CONSERVATION OF FOREST GENETIC RESOURCES IN THE UNITED STATES

Brad St.Clair[1], Sara Lipow[2], Ken Vance-Borland[3] and Randy Johnson[1]

[1] USDA Forest Service
Pacific Northwest Research Station
3200 SW Jefferson Way
Corvallis, OR 97331
E-mail: bstclair@fs.fed.us

[2] Oregon Department of Forestry
2600 State Street
Salem, OR 97310

[3] Department of Forest Science
Oregon State University
321 Richardson Hall
Corvallis, OR 97331

ABSTRACT

Conservation of genetic diversity is recognized as an important requirement of sustainable forest management. Gene conservation activities include *in situ* conservation of native stands in reserves and *ex situ* conservation in seed banks, genetic tests, seed and breeding orchards, and other plantations of known identity. We present an example from Oregon and Washington of a GIS-based "gap analysis" approach to determine the spatial distribution of protected *in situ* genetic resources. GIS coverages showing detailed distributions of eight tree species stratified into presumably unique genetic units using seed zones or ecoregions were overlaid with coverages of reserves to determine the locations of protected populations as well as gaps in protection. The gap analysis indicated that most species appear to have sufficient genetic resources conserved in *in situ* reserves. This approach may be valuable elsewhere, particularly in the eastern United States where fewer large reserves exist. Of particular note, for *ex situ* conservation, is a recent agreement between the USDA Forest Service National Seed Laboratory and the USDA Agricultural Research Service National Center for Genetic Resources Preservation to provide long-term storage of seed collections of valuable plant germplasm in their facility in Ft. Collins, Colorado. Protection from disease and insects is another important component of gene conservation.

INTRODUCTION

Conservation of genetic diversity has been recognized as an important requirement of sustainable forest management. The ability of forest trees to evolve to resist pests and adapt to changed climates depends on the genetic diversity present within a species. Genetic diversity is also essential for tree breeders in order to continue to achieve genetic improvement objectives, particularly when new traits become important, in response to changing product objectives, new disease or insect threats, or new environments. It is important that we properly manage and maintain genetic resources for future generations.

WHY CONSERVE GENETIC DIVERSITY?

Three reasons are often given for the conservation of genetic diversity: ecological, economic, and ethical (Ledig 1988).

An ecological rationale ecognizes that the diversity of life forms and ecosystem processes that shape the world are fundamentally a function of genetic diversity. Genetic diversity is the basis for evolutionary change that allows species to adapt to future biotic and abiotic environments. Gene conservation is important because we do not have a complete understanding of ecological processes; thus, we seek to save at least some of the pieces as insurance against poor or uninformed decisions in the management of our genetic resources.

An economic rationale recognizes the economic value of forests for timber and other forest products as well

as social benefits. Genetic variation allows humans to select for favored characteristics to better serve our needs and desires. Genetic variation is necessary for continued genetic gain in tree breeding programs and allows us to select for new products such as wood of a specified density or grain, different pulping characteristics, or new chemical derivatives. Genetic variation allows us to select for disease and insect resistance as new pest challenges arise and to select new seed sources for moving populations to better match future climates.

The third reason for conserving genetic diversity is ethical, moral or aesthetic. An ethical or moral rationale recognizes our obligation to protect genetic diversity for future generations, partly because we cannot predict what traits may be important in the future for evolution or for genetic improvement to address new desires or challenges. An aesthetic rationale simply states that people find beauty in a world that is diverse, and genetic diversity contributes to that biological diversity.

POPULATION CLASSIFICATIONS FOR GENE CONSERVATION

Populations are the basic unit of conservation in gene conservation programs. Genetic diversity exists and is maintained within and among populations. Thus, any evaluation of gene conservation must assess the amount and distribution of diversity of genetic variation in populations as well as the population size. Populations may be distinguished by management type and by geography.

Rowland Burdon of the New Zealand Forest Research Institute presented a classification of managed forest tree populations that is useful for considering genetic conservation (Fig. 1). His classification considers the amount of genetic variation within a population (the horizontal axis) and the amount of genetic gain that may be achieved (the vertical axis). The classification helps clarify the gene conservation objectives for different management populations and the population sizes required to meet those objectives.

At the base of his classification scheme is the gene resource population. This population represents all the genetic variation that is available to a species for future generations. It includes native stands, operational plantations, genetic tests, seed and breeding orchards, and seed stores. The large genetic diversity and large population sizes of the gene resource population make it the primary place for the long-term maintenance of genetic variation. The literature suggests that population sizes in the thousands are required for the maintenance of multiple copies of rare alleles (Yanchuk 2001) or the maintenance of quantitative genetic variation in potential adaptive traits given evolutionary forces (Lande 1995, Lynch 1996).

The breeding population is the group of parents that is used to advance to the next generation in a breeding program. Because it is a more highly selected set of parents, the breeding population represents increased genetic gain over the gene resource population, but contains less genetic diversity. The objective of this population is often continued genetic gain in traits of interest. A breeding population size of 30 to 50 maintains sufficient genetic variation for continued genetic gain for five to ten generations, but other constraints involving multiple traits and restricted inbreeding would suggest sizes over 100 (White 1992, Johnson et al. 2001, Yanchuk 2001).

The production population consists of seed orchard parents or clones used to produce genetically improved planting stock for operational plantations. These parents are typically the best selections from the breeding population. This population must carry sufficient genetic variation across a landscape to buffer stands from variations in climates or pests, but must also have sufficient genetic gain to justify the expense of tree breeding. Relatively few parents are required to capture much of the variation in a population; e.g., ten parents capture 90% of the genetic variation found in a population (Johnson and Lipow 2002).

Populations may also be defined by geographic variation in alleles or quantitatively-inherited traits. For gene conservation purposes, we are particularly interested in geographic variation in adaptive traits, that often vary gradually (i.e., clinally). Common garden studies are used to explore geographic variation in quantitatively-inherited adaptive traits. For example, common garden studies of coastal Douglas-fir (*Pseudotsuga menziesii*) in western Oregon and Washington indicate that populations differ in bud-set in a predominately longitudinal direction associated with elevation and minimum annual temperatures, whereas populations differ in bud-burst in a predominately latitudinal direction associated with summer drought (Fig. 2) (St.Clair et al. 2005). Using multivariate analyses, population variation in several traits was summarized in two traits, one trait largely associated with bud-set, germination rate, and growth, and the other trait largely associated with bud-burst and stem height:diameter ratio. Geographic variation in these two multivariate traits was overlayed to create a map of populations that are similar in a variety of traits measured in the study (Fig. 3). Results from common garden studies may be used to delineate seed and breeding zones, that are simply a summary of our best available knowledge of geographic variation in adaptive traits. In the absence of knowledge from common garden studies, we might use important climate variables, ecoregions, vegetation types or other information to serve as surrogates for genetic variation to delineate populations.

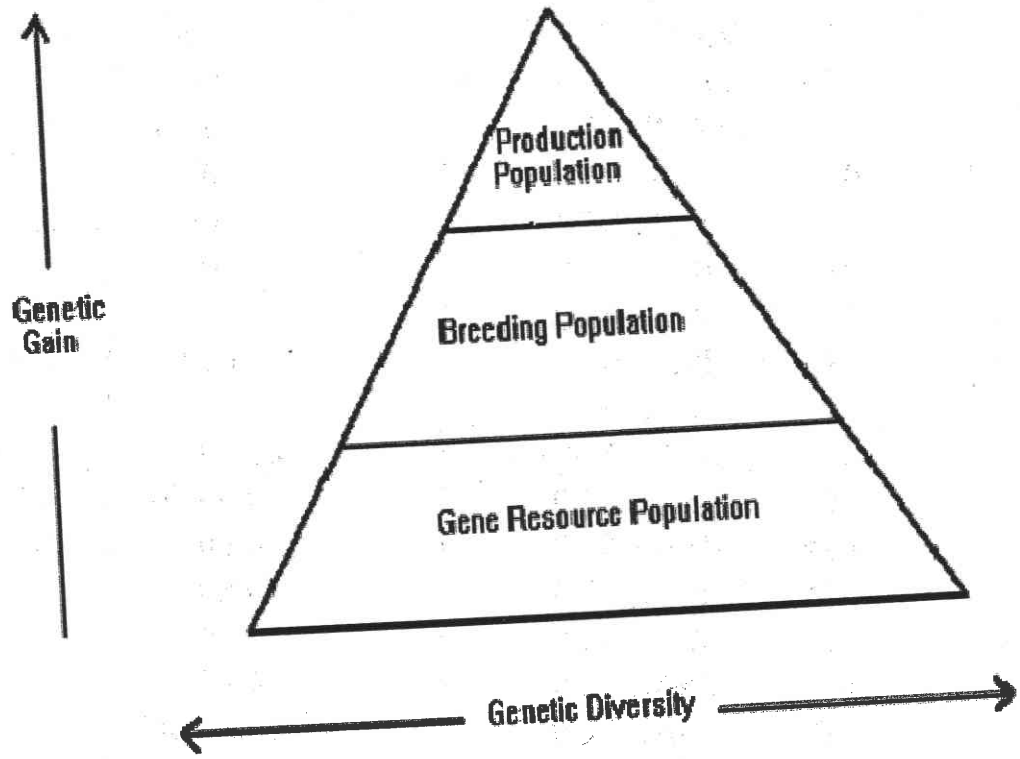

Figure 1. Conceptualization of gain versus genetic variation for a gene resource management program. (from Rowland Burdon, New Zealand Forest Research Institute)

Difficulties in delineating populations for gene conservation arise when a trait of interest is controlled by alleles at very low frequencies or when alleles can only be found in a few localized populations. Often this is the case when looking for pest resistance. One example is the MGR gene for blister rust resistance in sugar pine (*Pinus lambertiana*). Over the range of the species, the frequency of this allele is 0.022, although the frequency varies geographically from absent in the north to 0.087 in the south (Kinloch 1992). Another example is white pine weevil (*Pissodes strobi*) resistance in Sitka spruce (*Picea sitchensis*) in which resistance was found predominately in two localized British Columbia populations (Ying 1997).

GENE CONSERVATION ACTIVITIES IN THE UNITED STATES

Gene conservation activities have traditionally been classified as *in situ* and *ex situ*. *In situ* conservation is the conservation of genetic diversity in its original location, usually in protected areas with little active management, such as national parks, wilderness areas, research natural areas, and other reserves. The goal of *in situ* conservation is to protect and perpetuate the integrity of native gene pools and the natural evolutionary processes affecting those gene pools. *Ex situ* conservation is the conservation of genetic diversity at some place other than the original native habitat. *Ex situ* conservation includes collections of plant material in seed banks, tissue culture, genetic tests, seed and breeding orchards, and other plantations of known genetic identity. In the future, even DNA in genomic libraries may serve as *ex situ* collections. Breeding programs may be thought of as a type of *ex situ* conservation activity since the genetic material is removed from the original location before being planted back into the breeding zone.

Another type of activity that is not often thought of as either *in situ* or *ex situ* conservation is the use of seed zones and seed transfer guidelines for the movement of planting material to ensure adapted, productive stands. But seed zones also help to maintain some of the native genetic structure and locally-adapted gene pools, and thus serve an important gene conservation role. Seed zones and seed movement guidelines have been in use for decades for forest trees in the western United States (Kummel et al. 1944, Isaac 1949). The

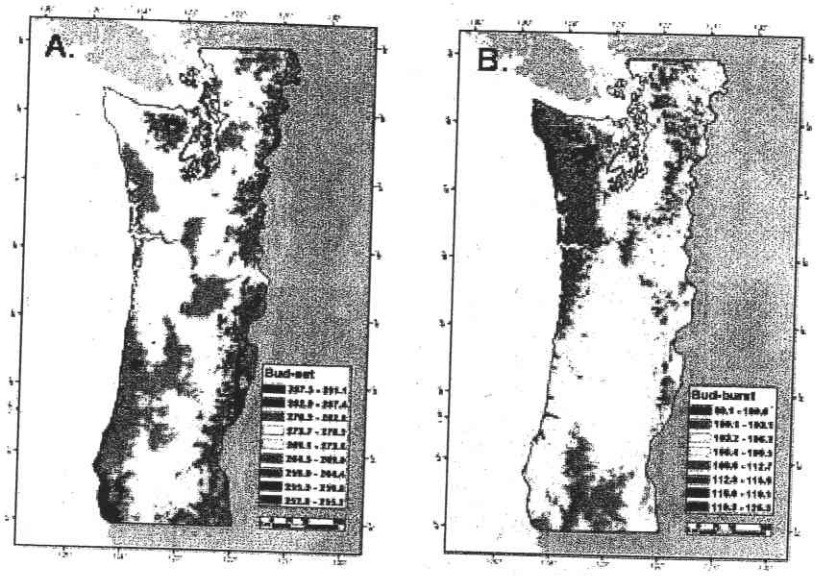

Figure 2. Geographic variation in first-year bud-set (A) and second-year bud-burst (B) in Douglas-fir from western Oregon and Washington. (from St.Clair et al. 2005)

widely-used seed zone maps for Washington and Oregon were published in 1966 and for California in 1970. Seed zones for Oregon and Washington were later revised for each species based on available knowledge of geographic patterns of genetic variation (Randall 1966, Randall and Berrang 2002). More recently, there is increased interest in seed zones for native shrubs, grasses and forbs due to increased use of these species in restoration projects (Johnson et al. 2004).

In situ conservation in the United States generally happens as a consequence of setting aside lands for other purposes. One exception is the "gene-pool reserve system" set up by the Washington State Department of Natural Resources (DNR) (Wilson 1990). The DNR set aside over 100 reserves in western Washington for the explicit purpose of the conservation of Douglas-fir genetic resources (although the genetic diversity of other species is also being protected in these reserves).

Because few formal gene conservation reserves exist for many species, a group of interested land managers in the western United States came together to fund a project to evaluate the role of current reserves in protecting genetic diversity for eight conifer species in western Oregon and Washington (Lipow et al. 2004, 2007). A "gap analysis" approach was used, similar to the approach previously used to identify gaps in species protection (Scott and Jennings 1997). Using GIS, maps of protected areas and tree distributions for each species were overlaid onto maps of seed zones or ecoregions, where seed zones or ecoregions represent genetic variation in adaptive traits. The tree distribution maps were stratified into three levels of stand density for purposes of estimating population sizes. Seed zones or ecoregions in which a species was considered poorly protected in *in situ* reserves were identified. A species was considered poorly protected if fewer than 5,000 trees or 10% of a species' population were found in reserves in each seed zone or ecoregion. The gap analysis indicated that most species appear to have sufficient genetic resources conserved in *in situ* reserves throughout their ranges. Some genetic gaps were found, however, for noble fir (*Abies procera*) in southwest Washington and for western white pine (*Pinus monticola*) and Sitka spruce in the Puget Sound. Western white

pine is of particular concern due to the impact of urbanization and blister rust (*Cronartium ribicola*), and because that area of its range has not been well sampled for blister rust resistance (Fig. 4).

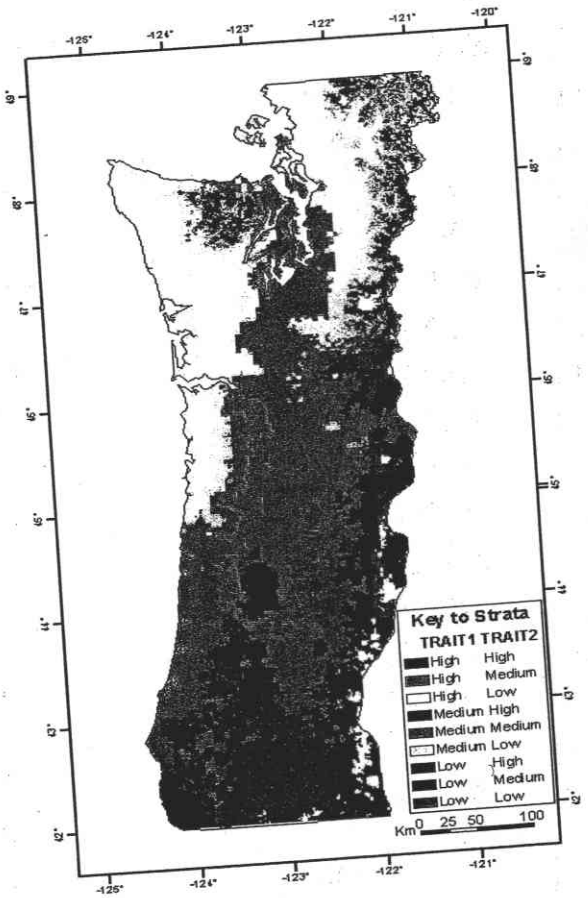

Figure 3. Map of areas of similar adaptive characteristics for Douglas-fir in western Oregon and Washington. (from St.Clair et al. 2005)

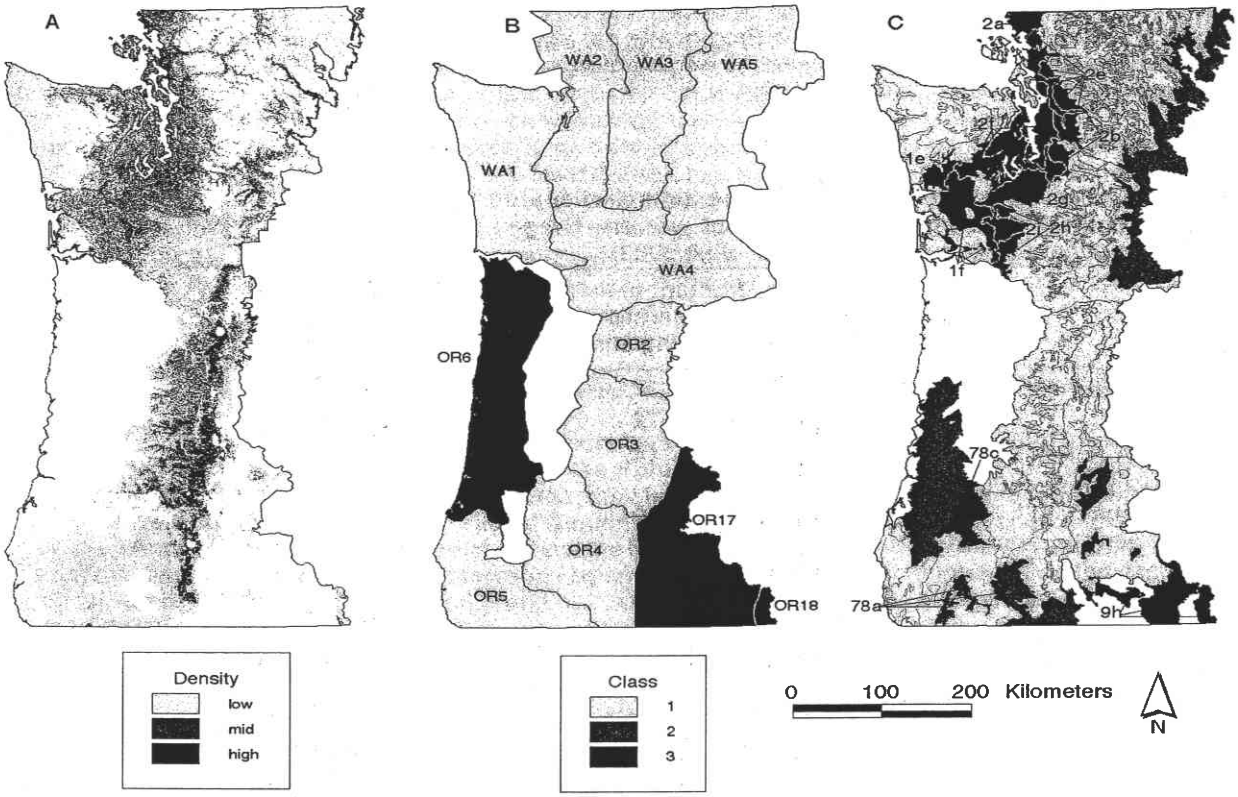

Figure 4. Distribution of western white pine (A), and results from the gap analysis for *in situ* gene conservation indicating seed zones (B) and ecoregions (C) with less than 5,000 individuals in protected areas. (from Lipow et al. 2004)

The findings from the gap analysis of sufficient protection of genetic resources for most species in most locations may not be surprising since Oregon and Washington have a high proportion of land in protected areas, particularly at higher elevations. A similar analysis was done in British Columbia with similar conclusions (Lester and Yanchuk 1996, Hamann et al. 2004). A gap analysis approach may be valuable elsewhere in the United States, particularly in the eastern United States where fewer large reserves exist. Fewer reserves may be required in the East, however, since climatic variation and the associated genetic variation in adaptive traits are generally more homogeneous.

Several organizations are actively involved in *ex situ* conservation by maintaining seed banks or *ex situ* plantations. The U.S. Forest Service maintains extensive seed collections of forest trees, many from first-generation selections in their tree improvement programs. Although the tree improvement programs have been de-emphasized in recent years, the seed banks are maintained in regional facilities (e.g., the Dorena Tree Improvement Center in Oregon). The Bureau of Land Management maintains seed stores for forest trees from their forestlands in Oregon. The Bureau of Land Management, the Agricultural Research Service, and the Forest Service's National Seed Laboratory (all federal agencies) have begun to maintain collections of native shrubs, grasses, and forbs. More recently, the Forest Service has entered into an agreement with the Agricultural Research Service for the long-term storage of up to 3,000 seeds of valuable germplasm of native plants at the National Center for Genetic Resources Preservation at Fort Collins, Colorado (http://www.nsl.fs.fed.us/nsl_ars_mou.html).

Tree improvement programs in the United States are also repositories for considerable genetic resources for species of economic interest. For example, a survey of organizations involved in Douglas-fir tree improvement indicates that over 33 000 parents are growing in over 1,000 first-generation progeny tests representing most of the range of Douglas-fir from British Columbia to California (Table 1) (Lipow et al. 2003). The genetic resources of other species in the region are represented in tree improvement programs to a lesser degree

(Lipow et al. 2002). Recognizing the value of Douglas-fir parents in progeny tests for gene conservation, members of the Northwest Tree Improvement Cooperative are thinning and maintaining a portion of the tests to preserve family identity for the future. A similar approach is being taken by the North Carolina State University – Industry Tree Improvement Program to set up genetic diversity archives to maintain unique genotypes, particularly those that may not be perpetuated in their mainline breeding populations (McKeand and Svensson 1997).

Table 1. Estimates of the numbers of parental selections included in first-generation Douglas-fir tree improvement programs throughout western Oregon and Washington, British Columbia, and northern California. (from Lipow et al. 2003)

Program	Number of first-generation breeding zones	Number of first-generation selections	Number of test plantations
Oregon and Washington			
NWTIC	72	19,421	620
USDA Forest Service [a]	14	3,152	110
USDI Bureau of Land Management [a]	9	2,219	60
Oregon Department of Forestry [a]	1	150	3
Washington Department of Natural Resources [a]	6	720	21
Weyerhaeuser Company	6	3,707	Not available
Other industry	16	1,809	47
California USDA Forest Service	9	1,800	36
British Columbia Ministry of Forests	2	650	102
Total	135	33,628	>999

[a] These organizations have independent programs in some regions, but in other regions they participate in NWTIC programs. Only the independent programs are listed here.

Tree improvement programs recognize the need to conserve genetic variation in breeding populations for purposes of continued genetic gain in advanced generations. Most breeding populations have between 200 and 400 parents, sufficient to allow continued genetic gain for several generations (White 1992, Johnson et al. 2001). For Douglas-fir tree improvement in western Oregon and Washington, several second-generation breeding programs have been initiated for different parts of the species range. Although a portion of the parents overlap between programs, each program has well over 200 unique, unrelated parents (Table 2).

Table 2. Number of first- and second-generation parents in Northwest Tree Improvement Cooperative Douglas-fir second-generation breeding programs.

Second-generation breeding program	Number of first-generation breeding zones combined into second-generation program	Number of first-generation parents	Number of second-generation parents
Washington Coast	5	1,203	294
Puget Sound	7	1,186	255
Washington Cascades	17	2,995	379
Vernonia	3	1,372	501
Trask Coast	11	2,541	444
Trask Inland	9	1,625	334
South Central Coast	6	2,048	423
North Oregon Cascades	14	3,208	394
Total	78	13,082	1,722

Another important component of gene conservation is protection of species from pests. Examples of concern over the loss of populations from disease and insects are numerous: chestnut blight (*Cryphonectria parasitica*), butternut canker (*Sirococcus clavigignenti-juglandacearum*), blister rust on white pines, pitch canker (*Fusarium moniliforme* var. *subglutinans*) on Monterey pine (*Pinus radiata*), *Phytophthora lateralis* root rot on Port Orford cedar (*Chamaecyparis lawsoniana*), emerald ash borer (*Agrilus planipennis*), and hemlock whooly adelgid (*Adelges tsugae*) to name a few. Research on and applied breeding for tolerance or resistance to pests is an important component of gene conservation work in the Forest Service, as well as an important component of work at universities, non-profits, and other organizations. Seed collections for populations at threat are also an important component. The Forest Service has seed banks for species in resistance breeding programs such as western white pine and sugar pine. Recently they have initiated seed collections of ash (*Fraxinus* spp.) in the Lake States for *ex situ* conservation to protect against population extirpation by the emerald ash borer. The Forest Service is working with CAMCORE to establish *ex situ* plantations of eastern (*Tsuga canadensis*) and Carolina hemlock (*T. caroliniana*) at risk from hemlock whooly adelgid (http://www.camcore.org/projects/hemlock.php).

CONCLUSIONS

Genetic conservation activities are being undertaken by a variety of organizations directed towards a range of native species in the United States. Although the Forest Service has always been concerned with gene conservation at the regional level and in research, they have taken a more active role recently with national-level agreements to store seed at the National Center for Genetic Resources Preservation and agreements for *ex situ* plantations of hemlock to protect against the hemlock whooly adelgid. Tree improvement programs also play an important role in gene conservation by maintaining first-generation parents and by maintaining genetic diversity in advanced generation breeding. *In situ* gene conservation is largely a result of reserves set aside for other purposes. A gap analysis was carried out in western Oregon and Washington to evaluate the effectiveness of current reserves for gene conservation purposes. Results indicated that most species are adequately protected. We recommend expanding this approach to other species in other regions.

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