some ecological effects of shelterwood harvesting and site preparation in white pine forests

Genetic diversity

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Background

Genetic diversity is the basis of all biodiversity because it provides raw material for adaptation, evolution, and survival of species, especially under changed environment and disease conditions. The Canadian Standards Association has identified genetic diversity as one of the criteria and indicators for registration, certification, and audit of sustainable forest management systems (CSA 1996a,b). Forest management practices may or may not affect genetic diversity in subsequent forest populations. For example, shelterwood harvesting in old-growth Douglas-fir (*Pseudotsuga menziesi*) appears to have no negative effects on genetic variation (Neale 1985) or mating systems (Neale and Adams 1985). In Norway spruce (*Picea abies*) no significant differences were found between virgin forests and naturally regenerated stands; however, planted stands were less genetically diverse (Gomory 1992). A few studies on genetic diversity of natural stands versus seed orchard clones in forest species have indicated that expected heterozygosities were similar in natural and managed populations (Savolainen and Karkkainen 1992). In white spruce (*Picea glauca*) natural regeneration has been shown to maintain genetic diversity, whereas plantations and phenotypic selections (plus trees) significantly reduced genetic diversity (Rajora 1999).

Eastern white pine is primarily regenerated under the shelterwood and seed-tree harvesting systems. In a finite population, genetic diversity is expected to decrease as population size decreases. In 2 old-growth white pine stands at Galloway Lake in Ontario, harvesting about 75% of white pine trees reduced genetic diversity by 25% to 50% in the post-harvest residual gene pools (Buchert *et al.* 1997, Rajora *et al.* 2000). However, these stands were small, on the edge of the normal range of white pine, and the genetic diversity of the post-harvest natural regeneration has yet to be analyzed. Information on genetic diversity inherent in white pine stands and the effects of shelterwood harvesting on genetic diversity has not yet been studied in the central part of the white pine range in Ontario. Understanding the effects of harvesting on local gene pools will facilitate the monitoring of such practices to ensure their effectiveness in maintaining long-term ecosystem productivity and health. If current silvicultural practices substantially reduce genetic diversity, it will be necessary to develop alternative practices that ensure genetic diversity is maintained in regenerated stands.

Objectives

The objectives of this study were:

- To determine genetic diversity inherent in 2 second growth white pine stands and evaluate genetic diversity changes associated with shelterwood cutting
- To generate benchmark information for developing genetically sound forest management practices, future monitoring of genetic diversity, and developing genetic biodiversity criteria and indicators for sustainable forest management

Methods

Two treatment plots were randomly chosen from a total of 15 plots, one from Block 1 (Stand 1) and one from Block 3 (Stand 3). These stands were approximately 14 km apart. In 1997, after stands were marked for harvest but before harvesting occurred, 100 cone-bearing white pine trees in each plot were numbered and mapped. Cones from individual trees were collected at maturity by shooting out the cone-bearing twigs. Cones were put into small burlap bags, labelled by tree number and date of collection, and kept at room temperature with good air circulation until they could be shipped to the Ontario Forest Research Institute, where they were unpacked and put onto drying racks. Seeds were manually extracted from cones, mounted on paper cards, and x-rayed. Filled seeds were separated from partially filled and empty seeds using x-ray images, and stored at –20°C until analysis.

Genetic diversity was determined by allozyme analysis. The genotypes of 100 white pine trees from Stand 1 and 95 white pine trees from Stand 3 were determined for 54 allozyme loci coding for 16 enzymes (Table 1). A minimum of 8 individual megagametophytes were analyzed per tree. Genotypes of individual trees and genetic interpretation of loci and alleles were inferred from the banding patterns in individual megagametophytes. A locus was considered polymorphic if more than one allele was observed at that locus. Allele frequencies, allele distribution in different frequency classes, number of unique and rare alleles, and the standard genetic diversity parameters were calculated for the pre-harvest gene pool and post-harvest residual trees.

Results

Both pre-harvest stands had high allozyme genetic diversity. Stand 1 had higher genetic diversity than Stand 3 (Table 1). Most of the genetic diversity resided among individuals within stands, with only about 3% difference between the 2 stands. Both stands had unique alleles; however, the number of unique alleles in Stand 1 was almost twice that of Stand 3. Removing 20% and 23% of the trees by shelterwood cutting in Stand 1 and Stand 3, respectively, reduced genetic diversity by about 5% (Stand 1) and 3% (Stand 3) for the percentage of polymorphic loci and about 7% for the number of alleles in both post-harvest residual stands. Harvesting did not affect heterozygosity in Stand 1, whereas observed heterozygosity was reduced by about 2% in Stand 3. The genetic diversity reduction in the post-harvest residual stands approximated theoretical expectations. Shelterwood cutting with 20 to 23% white pine tree removal as occurred in this study had only minor effects on genetic diversity compared to the 75% tree removal in the Galloway Lake study.

Future Work

Until the genetic diversity of the post-harvest natural regeneration and planted stock in both stands is assessed and the mating system (outcrossing and inbreeding rates) in post-harvest residual stands is analyzed, the study remains incomplete.

References

Buchert, G.P., O.P. Rajora, J.V. Hood and B.P. Dancik. 1997. Conserv. Biol. 11: 747-758.

CSA.1996a. Z808-96.

CSA. 1996b. Z809-96.

Gomory, D. 1992. For. Ecol. Manage. 54: 215-223.

Neale, D.B. 1985. For. Sci. 31: 995-1005

Neale, D.B. and W.T. Adams. 1985. Theor. Appl. Genet. 71: 201-207.

Rajora, O.P. 1999. Theor. Appl. Genet. 99: 952-959.

Rajora, O.P., M.H. Rahman, G.P. Buchert and B.P. Dancik. 2000. Mol. Ecol. 9: 339-348.

Savolainen, O. and K. Karkkainen. 1992. New For. 6: 329-345.

Table 1. Measures of genetic diversity in 2 white pine stands before and after shelterwood harvesting**.**

Stand	**Trees**	**Total (#)**	**Mean Alleles**	**Polymorphic Alleles per**	**Mean Loci**	**Heterozygosity**
	Observed/Expected	(#)	**Locus (#)**	(**%)**		
Stand 1 (Block 1)						
Pre-harvest	100	148	2.7	77	0.15	0.16
Post-harvest	80	138	2.6	74	0.15	0.16
Stand 3 (Block 3)						
Pre-harvest	95	126	2.3	63	0.12	0.13
Post-harvest	73	117	2.1	61	0.12	0.13