

# FRAGMENTATION AND THE EFFECTS OF POPULATION SIZE ON GENETIC DIVERSITY AND SEED SET IN *EREMAEA PAUCIFLORA* (MYRTACEAE)

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## INTRODUCTION

Land clearing for agriculture in the Western Australian wheatbelt has resulted in numerous fragmented and isolated vegetation remnants. *Eremaea pauciflora* is an insect pollinated, long-lived woody shrub. Prior to land clearing it was widespread and common in heath forming large populations (Fig. 1a). In the current landscape it occurs both as large populations in nature reserves and as small road verge populations (Fig. 1b). These small populations may be subject to increased risk of extinction.

This study investigates the genetic and ecological factors that influence the viability of *E. pauciflora* populations in these remnants.



Fig.1: *E. pauciflora* in a large undisturbed remnant (a), and a highly disturbed road-verge remnant (b).

## MATERIALS AND METHODS

Genetic diversity and seed set were measured in 19 populations with contrasting levels of isolation and ranging in size from 13 to ca.70,000 plants (Fig.3). Seed set was estimated for 10 fruit from 20 plants in 19 populations. Twelve polymorphic allozyme loci were assayed. Linear regression was used to assess the relationship between seed set, genetic diversity parameters and population size.



Fig.2: *E. pauciflora*; flowers Sept – Dec.

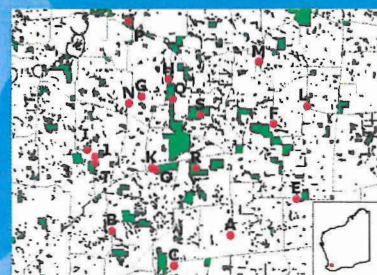


Fig.3: Geographical distribution of study sites within the Dongolocking region in Western Australia.

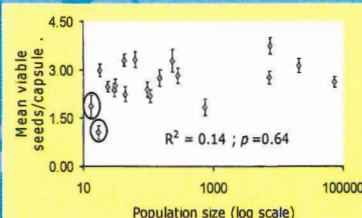


Fig.4: Relationship between viable seed set and population size.

## RESULTS

Although the two smallest populations (circled, Fig. 4) had the lowest viable seed set, overall there was no significant correlation between seed set and population size (Fig.4). Genetic diversity based on mean number of alleles per locus ( $A$ ), gene diversity ( $H_e$ ) and number of rare alleles per population showed no relationship with population size (Fig 5). Similarly, there was no significant correlation between the inbreeding coefficient ( $F_{IS}$ ) and population size (Fig. 6). The mean genetic distance (Nei's  $D$ ) and  $F_{ST}$  were low, and the UPGMA analysis showed no population structure based on geographical relationships between populations.

## DISCUSSION

Despite the large range in population size there were no observed trends with genetic diversity ( $A$ ,  $H_e$  and rare alleles) or fecundity (seed set). Seed set was not associated with the level of habitat disturbance within populations based on comparisons between linear (road verge) and non-linear (reserve) remnants. These results indicate that the reproductive biology of *E. pauciflora* may be resilient to the effects of fragmentation.

Mating system variation, seedling progeny fitness and patterns of gene flow are currently under investigation.

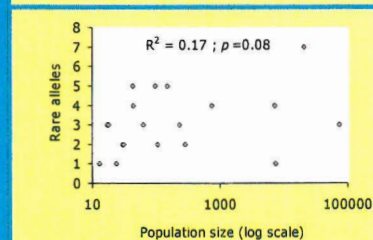
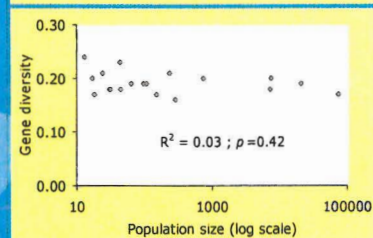
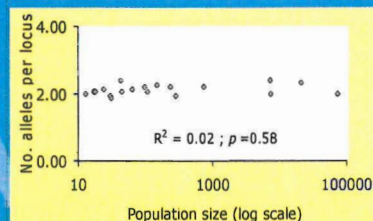


Fig. 5. Relationship between genetic diversity (mean number of alleles per locus, gene diversity, number of rare alleles) and population size

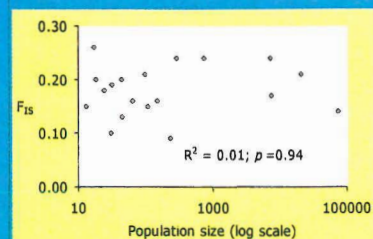


Fig.6: Relationship between  $F_{IS}$  (indirect estimates) and population size.