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Molecular ecological analysis of vegetation function in fragmented Australian biomes

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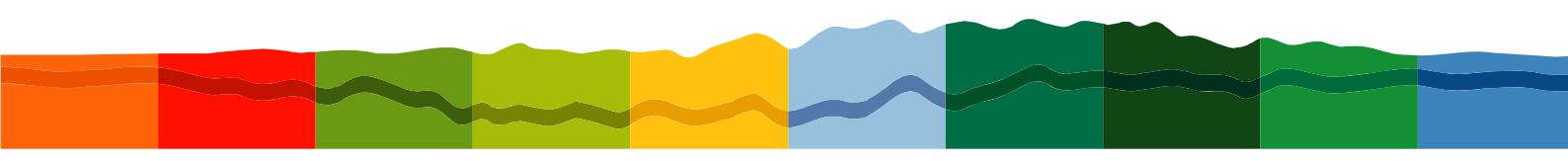

EXECUTIVE SUMMARY

1. The aims of this project were to quantify the strength and scale of reproductive interactions among native plant populations occupying remnant vegetation patches in fragmented cropping landscapes in New South Wales and Western Australia, assess their demographic significance in terms of progeny fitness and population viability and from this develop models of inter-patch interactions in relation to landscape configuration.

2. Reproductive function and interpopulation interactions were measured for two bird-pollinated plant species *Eremophila glabra* and *Banksia sphaerocarpa* in remnant native vegetation patches within intensively cropped agricultural landscapes in NSW and WA respectively, using a combination of molecular ecological analysis of pollen movement and mating, field-based assessment of reproductive output and glasshouse growth trials to measure seedling fitness.

3. In both study systems species exhibited significant reproductive dependence on interpopulation mating events with between 26-62% of all genotyped *Eremophila glabra* seed and 15-33% of *Banksia sphaerocarpa* seed resulting from interpopulation reproductive events. In *E. glabra* these events could be shown to be regularly taking place over scales of 5-10km. This is considerably greater than has been previously observed for any plant population system.

4. While interpopulation interactions for *Eremophila glabra* are common and likely to be demographically important, they are also spatially unpredictable with little evidence of spatial restrictions in matings across the observed 400km^2 landscape, though there was significant variation in the relative contribution of different populations to overall landscape mating events. There was some evidence of reduced gene flow into small populations of *Banksia sphaerocarpa,* which were isolated.

5. This significant role for interpopulation interactions was supported by the strong reproductive performance of populations in both landscapes in terms of fruit and seed production, regardless of population size or location.

6. Apart from making up a significant proportion of all inter-plant matings in both species, interpopulation fertilisation conferred no specific additional fitness advantage in *Eremophila glabra* with seedlings resulting from within-population and between-population mating showing no obvious differences in germination, growth or flowering. The lower overall fitness of *Banksia sphaerocarpa* seedlings from small populations that exhibited lower levels of inter-population mating than large populations with higher inter-population mating suggests that for this species, between population matings may result in fitter progeny.

7. Results suggest a stronger than expected reproductive functionality for populations of *Eremophila glabra* and *Banksia sphaerocarpa* occupying fragmented high intensity cropping landscapes, probably due to high levels of interpopulation interaction.

8. Management of high intensity cropping landscapes should take account of the need to maintain local remnant vegetation patches that show surprising reproductive resilience to spatial isolation over scales of several kilometres and therefore represent a significant opportunity to conserve on-farm biodiversity. The substantial amount of long distance mating interactions observed for the bird pollinated species studied here suggests that management needs to be coordinated among populations over scales of hundreds of square kilometres to take account of current reproductive dynamics.

1. PROJECT OBJECTIVES:

Remnant vegetation patches are critical elements of agricultural landscapes that perform a range of important ecological and hydrological services. However, vegetation fragmentation and current patterns of land degradation are imposing genetic and demographic constraints that threaten the long-term persistence of many remnant populations (Young *et al.*, 2005). Given the significant environmental capital that these remnants represent, it is vital to develop strategies that will maintain and enhance remnant function both within and among patches to ensure their long-term persistence within agricultural landscapes.

An important component of plant population dynamics is the movement of pollen and seed among populations. Indeed, one of the most important findings of the LWA CPI10 study is that gene flow among remnants is occurring across much broader scales than previously recognised (< 2km). This research also indicated that, while an understanding of the site-specific constraints to remnant population viability is important, the inter-connectedness of populations at the landscape level cannot be ignored and may be playing a crucial role in determining the demographic trajectories of these populations. However, currently almost nothing is known about the scale, intensity or temporal variation of gene flow among populations of native plants and how this is affected by landscape configuration.

Changes to the way genes move around landscapes may influence remnant populations in either a positive or negative manner. Novel genes moving into small and isolated populations may rescue these from the negative effects of genetic erosion and elevated inbreeding whereas this movement into locally adapted population may be disastrous if outbreeding depression results. A further negative effect highlighted by the Land & Water Australia CPI10 research, is that some remnants are experiencing elevated inter-specific gene flow such that up to 40% of progeny can be of hybrid origin (Young *et al.*, 2005). These factors are all likely to play an important role in determining the utility of patch populations either as foci for *in situ* conservation or, increasingly important, as a source of seed for revegetation activities.

The aim of this project is to use molecular ecological techniques and population models to develop an explicit understanding of the importance of gene flow and seed dispersal *among* populations for determining local species persistence, and how this is affected by landscape configuration. This project specifically builds on the findings of CPI10 regarding the effects of habitat fragmentation on the viability of single plant populations by extending the analysis to the development of more realistic multi-population remnant vegetation management models.

Specific objectives are to:

1. Quantify the strength, scale and temporal variation of gene flow through pollen and seed movement among vegetation patches in fragmented landscapes in south-east New South Wales and south-west Western Australia.
2. Determine the significance of gene flow for seed production, progeny fitness and population viability.
3. Produce spatially explicit models to describe current patterns of inter-patch gene flow in relation to landscape configuration. Develop "landscape leverage" analysis to quantify the influence of different patch populations on local ecological and genetic dynamics and use "landscape leverage" maps to predict effects of landscape changes (habitat loss, altered configuration, revegetation) on species persistence.
4. Develop guidelines to: a) maximise long-term plant population viability through coordinated management of multiple populations within landscapes at biologically appropriate scales and; b) improve revegetation success through the strategic placement of vegetation into the landscape that will maximise gene flow and population viability.

2. METHODS

2.1 Biomes

This research was conducted in two biomes - the Mallee woodlands of central western New South Wales and the Kwongan heathlands and shrublands of the Dongolocking region of south-west Western Australia (Fig. 1). Both of these ecosystems have been subjected to severe habitat loss and disturbance since European settlement, and the remaining native vegetation now exhibits a range of extent and condition types. These two biomes represent highly fragmented landscapes, with remnant vegetation physically isolated by intervening intensive cropping and grazing land use (Fig. 1c and 1f).

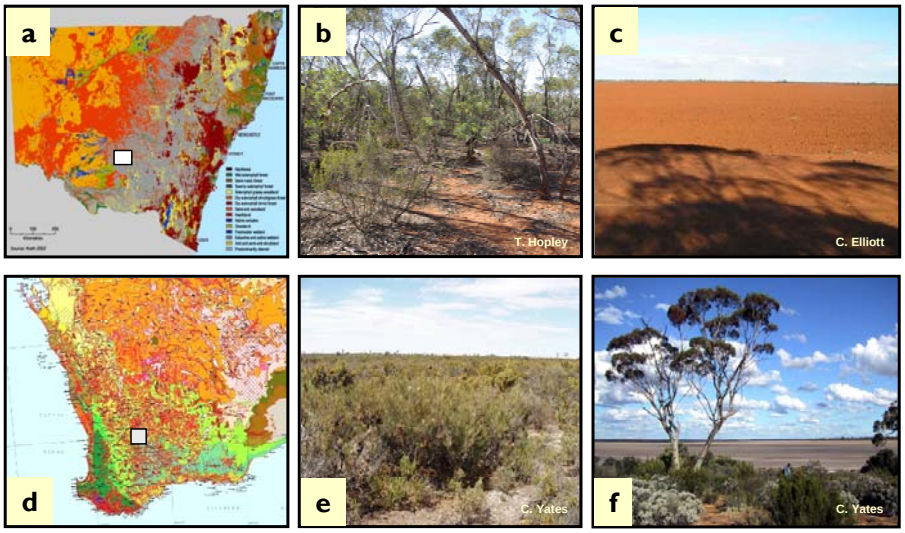

Figure 1: Location of study biomes – Mallee woodlands of NSW (a), typical Mallee woodland (b), typical fragmentation of Mallee woodland remnants (c), Kwongan shrublands of Western Australia (d), typical Kwongan shrublands (e), and typical fragmentation of Kwongan shrublands remnants (f).

2.2 Target taxa

Similar taxa were chosen for study within each biome with both being common and widespread, long-lived and primarily bird-pollinated shrubs. *Eremophila glabra* ssp. *glabra* (R.Br. (Ostenf.)) (Myoporaceae) was chosen in the western Mallee while *Banksia sphaerocarpa* var. *caesia* A.S. George (Proteaceae) was chosen in the Kwongan (Fig. 2). These life history traits were chosen as they were expected to be characteristic of species that would exhibit a reproductive response to changes in landscape structure due to their reliance on birds for pollination.

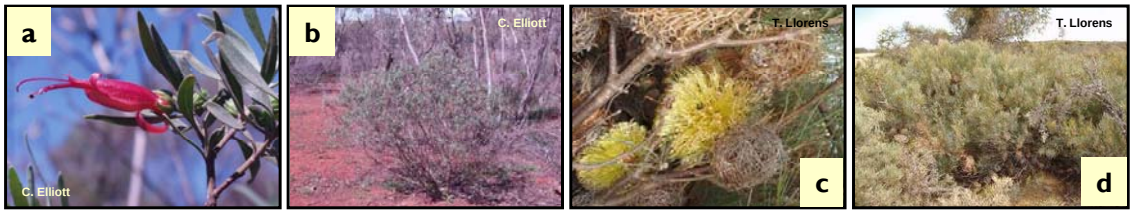

Figure 2: Target taxa - *Eremophila glabra* ssp. *glabra* (a and b) and *Banksia sphaerocarpa* var. *caesia* (c and d).

2.3 Landscape and population parameters and sampling

Reference landscape grids were delineated in each biome and intensively surveyed to locate all target taxa populations (Fig. 3). In New South Wales, one 20 x 20 km grid was used for reproductive and genetic analysis within which 15 remnants containing *Eremophila glabra* were identified; four of these remnants were chosen as focal populations to investigate gene flow and fitness parameters. Three additional replicate 20 x 20 km grids were used for collection of reproductive data from nine additional populations providing replicates of the three of the four focal populations in the first grid. Population classes included: 1) Interior (centre of large habitat patches); 2) Near (fragmented populations 3km from a large patch) and; 3) Far (fragmented populations 5km from large patch). A single 10 x 20 km grid was delineated in WA and 12 *Banksia sphaerocarpa* populations (four large and eight small) were selected for study, of which nine were chosen as focal sites for genetic and reproductive measurements. Populations were assessed for size, density and reproductive status (flowering) and isolation distance from other populations in the grids. Between 2005 and 2008 at each site leaf material was collected from 30-60 adult plants for genotyping. Within the focal populations

seed was also collected from 10-12 plants for growth trials and assessment of gene flow. Drought conditions during the study period limited our ability to undertake the temporal re-sampling of populations for seed material which was only available in quantity for NSW in 2005-06 and for Western Australia in 2006-07.

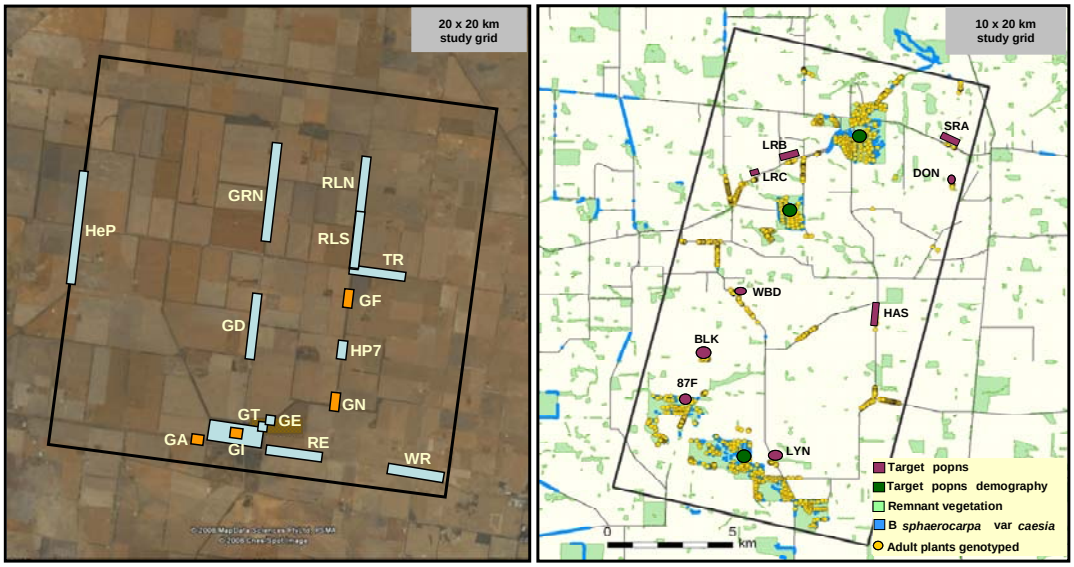

Figure 3: Study grids and populations for *Eremophila glabra* (left) and *Banksia sphaerocarpa* (right). Orange remnants on *Eremophila glabra* grid indicate focal populations.

2.4 Reproductive ecology

Ecological and fitness characteristics were estimated for each of the 96 maternal plants across the 12 study populations (four interior, four near, four far) in the four replicated landscapes for *Eremophila glabra* and for each of the 120 maternal plants across the 12 target populations (eight large and four small) for *Banksia sphaerocarpa*. Measurements of plant size, inflorescence and fruit production and seed set were made for each population.

2.5 Molecular ecological assessment of gene flow by seed and pollen

Leaves were genotyped from all sampled adults using co-dominant SSR markers developed and designed for each of the target species (Elliott, 2009; Nistelberger *et al.*, 2009) and the data used to generate gene frequency estimates for each population sampled within the grids. Seed grown in the fitness trials (see section 2.6 below), along with additionally germinated seed, were similarly genotyped and then subjected to paternity analysis to determine whether the pollen was derived from: 1) self-fertilisation; 2) outcrossed fertilisation from within the focal population or; 3) outcrossed fertilisation from a population external to the focal population. In this third case, for *Eremophila glabra*, genetic assignment testing was used to identify the most likely source of the immigrant pollen that gave rise to the seed. Due to the hexaploid nature of *Eremophila glabra* specific software was developed to undertake the assignment analysis. For *Banksia sphaerocarpa* the pattern of within-population pollen movement was explored by comparing the average distances over which successful pollen travelled between maternal and paternal plants and this was compared among populations. Relationships between pollen origin (selfed, outcrossed within-population or outcrossed external) and seedling fitness were explored using ANOVA.

2.6 Demographic significance of gene flow

For *Eremophila glabra,* 24 seeds from each of 10-12 plants collected from three of the focal populations in the four replicated landscapes representing three levels of isolation (interior, near, far) were sown under glasshouse conditions in a split-split-plot design and assessed for germination daily for 120 days. Up to ten of these germinants from each mother plant from each focal population were grown on for 12 months and assessed for i). vegetative fitness including: seedling height, width,

perpendicular width, number of branches, and ii). reproductive fitness as measured by: number of flowers and fruit produced and final survivorship. Fitness was then compared between population treatments and also seedling mating status (i.e. selfed, within-population outcross, between-population outcross).
For *Banksia sphaerocarpa* 20 seedlings for each plant from each focal population were grown under glasshouse conditions for 11 months in a nested design and fitness was measured as final seedling survival, height and weight. Nested ANOVA models were used to test for relationships between population size and each ecological and fitness characteristic measured.

2.7 Population genetic diversity and structure - *Banksia*

All non-target populations of *Banksia sphaerocarpa* within the Western Australia grid were genotyped for up to 40 plants as previously outlined and used to generate measures of genetic diversity, inbreeding and genetic structure which was estimated at both a broad scale among populations across the study landscape as well as at a localized scale among plants within populations.

3. RESULTS

3.1 Reproductive ecology

Neither of the two species in the different biomes showed strong effects of population size (*Banksia sphaerocarpa*) or isolation (*Eremophila glabra*) on overall reproductive output as measured by flowering effort, or seed set per fruit/cone. *Eremophila glabra* did show an overall reduction in fruit set in more isolated sites (Table 1). For all parameters measured there was significant variation between populations within treatments for both species. The variation in fitness measures was particularly evident in small populations of *Banksia sphaerocarpa* where some consistently showed values matching the large populations.

Table 1. Reproductive output of *Eremophila glabra* and *Banksia sphaerocarpa*

Trait	***Eremophila glabra***			***p***	***Banksia sphaerocarpa***		***p***
Site	**Interior**	**Near**	**Far**		**Large**	**Small**	
Flowers	21.76 (1.21)	20.72 (1.38)	24.27 (1.37)	ns	10.64 (1.04)	8.97 (0.67)	ns
Fruits or cones	10.4 (0.44)	5.31 (0.62)	6.73 (0.93)	<0.05	6.10 (0.62)	5.16 (0.42)	ns
Seeds per fruit	1.185 (0.04)	1.026 (0.03)	1.09 (0.03)	ns	0.95* (0.03)	0.78* (0.07)	<0.05

*proportion not count, (SE), ns = non significant

3.2 Gene flow

No seedling recruitment was observed in any *Eremophila glabra* or *Banksia sphaerocarpa* populations during the study period, limiting analysis to gene flow via pollen movement only. Neither species showed significant levels of self-pollination though this was slightly higher in *Banksia sphaerocarpa* than *Eremophila glabra*. The proportion of pollen from sources external to the focal populations was significant but varied both between the two study species as well as among populations within species for the two biomes. External pollen accounted for between 26-61% of the seed produced in *Eremophila glabra* (Fig. 4 left) but only 15-33% for *Banksia sphaerocarpa* (Fig. 4 right). The four small focal populations of *Banksia sphaerocarpa* showed lower (6.2-15.4%) external gene flow than large ones but this is still biologically significant, especially given the isolated status of the sites.

Assignment of pollen source for each *Eremophila glabra* focal site also indicated large differences among them in the amount of external pollen they received (Fig. 5). For example, fewer seedlings from GA (44%) and GI (39%) were assigned to within-population pollen sources than seedlings from GN (75%) and GF (62%). When seed were sired from external pollen sources there was also variation in the relative contributions of pollen from different populations. For example population GT contributed 8% to GA, 12% to GI, 6% to GN but nothing to GF. Importantly, these data show that pollen is moving over large distances. At population GA pollen moving at least 10 km from remnant GRN contributes to 5% of the seed crop. Approximately 2.5% of the GF seed crop is

pollinated by remnant HeP which is approximately 15 km away and this remnant also contributes to approximately 1% of the seed crop in other focal sites.

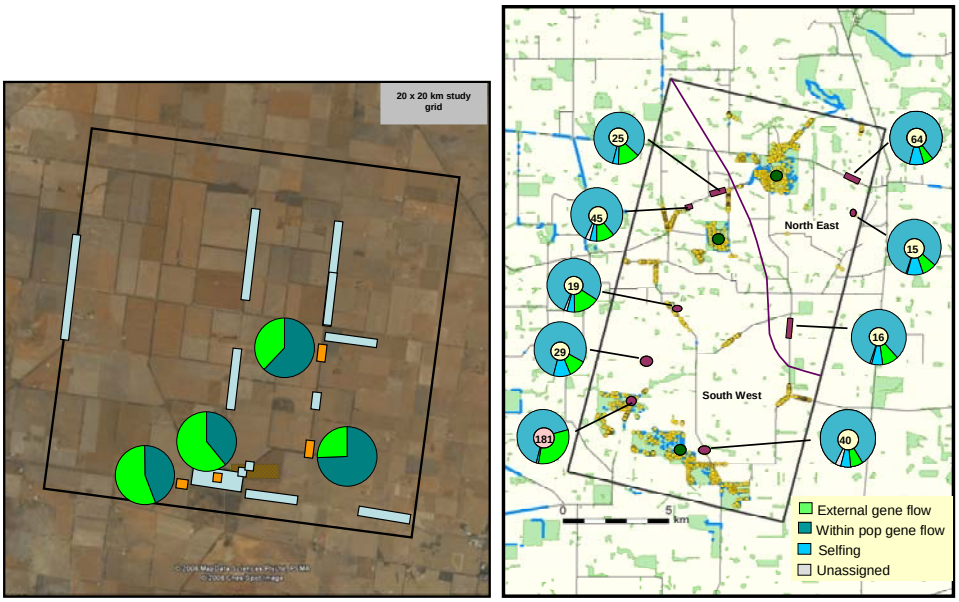

Figure 4. Proportion of seed crop pollinated by within and external pollen sources for *Eremophila glabra* (left), and proportion of seed crop resulting from self, within and external pollen sources for *Banksia sphaerocarpa* (right).

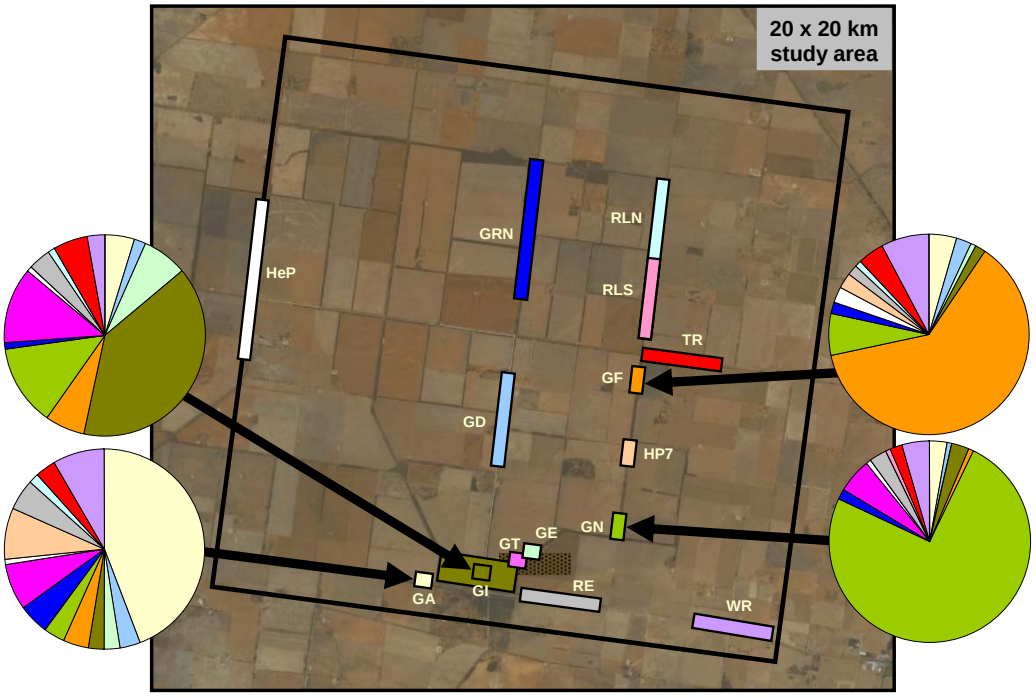

Figure 5. Proportion of *Eremophila glabra* seedlings assigned to potential pollen sources within the grid. Pie chart colours correspond with remnants colours on grid.

There was also unequal contribution of *Eremophila glabra* populations to the total seed crop with approximately 40% of the crop being pollinated by only three remnants (GT, WR and GN) (Fig. 6). At

the other end of the scale, a further five remnants (GD, GI, HeP, RLN and RLS) each contributed to <5% of the total seed crop assessed.

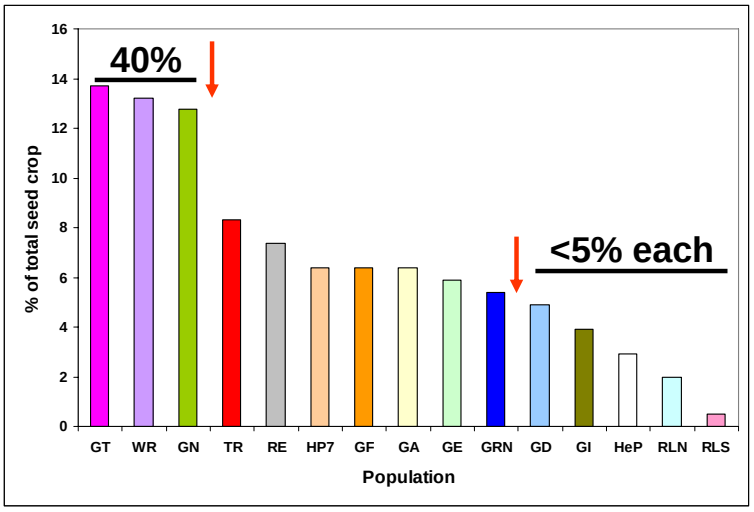

Figure 6. Total percentage of *Eremophila glabra* seed crop assigned to pollen sources within the grid. Population codes and colours correspond with populations in Fig. 5.

3.3 Demographic significance of gene flow

Seedlings from small populations of *Banksia sphaerocarpa* show reduced fitness in terms of poorer germination, shorter stature and showed a trend towards lighter plants (Table 2). Interestingly these are also the populations that exhibited reduced interpopulation mating. This was not evident for *Eremophila glabra* where seedlings grown from the three different population types (Interior, Near, Far) showed similar levels of fitness (though slightly reduced size). Nor was there any effect of pollen source on fitness, with *Eremophila glabra* seedlings produced as a result of outcrossing within populations growing just as well as those resulting from inter-population cross-pollinations. There was some evidence of lower fitness for the very small numbers of selfed *Eremophila glabra* individuals for growth variables.

Table 2. Seedling fitness for *Eremophila glabra* and *Banksia sphaerocarpa*

Trait	***Eremophila glabra***			***p***	***Banksia sphaerocarpa***		***p***
Site	**Interior**	**Near**	**Far**		**Large**	**Small**	
Germination	0.54 (0.02)	0.46 (0.02)	0.53 (0.02)	ns	.	.	
Size/height	23024*	20812*	19904 *	<0.001	38.57 (1.03)	36.30 (1.53)	<0.001
Flowers	11.40	14.10	15.83	ns	.	.	
Weight	.	.	.		5.84 (0.36)	5.19 (0.32)	<0.1

(SE) *volume in cm^3

3.4 Population genetic diversity and structure – *Banksia*

Genetic diversity and inbreeding measures for the nine focal sites indicate that more isolated remnants such as SRA, HAS and DON tend to have lower allelic richness (*A*) when adjusted for sample size as well as observed (H_O) and expected heterozygosity (H_E) (Table 3). Bottleneck analysis of all populations sampled in the grid (12 focal and 26 others) found no evidence of recent bottlenecks.

Table 3. Genetic diversity characteristics for nine *Banksia sphaerocarpa* var. *caesia*. focus populations using eight microsatellite loci.

Focal pop	Population size	N	*A*	*A*†	H_O	H_E	F_{IS}
BLK	29	29	12.75(2.17)	8.50(1.21)	0.68(0.08)	0.75(0.06)	0.12*(0.01)
DON	14	14	7.13(1.51)	6.56(1.34)	0.60(0.13)	0.60(0.12)	0.04 (0.01)
HAS	15	15	7.63(1.38)	6.81(1.13)	0.58(0.08)	0.66(0.09)	0.11*(0.01)
LRB	24	24	10.75(1.92)	7.97(1.07)	0.71(0.08)	0.76(0.05)	0.09*(0.01)
LRC	45	45	9.88(1.71)	6.46(0.99)	0.71(0.09)	0.70(0.07)	0.01 (0.01)
LYN	39	39	10.25(1.89)	7.13(1.07)	0.70(0.08)	0.70(0.08)	0.01*(0.01)
SRA	63	63	9.50(1.95)	5.66(0.86)	0.63(0.09)	0.66(0.09)	0.05*(0.01)
WBD	19	19	8.75(1.56)	7.06(1.16)	0.69(0.09)	0.67(0.08)	-0.01 (0.01)
87F	5000	181	17.00(2.20)	8.09(0.99)	0.72(0.05)	0.77(0.05)	0.04 (0.02)

N, number of individuals sampled; *A*, allelic richness; *A*† allelic richness adjusted for sample size using rarefaction; H_O, observed heterozygosity; H_E, expected heterozygosity; F_{IS}, Weir and Cockerham's fixation index. (SE).* $P<0.05$.

Broad landscape scale genetic structure was observed under principal coordinates analysis (Fig. 7) with populations being clearly divided into two geographical groups corresponding with those occurring in the north-east (blue) of the grid and those in the south-west (green). This pattern indicates a significant historical barrier to gene flow that may be associated with vegetation differences that are not apparent following fragmentation.

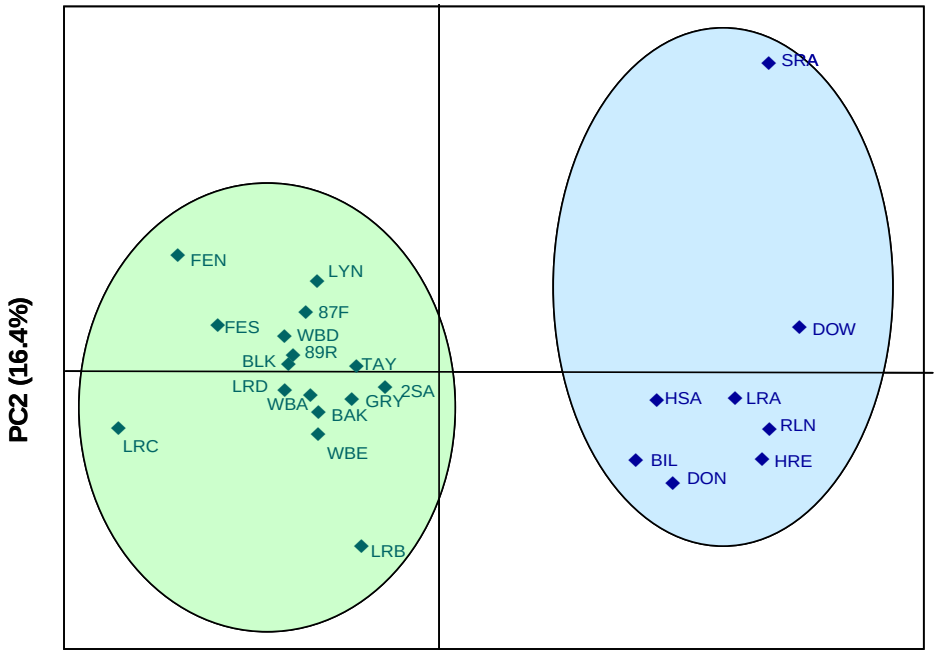

Figure 7. Principal Component Analysis of *Banksia sphaerocarpa* populations based on pairwise comparisons of Nei's genetic distance. Circles around populations indicate geographic boundaries and are not based on statistical analyses.

The correlation of kinship coefficients against distance within populations indicated the presence of significant fine scale genetic structure (Fig. 8) in three remnants (87F, LYN and HSA) and a strong trend within the other focus populations. This trend consistently showed a reduction in kinship with distance from the plant. It appears that population density may have an impact on the degree of fine

scale genetic structure. The pattern of fine scale genetic structure, that is the relationship between kinship coefficient and distance between plants, was comparable between the large population investigated (87F reserve) and the smaller, fragmented populations.

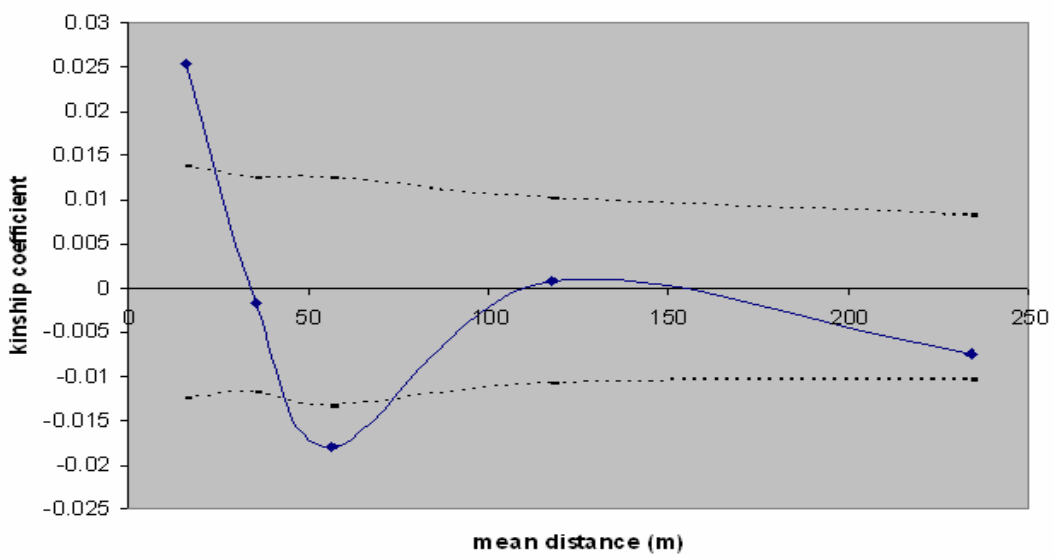

Figure 8. Correlogram for the focus population LYN (40 individuals) showing the average kinship coefficient (Loiselle *et al.*, 1995) per distance class plotted against the mean distance (m). 95% confidence intervals are shown.

Significant isolation by distance ($P<0.01$) was detected across the whole study grid and it was also detected in the south west group of populations ($P<0.01$), as defined in the PCA. It was not detected within the north-east populations. This indicates that in addition to the historical impediment to gene flow apparent between the north-west and south-east populations there has also been limited gene flow across the south-west populations and that limited landscape based gene flow was probably a characteristic of this species pre-fragmentation.

4. CONCLUSIONS

The study was undertaken during challenging environmental conditions with regard to the prevalence of drought and also required the development of new analytical software to cope with the polyploidy cytology of *Eremophila glabra*. Nevertheless, the results obtained represent the first dataset of its kind looking in detail at patterns of genetic variation, fitness and direct observation of interpopulation gene flow in response to habitat fragmentation across large (200-400km^2) landscapes in Australian biomes. As such, they provide significant insights into the functionality of fragmented remnant vegetation in high intensity cropping landscapes that have significant implications for biodiversity conservation planning and farm management.

Key objectives of this research were to: 1) Quantify the strength and scale of gene flow in fragmented plant communities; 2) Determine the demographic significance of this gene flow and; 3) Produce landscape models that describe inter-patch gene flow in relation to landscape configuration.

Overall results suggest that for both *Eremophila glabra* in the mallee woodlands of NSW and *Banksia sphaerocarpa* in the kwongon shrublands of Western Australia, inter-population gene flow by pollen is both numerically important and spatially extensive (though with some broad historical limitations in *Banksia sphaerocarpa*). Inter-population gene flow accounts for up to 26-61% of all observed *Eremophila glabra* mating events and 15-33% of all matings in *Banksia sphaerocarpa*. This represents a very significant contribution of interpopulation mating to overall reproductive dynamics in these two highly fragmented landscapes. The paternity analysis data from *Eremophila glabra* also showed that these mating events are commonly occurring between individuals in populations 5-10km apart. Taken

together, these results suggest significant ecological interdependency among *Eremophila glabra* populations right across the 400km^2 study landscape.

The demographic significance of the observed gene flow is in part a function of the large proportion of the mating events it makes up. Simply by contributing to up to half of the overall observed pollination events, inter-population matings are having a substantial impact on the reproductive dynamics of both the *Eremophila glabra* and *Banksia sphaerocarpa* population systems. Interestingly though, based on the seedling fitness data, they do not appear to make any extra contribution beyond this. *Eremophila glabra* seedlings grown from seeds produced by inter-population matings were no fitter in terms of growth or fecundity than those produced by matings within populations. In contrast for *Banksia sphaerocarpa*, there is some evidence that interpopulation matings may confer a compounding fitness advantage, as evidenced by higher overall fitness in large populations that experience higher interpopulation matings than seedlings from small populations that experienced lower gene flow.

The third key issue is the elucidation of the effect of landscape configuration and population parameters on the observed patterns of connectivity. Data to support this analysis are relatively sparse coming from the single fully mapped and genotyped *Eremophila glabra* landscape. The combination of the very large amounts of gene flow, the relatively large spatial scale of these events and the low variance in demographic and reproductive parameters among populations made quantitative analysis of relationships between population characteristics and landscape configuration and their relative contribution to overall mating dynamics difficult. Also, the additional resources indentified as being necessary to support this part of the project (see CPI13 Milestone Reports 1 & 2) were not available. As a result, no explicit GIS based modelling relating landscape structure to connectivity was undertaken. However several trends were clear: 1) Populations are highly variable in their contributions to overall mating dynamics within landscapes; 2) Patch size was not a good predictor of importance as a pollen source within the landscape; 3) Spatially proximity was not a good predictor of likelihood of mating interaction between populations.

Taken together the overall results of this study confirm and extend the results of the previous project CPI10 "Genetic and Ecological Viability of Plant Populations in Remnant Vegetation" showing that fragmented populations of plant species with highly vagile pollinators such as *Eremophila glabra* and *Banksia sphaerocarpa* can maintain significant reproductive function. Furthermore the data show that inter-population reproductive dynamics are critical to the maintenance of this function. While both species exhibit significant reliance on interpopulation dynamics, gene flow is more extensive in *Eremophila glabra* than *Banksia sphaerocarpa* but perhaps more important in terms of maintaining seedling fitness for *Banksia sphaerocarpa* than for *Eremophila glabra*.

These results strongly suggest that fragmented plant species must be managed for conservation at scales well beyond the individual population. More detailed assessment of the relationships between observed patterns of mating and landscape structure using these data sets could still prove informative with regard to developing explicit conservation strategies for these two species and for developing more landscape design guidelines for remnant vegetation. In particular, the identification of parameters that predict the relative importance of particular populations as pollen sources will be very useful in guiding landscape scale management for regional species persistence.

5. REFERENCES

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Appendix 1

6.1 Communications and achievements

Print (included in report)

- 2007: LWA Information brochure "Managing Genetic Diversity in Remnant Vegetation" (Technical Note 01/2007)
- 2007: Thinking Bush article "Genes ain't genes – genetic diversity affects remnant health"
- 2008: LWA Information brochure on using genetic tools in ecology – "CSI in the Bush" (Product code PN22012)
- 2009: CSIRO project information flyer – "Gene flow in fragmented landscapes"
- 2009: Thinking Bush article – "Tracking genes in fragmented landscapes"

Seminar

- 2008: Greening Australia vegetation workshop presentation – "Plant Genetics: Implications for Seed Production and Use"
- 2008: ANPC communications seminar – "Genetic Considerations for Seed Sourcing in Fragmented landscapes"
- 2008: Greening Australia Veg Futures Toowoomba presentation – "Provenance vs. seed quality – genetic issues in native seed sourcing for restoration and revegetation"
- 2009: Genetics Society of AustralAsia presentation "Gene flow among fragmented *Eremophila glabra* populations in the western mallee

Appendix 2

6.2 Scientific publications

- Nistelberger *et al.* (2009) **Molecular Ecology Resources**
- Elliott (2009) **Molecular Ecology Resource**