Changes in the Genetic Diversity of Eastern Hemlock as a Result of Different Forest Management Practices

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Abstract

Loss of populations and individuals within species to human-induced selective forces can result in loss of specific genes and overall genetic diversity upon which productivity, ecosystem stability, long-term survival, and evolution depend. This is particularly true for long-lived organisms, such as forest trees, because genetic diversity confers adaptability necessary for trees to persist across temporally and spatially variable environments. Forest management is an anthropogenic force by which forest managers selectively remove individual trees from a population leaving a residual stand to provide the gene pool for future generations. Very little is known about the influence of forest management and silvicultural practices on the genetic diversity within forest ecosystems. The goal of this research was to evaluate the impacts of forest management on genetic diversity of forest ecosystems.

Genetic diversity assessments were conducted on hemlock trees in stands that have resulted from long-term, active silvicultural experiments established between 1952 and 1957 on the Penobscot Experimental Forest in east-central Maine. In those experiments treatments include fixed diameter limit cuts, and selection cuts. Diameter limit cuts were imposed in 1952, 1973, and 1994 and trees 24 cm or larger were removed each year. For selection cuts, phenotypically superior trees were favored and inferior, unmerchantable and poor risk trees were removed in both 1957 and 1977. Stand-level genetic diversity estimates were obtained for stands representing each silvicultural treatment using starch-gel electrophoresis. These estimates was compared to genetic diversity and inbreeding estimates of an unmanaged control stand to determine genetic changes resulting from these long-term forest management experiments.

Our data indicate that eastern hemlock is low in genetic diversity relative to many north temperate conifer species. Compared to genetic estimates in unmanaged control stand, a series of selection cuts have had limited impact on the level of genetic diversity in the residual stand. Selection cuts did however result in a loss of rare alleles that may be valuable for future evolution. Trees remaining after repeated diameter-limit cuts, leaving only the very worst trees in terms of size and form, had significantly higher levels of heterozygosity, polymorphic loci, and effective number of alleles per locus. These counter-intuitive results reflect an apparent association between rare alleles and defective phenotypes in eastern hemlock. Several alleles that occurred at very low frequencies ($p < 0.03$) in the natural unmanaged stand occurred at much higher frequencies in the diameter limit cut because the defective residual trees preferentially possessed these rare alleles. That is, rare alleles conferred a negative fitness impact on eastern hemlock trees. In fact, 68% and 24% of the residual trees from the diameter limit cut possessed at least one or two rare alleles, respectively, compared to 26% and 6% and 32% and 2% for the unmanaged and selection cut stands, respectively. If rare alleles are disadvantageous, there may be a loss of fitness in the diameter limit cut stand compared to the unmanaged control stand. Because residual trees in the selection cut stand contained fewer rare alleles than the control stand, there may be increase in fitness resulting from repeated selection cuts, at least in the short term. However, in the long term this loss of rare alleles in the selection cut stand compared to the control stand may come at an evolutionary cost because rare alleles are the raw material for evolutionary change.

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