



Introduction

Habitat fragmentation, which reduces local population size and promotes isolation of remnant patches or population subdivision, may erode genetic diversity and increase population differentiation, affecting population viability in the short and long term (Young et al. 1996). These effects are due mainly to an increase in the level of inbreeding and genetic drift in forest fragments associated with small census sizes and reduced gene flow between fragments (Lande 1999). Fragmentation will promote local population differentiation if gene flow barriers are established allowing subpopulations to diverge due to genetic drift (Young et al. 1996).

Populations of long-lived woody perennials seem to be resilient to changes in genetic diversity due to long generation times. However, genetic losses may be more observable in seedling cohorts than in adult cohorts because seedlings may reflect reduced present-day levels of gene flow.

Questions addressed

1. Does genetic diversity and inbreeding differ between adult populations of trees in fragmented and continuous forests?
2. Is inbreeding in seedling cohorts higher than that in adults?
3. Is there spatial genetic structure among adult populations of bigleaf maple?

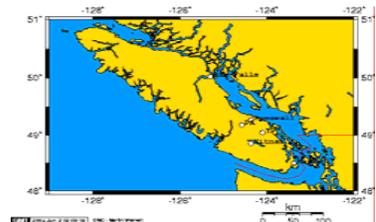


Fig 1. Geographic locations of sampled bigleaf maple populations

Methodology

Seedlings and bud tissues from adult trees were sampled from three continuous and three fragmented populations from Vancouver Island (Fig. 1). Spatial location of each tree was located using a hand held GPS. Samples were genotyped for ten allozyme loci (Table 1).

Table 1. Electrophoresis buffer systems and enzymes

Electrode Buffer	Gel Buffer	Current (mA)	Running time (hrs)	Enzymes
A. 0.04M citric acid, pH 8.0	1:20 dilution of electrode buffer	50	5	pgi-1, pgi-2, gdh, lap-1, lap-2.
B. 0.03M lithium hydroxide, 0.19 M boric acid, pH 8.3	10% electrode buffer, 90% gel, 0.05M Tris, 0.008M citric acid	80	7	aat-1, aat-2, idh, gpg-1, 6pg-2

Results & Discussions

All six seedling and adult populations possess similar levels of genetic variation regardless of whether populations were fragmented or continuous (Fig 2).

Genotypic frequencies deviated from Hardy-Weinberg expectations in both adults and seedlings populations (Table 2).

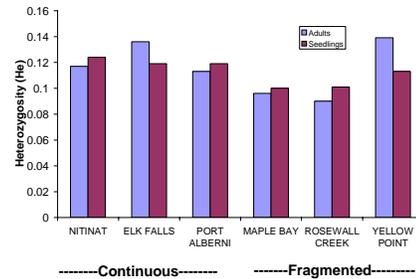


Fig 2. Genetic diversity in adults and seedlings populations

Table 2. Inbreeding coefficient F_{IS} .

Populations	F_{IS}
<i>Continuous</i>	
NITINAT	
adults	0.17*
seedlings	0.43*
ELK FALLS	
adults	0.19*
seedlings	0.07 ^{NS}
PORT ALBERNI	
adults	0.25*
seedlings	0.32*
<i>Fragmented</i>	
MAPLE BAY	
adults	0.27*
seedlings	0.10 ^{NS}
ROSEWALL CREEK	
adults	0.16*
seedlings	0.58*
YELLOW POINT	
adults	0.13*
seedlings	0.33*

* $P < 0.05$, ^{NS} not significant

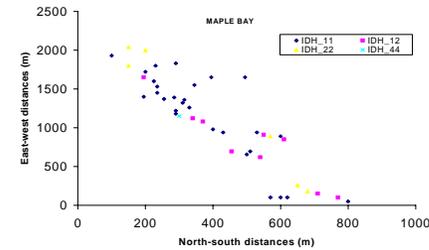


Fig 3. Spatial distribution of genotypes at the IDH locus in a fragmented population

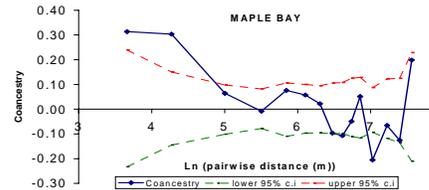


Fig 4. Spatial correlogram of coancestry coefficient in a fragmented population

Analysis of spatial genetic structure indicates non-random distribution of genotypes in fragmented populations (Fig 3).

We found a significant positive autocorrelation among individuals located up to 300 m apart in all three fragmented populations e.g. (Fig 4) This could be due to assortative mating or restricted dispersal of pollen or seed among bigleaf maple populations.

Conclusions

We found no effect of habitat fragmentation on genetic diversity and inbreeding in bigleaf maple populations.

We found evidence of inbreeding in both seedlings and adult populations but higher in seedlings than adults populations of bigleaf maple.

There is evidence of spatial structuring of genotypes with localized mating in bigleaf maple populations.

References

Lande, R .1999. Extinction risks from anthropogenic, ecological and genetic factors. *In* L. A. Landweber and A. P. Dobson, editors. Genetics and the extinction of species: Princeton University Press, Princeton, New Jersey.

Young, A.G., Boyle, T and Brown, T. 1996. The population genetic consequences of habitat fragmentation for plants. *Trends in Ecology and Evolution*. 11: 413-418.

Acknowledgements

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