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

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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 declivities 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 (Dest = 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.

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