

THE EFFECT OF ALTERNATIVE SILVICULTURAL SYSTEMS
ON GENETIC DIVERSITY IN DOUGLAS-FIR ^{1/}

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Abstract.--The genetic composition (20 allozyme loci) of remaining overstory trees in two-story and group selection plots (6-8 ha) were compared to uncut stands in each of three replications, to assess the impacts of harvesting on genetic diversity in Douglas-fir. In addition, the genetic composition of seven artificial seedling stocks used to reforest the harvested units was examined. Neither harvesting nor artificial reforestation appreciably altered levels of genetic diversity compared to uncut stands.

Key words: Pseudotsuga menziesii var. menziesii (Mirb.) Franco, isozymes, artificial reforestation,

INTRODUCTION

An issue of particular concern today in the practice of forestry is the extent to which management may alter levels of biodiversity in our forests. One important component of biodiversity is genetic variation within species at the population or stand level. This variation is not only vital to adapting species to pest attack and climatic extremes in current environments, but also to their continued evolution in the face of new environments in the future (Ledig 1986). Variation within populations is also the primary source of genetic diversity employed by breeders in tree improvement programs. Despite the importance of genetic variation within populations, little data is available to assess the potential implications of alternative management practices on levels of diversity (Savolainen and Kärkkäinen 1992).

A recent study established by the College of Forestry at Oregon State University, provides an excellent opportunity to address impacts of forest management on biodiversity in a well controlled and replicated experiment. Plant and animal communities under alternative silvicultural regimes are being compared, over time, to those in uncut, mature stands, in each of three replicated blocks. The study summarized in this paper adds genetic composition of the dominant tree species to the higher levels of biodiversity already being

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addressed. The overall objective is to assess the impact of three silvicultural systems (group selection, two-story, and clearcut) on the genetic composition of Douglas-fir [*Pseudotsuga menziesii* var. *menziesii* (Mirb.) Franco] stands when followed by either natural or artificial regeneration. Natural regeneration in harvested areas has not been sufficient as yet to warrant sampling, but data is available on the genetic composition of overstory trees and the artificial stocks used to regenerate the sites. Thus, in this preliminary report, we address the following issues: 1) To what extent does partial harvesting influence the genetic composition of overstories? 2) Do artificial planting stocks differ substantially in genetic composition from uncut stands? 3) To what extent do different sources of planting stock suitable for the same area differ in genetic composition?

Based on the few previous reports of genetic impacts of alternative silvicultural systems (Neale 1985, Savolainen and Kärkkäinen 1992), as well as evidence for high within-population genetic variation and strong gene flow in conifers (Ellstrand 1992, Hamrick et al. 1992), we expected to find little, if any, impact of harvesting in group selection or two-story systems on genetic diversity. Furthermore, unless seed stocks come from very limited numbers of parent trees, artificial regeneration should also possess high levels of diversity (Adams et al. 1992). Given the paucity of actual observations, however, and concerns expressed in professional literature regarding negative genetic impacts of forest management (e.g. Society of American Foresters 1991), the need for additional published data is evident.

METHODS

Study Sites

The study was carried out on the College of Forestry Research Forests, located in the Willamette Valley near Corvallis, Oregon. Distances between the three replicates (blocks) ranged from 3.4 to 7.2 km. Each block was subdivided into stands of approximately 8 ha, which were subjected to one of the treatments: clearcutting, partial harvesting (group selection and two-story systems), or left uncut. Harvesting was done in two of the blocks in 1990 and in the third block in 1991. In the group selection treatment, all mature trees were removed in 0.20 ha patches scattered throughout the stand. In total, approximately 25% of the stand was harvested. In the two-story treatment, stands were selectively thinned to an average of 18% of the most vigorous trees distributed relatively evenly over the entire area (about 23 trees/ha). With the exception of the few scattered individuals left (and later topped) for wildlife habitat, all trees were removed in the clearcut treatment. Each harvested area was replanted with one or more of a total of seven Douglas-fir seedling stocks originating from two seed zones overlapping the boundaries of the forest. Seed sources were commercial collections in wild stands from two elevational bands (0-152 m, 152-305 m) in seed zone 262 and one elevational band (0-152 m) in zone 252 (Western Tree Seed Council 1966). The seven stocks also differed by the nursery in which they were raised (three) and by stock type (i.e., 1-1 or plug-1). Planting of the harvested areas was begun in the winter of 1990/91 and completed the following winter.

Sampling

One stand of each treatment type (uncut, group selection, two-story, and clearcut) was chosen for sampling in each replicate block. In all stands with overstory trees (i.e., all except clearcuts), a sampling area of approximately 5.0 ha was laid out and twig samples containing dormant buds collected from 120 mature trees located systematically on a grid within this area. In total, 1080 (3 treatments x 3 replicates x 120 trees) overstory trees were sampled. Dormant buds were also collected from 120 seedlings of each of the seven stocks used in planting the harvested areas. Since the seedling stocks were not allocated according to any particular experimental design, and there was no reason to expect samples of the same stock to differ appreciably among planting locations, each stock was sampled in only one area. Immediately after collection, the bud samples from each overstory tree or seedling were sealed in a labeled plastic bag and placed on ice. Subsequently, the samples were kept in a cold (3°C) room until laboratory analysis.

Isozyme analyses

Isozyme analyses were performed on the bud tissues according to procedures described by Adams et al. (1990). In total, 14 enzyme systems (ACO, PGM, PGI, LAP, SDH, GDH, SOD, GOT, G-6PD, F-EST, 6-PGD, IDH, DIA and MDH) and 20 loci were assayed. Genetic diversity statistics [average number of alleles per locus (A), percent of polymorphic loci (P, 99% criterion), and observed (H_o) and expected (H_e) heterozygosities] were estimated for each mature-tree and seedling population sampled. In addition, the extent of genetic differentiation among populations was evaluated by calculating Nei's unbiased genetic distances (Nei 1978) and chi-square statistics for testing heterogeneity of allele frequencies (Workman and Niswander 1970). All calculations were performed using the "BIOSYS" computer program (Swofford and Selander 1989).

RESULTS

Impact of harvesting on the genetic composition of overstory trees

Nineteen of the 20 loci were polymorphic in at least one of the nine stands sampled, and on average, levels of polymorphism in these populations were consistent with earlier studies in this species (Neale 1985, Moran and Adams 1989). Partial harvesting appears to have had little influence on the genetic composition of overstory trees. On average, allele frequencies in the group selection and two-story treatments differed significantly ($P < 0.05$) from the uncut stand in the same replication at 6 of the 20 loci (range 4-9). The largest allele frequency difference at any one locus, however, averaged only 0.07 (range 0.02-0.16). In addition, mean genetic distances between the uncut and group selection stands (0.0017), and between the uncut and two-story stands (0.0023), were small and no greater than the average genetic distance observed among the three uncut stands (0.0027). Estimated levels of genetic diversity also varied little among the three stand types (Figure 1).

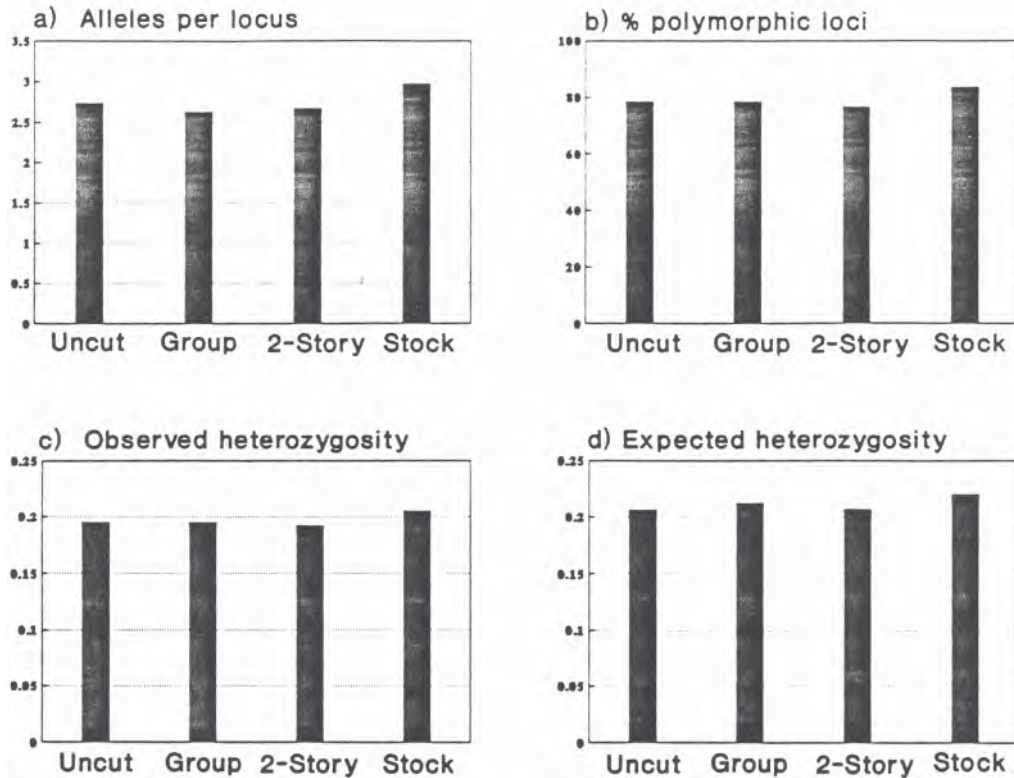


Figure 1. Average number of alleles per locus (a), percent of polymorphic loci (b), observed (c), and expected (d) heterozygosities in Douglas-fir overstory trees and planting stocks.

Genetic composition of planting stocks

Despite the variety of seed sources, nurseries and stock types involved, genetic distances between all pairs of the seven planting stocks never exceeded 0.002 (mean distance 0.0006). The mean genetic distance between the planting stocks and uncut stands in each replication was also small (0.0018, range 0.001-0.004). Levels of genetic diversity in the planting stocks were quite consistent with those found in the uncut stands (Figure 1).

DISCUSSION

The lack of significant changes in levels of genetic diversity due to harvesting confirms results from an earlier investigation in Douglas-fir, where two pairs of shelterwood and adjacent uncut stands were compared (Neale 1985). The numbers of leave trees in the shelterwoods were similar to those remaining after harvesting in the two-story stands in this study. Apparently, reduction in numbers of overstory trees would have to be much greater before losses in allelic diversity due to genetic drift are detectable. Furthermore, even if selection

of overstory trees alters the genotypic mean of the stand for traits selected, the impact on allelic frequencies at individual isozyme loci is expected to be slight, even if the loci directly influence the traits under selection (Lewontin 1984). Thus, both theory and observation confirm that harvesting, per se, has little influence on levels of genetic diversity, as long as numbers of overstory trees are not drastically reduced.

In most cases it is expected that natural regeneration will possess as much or more genic diversity than present in overstory trees. This is because overstory trees not only mate among themselves, but also outcross with trees in neighboring stands. The effective number of parents in overstories, however, could be dramatically reduced in poor seed years, where only a few trees produce pollen and seeds. Therefore, if stands are naturally regenerated in poor seed years, genic diversity in offspring might actually be less than in the overstory.

Levels of genic diversity in artificial stock are primarily a function of the number of parents from which seed is collected. Although the number of parents contributing to commercial seed lots is generally unknown, attempts are made by most forestry organizations in the Pacific Northwest to ensure that wild stand collections include at least 15-30 scattered trees (Adams et al. 1992). In addition, it is recommended that seed orchards contain at least 50 unrelated clones or families. Such numbers seem more than adequate to ensure high levels of genetic variability in planting stock.

The fact that little differentiation was found among the planting stocks at isozyme loci, is not unexpected if relatively large numbers of parents were involved in each stock. In previous studies, genetic distances between coastal Douglas-fir populations, even over fairly wide geographical distances, were shown to be quite small (Merkle and Adams 1987, Li and Adams 1989, Moran and Adams 1989). Thus, isozymes are not very useful for verifying geographical source of parentage (Adams 1983). In this study, it can be assumed that the geographical sources of the planting stocks are appropriate, because the seed originated from the same or adjacent seed zone as the planting locations. Furthermore, there is no evidence that artificial planting stocks contain less genic diversity than found in natural stands.

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