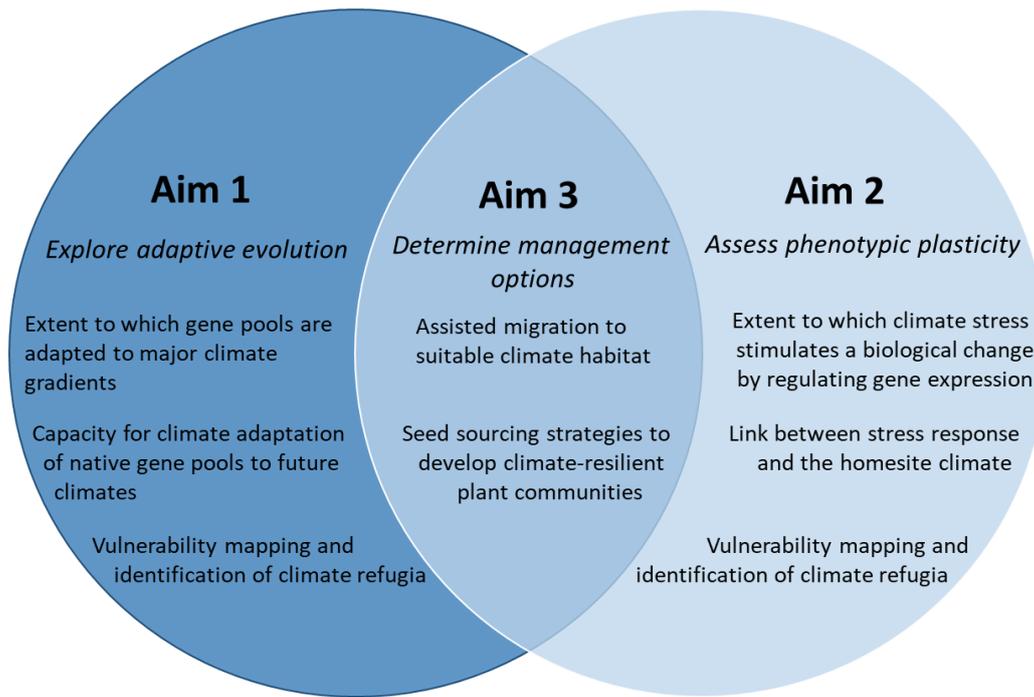# Progress Report 2023

**GRANT PROGRAM:** Malcom Reed Grant (2023 – 2025).

**PRINCIPAL INVESTIGATOR:** Ellen Gunn (PhD student) – ellen.gunn@utas.edu.au.

**PROJECT TITLE:** To move or not to move? Understanding climate adaptation to inform forest management options.

**PROJECT BACKGROUND AND SUMMARY:** Climate is a major agent of selection that defines a species' geographic distribution and helps shape adaptive variation, allowing a species to maintain fitness in their local environment. However, as modern-day climate change causes rapid shifts in local conditions, a mismatch between the adaptations driven by historic selective forces and current homesite conditions is causing maladaptation – the decrease in population fitness. Already, there are many cases where Australia's unique flora are reaching their ecological and physiological tipping points, resulting in range-wide dieback. To maintain fitness in their perturbant environment, trees must either evolve and adapt through changes in their genetic composition (adaptive evolution) or persist by developing alternative phenotypes without changing their genetic composition (phenotypic plasticity). Using the ecologically and economically important ash eucalypts (*Eucalyptus regnans*, *E. tasmaniensis* [formally *E. delegatensis*], and *E. obliqua*) that dominant the temperate forest ecosystems of Australia, this project will use a novel framework to investigate the genetic (adaptation) and nongenetic (phenotypic plasticity) responses of forest trees to climate change to evaluate the extent to which plant populations are adapted to future climates and elucidate the capacity of plants to respond plastically to climate stress. This project will be investigated through three aims (Figure 1) that will explore the extent to which plants can (i) adaptively evolve or (ii) change their phenotype through reversible nongenetic processes (phenotypic plasticity) to (iii) better inform management options to conserve plant gene pools and restore their unique ecosystems.
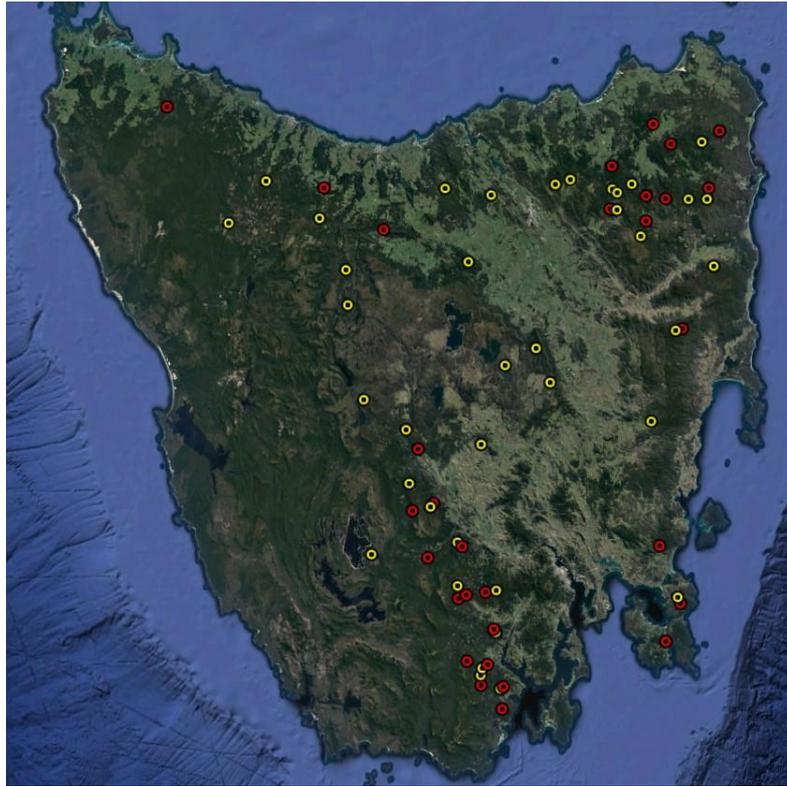
**Figure 1**. Conceptual framework demonstrating the inter-relationship among the three project aims and the expected outcomes.


**PROJECT PROGRESS:**

*Aim 1 – Explore adaptive evolution*

A total of 506 seedlings have been grown from seed sourced from 39 *Eucalyptus tasmaniensis* and 30 *E. regnans* populations across their native range in Tasmania (Figure 2). Due to unexpected delays in acquiring the seed and germination issues, seed was germinated 3 months later than anticipated. This has resulted in a slight delay to the originally proposed timeline; however, we have put in place a number of actions to ensure this delay does not affect the timeframe of deliverables.

**Figure 2.** Locations of the 39 *Eucalyptus tasmaniensis* (yellow points) and 30 *E. regnans* (red points) populations from which seed was sourced for aim 1. These sampling locations span each species' native range in Tasmania.

To link seedling phenotype to genotype and homesite environment, morphological traits representing growth (e.g., height, number of fully expanded nodes), plant development (node of ontogenetic change), resource allocation (e.g., glaucousness, leaf oil gland density) and function (e.g., specific leaf area, leaf thickness) have been measured on each seedling. This data is currently being analysed and associated with the environmental variables of each population and will form the basis of the first experimental chapter of my thesis.
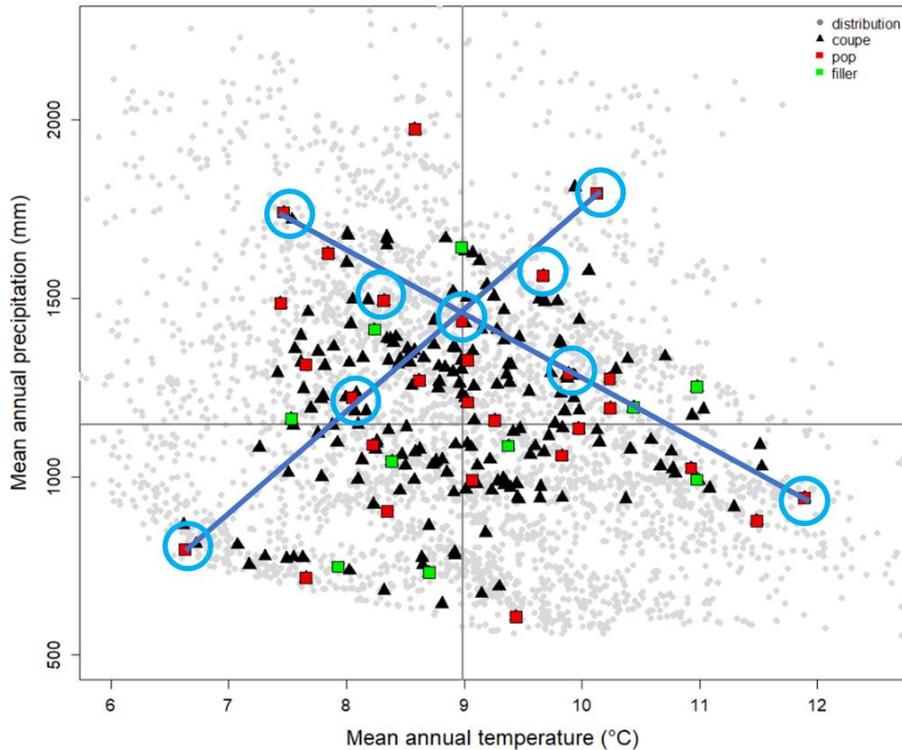
Leaf material for DNA extractions have been collected from each of the 506 seedlings (Figure 3) with the DNA extractions expected to be completed in early 2024. The DNA extraction method has been fine-tuned and all required laboratory supplies and consumables purchased and prepared (solutions made and tested, and leaf tissue collected and stored). High quality DNA will be sent to Diversity Arrays Technology (DArT) for genotyping in the first quarter of 2024. This genotyping data will be used in a genome-environment association analysis (GEA) to detect signals of climate-associated adaptation. To expedite and streamline the GEA analysis, I have developed and tested a step-by-step analysis pipeline, meaning that a publication should be completed in the first quarter of 2025, as originally proposed.

**Figure 3.** Seedlings for aim 1 growing in the glasshouse facilities at the University of Tasmania.

### *Aim 2 – Assess phenotypic plasticity*

To address the second aim of this project, seed from 9 populations of *Eucalyptus tasmaniensis*, *E. regnans*, and *E. obliqua* were germinated and grown into seedlings for use in a controlled drought experiment. Populations were selected based on their location along a temperature and precipitation gradient (Figure 4) to help pull apart the effects of these key climate variables on drought tolerance. Throughout this drought experiment, the performance of each population under drought stress will be assessed visually and by continually monitoring the water potential within plants, and DNA will be extracted at four time points to explore changes in the DNA-methylation profile of populations that may be associated with a plastic (non-genetic) response to drought stress.

**Figure 4.** Sampling design for the nine populations of *E. tasmaniensis* selected for the drought experiment (aim 2) based on their location along a temperature and precipitation gradient (blue lines). Red squares represent all the populations sampled for both aim 1 and aim 2, with those circled in blue being the nine selected for aim 2.

The seedlings for this experiment faced the same germination hurdle as those grown for aim 1. As a result, the drought experiment has been slightly delayed. However, this delay will mean the seedlings will be droughted towards the end of summer, starting in the first quarter of 2024, which we believe will benefit this experiment by providing a more realistic hot and dry drought scenario.

The seedlings have now been planted into their communal experimental pots and arranged into their experimental design (Figure 5) to give them time to acclimate prior to commencing the drought experiment. Once the plants have acclimated, I will estimate the critical cavitation threshold at which the water system of each population fails and take morphological measurements representing growth, plant development, resource allocation and function (the same that were taken for aim 1) so that these traits can be linked to population performance under drought stress.

**Figure 5.** Seedlings for aim 2 growing in the glasshouse facilities at the University of Tasmania.

### *Aim 3 – Determine management options*

The final aim of my project will utilise the findings from aim 1 and aim 2 to develop informed management options for forests in the light of predicted climate change. Progress on this aim is still anticipated for 2024 and 2025.

### *Communication*

During 2023 I was given the opportunity to present an introduction to this project at the International Congress of Genetics, a congress held every five years. This was a highly valuable opportunity to discuss this work with the global scientific community, and to bring awareness to the importance of this work in protecting native Australian flora.

I also presented at Sustainable Timber Tasmania's annual general meeting, which gave me the opportunity to have valuable discussions with forest managers about how the outcomes of this project may be implemented within their practices to help improve the climate resilience of native forests.