

Healthy Forests Restoration Act Projects Title IV-Accelerated Information Gathering

Project Title: Genetic diversity of western white pine (*Pinus monticola* Dougl.) revealed by genetic markers: Improving the white pine blister rust resistance breeding program and understanding the importance of natural regeneration after biotic and abiotic disturbances (**Accelerated Information Gathering**)

Significance: Western white pine (*Pinus monticola*; WWP), once a major component of western forests, has declined precipitously in the last 70 years for a variety of reasons -- foremost among them being the introduction of blister rust caused by *Cronartium ribicola*.



The introduction of blister rust to the west coast of North America in the early 1900s created a disease epidemic across most of the range of WWP. For example, less than 10 percent of the historic 5 million acres of WWP cover type remains in today's Inland Northwest forests. Genetic diversity is a major determinant and indicator of the ability of forest tree populations to maintain adaptability and respond to biotic and abiotic disturbances, thus it is recognized as an indicator of sustainability. When forest tree populations suffer dramatic reductions in genetic diversity, they may become more vulnerable to environmental stress- or pest-related reductions in overall health, productivity, and fitness. Restoring WWP to the Pacific Northwest requires a basic understanding of post-epidemic genetic diversity and population structure within its natural range, and identification and maintenance of valuable or unique populations for species management and conservation.

Approach: We have collected 15 natural WWP populations (a total of 450 tree samples) representing six Pacific Northwest regions: Interior, Coastal, North Central Cascade, South Central Cascade, Siskiyou, and South Cascade-Sierra. Each region was represented by at least two sampling populations. We will examine WWP groups defined by physical and morphological data, blister rust-resistance data, and genetic marker data. We will develop protocols for identifying valuable or unique WWP populations and prioritizing them for WWP management, restoration, and conservation.

Outcomes: This study will 1) provide baseline information regarding population genetic structure of WWP at the landscape level, 2) identify valuable and unique WWP populations for species management, restoration, and conservation programs, and 3) develop molecular tools for further characterizing rust resistance and adaptive traits in WWP.



Benefits: Results from this study will provide baseline information for WWP restoration and conservation programs to ensure that restored populations are sufficiently genetically diverse to maintain themselves in the long term. In addition, forest managers, practitioners, and/or policymakers will be able to recognize the importance of valuable and unique WWP populations for species restoration-conservation. This information can be incorporated into the future Forest Plan revisions.

Contacts: Mee-Sook Kim, Ned B. Klopfenstein, Paul J. Zambino, and Dennis E. Ferguson (USDA Forest Service, Forestry Sciences Laboratory, Rocky Mountain Research Station, Moscow, ID); Steve J. Brunsfeld (Dept. Forest Resources, University of Idaho, Moscow, ID)