

Synthesizing Genetic Divergence and Climate Modeling to Inform Conservation Planning for Ponderosa Pine¹

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Geological, climatological and ecological processes partially or entirely isolate evolutionary lineages within tree species. These lineages may develop adaptations to different local environmental conditions, and may eventually evolve into distinct forms or species. Isolation also can reduce adaptive genetic variation within populations of a species, potentially compromising their ability to respond to climate change. Dramatic climate changes during the Pleistocene, for example, caused species ranges to contract and fragment into isolated glacial refugia before expanding and reconnecting. The genetic signals of these processes remain in several species, and may be useful in guiding gene conservation strategies. Such within-species evolutionary differences should be considered when predicting species responses to climatic conditions. We considered within-species evolutionary differences within a climate context for ponderosa pine (*Pinus ponderosa*), applying results from range-wide molecular marker assessments and nonparametric multiplicative regression climate models. In this widespread western North American species, we detected and mapped 10 mitochondrial (mtDNA) haplotypes from 3,100 trees across 104 populations. Each haplotype is an evolutionarily distinct unit that may be evolving separately and responding differently to climate change. Our analyses, in fact, indicate strong relationships between genetic lineages and climate. Most important were differences in seasonal precipitation regimes between the Rocky Mountain and Pacific evolutionary lineages, but other precipitation differences were also apparent among haplotypes. This synthesis of phylogeography, population genetics, and climate modeling should assist management and conservation planning for this widespread and ecologically important forest tree species in the face of climate change.

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