



Understanding the genetic architecture underlying cold adaptation

Ting Yin, Katarina Stuart, David Field

Affiliations : Applied BioSciences, Macquarie University, NSW, Australia

Background

Alpine ash is an ecologically important Australian montane eucalypt that is increasingly affected by climate change, altered fire regimes, and regeneration challenges.

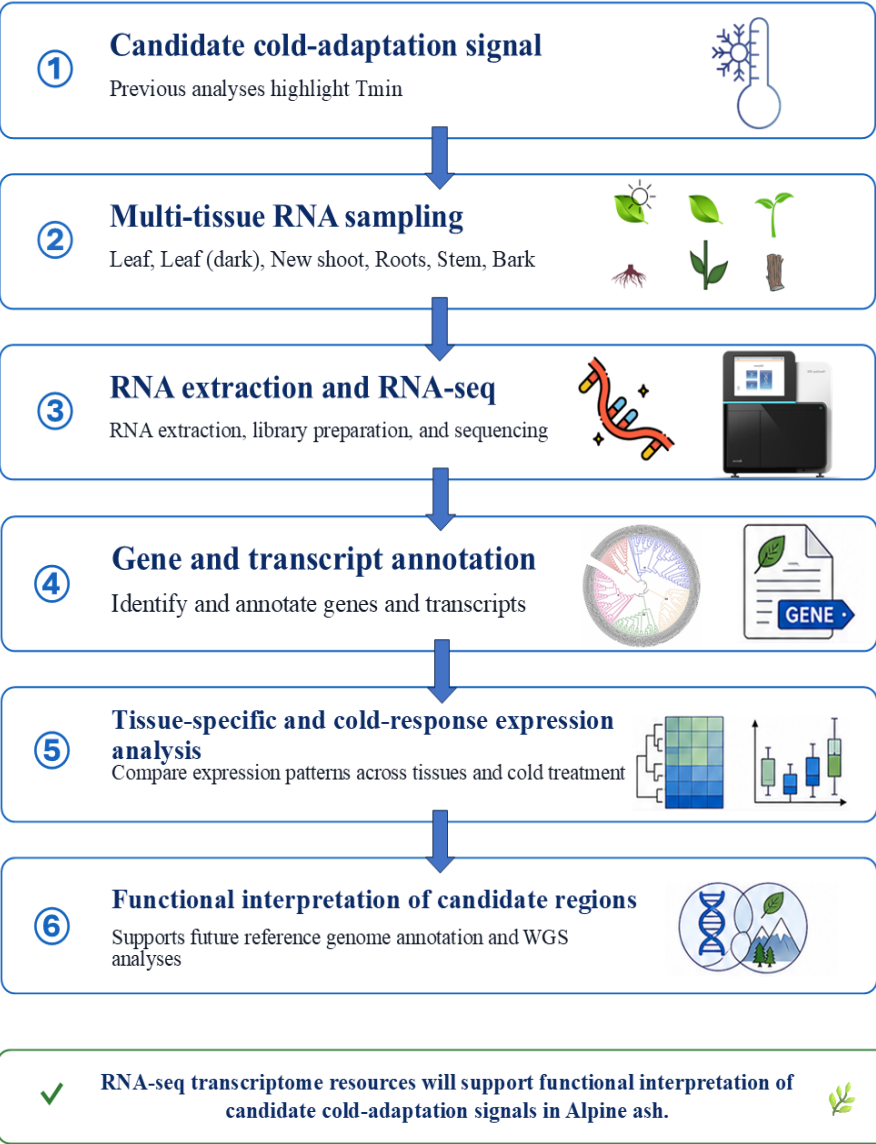
Our preliminary landscape genomic analyses identified minimum temperature (Tmin) as one of the strongest and most consistent environmental association signals.

However, existing reduced-representation genomic data and reliance on the reference genomes from related eucalypts limit gene discovery and the resolution of genomic architecture in Alpine ash.

Aims

- 1 Generate a high-quality reference genome for Alpine ash.
- 2 Identify and annotate novel genes and transcripts using RNA-seq Multi-omic RC funded component
- 3 Resolve the genomic architecture of cold adaptation using whole-genome resequencing.

Method



Results

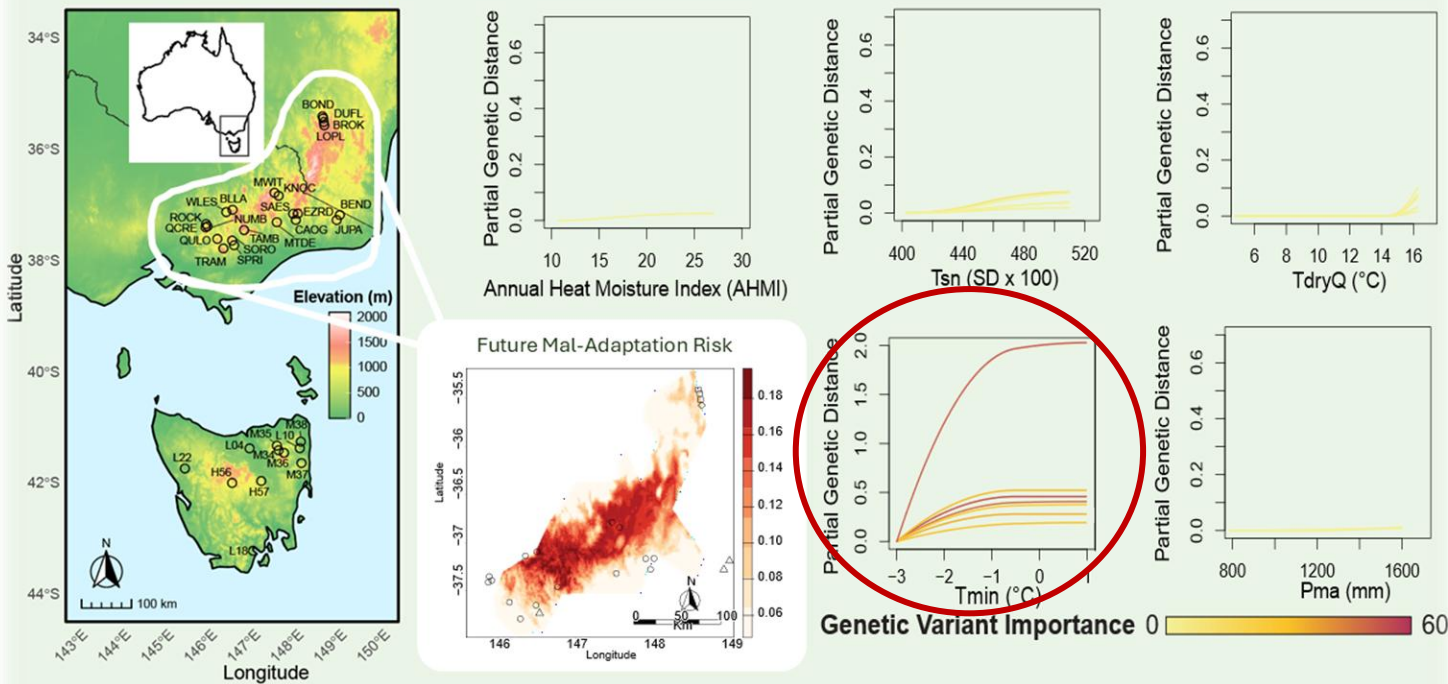


Figure 1. Strong genomic signals of adaptation to minimum winter temperature (Tmin)

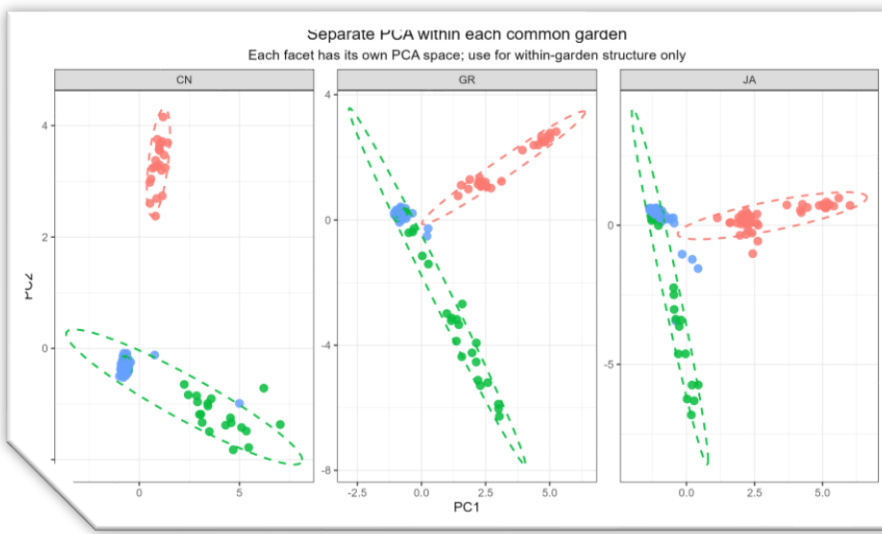


Figure 2. Strong genetic population structure is present in Alpine ash

We will use common garden experiments, coupled with genetics and transcriptomics, to investigate the adaptive responses of Alpine ash to different climatic conditions across its range, including variation in minimum winter temperature (Tmin).

To investigate these patterns, we collected RNA samples from the common gardens to develop transcriptomic resources that will support the functional interpretation of candidate regions associated with Tmin and cold adaptation.



Figure 3. RNA sampling for transcriptome development and functional interpretation

Conclusion

- Existing genomic analyses highlight cold adaptation as a key axis of variation in Alpine ash.
- RNA-seq transcriptome resources will improve gene discovery, annotation, and functional interpretation of candidate regions associated with Tmin and cold adaptation