

The California Forest Germplasm Conservation Project: A Case for Genetic Conservation of Temperate Tree Species

Tremendous species diversity, together with accelerating deforestation and land development, has been a formula for rampant extinction and community collapse in tropical forests. Conservationists have brought the crisis of tropical forests to the attention of the international community, showing that continued efforts are needed to conserve the biotic riches of these regions. The forests of temperate latitudes, although less in worldwide focus, also have urgent conservation needs, but of a somewhat different nature. As in tropical forests, biodiversity in temperate forests is high, and the threats faced are many. This great diversity resides not so much in high species numbers, but in the genetic variation that exists within species.

Genetic variation is not as readily tabulated and described as are species numbers, and its magnitude, distribution, and importance have not been impressed on the conservation community. The sum of information about genetic variation, called genetic architecture (Libby & Critchfield 1987), refers to the hierarchical patterns of genetic variation within and among species, races, populations, stands, and individuals. Knowledge of genetic architecture has long been valuable to forestry, where studies of geographic variation in survival, growth, and form date to the 1700s (Langelet 1971). In the last

chemical, and molecular variation has also been described. What emerges from these studies is that temperate, wind-pollinated trees, especially conifers, are among the most genetically variable organisms known. Using the few statistical measures (molecular data) that can be compared across taxonomic kingdoms, trees rank with some invertebrates (e.g., *Drosophila*) as containing the greatest allelic diversity within species of all taxa studied (Selander 1976, Hamrick et al. 1979). The current genetic picture depicts temperate tree species as unique moieties of great genetic variation containing highly heterozygous individuals that differ substantially from one another within stands and over geographic distance. The patterns reflect evolutionary history and recent adaptation. Continued survival and evolutionary success of species depend at least in part and perhaps substantially on the retention of these mosaics of intraspecific variation. Thus in temperate forest trees, species extinction is rarely a problem, and conservation biology should focus especially on the within-species level.

This is not meant to imply that temperate tree species are more variable genetically than tropical species. The general situation in tropical species simply is little known, although the few available

of genetic variation (Hamrick & Loveless 1986). That we do know of the high variation for temperate species creates a conservation imperative that should not be overlooked because of the lower species diversity of temperate compared to tropical forests.

This imperative is motivated not only by the genetic richness of temperate trees but also by the grave risks that threaten to contaminate, disrupt, and reduce this wealth. Many of the threats are similar to those facing tropical forests, whereas others are of minor impact in the tropics. Different threats affect different levels of genetic variation. In temperate forests, urbanization and land conversion threaten the survival of species occasionally and of populations often. Indiscriminate or poor forest and landscape management also alters and reduces the quality of genetic variation. For example, very large clear cuts or fires affect variation within populations. Natural regeneration from single or few remaining trees in such areas means that genetic variation in the next forest is reduced, and subsequent generations may become increasingly inbred. Even worse, the planting stock used to reforest such burns or clearcuts may be nonlocal, which introduces unknown and perhaps maladapted genotypes into a region and changes the pattern and level of ge-

duce. High grading was a common forestry practice, now discouraged, whereby the best trees were removed each harvest cycle and the less useful were left to reproduce. Centuries of such dysgenic selection modified the gene pools of once vigorous timber-producing forests of *Pinus densiflorus* and *P. thunbergiana* in Japan and particularly in Korea to stunted and malformed trees. Similar examples occur with *P. brutia* in Turkey and *P. roxburghii* in the Himalayas.

The indiscriminate ornamental planting of native species, especially with plants of unknown origin, disrupts genetic integrity at the population and individual level through gene contamination. For instance in California, one of the five native populations of Monterey pine (*P. radiata*) occurs in a small area on the urbanized Monterey peninsula, where ornamental Monterey pines are extensively planted. These trees came from New Zealand nurseries whose germplasm sources are southern hemisphere land races of unknown native origin. The old age and large number of the ornamentals at Monterey suggest that they contribute considerably to the pollen clouds of the native stands.

Even prudent forest management practices alter the genetic architecture of native species. Modern tree breeding, which is at an early stage compared to agronomic crop improvement, has the explicit goal of changing the natural genetic composition of commercial forests. Although tree breeders are committed to maintaining vigorous and genetically diverse forests, at least for traits of present value, natural gene pools will be altered as native trees are replaced by or interbred with genetically "superior" trees. Over the long term, tree breeding could greatly reduce genetic variation and increase inbreeding within improved lines. The relatively young state of tree breeding and the great genetic diversity in temperate forests create

opportunity for careful planning remains.

Recognizing these risks, forest geneticists and tree breeders have sought ways to minimize genetic erosion. Current forestry practice has established seed and breeding zones with well-defined transfer rules, has allowed or encouraged natural regeneration on many forest sites, and in tree-improvement programs has used large numbers of unrelated parents and kept strict pedigree control. Many forestry and tree-improvement programs maintain excellent seed banks with strict genetic control over entries. Theoretical models have been developed for establishing genetic-conservation programs that parallel main breeding efforts (e.g., Namkoong 1984).

Programs run by the Food and Agriculture Organization of the United Nations, the research stations of the U.S. Forest Service (notably the Pacific Southwest station), the Canadian Tree Improvement Council, and several private groups have directly tackled the problems and opportunities of genetic conservation in temperate forests. Another program is the California Forest Germplasm Conservation Project (CFGCP), a two-year-old program based on the Berkeley campus of the University of California. Funded by annual grants from the California State Environmental Protection Program, this program undertakes practical genetic-conservation activities, provides genetic-conservation information services, and conducts genetic research. The scope of the CFGCP includes rare and/or endangered species and widespread, commercially valuable species that are not endangered at the species level but have important populations that are or may be at risk.

The main goal of the CFGCP's practical genetic-conservation work is to gather and maintain ex situ collections of California tree species. One project involves repropagating a de-

Monterey pine is the most widely planted and intensively managed exotic conifer in the world, and diverse germplasm correctly identified to origin is highly valued. None of the five small native populations, however, is adequately protected; one population is in danger of extinction while three others are threatened. Several collecting trips led by pine geneticist W. J. Libby provided seeds for replicate hedge orchards, which were established in 1963 and 1966 and contained a systematic and unbiased collection of clones from all native populations. Each plant was maintained in a physiological state whereby shoot cuttings could be easily rooted. These clones and their seedling offspring were being tested worldwide and served as a major germplasm reserve for the species. Maintenance funding was withdrawn, however, and the plantations suffered heavy mortality. In 1985 the CFGCP contracted Applied Forest Genetics (Pt. Richmond, California), a company specializing in clonal forestry, to repropagate the surviving clones and to raise replacement seedlings from seed reserves. Clonal propagules of these plants will be outplanted in two plantation sites where long-term protection and maintenance can be better assured.

The CFGCP has also established a small but diverse and expanding seed bank of California conifers (of which there are 53 arborescent species). Many of the species in the collection are poorly represented or unrepresented in seed banks elsewhere. The seeds are usually collected during research expeditions and derive from large population samples throughout the species ranges in California. Seeds from single trees are kept separate and are prepared for long-term cold storage. All entries are inventoried in a microcomputer data base. We distribute small subsamples of seeds to conservation scientists for research and practical genetic conservation. Research studies that use these seeds provide genetic infor-

ing them more valuable for future use.

The information services objective of the CFGCP is met through both data compilation and education. GENREC, a genetic consulting group, was contracted to prepare a micro-computer data base of natural reserve lands in California that contains any of the 86 native tree species. This data base, available to the public, is cross-referenced with information and references on over 250 areas, and serves as a valuable tool for evaluating the adequacy of protection for each species and for conservation planning.

The CFGCP has participated in seminars and short courses, has cosponsored three graduate seminars on conservation biology at the University of California, Berkeley, and is involved in organizing a curriculum on conservation biology at that campus. In July 1988 the CFGCP will cosponsor a satellite conference on forest genetic-conservation to be held in conjunction with the Western Forest Genetics Association meeting in Davis, California.

Two kinds of genetic research are conducted by the CFGCP, genetic natural-history research on basic genetic parameters of tree species, and genetic-conservation research on use of basic genetic data in problem solving. The former provides baseline or inventory information on geographic variation and genetic architecture, mating systems, gene flow, selection indices, and genome organization (inheritance and map distance), all of which are essential for monitoring genetic changes and planning effective genetic management. We use the technique of enzyme electrophoresis, which is especially valuable for conifers, as both haploid and diploid tissues can be analyzed.

The conifers we have studied or plan to study in the coming year include the wide-ranging commercial species Douglas-fir and ponderosa

bigcone Douglas-fir, the 10 California cypress species, and Port Orford-cedar. Patterns of variation within and among the species are described with special reference to risk assessment and genetic monitoring (e.g., Millar et al. 1987, Millar 1987). For example, in several of the California cypresses, seeds collected in the 1930s from many of the same populations we have sampled are available, and changes in allele frequency and variance over 50 years can be analyzed.

The CFGCP also applies these baseline data to problems of conservation biology, such as determining minimum population sizes for in situ reserves and determining optimal sampling for ex situ collections. Efforts have focused on the application of empirical data to available models. For example, we have estimated priorities for ex situ sampling, including the intensity of collecting at a site versus the number of sites to sample, and we have estimated numbers of plants to sample given different gene diversity levels among populations (Millar 1987). Using equilibrium formulae for heterozygosity, we estimated for different species the number of individuals that would be required to maintain present levels of average heterozygosity in native populations throughout California.

In the next few years, the CFGCP plans to continue similar work on California conifers and to begin work on angiosperm trees. The California oak communities have been identified as a major conservation concern: Several species that were once wide ranging (e.g., *Quercus lobata*) have been reduced to small and highly fragmented populations. Because these species occur in hardwood rangelands, natural regeneration has been disrupted, and the oaks appear to be reproducing poorly. No genetic research has been done on the California oaks or related species. With colleagues at

hope of contributing to effective conservation management of temperate hardwood communities.

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References and Notes

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