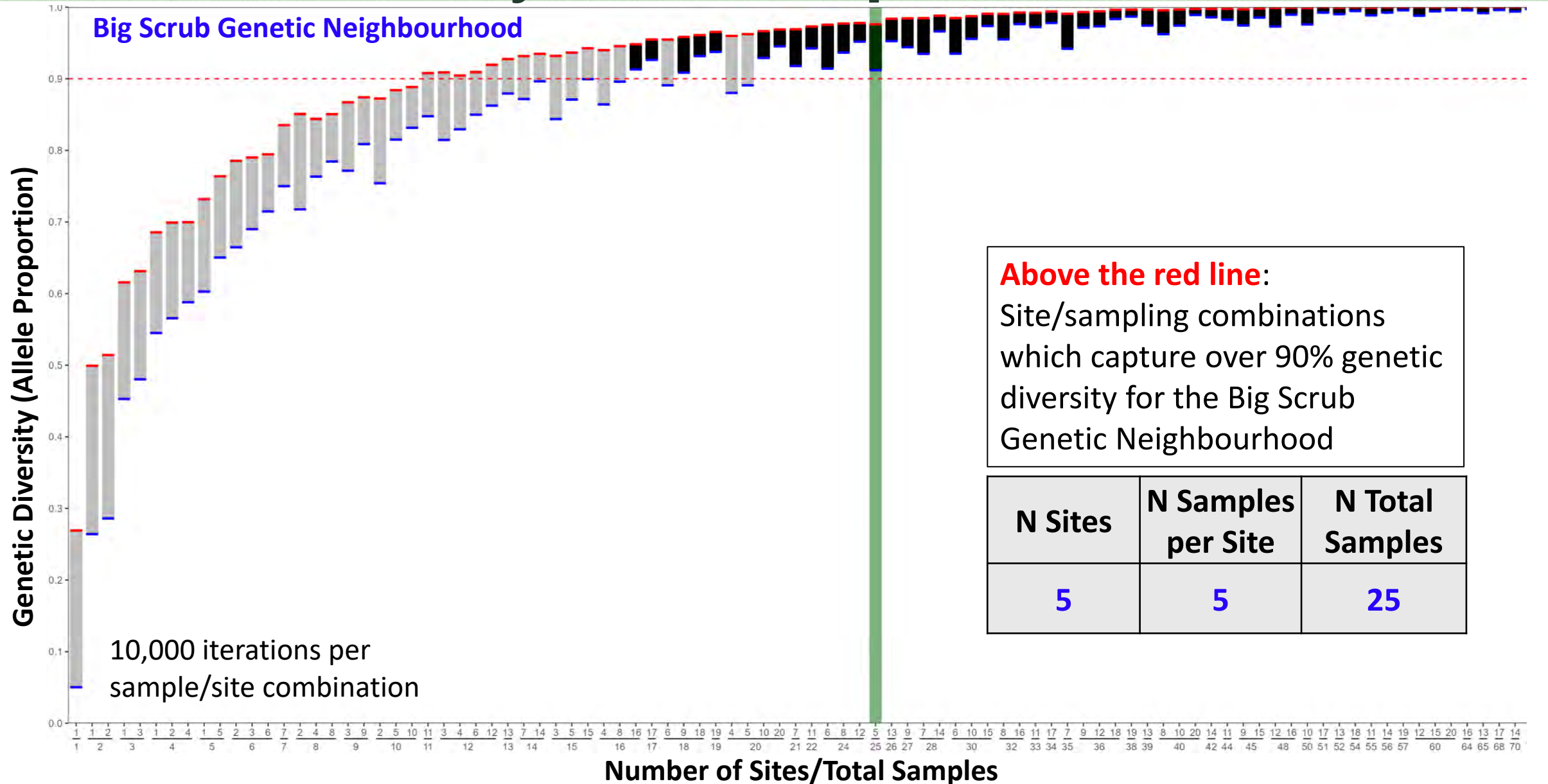
Bragg, J.G., Cuneo, P., Sherieff, A. and Rossetto, M., 2020. Optimizing the genetic composition of a translocation population: Incorporating constraints and conflicting objectives. Molecular Ecology Resources, 20(1), pp.54-65.1

Example using *Diploglottis australis*

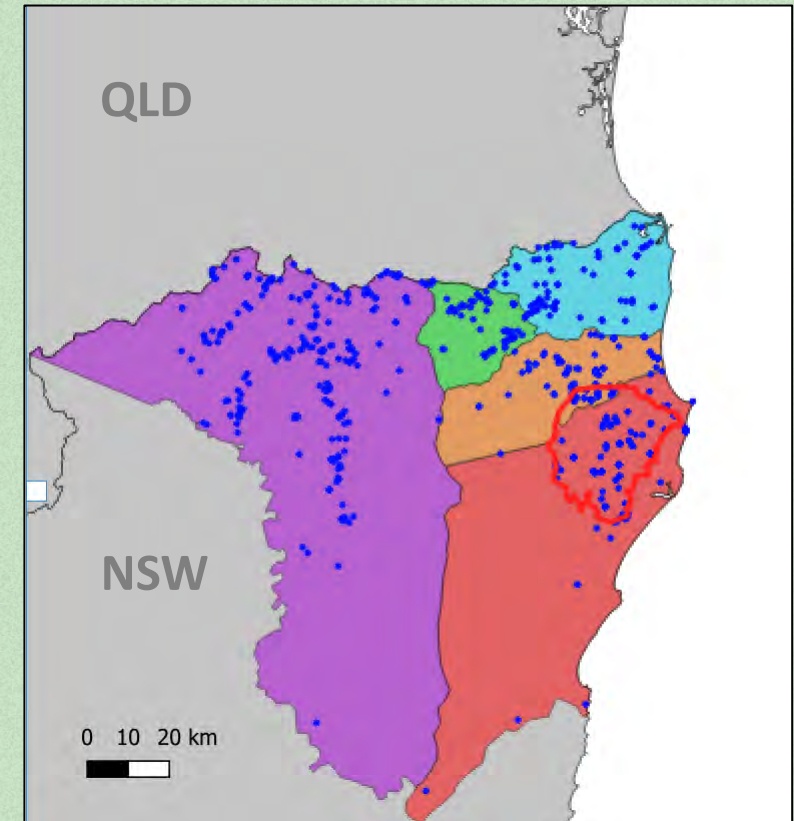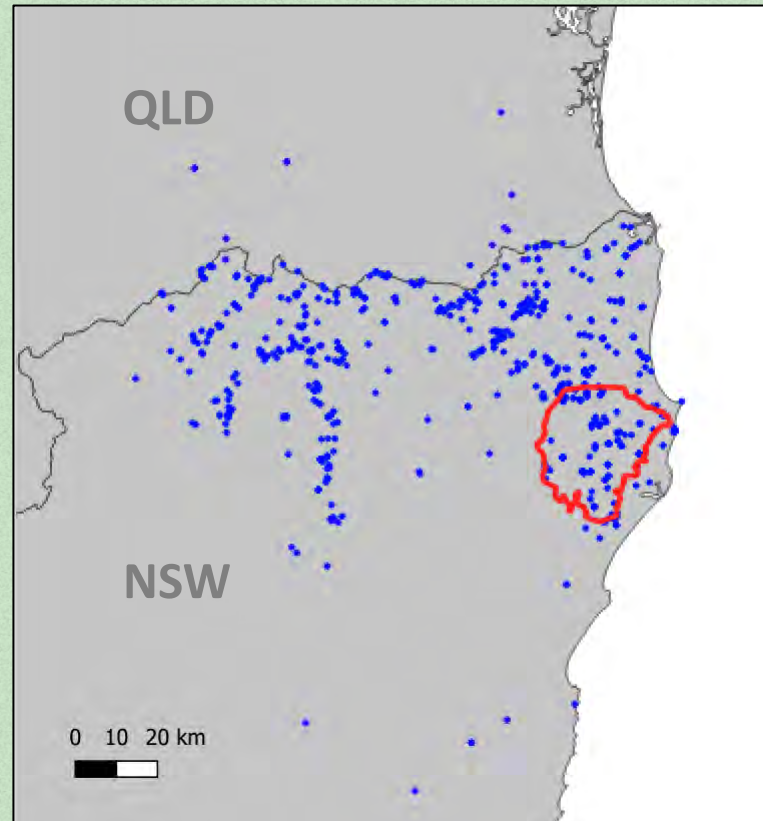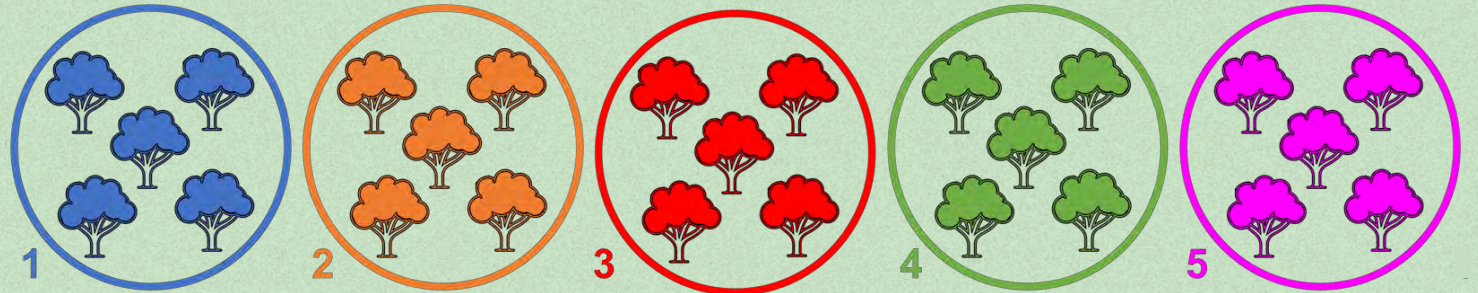Analyse data from the **Big Scrub Genetic Neighbourhood**

How many sites/samples to collect?
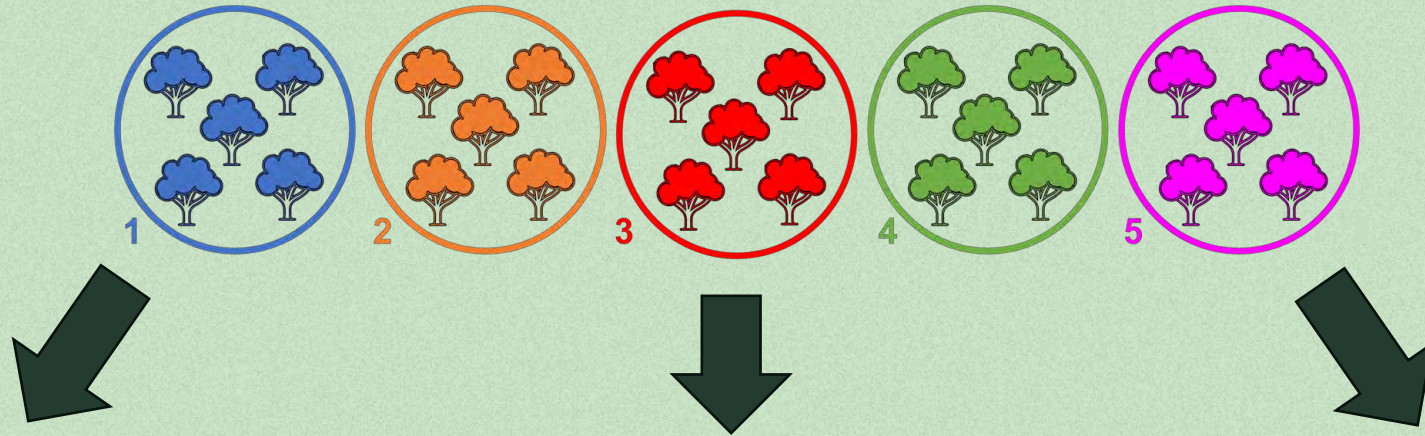
Example: Sample 5 trees from 5 sites

- Sample 5 sites geographically spread across the genetic neighbourhood

- Multiple species with similar genetic neighbourhoods can be sampled at the same time

= ALA Records   = Big Scrub

Broadly applicable guidelines

Seed

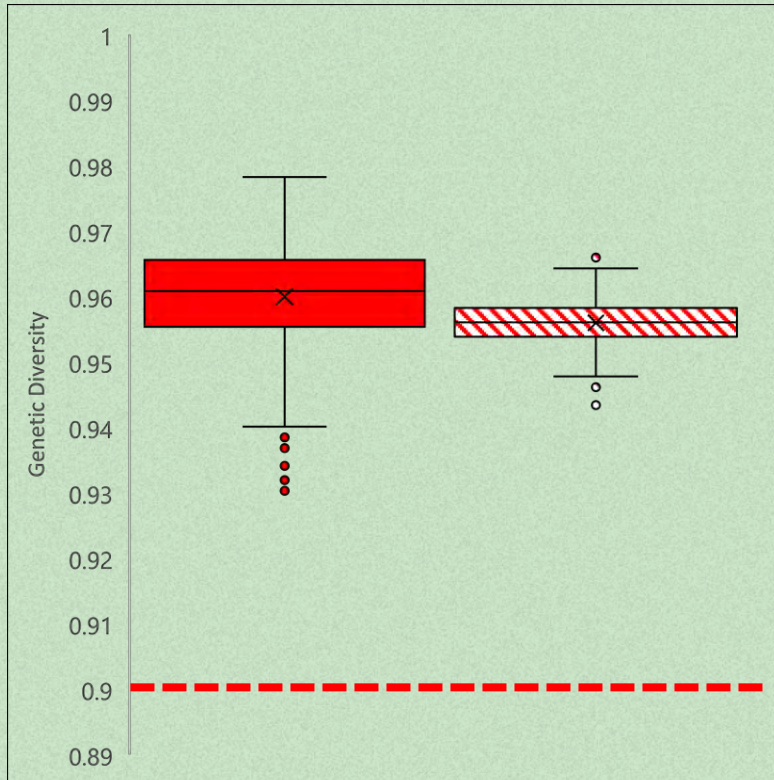**Cuttings**

In-situ "Seedling Bank"

Source material at each site from unique maternal lines
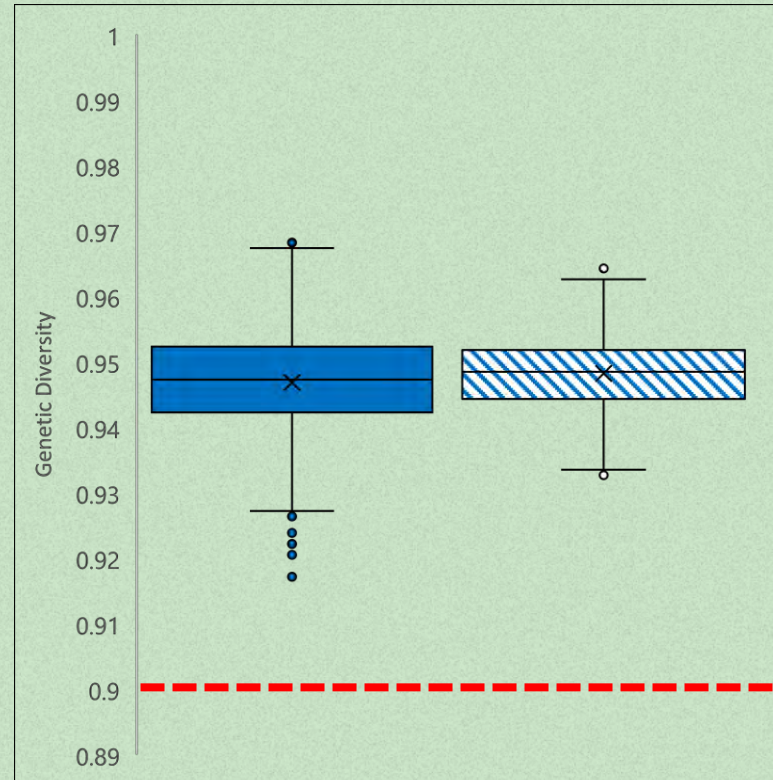
Testing the concept - nursery pilot trial

Sloanea australis
4 trees from **5 sites (20)**

Neolitsea dealbata
5 trees from **6 sites**

Firewheel
Rainforest Nursery

Over 90% of common alleles are represented in the collections

■ Randomly selecting X sites across the genetic neighbourhood

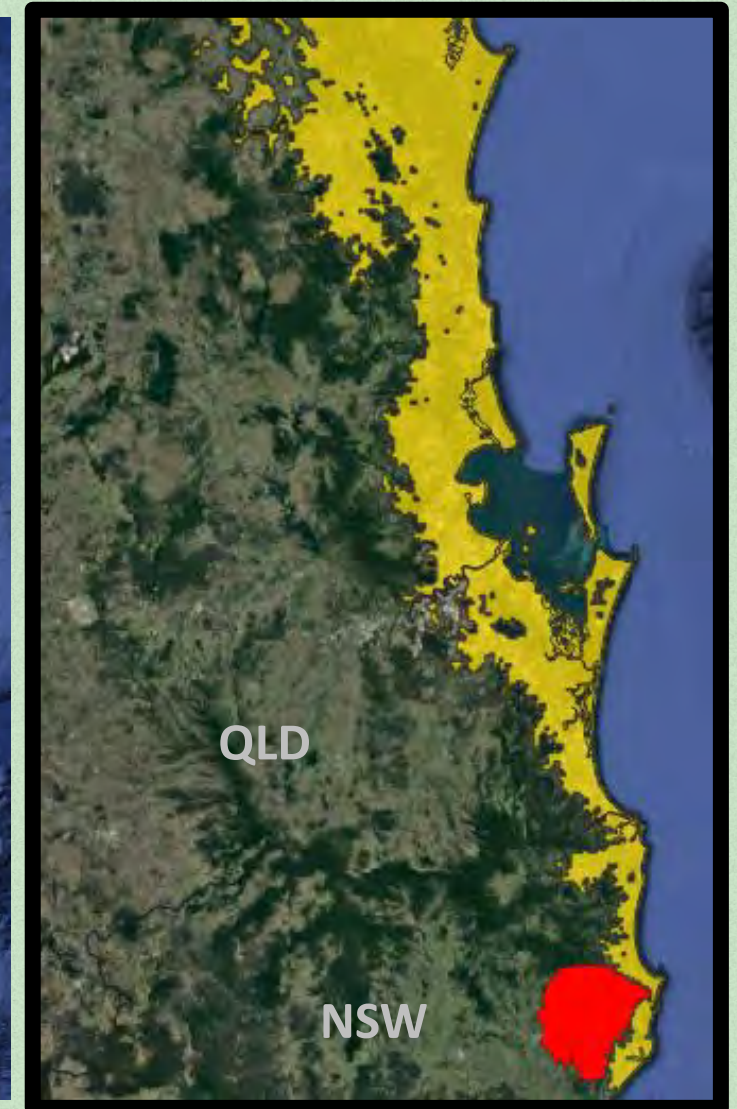▨ Nursery cuttings successfully propagated from X sites

Incorporating climate resilient material

- Dependant on species distribution north of the Big Scrub

- Sample additional climate-resilient material from areas closely related to the local genetic neighbourhood

QLD

NSW

QLD

QLD

Big Scrub Target Area

2070 Future climate match

Regional future climate matching tool developed by Peter D. Wilson

Benefits of genetically-informed restoration

Credit: Big Scrub Rainforest Conservancy

- More feasible and cost-effective than ever before
- Can undertake large, multispecies project in a relatively short timeframe
- Maximise positive impacts of high genetic diversity and climate-adapted genotypes
- minimise negative impacts of outbreeding depressions and maladaptation
- Establish adaptable and self-sustaining populations

Thankyou ☺

Big Scrub Rainforest Conservancy – Science Saving Rainforests project

ReCER – Botanic Gardens of Sydney

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Rossetto, M., Yap, J.Y.S., Lemmon, J., Bain, D., Bragg, J., Hogbin, P., Gallagher, R., Rutherford, S., Summerell, B. and Wilson, T.C., 2021. A conservation genomics workflow to guide practical management actions. *Global ecology and conservation*, *26*, p.e01492.