

Genetic Effects of Diameter-Limit Cutting

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The long-term health and productivity of forests is influenced by genetic diversity that enhances resiliency in response to environmental change. Loss of specific genes and a reduction of overall genetic diversity could affect productivity, ecosystem stability, long-term survival, and evolution. Harvesting trees removes genes from a forest. The effect of this removal depends on the: 1. heritability of traits, especially growth; 2. inherent variability of a site; 3. age structure of a stand; 4. intensity and timing of the manipulations; 5. amount of advance regeneration; 6. size and degree of isolation of the stand; 7. original level of genetic diversity; and 8. number and genetic make-up of residual trees. It is important to consider the short- and long-term impacts on the quality and sustainability of the residual stand following harvesting.

The genetic diversity of the residual stand following harvest can be changed in several ways. Through selection of certain phenotypes (outward appearance of individual) there could be a loss of or change in genetic diversity if there is a strong phenotype-genotype relationship or growth-genetic diversity relationship. Also, the genetic diversity of a stand could be compromised if there is a large reduction in population size, which might result in increased inbreeding or a poorly adapted residual stand.

One way that we have assessed the genetic implications of diameter-limit cutting was by simulating the effect of different cutting strategies on red spruce populations of known genetic diversity. Selecting 25%, 50% and 75% of trees to remove at random resulted in the loss of only one allele (one of multiple forms of a gene), and no significant change in heterozygosity (a measure of the proportion of the genes that are genetically variable). Selecting the fastest growing trees to be removed (based on basal area increment) led to a loss of 2, 4 and 15 alleles, respectively, for the three cutting intensities. Only at the highest removal intensity (75% of fastest

trees removed) was there a significant reduction in heterozygosity.

In another study we assessed the genetics of a 300-tree white pine population, mapped the tree location and measured several tree age and growth characteristics, resulting a genetically-mapped forest. The stand had three age classes, with the oldest comprised mainly of wolf trees. Heterozygosity increased with age, except for the old wolf trees. Data also show a tendency for trees of poorer crown positions to have more rare alleles. In this study, a simulated harvest indicated that cutting the old trees (≥ 29 inches dbh) reduced the genetic diversity in the stand. Cutting mostly overtopped trees in this case study decreased the number of rare alleles.

We also evaluated the influence of long-term silvicultural selection on the genetic structure of an eastern hemlock forest at the Penobscot Experimental Forest in Maine. Plots in this forest received one of the following three treatments: 1) selection cuts in which small and poor-formed trees were preferentially removed in 1957 and 1977, 2) diameter-limit cuts in which trees 24 cm in diameter and larger were removed in 1952, 1973, and 1994, or 3) no harvesting (an unmanaged control). Because of an association between the occurrence of rare alleles and tree phenotypes, phenotypically based tree removals were associated with a shift in allelic frequency. Where smaller trees with inferior phenotypes were preferentially removed (selection cut), the number of rare alleles was lower and estimates of future genetic potential were lower relative to the control. Because of the theoretical long-term evolutionary benefit of unique gene forms, the loss of rare alleles could diminish the potential of populations to adapt to and survive ongoing environmental change. In contrast, trees in the diameter-limit cuts had fewer rare alleles, more low-frequency alleles, more lost alleles and interestingly were higher in heterozygosity. It appears that the increase in

heterozygosity of trees in the diameter-limit cut was due to an increase in frequency of alleles that were rare in the control stand, thus increasing low-frequency alleles and increasing heterozygosity. However, productivity was low in this stand where the frequency of characteristically rare alleles was artificially amplified.

Differences between the three management strategies are evident in the effects on rare alleles. Rare alleles are generally thought to have deleterious effects on the growth and overall fitness of a tree. So, cutting smaller trees may remove some of these undesirable alleles from a population, and selection system cutting in an uneven-aged stand may have positive short-term effects on growth. This will presumably improve the short-term fitness of the stand as well. Yet the rare alleles reduced by selection system cutting and amplified by the diameter-limit cut may be vital to long-term adaptation and

evolution of future generations. Findings from other researchers have found similar increases in rare alleles associated with poor quality, slow growing phenotypes.

Findings in our work that are supported by work of other researchers for a variety of conifer species have shown that limited removal of the largest or fastest-growing trees does not appear to significantly alter the population genetics. Yet repeated heavy removal of larger diameter trees may affect the residual stand. Findings suggest that the smallest and slowest growing trees in a population may contain high frequencies of alleles that are rare in the whole population. These individuals should not be left as the only residual trees. It appears that managers should leave trees of a range of sizes to insure that regenerating offspring have the maximum number of alleles. Maintaining this genetic diversity may be critical to the long-term survival and adaptability of a species.

Citation

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