

**The conservation genetics of  
endangered *Eucalyptus camaldulensis*  
Dehnh. subsp. *camaldulensis* (River Red  
Gum) in an eastern Australian floodplain**



**Penelope Nelson**

B.Sc. (JCU)

M.Nat. Res. (NE)

A Thesis Submitted for the Degree of Doctor of Philosophy  
Faculty of Arts and Sciences

School of Environmental and Rural Science

University of New England

Armidale, New South Wales

Australia

May 2011

## Acknowledgements

I would like to extend a warm thankyou to my primary supervisor Professor Caroline Gross for her ongoing support and friendship throughout my candidature. I would also like to thank co-supervisor Doctor Mohammad Fatemi, especially for his patient and calm guidance in the lab. Together you have helped me develop confidence in myself; a gift of immeasurable value.

I would also like to extend my gratitude to a team of people who helped me in one way or another throughout this project. I would like to thank Simone Simpson and Wendy Waters for their friendship and assistance in the field. A special thankyou to Ian Simpson for both field assistance and greenhouse support – both me and my ‘babies’ are most grateful. I would also like to thank Mick Faint for providing me with what I needed in the greenhouse. Thankyou also to Azi Haddadchi who shared my office and my thoughts and kindly helped me wash the dirt from a million roots.

I would also like to thank facilitators and landowners: Lorna Adlem at the Hunter –Central Rivers CMA for support and site data, Rio Tinto Coal and Allied for access to sites, James Wearne for driving around mine sites and catching fish, John Taylor and Scott Wheatley for access to their properties and Michael Baer at the Singleton Army base for giving me site access. I would also like to thank Shirley Fraser (UNE) for finding money for me when I was broke and helping me with the paperwork.

Many people also assisted me in writing and analysing data. I would like to thank Suzanne Hoebee for reading through early drafts and looking through my analysis. I would also like to thank the online community: Lou Jost who answered my queries and helped me to think about numbers. I would also like to thank Peter Smouse for responding to my emails and helping me through data analysis at difficult times. I would also like to thank Liisa Atherton for her careful proofreading.

A special thankyou to the funding bodies - this project would not have been possible without funding support from the Hunter-Central Rivers CMA (to C.L.Gross), the University of New England and the Australian government.

And last but not least thankyou to my beautiful family (Joseph Bell, Elly Bell and Jack Bell) who provided me with emotional support and encouragement throughout. Who willingly ate beans (again) and didn’t mind talking trees ad nauseum; who clumped around field sites in the rain and kept me cheerful. I couldn’t have finished this beast without you.

## Abstract

Of primary concern to conservation biologists is that the level of genetic variability remaining within fragmented remnant populations may be insufficient for maintaining reproductive and evolutionary processes. The consequences and contributions of genetic deficiencies on the persistence of remnant communities, however, are not consistent across species. Plant breeding systems, historical mating patterns and pollinator behaviour can impact upon the susceptibility of a species to genetic decline; while the extinction threat presented by environmental factors may render genetic concerns redundant, at least in the immediate future. Thus, to accurately assess the resilience of remnant communities, genetic diversity and the impact of genetic diversity on individual fitness should be considered within the context of environmental factors and a range of time scales.

*Eucalyptus camaldulensis* is a dominant species of tree in many riparian and floodplain ecosystems in Australia. In the Hunter Valley catchment region, the distribution of the species has been reduced to a series of disconnected remnants along small stretches of river and floodplain habitats. *Eucalyptus camaldulensis* is a niche specialist in which several critical life-stages are water dependant. The species is also known to hybridize with closely related species and exhibits a complex breeding system that enables post-zygotic selection based on the fitness of zygotes and available resources. Hence, the ecological viability of remnants, the level of inherent genetic variability, the impact of genetic variability on progeny performance and the breeding response of individuals to altered mating opportunities are potentially complicated. This research investigated key genetic and non-genetic attributes in thirteen remnant communities to assess genetic resources and their contribution to population persistence.

Nine microsatellite markers were used to assess the levels and distribution of genetic variability within and among thirteen populations in the Hunter Valley. High levels of genetic diversity were detected ( $He = 0.60-0.81$ ) that were not dissimilar to other widespread eucalypt species. Genetic differentiation based on these neutral markers

was predominantly low ( $D_{est} = 0.196$ ,  $F_{ST} = 0.05$ ) however pairwise comparisons indicated differentiation was pronounced between some remnants suggesting that they may be, or may have been reproductively isolated. Comparisons of genetic diversity between individuals grouped by age (diameter at breast height) indicated that declines in levels of genetic diversity were detectable in most remnants. Older trees (possibly in excess of one-hundred years) exhibited higher levels of genetic diversity compared with younger trees and low levels of genetic diversity in the younger trees were not accompanied with high inbreeding coefficients indicative of inbreeding.

Assessments of geographic and demographic attributes of remnant populations suggested that specific attributes (high density, high number of young trees, and low edge to area ratios) were associated with stands that inhabited creek margins while opposite traits were associated with the majority of populations occurring in floodplain habitats. However, while the age-class structure indicated that successful recruitment was more apparent in riparian remnants, a negative correlation was detected between the genetic diversity and the edge to area ratio (Shannon's Diversity Index,  $r = -0.60$ ) indicating that riparian remnants were also characterised by relatively low levels of genetic diversity.

Further investigation into the spatial genetic structure of habitat types indicated that genetic structure in episodic neighbourhoods (where individuals recruit at the same time in response to flood water) typical in floodplain habitat differed from linear neighbourhoods of saplings typical of riparian habitat. Floodplain neighbourhoods exhibited genetic structure consistent with limited seed dispersal while riparian neighbourhoods exhibited relative high levels of genetic diversity and little genetic structure. The degree to which genetic patterns established in recruitment neighbourhoods reflected population-wide genetic structure was variable. At the population level, genetic structure was relatively strong in two populations but weak and non-existent in another two.

The impact of individual genotype on seedling growth indicated that inbreeding depression was operating. Positive correlations between seedling traits and the degree of heterozygosity (e.g. height x heterozygosity,  $r = 0.82$ ) were detected. Investigations into the mating system detected significant variation among trees (0.383–0.981 tm) sampled in the Hunter Valley. In combination, these results indicate that under

certain circumstances, high levels of selfing or close sibling mating were occurring, and if widespread, the resulting increased homozygosity could significantly impact upon individual fitness.

While remnant populations exhibited high levels of genetic diversity, this study demonstrated that lower levels of genetic variability were found in younger trees compared with older tree in six remnants. The results also indicated that populations with negligible recruitment can exhibit high levels of variability while populations with high levels of recruitment may be genetically impoverished. This is likely to occur in other species, particularly those in which critical life-stages depend on specific environmental attributes. The viability of *E. camaldulensis* populations is intimately linked to inundation, (a lack of inundation immediately impacts upon recruitment opportunities), however, long term fitness declines are possible, even in habitat that supports recruitment, if genetic variability continues to decline. High levels of genetic diversity residing in non-viable habitat may need to be conserved via seed collection to guarantee long-term conservation of genetic resources. However, further work is required to determine if the variation that may potentially be lost is of adaptive significance.

# Table of Contents

<b>Declaration</b>	<b>i</b>
<b>Acknowledgements</b>	<b>ii</b>
<b>Abstract</b>	<b>iii</b>
<b>List of Figures</b>	<b>x</b>
<b>List of Tables</b>	<b>xii</b>
<b>1 Introduction</b>	<b>1-1</b>
1.1 <i>General introduction</i>	1-1
1.2 <i>Thesis outline</i>	1-3
<b>2 Study Species</b>	<b>2-7</b>
2.1 <i>The Species</i>	2-7
2.2 <i>Taxonomic description</i>	2-7
2.3 <i>Hybridisation between <i>Eucalyptus camaldulensis</i> and its relatives</i>	2-8
2.4 <i>The Reproductive ecology of <i>Eucalyptus camaldulensis</i></i>	2-10
2.5 <i>Niche habitat, recruitment, and survival in <i>Eucalyptus camaldulensis</i></i>	2-11
2.6 <i>Level and distribution of genetic diversity in <i>Eucalyptus</i> species</i>	2-12
<b>3 The Hunter Valley</b>	<b>3-17</b>
3.1 <i>Climate and location</i>	3-17
3.2 <i><i>Eucalyptus camaldulensis</i> in the Hunter Valley</i>	3-17
3.3 <i>Historical distribution of <i>Eucalyptus camaldulensis</i> in the Hunter Valley</i>	3-18
<b>4 Genetic decline detected in small disjunct populations of <i>Eucalyptus camaldulensis</i> Dehnh. subsp. <i>camaldulensis</i> (River Red Gum)</b>	<b>4-32</b>
4.1 <i>Abstract</i>	4-32
4.2 <i>Introduction</i>	4-32
4.3 <i>Methods</i>	4-35
4.3.1 <i>Study sites</i>	4-35
4.3.2 <i>Material collection and DNA extraction</i>	4-35
4.3.3 <i>Polymerase chain reaction</i>	4-36
4.3.4 <i>Microsatellite performance</i>	4-37

4.3.5	Genetic diversity and genetic structure	4-37
4.3.6	Temporal analysis	4-39
4.4	<i>Results</i>	4-40
4.4.1	Microsatellite performance	4-40
4.4.2	Genetic diversity and genetic structure	4-41
4.4.3	Temporal analyses	4-42
4.5	<i>Discussion</i>	4-43
4.5.1	Levels of genetic diversity	4-43
4.5.2	Distribution of microsatellite diversity	4-47
4.5.3	Conservation and management implications	4-48
4.6	<i>Conclusion</i>	4-50
<b>5</b>	<b>Population viability in episodic recruiters: exploring the correlation between genetic and non-genetic attributes of <i>Eucalyptus camaldulensis</i> Dehnh. <i>camaldulensis</i> (Myrtaceae) populations</b>	<b>5-61</b>
5.1	<i>Abstract</i>	5-61
5.2	<i>Introduction</i>	5-61
5.3	<i>Methods</i>	5-64
5.3.1	Site assessment	5-64
5.3.2	Material collection and DNA extraction	5-65
5.3.3	Polymerase chain reaction	5-66
5.3.4	Genetic parameters	5-66
5.3.5	Statistical analysis	5-66
5.4	<i>Results</i>	5-67
5.4.1	Site assessment	5-67
5.4.2	Correlation analysis between genetic parameters	5-68
5.4.3	Correlations analyses between non-genetic parameters	5-68
5.4.4	Correlations analyses between genetic and non-genetic factors	5-68
5.5	<i>Discussion</i>	5-69
5.5.1	Correlation analysis	5-69
5.5.2	Uncorrelated variables	5-72
5.5.3	Conservation and management implications	5-72
5.6	<i>Conclusion</i>	5-73
<b>6</b>	<b>Habitat type promotes variable genetic structure in a water dependant tree, <i>Eucalyptus camaldulensis</i> Dehnh. subsp. <i>camaldulensis</i> (River Red Gum).</b>	<b>6-80</b>
6.1	<i>Abstract</i>	6-80
6.2	<i>Introduction</i>	6-80

6.3	<i>Methods</i>	6-82
6.3.1	Genetic structure sampling	6-82
6.3.2	Seed sampling	6-83
6.3.3	DNA extraction and polymerase chain reaction	6-84
6.3.3.1	Spatial autocorrelation	6-84
6.3.4	Neighbourhood & population genetic similarity	6-85
6.3.5	Levels of genetic diversity	6-85
6.4	<i>Results</i>	6-86
6.4.1.1	Neighbourhood scale	6-86
6.4.1.2	Population scale	6-86
6.4.1.3	Combined population and neighbourhood scale spatial autocorrelation analysis	6-86
6.4.2	Neighbourhood & population genetic similarity	6-87
6.4.3	Hierarchical statistics	6-87
6.5	<i>Discussion</i>	6-87
6.5.1	Neighbourhood level genetic diversity and genetic structure	6-87
6.5.2	Population genetic structure	6-89
6.5.3	Population and neighbourhood scale genetic structure	6-90
6.5.4	Spatial genetic structure and genetic diversity	6-91
6.5.5	Inbreeding coefficient	6-91
6.6	<i>Conclusion</i>	6-92
<b>7</b>	<b>Heterozygosity associated with superior growth traits in <i>Eucalyptus camaldulensis</i> Dehnh. subsp. <i>camaldulensis</i> (River Red Gum): an evaluation of open pollinated seeds</b>	<b>7-100</b>
7.1	<i>Abstract</i>	7-100
7.2	<i>Introduction</i>	7-100
7.3	<i>Methods</i>	7-103
7.3.1	Sampling	7-103
7.3.2	Tree, capsules and seed measurements	7-103
7.3.2.1	Capsules	7-103
7.3.2.2	Individual seed and seedling measurements	7-104
7.3.2.3	Offspring fitness of individual parent trees	7-104
7.3.3	Material collection and DNA extraction	7-105
7.3.4	Polymerase Chain Reaction	7-105
7.3.5	Estimation of individual and family outcrossing rates and genetic variability	7-106
7.3.6	Fitness and genotype interaction	7-107



7.3.6.1	Individuals	7-107
7.3.6.2	Parent trees	7-107
7.4	<i>Results</i>	7-108
7.4.1	Individual level analyses	7-108
7.4.2	Parent tree analyses	7-109
7.4.3	Population level analyses	7-110
7.5	<i>Discussion</i>	7-110
7.5.1	Heterozygosity-fitness correlations	7-111
7.5.2	Individual outcrossing rates	7-112
7.5.3	Population outcrossing rates	7-113
7.5.4	Selective seed abortion	7-114
7.5.5	Growth and seed traits	7-114
7.6	<i>Conclusion</i>	7-115
<b>8</b>	<b>Discussion and Conclusions</b>	<b>8-122</b>
8.1	<i>Introduction</i>	8-122
8.2	<i>Are remnant populations of Eucalyptus camaldulensis genetically impoverished?</i>	8-123
8.3	<i>Is a lack of genetic variability a possible cause of recruitment failure?</i>	8-127
8.4	<i>What impact does habitat and environmental factors have on remnants and how does this relate to remnant genetic diversity and structure?</i>	8-129
	<b>References cited</b>	<b>136</b>
	<b>Appendix 1.</b>	<b>151</b>
	<b>Appendix 2.</b>	<b>152</b>
	<b>Appendix 3.</b>	<b>153</b>
	<b>Appendix 4.</b>	<b>154</b>
	<b>Appendix 5.</b>	<b>156</b>
	<b>Appendix 6.</b>	<b>163</b>

## List of Figures

Figure 1. Chapter overview	1-6
Figure 2. <i>Eucalyptus camaldulensis</i> understory ( <i>Silybum marianum</i> ) in the floodplain component of the Lemington site, October 2007	3-22
Figure 3. The landscape context of remnant <i>Eucalyptus camaldulensis</i> sites: Lemington coal mine and agriculture.	3-22
Figure 4. <i>Eucalyptus camaldulensis</i> remnants in the Hunter Valley, NSW. Black circles denote study sites. White circles are known remnant populations that were not included in this research.	3-23
Figure 5. Looking upstream (east) from Redbournberry site (July 1906) showing degraded river margin and the extent of land clearing. Reproduced with permission, State Library NSW (accessed via trove: <a href="http://trove.nla.gov.au">http://trove.nla.gov.au</a> )	3-25
Figure 6. A large tree (dbh > 200 cm) at Redbournberry site taken in 2010 surrounded by a number of younger trees, <i>Casuarina cunninghamiana</i> and an understory of exotic weeds, October 2007	3-26
Figure 7. Redbournberry site, July 1906, showing evidence of sapping and the denuded and degraded river bank.	3-27
Figure 8. An early photograph (early 1900s) taken near Muswellbrook in the centre of the study range displaying minimal riparian vegetation	3-28
Figure 9. Remnant population at the Denman site showing mature trees growing along the margin of a permanent lagoon, August 2010	3-29
Figure 10. Historical references to gum trees in riparian habitat in the Hunter Valley	3-30
Figure 11. The history of floods recorded at Muswellbrook	3-31
Figure 12. <i>Eucalyptus camaldulensis</i> study sites in the Hunter Valley, NSW, Australia	4-51
Figure 13. Percentages of detected allelic variability present in combinations of <i>Eucalyptus camaldulensis</i> remnants in the Hunter Valley	4-55
Figure 14. Graphical representation of cluster assignment for K=7. Each bar represents an individual <i>Eucalyptus camaldulensis</i> tree and each colour denotes an inferred cluster. Individual trees are grouped by population	4-56
Figure 15. The correlation between the level of differentiation (Dest) between remnant <i>Eucalyptus camaldulensis</i> populations and geographic distance	

- (GGD = geographic distance in meters) via the Mantel test.  $p$  = significance of correlation based on 999 permutations. 4-60
- Figure 16. The location of remnant *Eucalyptus camaldulensis* sites studied in the Hunter Valley catchment 5-75
- Figure 17. Variable age-class structure in *Eucalyptus camaldulensis* remnant populations estimated by diameter at breast height (dbh cm) classes 5-76
- Figure 18. Correlation (Pearson's  $r$ ) between the edge to area ratio and structural characteristics (age-class distribution, density) measured in nine remnant populations of *Eucalyptus camaldulensis* 5-77
- Figure 19. Correlation (Pearson's  $r$ ) between genetic and non-genetic parameters in remnant populations of *Eucalyptus camaldulensis* 5-78
- Figure 20. Maps of neighbourhood and population scale sampling units in four remnant populations of *Eucalyptus camaldulensis*: a) Camry Allyn, b) Sandy Hollow, c) Bylong, and d) Lemington. Dark areas depict the river and enclosed areas are the mapped individuals in the neighbourhood scale sampling units 6-94
- Figure 21. Principal co-ordinate analysis of genetic proximity of population scale samples and neighbourhood scale samples in four remnant populations of *Eucalyptus camaldulensis* 6-98
- Figure 22. Decreasing correlation (Pearson's  $r$ ) of re-sampled attributes in *Eucalyptus camaldulensis* seedlings (leaf number and leaf length) at 2, 4, 6, 8, 10, 12, and 14 weeks 7-118
- Figure 23. The mean weight of seeds (mg) per capsule collected from eight *Eucalyptus camaldulensis* trees plotted against the mean number of seeds germinated (n seeds) per capsule 7-118
- Figure 24. The mean weight of seeds (mg) per capsule collected from eight *Eucalyptus camaldulensis* trees plotted against percentage of seeds germinated (% germinated) per capsule 7-119
- Figure 25. Correlation (Pearson's  $r$ ) between the proportion of heterozygous loci and seedling height in progeny from an individual *Eucalyptus camaldulensis* tree (DRT2) with individuals designated as selfed ( $t_m < 1$ ) outcrossed ( $t_m \geq 1$ ) 7-119
- Figure 26. Pairwise assessment of the percentage of shared alleles (middle row) and those unique (above and below) to each *Eucalyptus camaldulensis* remnant 153

## List of Tables

- Table 1. Genetic diversity parameters for *Eucalyptus* species. np = number of primers or probes, n pops = the number of populations,  $H_T$  = total heterozygosity across all populations,  $H_e$  = mean heterozygosity within population,  $F$  = the mean inbreeding coefficient within populations.  $F_{ST}$ ,  $G_{ST}$ ,  $R_{ST}$  and  $Q_{ST}$  are alternate measures of genetic differentiation 2-15
- Table 2. Attributes of studied remnant populations of *Eucalyptus camaldulensis*, population size = the number of individual plants (all plants with a diameter at breast height (cm) >2.5) 3-24
- Table 3. Microsatellite performance; all loci were 100% polymorphic 4-52
- Table 4 Genetic parameters for 13 remnant populations of *Eucalyptus camaldulensis* in the Hunter Valley catchment area 4-53
- Table 5. Genetic differentiation ( $D_{ST}$ ) between remnant *Eucalyptus camaldulensis* stands in the Hunter Valley calculated following Jost (2008) 4-54
- Table 6. Genetic diversity and allelic richness measures of *Eucalyptus camaldulensis* trees in the Hunter Valley. Trees were pooled from 13 populations and placed in dbh cohorts. Diversity measures were averaged over nine loci. Rarefied parameters were determined by the lowest sample size (n=30) in each group. 4-57
- Table 7. Significant p values calculated from the binomial distribution n=9 (loci) for the probability (p=0.5) of increased genetic diversity (a)  $I$  = Sannon's Diversity Index, b)  $AR$  = allelic richness and c)  $PAR$  = private allelic richness) between *Eucalyptus camaldulensis* trees grouped by dbh (cm) pooled from 13 populations across the Hunter Valley 4-58
- Table 8. A comparison of genetic diversity between *Eucalyptus camaldulensis* trees grouped by diameter at breast height in recently fragmented populations in the Hunter Valley 4-59
- Table 9. Pearson's correlation ( $r$ ) (below diagonal) and p values (above diagonal) for genetic, geographic and stand structure parameters in *Eucalyptus camaldulensis* remnants. Genetic diversity was correlated with edge to area ratio, density and nearest neighbour distance. 5-79
- Table 10. The mean pairwise kinship coefficient (Loiselle et al. 1995) and standard error (SE) within eight distance classes in riparian and floodplain recruitment neighbourhoods ( $N_f$  = floodplain,  $N_r$  = riparian) within remnant populations

(CA = Camyr Allyn, L = Lemington, B = Bylong and SH = Sandy Hollow) of <i>Eucalyptus camaldulensis</i> in the Hunter Valley	6-95
Table 11. The mean pairwise kinship coefficient (Loiselle et al. 1995) and standard error (SE) within five distance classes at the population scale (P) in remnant populations (CA = Camyr Allyn, L = Lemington, B = Bylong and SH = Sandy Hollow) of <i>Eucalyptus camaldulensis</i> in the Hunter Valley	6-96
Table 12. The mean pairwise kinship coefficient (Loiselle et al. 1995) and standard error (SE) within distance classes in remnant populations (CA = Camyr Allyn, L = Lemington, B = Bylong and SH = Sandy Hollow) of <i>Eucalyptus camaldulensis</i> in which recruitment neighbourhoods in floodplain (Nf) and riparian habitat (Nr) have been analysed in conjunction with population scale samples (P)	6-97
Table 13. Genetic diversity measures calculated from four microsatellite primers in four populations	6-99
Table 14. Correlation analysis (Pearson's r) between seedling traits (pooled from 8 <i>Eucalyptus camaldulensis</i> trees) and the proportion of heterozygous loci, and between seedling traits (pooled from 8 <i>Eucalyptus camaldulensis</i> trees) and the individual outcrossing rate (tm)	7-116
Table 15. Correlation (Pearson's r) between seedling traits and the proportion of heterozygous loci, and between seedling traits and the individual outcrossing rate (Ritland 2002) calculated from seedlings sourced from a single adult <i>Eucalyptus camaldulensis</i> tree in the Dartbrook remnant (DRT2)	7-117
Table 16. Genetic parameters calculated from progeny arrays sourced from adult <i>Eucalyptus camaldulensis</i> trees (CAA, CAB, CAC, DEN1, DEN2, DEN3 DRT1 and DRT2) from three populations: Camyr Allyn (CA), Denman (DEN) and Dartbrook (DRT)	7-118
Table 17. Single and multi-locus mating system estimates for three populations of <i>Eucalyptus camaldulensis</i> populations based on seed sourced from individual trees from Dartbrook (2 trees), Denman (3 trees) and Camyr Allyn (3 trees)	7-120
Table 18. Significant differences between mean growth traits of progeny from parent trees (CAA, CAB, CAC, DEN1, DEN2, DEN3, DRT1, DRT2) of <i>Eucalyptus camaldulensis</i>	7-121
Table 19. Embra (Brondani et al. 2006) and Eg (Benson 1991) primers: annealing temperatures, sequences, fragment size range (base pairs) and the chapter which primers were used	151
Table 20. Polymerase Chain Reaction protocol (see Table 19 for annealing temperatures)	152

Table 21. Correlation (Pearson's $r$ ) between seedling traits and heterozygosity within outcrossed ( $t_m \geq 1$ ) progeny of <i>E. camaldulensis</i> pooled from eight parent trees	154
Table 22. Correlation (Pearson's $r$ ) between seedling traits and heterozygosity within selfed ( $t_m < 1$ ) progeny of <i>E. camaldulensis</i> pooled from eight parent trees	155
Table 23. Correlation (Pearson's $r$ ) between <i>Eucalyptus camaldulensis</i> seedling traits and genotype (heterozygosity, outcrossing rate) from seedlings sourced from the same parent tree (CAA)	156
Table 24. Correlation (Pearson's $r$ ) between <i>Eucalyptus camaldulensis</i> seedling traits and genotype (heterozygosity, outcrossing rate) from seedlings sourced from the same parent tree (CAB)	157
Table 25. Correlation (Pearson's $r$ ) between <i>Eucalyptus camaldulensis</i> seedling traits and genotype (heterozygosity, outcrossing rate) from seedlings sourced from the same parent tree (CAC)	158
Table 26. Correlation (Pearson's $r$ ) between <i>Eucalyptus camaldulensis</i> seedling traits and genotype (heterozygosity, outcrossing rate) from seedlings sourced from the same parent tree (DEN1)	159
Table 27. Correlation (Pearson's $r$ ) between <i>Eucalyptus camaldulensis</i> seedling traits and genotype (heterozygosity, outcrossing rate) from seedlings sourced from the same parent tree (DEN2)	160
Table 28. Correlation (Pearson's $r$ ) between seedling <i>Eucalyptus camaldulensis</i> traits and genotype (heterozygosity, outcrossing rate) from seedlings sourced from the same parent tree (DEN3)	161
Table 29. Correlation (Pearson's $r$ ) between <i>Eucalyptus camaldulensis</i> seedling traits and genotype (heterozygosity, outcrossing rate) from seedlings sourced from the same parent tree (DRT1)	162
Table 30. Correlation (Pearson's $r$ ) between mean seed and seedling traits of progeny sourced from eight parent trees ( $n = 8$ )	163