

Comparison of Genetic Diversity and Population Structure of Pacific Coast Whitebark Pine Across Multiple Markers

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Abstract—Analysis of “neutral” molecular markers and “adaptive” quantitative traits are common methods of assessing genetic diversity and population structure. Molecular markers typically reflect the effects of demographic and stochastic processes but are generally assumed to not reflect natural selection. Conversely, quantitative (or “adaptive”) traits can be associated with climatic or other environmental variables that drive natural selection, but may not reflect the past demographic processes, such as bottlenecks, post-glacial recolonization, and population isolation. The genetics of whitebark pine has been studied using both molecular markers and adaptive traits, but never from a common set of samples so that the results could be directly compared. In addition, previous studies have not included samples from the Olympic Mountains in northwestern Washington, the westernmost distribution of whitebark pine that is geographically isolated from the rest of the species range.

We have analyzed genetic diversity and population structure using isozymes (88 populations ~30 individuals/population), organelle DNA (88 populations, ~30 individuals/population for chloroplast DNA [cpDNA] and ~8 individuals/population for mitochondrial DNA [mtDNA]), and genomic DNA (13 populations that were a subset of the 88, 22–28 individuals/population). Seedling quantitative traits were assessed in a common garden (92 families from 50 locations), mostly in Oregon and Washington, including the Olympic Mountains. Genomic DNA was analyzed with amplified fragment length polymorphisms (AFLPs) from 13 locations which also were analyzed with isozymes and organelle DNA (cpDNA and mtDNA), and 10 of which also had seedling traits measured. Twenty-five sites had assessments of isozymes, organelle DNA and measurements on seedling traits.

The Olympic Mountain populations had lower genetic diversity and were differentiated from all other populations by isozymes, nuclear and organelle DNA. Genetic diversity varied by marker type but among non-Olympic populations was generally within the ranges reported in other studies. Among non-Olympic populations, there was only weak genetic structure based on isozymes separating the Oregon and Washington populations. Isozyme analysis distinguished two population “groups”: the Olympics and everything else. Analysis of organelle and nuclear DNA showed more distinct population separation, with three “groups”: the Olympics, Oregon and southwestern Washington, and northern and eastern Washington, although the locations of the boundaries among haplotypes varied by marker type. Populations also differed significantly based on seedling traits. Mean date of needle flush was more than 3 weeks later in southern Oregon populations than populations from northern Washington and British Columbia. Date of needle flush was strongly associated with several winter and spring temperature variables, growth was associated with winter temperature and fall and winter precipitation, and needle length was associated with spring and summer maximum temperature. The Olympic populations were not differentiated from other populations based on these quantitative traits. This result illustrates that information from neutral molecular markers and adaptive traits is complimentary but completely independent based different ecological and evolutionary processes. These results also show that Olympic peninsula populations are genetically distinct and warrant conservation. In combination, the results across multiple genetic markers indicate that seed can be moved within the northern and eastern parts of Washington, and within southwestern Washington and Oregon, but should not be moved between these regions. In addition, seed should not be moved into or out of the Olympic peninsula populations.

The content of this paper reflects the views of the author(s), who are responsible for the facts and accuracy of the information presented herein.