



Phylogeography and refugia of disjunct populations of *Eucalyptus regnans* in south eastern Australia



Paul Nevill, Gerd Bossinger and Peter Ades
School of Forest and Ecosystem Science and
CRC for Forestry
University of Melbourne, Creswick, Australia
Email: p.nevill@pgrad.unimelb.edu.au

What is Phylogeography

Phylogeography is a method of inferring historical biogeographical scenarios at the within-species level using molecular markers

The landscape is made up of **refugia** and **recolonised** areas

What are **refugia**?

Locations in which species have persisted while going extinct elsewhere

How do we identify refugia and recolonised areas?

REFUGIA

HIGH CHLOROPLAST DIVERSITY OR UNIQUE CHLOROPLAST TYPES

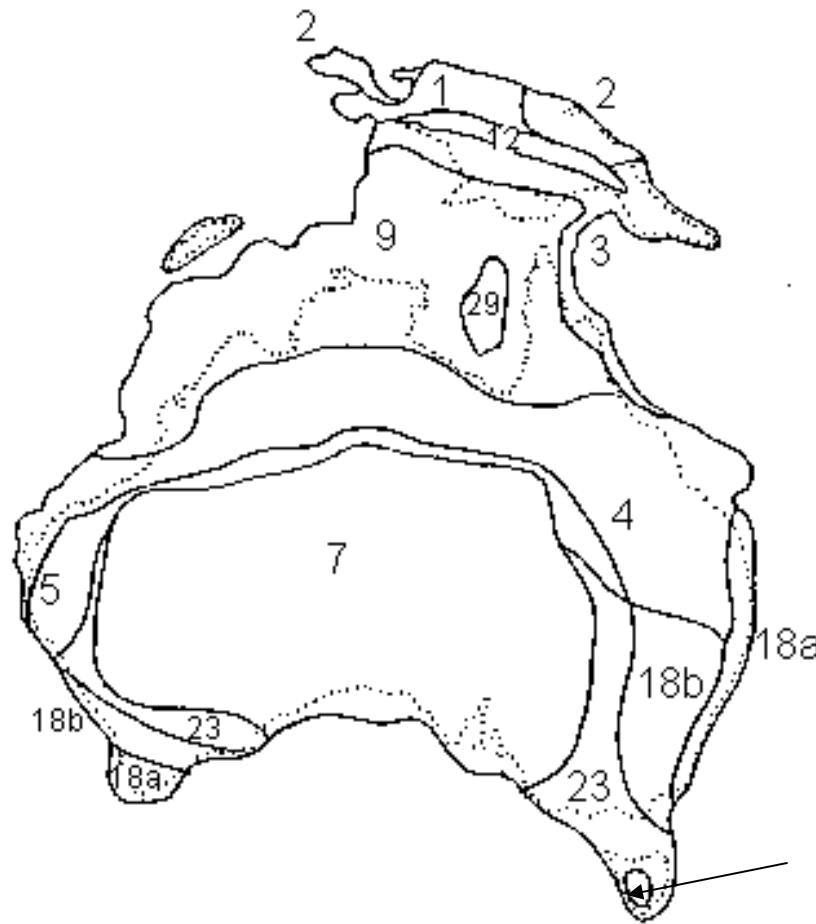
RECOLONISED

LOW CHLOROPLAST DIVERSITY OR FIXATION OF CHLOROPLAST TYPE OVER AREA

Quaternary Australia

23 Temperate semi desert (sparse shrubland or grassland)

18b Semi-arid temperate woodland or scrub



Ice sheet or alpine desert

Reconstructed vegetation cover, 18000 C14 years ago.



Can we move seed between regions without disrupting patterns of intraspecific genetic variation?

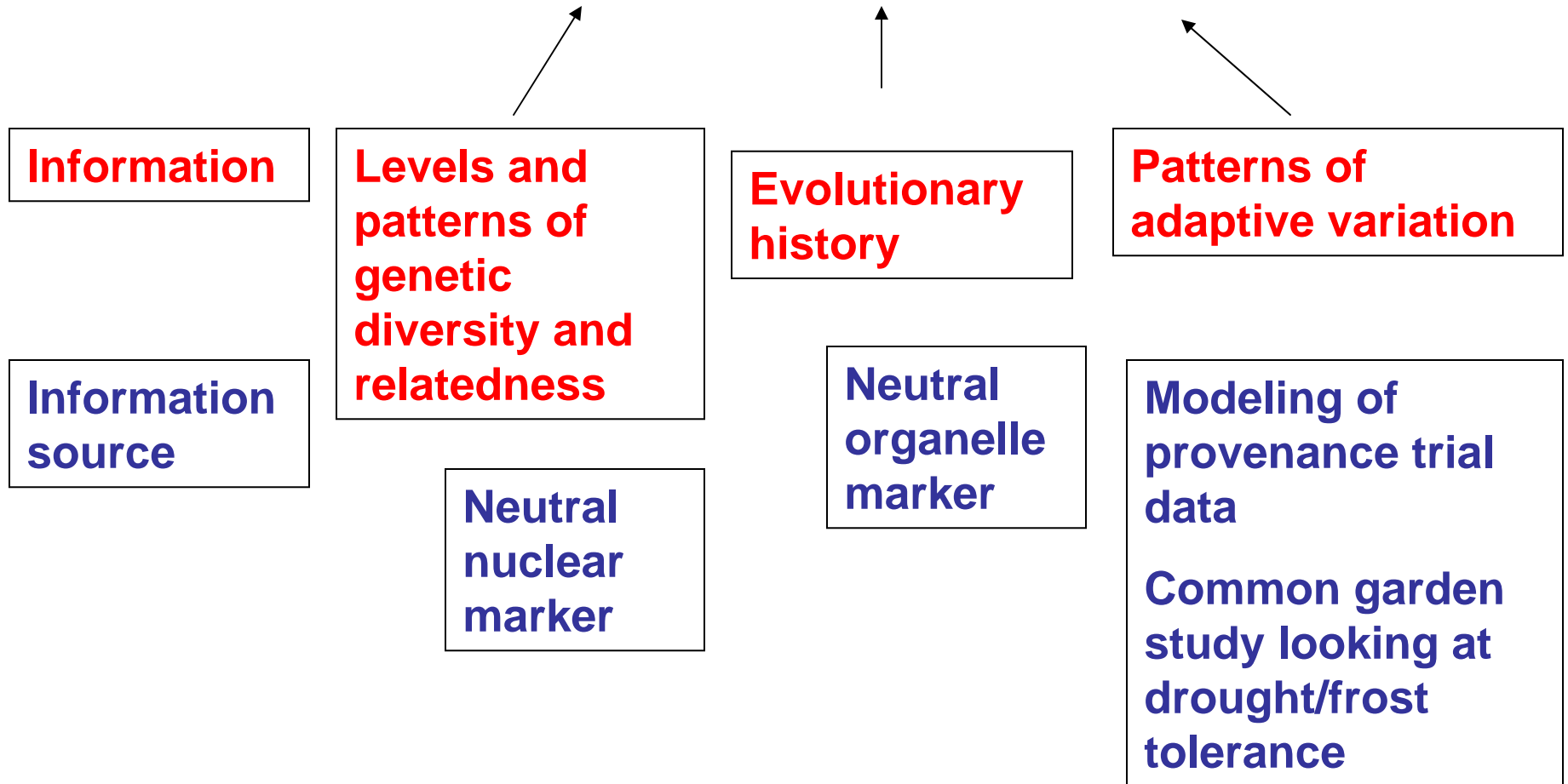


How did the species respond to past climate change



What impact are forest regeneration practices having on gene pools?

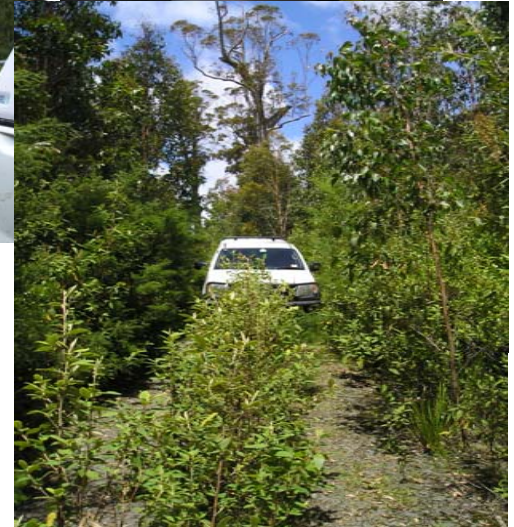
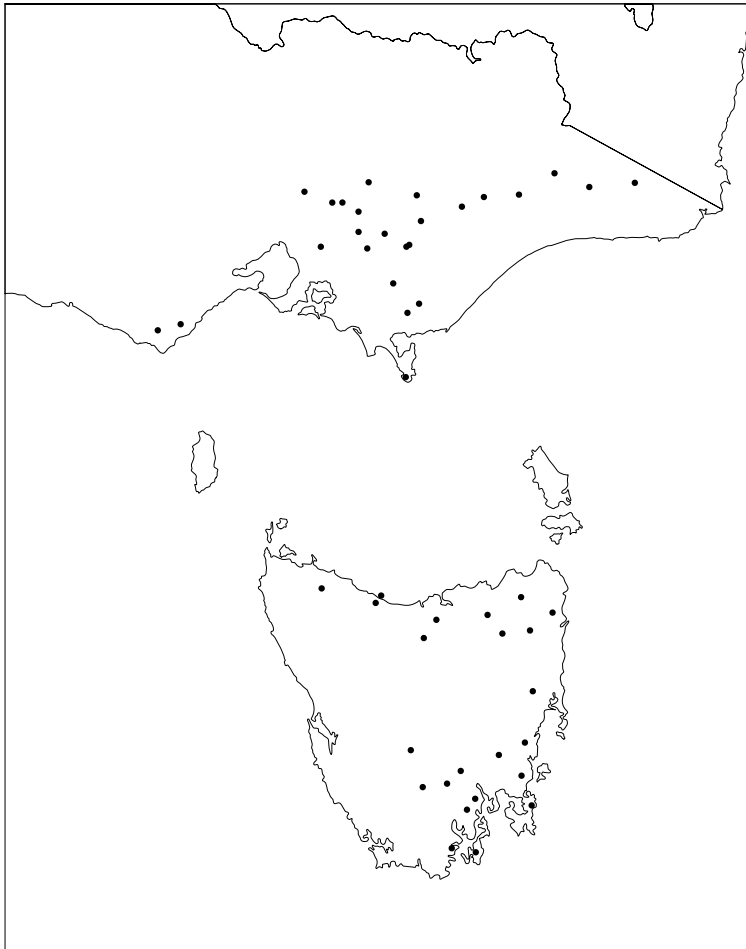
Gene pool management guidelines



Aims of study

- Describe levels of diversity and geographical distribution of chloroplast haplotypes
- Identify regions likely to share the same evolutionary history
- Identify likely refugia and recolonised areas
- Provide baseline data for gene pool management

Sample collection



Chloroplast DNA

Why chloroplast DNA?

- Uniparentally inherited
- Does not recombine
- Slow mutation rate

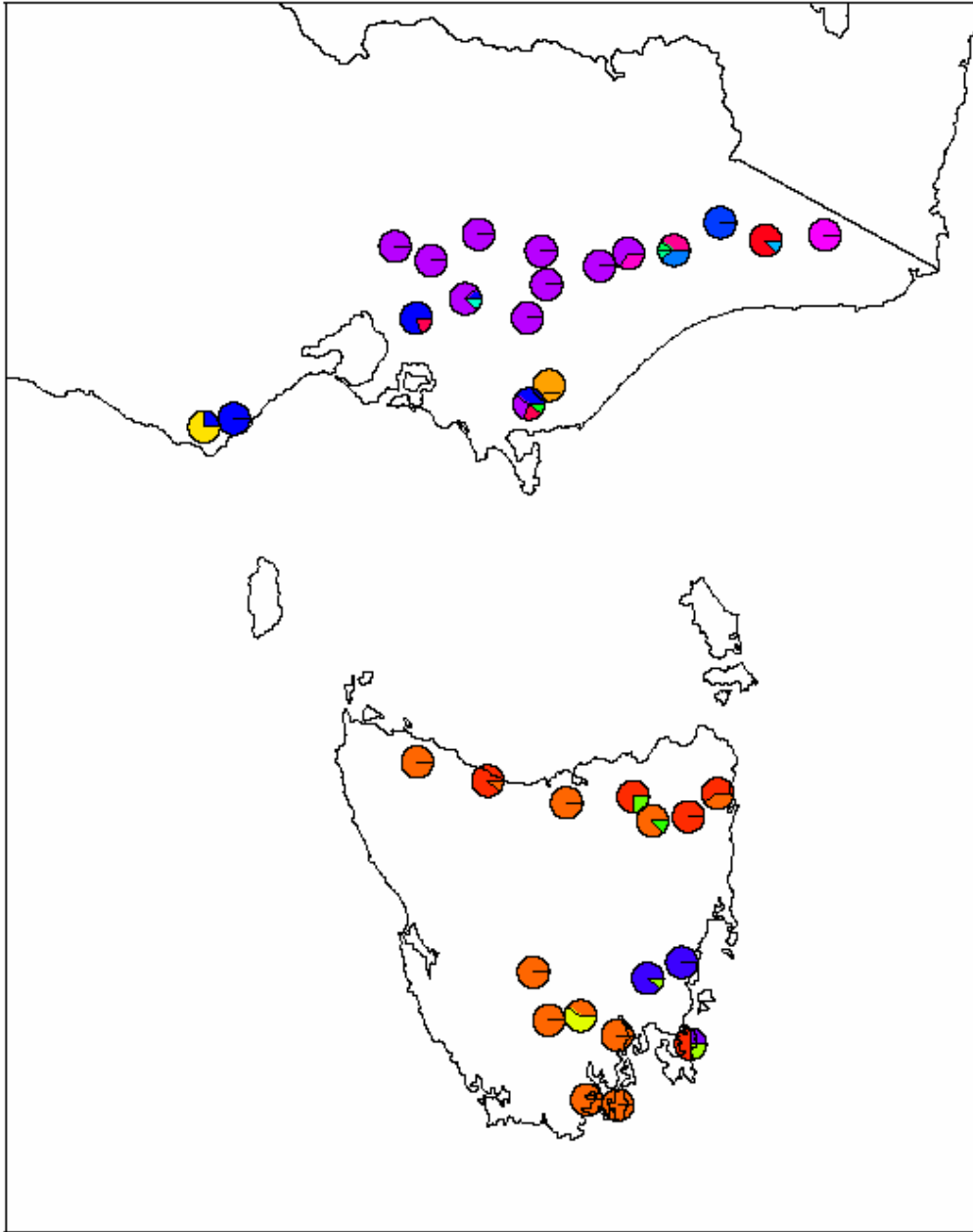
So, patterns of diversity are highly preserved

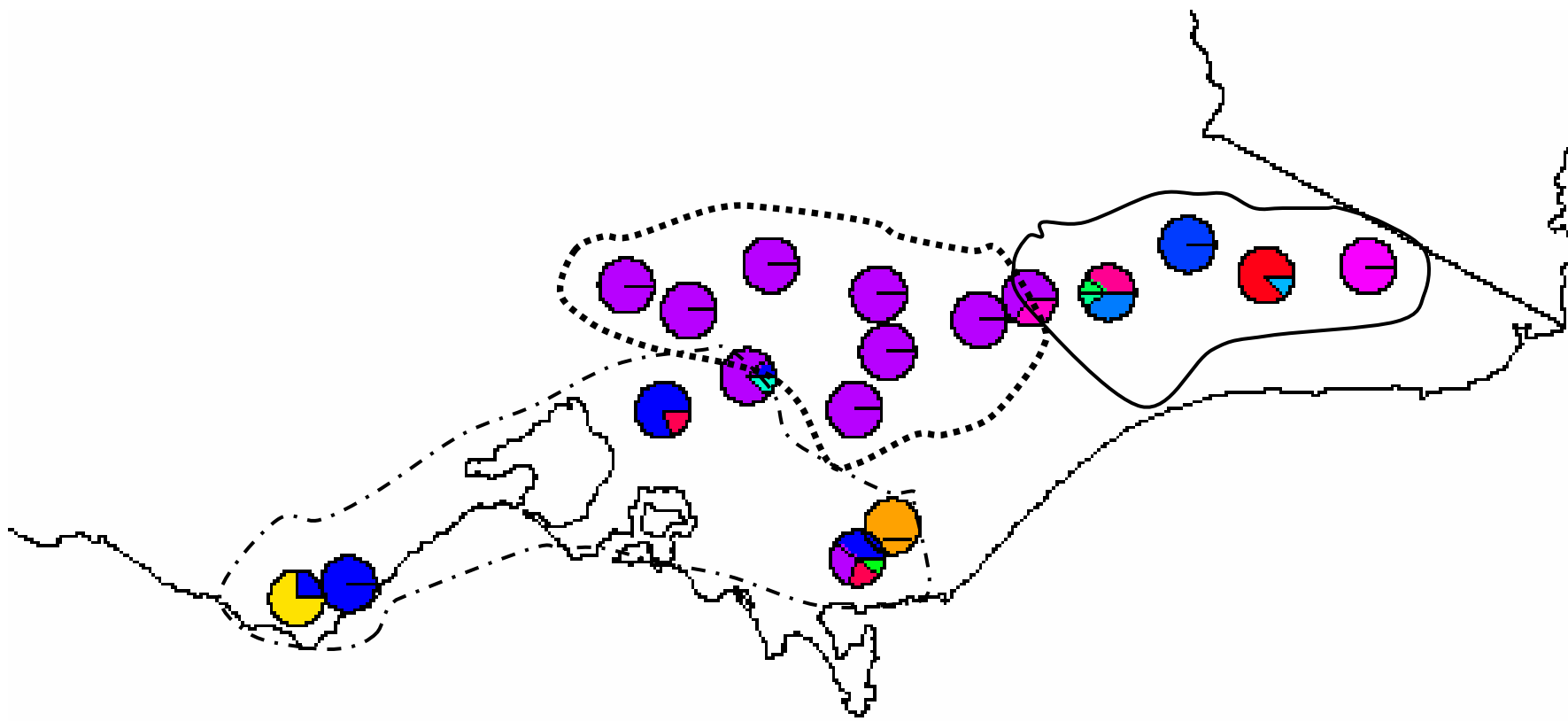
Analysis

- **Diversity parameters**
 - Number of haplotypes, Mean number of haplotypes, Haplotype diversity (based on ordered and unordered alleles) .
- **Geographic structure and relationships of haplotypes**
 - Haplotype map
 - AMOVA
 - Minimum Spanning Network
 - Bayesian analysis
- **Coalescence Modeling** (Next stage of analysis)

Results

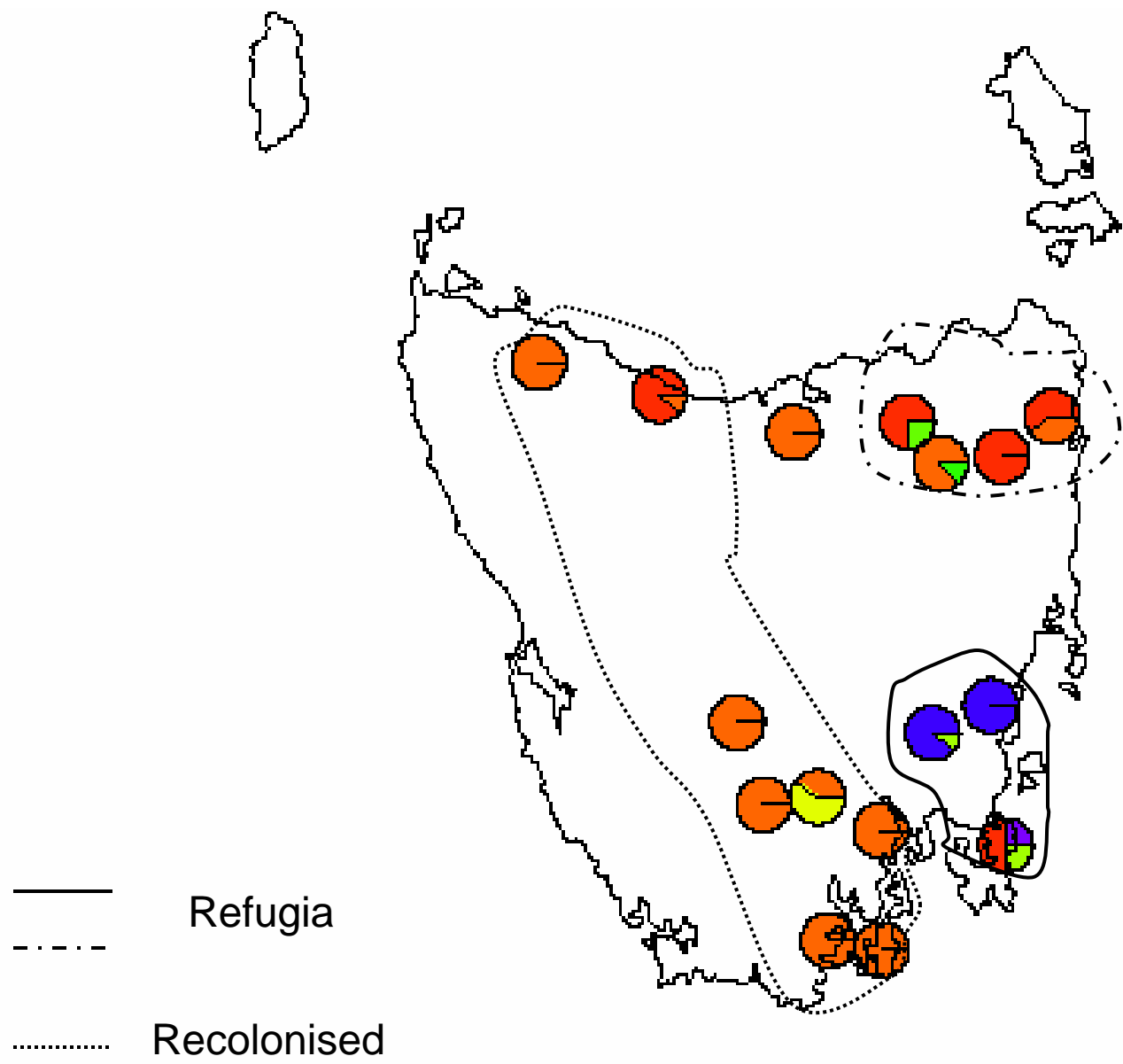
- 15 cpSSR markers screened
- Five cpSSR markers identified that are polymorphic and easy to score
- 400 individuals of *E. regnans* genotyped
- 35 haplotypes identified





— Refugia

..... Recolonised



Summary of main findings

- *E. regnans* chloroplast is variable and highly geographically structured
- Higher chloroplast diversity in putative refugia
- Lower chloroplast diversity in areas likely to have been re colonized since LGM
- Areas of same evolutionary history defined

Output to industry

- Improved seed transfer guidelines
- Baseline genetic parameters for monitoring managed forests
- Identification of Evolutionary Significant Units (ESUs)



Acknowledgements

This project is funded by an APA and the CRC for Forestry. Thankyou Vicforests and Forestry Tasmania for assistance with field work

