# Defining restoration seed zones in the genomics era
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## Abstract

A major challenge faced by restoration practitioners is how to achieve successful revegetation outcomes in a rapidly changing world. There is an imminent shift in seed sourcing techniques for restoration, away from strict local provenancing and towards seed sourcing based upon the genetic architecture of restoration species. A principal reason for this shift is that climate change is altering conditions faster than some plants can adapt, creating potential for local provenances to become maladapted. Consequently, there is an urgent need to study the genomic basis of adaptation to climate change, as only with this information is it possible to underpin the restoration of more resilient plant populations to climate change with real data.

## Introduction

My research explores the use of genomics as a tool to increase our understanding of plant population structure and adaptation to environmental variables. Central to my PhD is a range-wide study of population structure and adaptation to environmental variables in the arid zone specialist plant, *Maireana sedifolia*. To do this, I attempted to incorporate rangewide genomic analysis with a common garden trial.

Objectives of my PhD research:

1. Define seed transfer zones from neutral genomic data
2. Compare the neutral seed transfer zones with those inferred from adaptive genomic data to define adaptive seed transfer zones
3. Explore the congruence between neutral and adaptive seed transfer zones, and adaptive and functional phenotypic variation to cross-validate the genomic methods with established phenotyping approaches – **I received funding support from Nature Foundation SA for this objective**

The goal of my NFSA funded year was to complete the collection of cuttings from across aridity gradients in both the east and west genetic clusters, and establish a common garden trial. I also planned to measure key functional traits in situ of the individuals from which cuttings were obtained, and pending the establishment of the cuttings, begin part 1 of the common garden trait measurements. I had also planned to complete the analysis of the neutral genomic dataset and begin the analysis of the adaptive genomic dataset.

## Progress, methods and results for each component

1. Define seed transfer zones from neutral genomic data

The analysis for this component is complete (Figure 1.). Genetic diversity did not vary greatly across the species range, suggesting that inbreeding is not a concern. We found evidence for two distinct genetic clusters which provided the basis of delineating two separate seed transfer zones, divided into the more arid western zone and the more mesic eastern zone. There is evidence of admixture between the two genetic clusters in the more arid areas of the eastern seed transfer zone which will be further explored in the adaptive analysis, with a focus placed on the design of climate-adjusted provenancing based upon environmental adaptation.

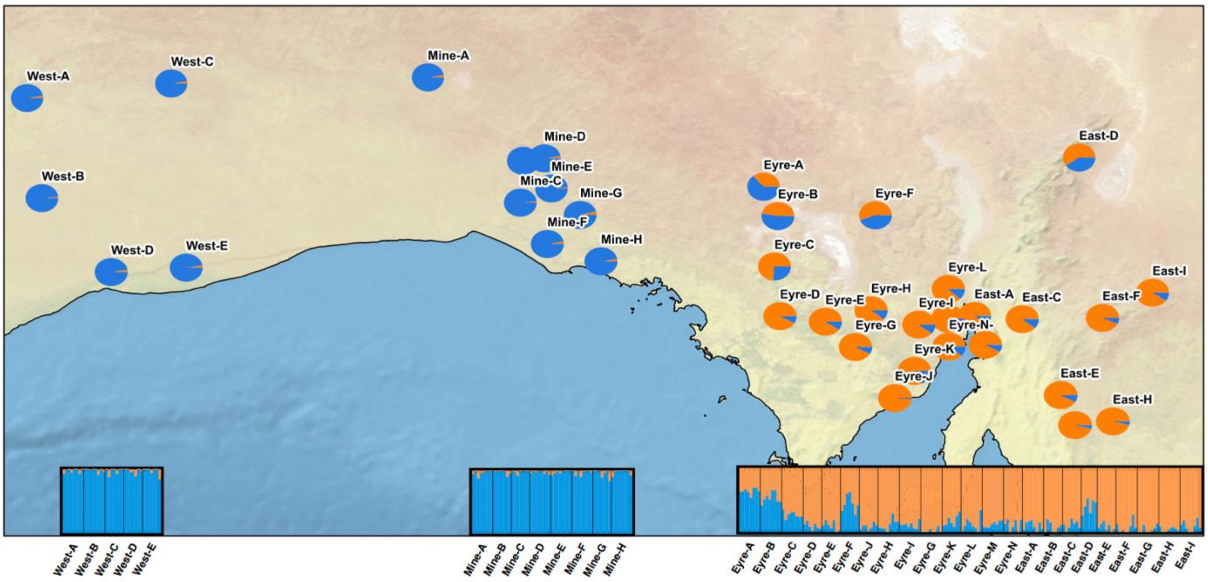


**Figure 1:** Neutral genetic population structure from a preliminary ADMIXTURE analysis. There have been two clear genetic clusters identified, with an east/west divide. Pie charts at each sampling site show the overall proportion of individuals assigned to the two genetic clusters (blue represents the western cluster, orange represents the eastern cluster).

2. Compare the neutral seed transfer zones with those inferred from adaptive genomic data to define adaptive seed transfer zones

This objective has been impacted by COVID-19 travel restrictions. To complete this objective, I still require further training in the techniques to analyse genomic data for adaptation and selection. I received funding to combine attendance of a highly relevant population genomics workshop in Berlin in May 2020 (https://www.physalia-courses.org/courses-workshops/course9/), with relevant training and work alongside my co-supervisor Dr Matt Christmas (https://katalog.uu.se/profile/?id=N17-740) based at Uppsala University, Sweden to achieve this objective. However, this trip has been cancelled and there has been some delay to the analysis. However, with online resources and collaboration with Dr Matt Christmas, this is still progressing with a projected completion date of 13/7/2021.

As the objective is ongoing, future results will be shared with **Nature Foundation SA.**

3. Explore the congruence between neutral and adaptive seed transfer zones, and adaptive and functional phenotypic variation to cross-validate the genomic methods with established phenotyping approaches – **I received funding support from Nature Foundation SA for this objective**

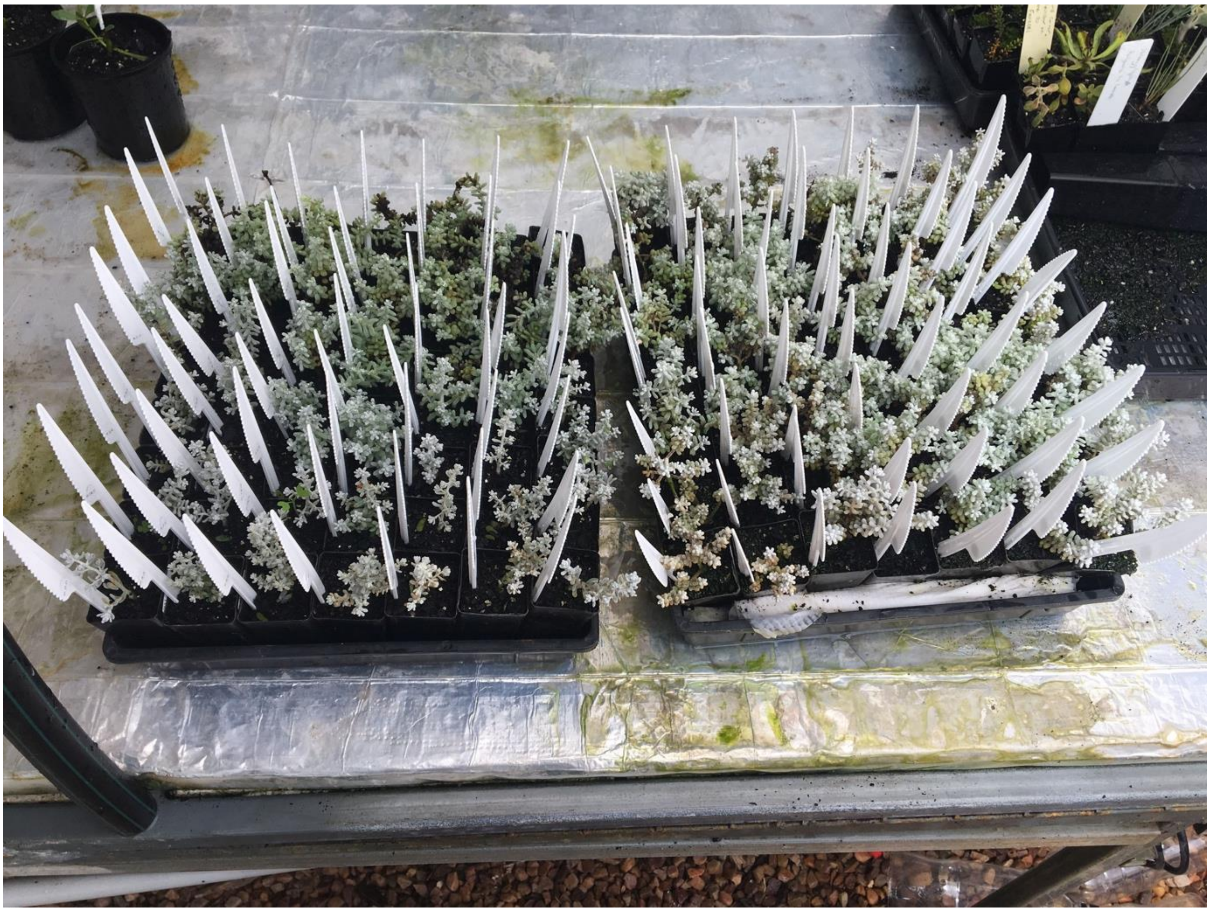
*Fieldwork and sample collection*
Fieldwork was completed successfully in November 2018. For logistical reasons, the Gawler Ranges were sampled rather than the Nullarbor. Cuttings were taking and propagated from four sites each along two aridity gradients. Further samples were collected from 10 individuals at each site for functional trait measurements

and further molecular analysis (e.g. isotopes) pending the successful establishment of the trial. Fieldwork was completed in less time than originally planned, with the project being completed under budget.

*Cuttings and samples being collected*

*Common Garden Trial*

Cuttings were established and kept at the Australian Arid Lands Botanic Gardens, Port Augusta. Throughout my research, they have provided expert advice about *Maireana sedifolia*, as they propagate the species commercially. Unfortunately, establishment of cuttings failed, caused by a heatwave over the 2018/2019 Christmas break, which caused some cuttings to die and some to receive considerable damage. We were informed by horticultural staff at the Australian Arid Lands Botanic Gardens that only 6 cuttings survived, leaving us without the numbers needed for effective sample sizes.



*Collected cuttings at the Australian Arid Lands Botanic Gardens*

*Trait measurements*
The initial phase of leaf trait measurements (of the in-situ plants) was completed in December 2018. However, since only 6 cuttings survived the first year of the common garden trial, the decision has sadly been made not to pursue the phenotypic trait component of this research.

## Discussion

The failure of the common garden trial caused a great disappointment to the team – a lot of hard work went into the collections and initial trait measurements and the addition of phenotypical data to the genomic dataset would have provided an extra dimension to the project. Fortunately, we can still answer many of the overarching questions of the research with the genomic data. We can still explore adaptation across the species range and answer some of the questions arising over the breaks in gene flow and the admixture that we can see between the genetic clusters. We are currently preparing a manuscript which includes both the neutral and adaptive analyses, with the neutral analyses complete and the adaptive analyses in progress.

We would like to thank **Nature Foundation SA** for their valued contribution to this project. We will notify **Nature Foundation SA** of any updates to this research and will acknowledge them in all resulting publications.