

Conserving Genetic Diversity in Ponderosa Pine Ecosystem Restoration¹

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Abstract

Restoration treatments in the ponderosa pine (*Pinus ponderosa* P. & C. Lawson) ecosystems of the southwestern United States often include removing over 80 percent of post-EuroAmerican settlement-aged trees to create healthier forest structural conditions. These types of stand density reductions can have negative effects on genetic diversity. Allozyme analyses were used to evaluate potential impacts of restoration treatments on genetic diversity of five ponderosa pine populations located 2 to 3 km apart within the U.S. Department of Agriculture Forest Service Fort Valley Experimental Forest, located north of Flagstaff, Arizona. Results revealed allele frequencies varied significantly among pre-settlement clusters of trees within and among populations, and trees within clusters had lower than expected heterozygosity levels. These results indicate the clumpy stand structure typical of reference stand conditions represent “genetic neighborhoods”. A combination of limited seed movement created by seeds dropping below parent trees within existing tree clusters along with kin-structured clusters created by scatter-hoarding animals likely created the genetic neighborhoods within the clumpy stand structure in Fort Valley pre-settlement populations. Gene flow among clusters in Fort Valley is not sufficient to overcome the family structure created by half and full siblings and parent-progeny kin relationships existing within individual clusters and suggests restoration prescriptions for clustered versus more evenly dispersed trees might be needed to protect evolutionary genetic patterns. Post-settlement trees averaged 150 years younger and were likely offspring of pre-settlement trees, since the pre- and post- trees sampled were interspersed. Compared to pre-settlement populations, post-settlement trees had slightly greater heterozygosity and allelic richness, and allele frequencies between these two age groups varied significantly. Post-settlement trees did not contain unique alleles, and genetic difference between age groups could be explained by different microclimate and thus selective conditions under which the two age groups became established. Simulated removal of 50 percent of post-settlement trees did not reduce genetic diversity, but 75 percent removal resulted in decreased allelic richness in the thinned population, particularly among rare and low frequency alleles. The loss of these alleles could be disadvantageous if they have adaptive significance to changing environments such as experienced between the two age groups. Maintaining some post-settlement populations with higher tree densities across the landscape could conserve low frequency alleles. Overall results of this study provide evidence of rapid evolution in ponderosa pine and indicate restoration treatments must consider genetic diversity to ensure adaptive potential is conserved.

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