GENETIC VARIATION AND POPULATION STRUCTURE IN BIGLEAF MAPLE: A COMPARISON OF ALLOZYME MARKERS AND QUANTITATIVE TRAITS

Mohammed N. Iddrisu and Sally N. Aitken

Department of Forest Sciences, University of British Columbia, Vancouver BC, V6T 1Z4

INTRODUCTION

Knowledge of genetic variation and population structure provides information necessary for understanding and conserving the evolutionary potential of populations (Wright 1951). Levels of genetic variation and degree of genetic control also vary among traits, ages and environments (Mullin et al. 1995).

The use of molecular markers has several limitations in providing information that could be used to define conservation and management strategies (Lynch 1996). This is because the primary aim of conservation genetics is to quantify and maintain the evolutionary potential of a species. For this reason sampling for genetic variation studies should include genetic variation for traits affecting fitness, many of which are polygenic (Petit et al. 2000). Most molecular markers are considered selectively neutral, while the pattern of quantitative trait variation is likely to be driven by environmental factors resulting in different selection pressures in different locations (Petit et al. 2000). A combination of molecular and quantitative measures of genetic variation allows insights into the different modes of phenotypic evolution in sub-divided populations.

OBJECTIVES

To determine the magnitude of genetic variation and genetic relationship in growth and phenologocal traits (bud flush) and compare popuation differentiation for genetic markers (F_{ST}) and quantitative traits (Q_{ST}).

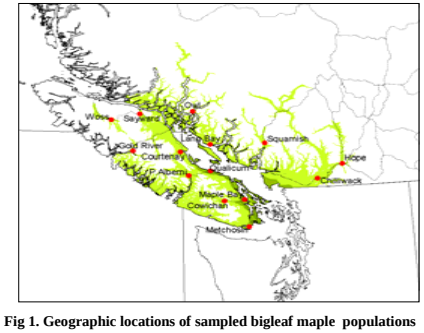

Fig 1. Geographic locations of sampled bigleaf maple populations

STUDIED POPULATIONS

Seeds from 14 populations comprising 10 families per provenance were collected from across the portion of the species range of distribution in British Columbia (Fig. 1) by the BC Ministry of Forests and used to establish a common garden test in Surrey, BC. The experiment was laid out in a split-plot design in four randomized blocks with provenances as main plots with five-tree family rows as subplots.

METHODOLOGY

Quantitative traits:

Height growth was measured at the end of years two (1998), three (1999) and four (2000). Diameter was measured for all provenances at the end of the growing season in year three (1999). Phenological data (bud flush) was monitored and recorded two to three times a week from March 2002 to mid-May 2002. Julian bud flush data was defined by when the first unfolded leaf was observed. With the exception of bud flush, height and diameter measurements were performed by the BC Ministry of Forests.

Analysis of variance (ANOVA) was conducted using PROC GLM (SAS Institute Inc. 1990) for height, diameter and bud flush traits using the following general linear models:

$$Y_{ijkl} = \mu + B_i + P_j + PB_{ij} + F(P)_{k(j)} + F(P)B_{k(ij)} + \varepsilon_{l(ijk)}$$

Where:
Y = measurement of seedling ***l*** from family ***k*** in provenance ***j*** in block ***i***
μ = overall mean;
B_i = effect of block
P_j = effect of provenance
PB_{ij} = interaction effect of block with provenance
$F(P)_{k(j)}$ = effect of family within provenance
$F(P)B_{k(ij)}$ = interaction effect of block with family within provenance
ε = experimental error.

Isozyme Variation:

Vegetative buds were collected from two out of the four blocks representing approximately 1400 trees from the 14 provenances in the common garden experiment described above and analyzed by isozyme electrophoresis for 10 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 hydrooxide, 0.19 M boric acid. pH 8.3	10% electrode buffer, 90% gel, 0.05M Tris, 0.008M citic acid	80	7	aat-1, aat-2, idh, gpg-1, 6pg-2

RESULTS

Genetic variation in growth traits for bigleaf maple seedlings both among and within provenances was detected at an early age.

All variance components were significant for bud flush and height at all ages but not significant for diameter.

The narrow-sense heritabilities for individual (h^2_i) and family (h^2_f) were moderately low and remained stable for height (Table 1).

The proportion of inter-population genetic differentiation among populations (F_{ST}) indicated that the vast majority of total variation resided within populations, with around 9% of the total variation occurring among populations.

Table 2. Heritabilities & population differentiation for quantitative traits Q_{ST}

Trait	h^2_i (SE)	h^2_f (SE)	Q_{ST}
Height-2	0.15 (0.06)	0.37 (0.04)	0.26
Height-3	0.17 (0.02)	0.38 (0.01)	0.16
Height-4	0.18 (0.05)	0.40 (0.01)	0.12
Bud flush	0.29 (0.01)	0.91 (0.02)	0.12

F_{ST} (isozymes) =0.09

Fig 2. Common garden experiment at Surrey BC.

CONCLUSIONS

The substantial within-population variation observed in this study coupled with the moderate heritabilities and moderate genetic correlations among growth traits and bud flush suggest an opportunity for genetic improvement and early selection for these traits.

Bigleaf maple has adapted to varying environmental conditions, with natural selection favouring different phenotypes in different environments.

RECOMMENDATIONS FOR FURTHER STUDIES

The study of quantitative variation in bigleaf maple needs to be extended to include more test sites as well measurements of more traits and more growing seasons in order to investigate the degree of genotype by environmental interaction and juvenile-mature correlations.

REFERENCES

Lynch, M. 1996. A quantitative-genetic perspective on conservation issues. In Conservation Genetics: case studies from nature. Avise, J. C. and J. L. Hamrick (eds). Chapman and Hall. New York, Pp. 471-501.

Mullin, T.J., Adams, G. W., Simpson, J.D. , Tosh, K. J., and Greenwood, M.S. 1995. Genetic parameters and correlations in test of open-pollinated black spruce families in field and retrospective nursery test environments. Canadian Journal of Forest Research, 25: 270-285.

Petit, C., Freville, H., Mignot, A., Colas, B., Riba, M., and Imbert, E. 2000. Gene flow and local adaptation in two endemic plant species. Biol Cons 100: 21-34.

Wright, S. 1951. The genetic structure of populations. Annals of Eugenics, 15: 532-554.

ACKNOWLEDGEMENTS

Funding:
- Financial support from Canadian Commonwealth Scholarship Program
- BC Ministry of Forests
- National Science and Engineering Research Council of Canada (NSERC) Industry Research Chair in Population Genetics
- Centre for Forest Gene Conservation via Forest Genetics Council from the Forest Investment Account BC