

Genetic diversity and adaptation in
Eucalyptus pauciflora

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(M.Sc.)

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Abstract

Restoration of degraded land to combat habitat degradation and deforestation requires understanding on adaptive potential of the species. Local adaptation and the geographic scale over which the local adaptation occurs raise issue on how well the existing genotypes will succeed in the face of increasing pressures from climate change and anthropogenic disturbances leading to new environment. This thesis examines genetic factors affecting the success of restoration plantings of the *Eucalyptus pauciflora* subsp. *pauciflora* on the island of Tasmania. Open-pollinated seed and DNA samples were collected from 281 trees from 37 native Tasmanian populations across the distribution and environmental range of the species and used to provide a quantitative and molecular genetics framework to understand local adaptation and guide future environmental planting decisions.

It specifically aims to: i) determine the mating system parameters of *E. pauciflora*, and to explore whether population variation is related to the degree of forest fragmentation or altitude; ii) assess the spatial pattern of genetic diversity in chloroplast and nuclear molecular markers, to understand historical and contemporary barriers to gene flow; iii) explore climate adaptation of the species, through assessing quantitative genetic variation in seedling morphology and growth in a glasshouse trial; iv) determine the effects of inbreeding, local climate and translocation from mainland Australia on genetic variation in performance in Tasmanian field trials up to age 3 years; and vi) provide the seed collection guideline based on the above observations.

Molecular research showed that Tasmanian *E. pauciflora* has a high outcrossing rate ($t_m = 0.90$). Outcrossing rates differed among populations, but this variation was not correlated with the degree of forest fragmentation nor with altitude. Nevertheless, fragmentation did affect early reproductive output by reducing the number of germinants per gram of capsule content. Chloroplast haplotypes showed clear geographic structure suggesting three low-altitude glacial refugia and recent colonization of high altitude areas. There was little population differentiation in neutral nuclear markers, but populations within 27 km were more similar than average. Similar significant quantitative genetic structure was also detected in the glasshouse trial,

suggesting an operational limit for the definition of a ‘local’ population. Population genetic variation was found for 24 of the 25 seedling traits studied. In several cases this population differentiation exceeded neutral expectations arguing for the action of disruptive selection and that local adaptation has over-ridden historical and contemporary gene flow. This is supported by significant correlations with population altitude and climate variables, with many seedling traits best related to the maximum temperature of the warmest month at the site of origin.

Integrating mating system parameters into the analysis of the two field trials revealed inbreeding depression for growth at the family level, but at the population level outcrossing rate did not affect performance. However, population differentiation was evident for early-age growth, survival, and susceptibility to drought and herbivory. Population differences in early performance appeared to reflect a trade-off between fast growth and herbivore susceptibility, with low altitude populations initially growing faster but rapidly losing their advantage through increased herbivory. Drought and high temperatures at one trial reshaped the fitness profile of the planting, selecting against populations from more moist areas. At both trials the Tasmanian populations outperformed those from the mainland, arguing against the need for seed translocations from mainland Australia.

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Table of Contents

Declarations	i
Authority of access	i
Statement of publication	ii
Statement of co-authorship	iii
Abstract	v
Acknowledgements	vii
Table of Contents	x
List of Tables	xiii
List of Figures	xvii
CHAPTER 1. INTRODUCTION	1
1.1 Habitat fragmentation and tree decline	1
1.2 Genetic issues in restoration: adaptation versus genetic pollution	2
1.3 Evolutionary potential: genetic variation within population, genetic structure, gene flow and adaptability	4
1.4 Study system	6
1.4.1 Choice of species for the study: <i>Eucalyptus pauciflora</i>	6
1.4.2 Biology of <i>Eucalyptus pauciflora</i> (Myrtaceae)	6
1.5 Thesis structure, objectives and hypothesis	11
CHAPTER 2. THE EFFECT OF FOREST FRAGMENTATION AND ALTITUDE ON THE MATING SYSTEM OF <i>EUCALYPTUS PAUCIFLORA</i> ..	14
Abstract	14
2.1 Introduction	14
2.2 Materials and methods	18
2.2.1 Sample collection	18
2.2.2 Progeny growth and sampling	18
2.2.3 DNA extraction and microsatellite analysis	20
2.2.4 Mating system analysis	21
2.2.5 Statistical analysis	22
2.3 Results	22
2.4 Discussion	26
2.5 Acknowledgements	32

CHAPTER 3. MOLECULAR GENETIC DIVERSITY AND POPULATION STRUCTURE IN <i>EUCALYPTUS PAUCIFLORA</i>	33
Abstract	33
3.1 Introduction	34
3.2 Materials and methods	36
3.2.1 Sample collection and DNA extraction	36
3.2.2 Molecular methods	36
3.2.3 Chloroplast microsatellite analysis	38
3.2.4 Nuclear microsatellite analysis	40
3.3 Results	41
3.3.1 Chloroplast haplotype diversity	41
3.3.2 Nuclear microsatellites	50
3.4 Discussion	55
3.5 Conclusion	59
3.6 Acknowledgements	59
CHAPTER 4. EVIDENCE FOR CLIMATE ADAPTATION IN EARLY-LIFE CYCLE TRAITS OF A WIDE-SPREAD EUCALYPT	60
Abstract	60
4.1 Introduction	61
4.2 Materials and methods	63
4.2.1 Sampling sites and experimental design	63
4.2.2 Traits measured	66
4.2.3 NIR spectroscopy	66
4.2.4 Morphological data analysis	67
4.2.5 NIR data analysis	71
4.3 Results	72
4.3.1 Genetic variation between populations	72
4.3.2 Genetic variation within populations	78
4.3.3 Inter- and intra-population genetic correlation	81
4.4 Discussion	83
4.4.1 Genetic variation between and within populations	83
4.4.2 Genetic differentiation is poorly associated with geographic distance	84
4.4.3 Genetic differentiation is strongly association with altitude and climate of origin	85
4.4.4 Correlation between traits and possible effect on adaptation	88

4.5 Conclusion	91
4.6 Acknowledgements	91
CHAPTER 5. GENETIC VARIATION IN SEEDLING PERFORMANCE IN FIELD TRIALS OF <i>EUCALYPTUS PAUCIFLORA</i>	92
Abstract	93
5.1 Introduction	94
5.2 Materials and methods.....	96
5.2.1 Genetic material.....	96
5.2.2 Field trials	96
5.2.3 Site preparation	97
5.2.4 Planting stock preparation and planting.....	100
5.2.5 Trial design and layout	100
5.2.6 Trait assessment.....	101
5.2.7 Statistical analysis	102
5.3 Results	106
5.3.1 Tasmania versus mainland populations	106
5.3.2 Genetic variation among populations within Tasmania and within the mainland	108
5.3.3 Association of traits with mating system parameters and climatic variables	111
5.3.4 Genetic variation within Tasmanian populations	115
5.3.5 Local versus non-local populations.....	115
5.4 Discussion.....	116
5.4.1 Population differentiation and association with altitude and temperature of origin ..	116
5.4.2 Population differentiation is not affected by variation in outcrossing rate.....	120
5.4.3 Local adaptation to the experimental sites	121
5.5 Acknowledgements	123
CHAPTER 6. DISCUSSION AND CONCLUSION.....	124
6.1 Minimal impact of habitat fragmentation on genetic variation in fitness traits in <i>Eucalyptus pauciflora</i>	124
6.2 Molecular markers provide insights into past migration and contemporary gene flow.....	125
6.3 Altitude and temperature of warmest month - key drivers of population divergence.....	126
6.4 Delineation of local seed source.....	127
6.5 Is there direct evidence that local populations are better adapted – implications for choosing a seed sourcing strategy for restoration	128
REFERENCES.....	130