

Prioritization of Gene Conservation Activities in the Face of Changing Climates¹

J. Bradley St.Clair,² Andy Bower,³ Vicky Erickson,⁴ and Glenn Howe⁵

Several analyses have been done or are underway to evaluate the vulnerability of individual forest tree species to climate change. Species vulnerability assessments allow managers to allocate limited resources to the management of those species that are most threatened. But we also know that threats to individual populations of species may vary across the landscape, and that populations may contain unique and potentially valuable genetic variants that should be conserved. We propose a framework for prioritizing populations within species for gene conservation activities in which maps of risk of extirpation are overlaid with maps representing genetic variation and the species range. The average risk of extirpation is determined for each genetic classification representative of genetic variation—for example, seed zones as representative of adaptively significant variation, or, if available, maps of geographic variation in adaptive traits as determined from common garden studies. The highest priority is given to those zones with the highest risk of extirpation due to immediate factors other than climate change—fire, disease, insects, invasive species, and human development (although those factors may be indirectly related to recent climate change). The risk associated with each factor is overlaid with the genetic classification, and an average risk for each zone determined. Zones with the highest average risk are given the highest priority for *ex situ* collections. Meanwhile, zones with lower average risk may be the best candidates for *in situ* reserves since they may be expected to be most stable. The second highest priority is given to those populations that are at risk because they are expected to be outside of the future climatic niche of the species based on the best available models. Those populations may, however, have some potential for migration to new locations over time. The potential for migration within each zone may be evaluated using the average climate velocity for each zone. The third highest priority is given to those populations which lay within the future climatic niche of the species, but are at highest risk of maladaptation. Measuring risk of maladaptation involves knowledge of those climates that are most strongly associated with adaptive genetic variation. Such knowledge may come from genecology studies in which differences in adaptive traits are directly associated with differences in climates of seed sources. Average differences may be determined for each zone between current and future climates or associated traits, and higher priority for gene conservation given to those zones with the greatest differences. Consideration may also be given to the potential for migration for those higher priority zones of high risk of maladaptation. In all cases, special considerations may be given to disjunct populations and populations at the trailing edge of climate change. These populations are likely to be small with a greater risk of extirpation and higher likelihood of harboring unique variation. Trailing edge populations, in particular, may contain genetic variation associated with adaptation to warmer climates.

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² USDA Forest Service, Pacific Northwest Research Station, 3200 SW Jefferson Way, Corvallis, OR 97331.

³ USDA Forest Service, Olympic National Forest, Olympia, WA 98512.

⁴ USDA Forest Service, Pacific Northwest Region, Pendleton, OR 97801.

⁵ Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR 97331.

Corresponding author: bstclair@fs.fed.us.