

The Conservation of Diversity in Forest Trees

Why and how should genes be conserved?

F. Thomas Ledig

Deforestation, pollution, and climatic change threaten forest diversity all over the world. And because forests are the habitats for diverse organisms, the threat is extended to all the flora and fauna associated with forests, not only forest trees. In a worst case scenario, if the tropical forest in Latin America was reduced to the areas now set aside in parks and reserves, 66% of the world's plant species would go extinct, along with 69% of the birds and correspondingly high proportions of the other fauna (Myers 1984).

But immediate loss of species is not the only danger. Among the surviving species, many populations will be lost, taking with them much of the genetic diversity upon which long-term survival and evolution depend. A really alarming thought is: What if the loss of biological diversity does irreversible damage to our planetary life-support system?

At the root of this threat is human population growth. And to support our expanding population, we concentrate our agriculture on just a few species—20 species supply most of the world's food (US Committee on Genetic Vulnerability of Major Crops 1972). In these species, the genetic base is greatly reduced, both purposefully, to facilitate management, and by chance. This reduction leads to another problem of gene conservation: the

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uniformity and, therefore, vulnerability of our food and fiber supply.

Therefore, three different objectives are included under the rubric of gene conservation:

- Protection, particularly of domesticated plants, from genetic vulnerability—a uniformity that leaves them vulnerable to new environmental or biotic challenges
- Protection of endangered species
- Preservation of genes for future use.

These three objectives, in fact, have a common thread—the maintenance of genetic diversity.

My objective in this article is to outline the scope of gene conservation in relation to wild plants and, most particularly, forest trees. The important questions are: why conserve, what should be conserved, and how can it be conserved?

Vulnerability

The question of genetic vulnerability is most pertinent for domesticated crops, not wild plants. National attention was focused on genetic vulnerability by the corn blight of 1970 (US Committee on Genetic Vulnerability

of Major Crops 1972). In the United States, 75% of the corn crop was descended from a single mutant that was susceptible to the corn blight fungus.

In all the major crops in the United States, a few varieties account for most of the acreage. Seed companies or public agencies lower their cost if they can conduct one breeding program rather than many. In addition, there is a legitimate demand for crop uniformity to facilitate management and reduce the costs of cultivation, handling, and processing.

The corn blight was not the first instance in which uniformity had led to epidemics. World history has been altered by similar events, such as the Irish potato famine of the 19th century. Potatoes were the staple crop of Ireland. They were vegetatively reproduced, and most of the country grew a single clone (US Committee on Genetic Vulnerability of Major Crops 1972). When late blight struck, thousands of people died and others emigrated. The first great postcolonial wave of immigration to the United States (in the 1840s) was a result of that famine.

Breeding has not yet resulted in dangerous uniformity in forestry. Most tree breeders strongly emphasize the maintenance of variability (Zobel 1978). Usually, breeding programs in forest trees begin with selections from wild, undomesticated populations. Breeders have restricted these initial selections to one per wild stand and brought the selections from different stands together in seed orchards where they intercross, generating

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more variability than would be found in natural stands (Zobel et al. 1972). In advanced generations, breeders plan to maintain multiple populations to reduce the problem of inbreeding and counter genetic uniformity (Burdon et al. 1978). Given the commitment of breeders to maintain variability and prevent inbreeding, one might believe that there is no threat that tree crops will become as vulnerable as most agricultural crops are. However, dangers do exist. Some lines and clones are so outstandingly superior in favorable environments (Zobel et al. 1972) that growers could decide to plant crops of restricted parentage, or even single clones, in a gamble to maximize profits. Thus, the results of breeding can be misused.

Species preservation

International concern about species diversity is a result of three major considerations—*economic*, *ecologic*, and *esthetic*. Some conservationists may add a fourth concern, *ethical*.

Economic concern is apparent because the loss of a species means the loss of not one gene, but a whole genetic library. Many of our medicines, insecticides, herbicides, and other chemicals come from plants or are based on plant models. Of all prescription drugs, 25% come directly from plants (Farnsworth and Soejarto 1985). But most plants have not yet been investigated for potentially useful compounds. The National Cancer Institute took 25 years to test 35,000 species for antitumor activity. Tests for antitumor activity use crude extracts and reveal nothing about other potential uses of the plant chemicals. At the present rate of extinction, thousands of species will be gone before they can be evaluated. The extent of consequent economic loss is not predictable, but potentially enormous (Oldfield 1984).

Ecologic concerns arise because the loss of species could mean the loss of entire ecosystems through a cascade effect (Ehrlich and Ehrlich 1981). Terborgh (1986) provided an example from the tropics. Less than one percent of the local plant diversity in the Amazon of Peru seems to support almost all of the frugivores for three months of the year. The frugivores include the primates, birds, and ro-



Figure 1. Sugar pine in the Sierra San Pedro Martir of Baja California, an area of unique diversity for the species.

idents. If these keystone plant species—the palms, figs, and a few nectar sources—were lost, the frugivores would be lost. And if the frugivores were lost, most of the other plant species that depend on them for seed dispersal would be lost. Thus, if a few keystone species are removed, a whole ecosystem could collapse. And if we drastically modify or destroy an ecosystem, will we disrupt the biogeoclimatic cycles that support all life on Earth?

The third reason for protecting endangered species is esthetic (for a discussion of the cultural importance of biotic diversity, see Office of Technology Assessment [OTA] 1987). Esthetic reasons are the hardest to pin down, but I believe that diversity is necessary to the health of humanity. Some sense of diversity seems necessary for sanity. Even if I never see a highland gorilla or an African lobelia, I feel better knowing they are still there. And I feel diminished knowing that the wild Cal-

ifornia condors are now gone.

Concerns for the safety of endangered species are great enough that they have sparked legislation applicable to the conservation of biological diversity. The Endangered Species Act was passed in 1973, in part as a result of economic and ecologic factors, but mostly in response to esthetics. In the continental United States, only two tree species are formally listed as endangered. Information on another four species supports proposing them for endangered status, and another nine species and two varieties need further study (US Fish and Wildlife Service 1985).

The Endangered Species Act was closely followed by the Forest and Rangeland Renewable Resources Act in 1974 and the National Forest Management Act in 1976 (Norse et al. 1986). These latter acts require the national forests to prepare land management plans that "provide for diversity of plant and animal communities." The plans are being released for comment now by each of the 156 national forests. They are written with a 50-year planning horizon, but they will be revised every 15 years. Within the past year the Sierra Club Legal Defense Fund and other groups have brought several suits under the National Forest Management Act, charging that some national forests have failed to provide for diversity.

At present no laws provide specifically for protection of populations or genes. Only named taxa (species, subspecies, or varieties) are addressed in the forest management plans. But, the National Forest Management Act could be used to justify the conservation of genetic resources on the intra-specific level.

Preservation of genes

Why preserve genes? They are the raw materials for breeding and continued evolution. Although markets may change and new pests may appear, breeders will not be able to respond without a pool of genes. An example of a change in market conditions is the increased demand for tissue, newsprint, and printing paper from southern pines (Zobel and Talbert 1984). Initially, the major paper product from southern pines was kraft bags and corrugated boxes. Breeders select-

ed trees that had wood of high specific gravity because they gave good pulp yields and resulted in bags with desirable properties (e.g., high tear strength). But wood of somewhat lower specific gravity is preferable for tissue and printing papers. Fortunately, trees that had been selected for growth and form before they were known to have low specific gravity, had been clonally propagated and preserved in research orchards, called clone banks, and therefore were available to breeders when demands changed.

The literature is full of examples of new pests, either introduced, like chestnut blight (McKay and Jaynes 1969), or those that arose in response to agricultural practices, such as native insects that became significant pests of introduced crops (Holling and Goldberg 1971). And recall the terrible new diseases that have appeared in our own species in the last 20 years—Legionnaires disease, Lyme disease, acquired immunodeficiency disease (AIDS), and Tahoe disease.

What genes do we want to save? All if we could, because it is impossible to predict what may be useful in the future. Preservation of genes takes on special importance now that they can be transferred between virtually any organisms using recombinant DNA technology.

How do we save these genes? Will we save enough genetic information if we save one individual? One population? Many populations? Our options are to systematically sample or to launch studies of a species' genetic architecture to identify representative and unique genetic resources.

Systematic samples. Without specific information, our best approach is to preserve samples systematically—both from representative populations and from extreme or unusual populations. For example, when the Institute of Forest Genetics undertook a major collection in sugar pine (*Pinus lambertiana* Dougl.), the scientists knew only that elevational variation was pronounced (Harry et al. 1983). So they sampled from various elevational transects in the Sierra Nevada, systematically covering the latitudinal range, and they sampled the Transverse Ranges and a few sites in the Klamath Mountains—all as representative of

the body of the species. But they also sampled from Junipero Serra Peak in Alta California and the Sierra San Pedro Martir in Baja California (Figure 1) as unusual sites, representing relictual populations or populations that were, perhaps, adapted to special conditions. In fact, sugar pine from both areas proved unique. Sugar pine from Junipero Serra had an unusually high frequency of a major gene for blister rust resistance, and the Baja sample is unusually blue in foliage color, which might be useful in breeding for droughty conditions.

Unfortunately, representative populations have already disappeared from the ranges of many wild species. Forests have been eliminated at lower elevations, and the land converted to agriculture. West of the Cascades in Washington and Oregon, forest land has decreased five percent since 1952 (Harris 1984). And even where forests were not eliminated, early loggers selectively removed the best trees, a practice that may have eroded the genetic resource. It is especially unfortunate that low-elevation populations were eliminated, because those were the populations likely to carry genes for high productivity under domesticated conditions (i.e., adapted to fertile soils). But they were lost before anyone even considered their genetic value.

Genetic architecture. So far, conservationists have been forced to proceed with little data on the distribution of genetic variation and have followed a common-sense, systematic scheme for sampling genetic resources. But we do have the technology to get information on the distribution of genetic variation quickly, refine efforts, and decide where the representative genes are and where unique genes or gene combinations exist. That technology is the electrophoretic separation of proteins and the analysis of variants called isozymes to quantify gene frequencies (Conkle and Adams 1977). Most of the rapidly accumulating information on wild species of plants and animals comes from isozyme analysis.

Several conifers have already been subjected to genetic analysis, but unfortunately, generalizing results to new species is difficult. Species of limited distribution have a tendency



Figure 2. Torrey Pine, a rare and genetically depauperate species, at La Jolla, California.

toward little variation and widespread species tend to have greater variation (Ledig 1987). But the exceptions are striking. Loblolly pine (*Pinus taeda* L.) has a wide range and is highly variable (Conkle 1981), but red pine (*Pinus resinosa* Ait.) also has a wide range and is genetically depauperate (Fowler and Morris 1977). Torrey pine (*Pinus torreyana* Parry ex Carr) is restricted to two small populations, each of which is completely depauperate but genetically unique (Figure 2; Ledig and Conkle 1983). Santa Lucia fir (*Abies bracteata* D. Don.) has a small, fragmented range and is almost depauperate also, but its populations are not unique (Ledig 1987).

Great Basin bristlecone pine (*Pinus longaeva* D. K. Bailey) also has a fragmented range. It is restricted to mountaintops, but it has high levels of diversity with no differences among populations. Over 90% of the total variation can be found on any one mountaintop (Hiebert and Hamrick 1983). Even more complicated patterns have emerged: western white pine (*Pinus monticola* Dougl.) is uniform across most of its range but highly variable in California (Steinhoff et al. 1983).

Electrophoresis provided a tool to locate genetic resources. But we can

not yet generalize from plant species to plant species, and the number of species that remains to be studied is huge. For trees alone, there are 684 native species in the continental United States (Little 1981). Even with isozyme electrophoresis, it will be a long time before they are all adequately studied, let alone all the temperate herbaceous flora or the far greater botanical riches of the tropics.

Conservation efforts

Identifying genetic resources is only part of the job. Once identified, how do we save them? Conservation efforts are usually classed as *in situ* and *ex situ*, meaning in the natural position (or in place) and out of the natural position, respectively.

Ex situ preservation. *Ex situ* preservation is accomplished in botanical gardens, test plantations, seed orchards, clone banks, seed storage banks, tissue cultures, and DNA libraries. The major problems are a lack of long-term, continuous funding and adverse changes in the preserved materials.

Botanical gardens and arboreta are common, but they preserve too small a genetic base, usually maintaining single trees, or, at the most, a few specimen trees of any given species.

Provenance, or seed source, tests use a common garden environment to compare offspring from a range of populations. They maintain a broader genetic base than arboreta, but are usually restricted to commercial or potentially commercial woody plants. In addition, they have a lifetime of only 50 to 100 years, and are not self-perpetuating. No provisions are made for replacement once test results are complete. Another problem is that selection takes place in an environment alien to most of the sampled populations; therefore, genes for which a population was saved may be lost by mortality.

For example, the Institute of Forest Genetics sampled Coulter pine (*Pinus coulteri* D. Don) throughout its range from the Sierra de Juarez of Baja California to the San Francisco Bay Area of Alta California. Seeds from several populations were sown and the progeny were raised in research gardens in Placerville, California, at a

latitude near the northernmost limit for native Coulter pine. The seedlings were then planted in a replicated, randomized test. First-year survival in the progeny from Chalk Peak, which is south of Monterey, was only 24%, but in progeny from San Benito Mountain, 87%. Selection among populations is already obvious, and it is likely that mortality within populations was also selective, eliminating the very diversity we should hope to preserve.

Seed orchards are plantations established for the production of commercial quantities of seed of important timber species. These orchards frequently are established with grafted clones. For species like loblolly pine, these orchards preserve hundreds of clones. However, in an active breeding program, a seed orchard lasts only about 20 years before it is replaced by the next generation of breeding.

Clone banks, like seed orchards, are another tool of the breeder but have a broader base and a longer life. Like seed orchards, clone banks are usually established with grafted clones. Unlike seed orchards, the purpose of clone banks is long-term preservation. Over 8000 clones of loblolly pine alone are preserved in clone banks in the southeastern United States (McConnell 1980). However, because of their costs, clone banks are generally established only for the most important commercial species.

Seed storage is more important for conservation of most species. It is the most obvious way to preserve samples of the genetic resource, yet is not without limitations (Roberts 1975). The most important limitation is that not all seeds can be stored. For example, seeds of poplars (*Populus* spp.) or oaks (*Quercus* spp.) remain viable for only a few weeks to a year. Poplars and oaks alone represent approximately 20% of all tree species in the continental United States. In the tropics, species that can be stored as seed are even less common (Ellis et al. 1985). Conifer seed can be stored for decades, but eventually seed must be renewed by growing new trees, a second limitation. The process of growing plants to produce fresh seeds is expensive, and, during the process, selection may modify the genetic resource in the same way that selection modifies provenance tests. A third lim-

itation is that not even stored seeds are immune to change. Mutations accumulate rapidly, even at low temperatures (Roberts 1975).

Finally, adequate facilities for long-term seed storage of forest trees do not yet exist (Belcher 1980). The National Seed Laboratory in Fort Collins was established for crop plants such as small grains, cotton, tobacco, and soybeans. The storage conditions used, open containers at 4°C, would be unsuitable for most tree species. The National Tree Seed Laboratory at Macon, Georgia, uses better conditions—sealed containers at -7°C. But it can handle only 5900 samples, and those mainly for a short term. Crop species in the National Seed Laboratory are represented by many samples (e.g., more than 40,000 seed samples for the grain crops—wheat, barley, oats, rye, rice, sorghum, and maize; White and Hyland 1973), so 5900 samples are too few to cover the 684 tree species native to the United States. The National Tree Seed Laboratory's primary functions are to test seed and act as a clearing house for seed exchange. Therefore, we are left with no long-term seed storage facility for forest trees or for the much greater number of woody shrubs and other wildland plants.

Tissue culture is promising, but genetic change occurs at even more rapid rates in unorganized tissue or cells than in seeds (Chaleff 1983, D'Amato 1975). Another problem with tissue culture is that we cannot yet regenerate whole plants from cultured tissues of most species. Only a few species have been regenerated successfully.

What about DNA libraries? DNA of forest trees can be fragmented and the fragments incorporated in bacterial DNA and perpetuated in bacterial cultures (Kinlaw et al. in press). But that would require maintenance of 10^6 to 10^7 cultures to preserve the DNA from a single tree. Therefore, the possibility of maintaining DNA from a large sample of trees is unthinkable.

The alternative is to read the DNA sequence to provide a blueprint for its reconstruction, and thus make the bacterial cultures superfluous. However, reading the DNA and making sense of it is a monumental task. Consider the current proposal to sequence the entire human genome. That project, if approved, could take

as much as 30,000 person-years and upwards of two billion dollars (Roberts 1987). The human genome has three billion nucleotide pairs, while conifer genomes have many more. The sugar pine genome is 5.5 times longer than the human genome (Dhillon 1980). Can we imagine sequencing the DNA of even one tree, let alone the range of variation within one tree species or representatives of all our tree species and wildland plants?

To summarize, all *ex situ* techniques have disadvantages. For example, genetic change is a problem in provenance tests, seed banks, and tissue culture. But the major problem is continuity. *Ex situ* conservation depends on continuity in policy and funding. If we establish a seed bank today, will it continue to be funded five years from now? How much faith can we place in governments, their stability, and consistency? The same questions may be asked of *in situ* conservation, but *in situ* reserves are often less costly.

***In situ* conservation.** The best solution for most species is to leave them *in situ*. *In situ*, the problem is not to preserve samples of genes; whole co-adapted gene complexes and biological communities must be preserved. Whatever keeps the population functioning as a viable, natural unit must be intact. This task requires protection, and perhaps management, of the whole support system—for example, the pollinators, seed dispersal agents, and the characteristic patterns of disturbance.

At first glance it would seem that many categories of public lands already function as *in situ* gene banks in the United States. About 28.5 million ha of federal land is in national parks, monuments, and preserves.¹ Another 11.5 million ha are in 327 wilderness areas (US Forest Service 1985a). Together these public lands cover a large area, but the problems of conservation are not solved.

These lands are almost invariably a biased sample of the resource. They are concentrated at high elevation. And while high mountain areas may be our greatest scenic treasure, biolog-

ically they are least diverse (Harris 1984). In addition, the restrictions on management of national parks and wilderness areas may preclude measures necessary for preservation of the genetic resource. For example, seral species may require disturbance in order to regenerate themselves, but protection has reduced the incidence of fire, often the primary agent in retarding succession.

Research Natural Areas (RNAs) are more suitable for conserving genetic resources in some ways. RNAs are a network of field sites established on federal lands for ecological research (Federal Committee on Ecological Reserves 1977). One of their stated functions (US Forest Service 1985b) is to "preserve and maintain genetic diversity." The areas are systematically located to preserve representative plant communities; therefore, they are not concentrated at high elevations. The minimum size of an RNA is 121.4 ha (300 acres), but the 150 established by the Forest Service, as of 1985, averaged 470 ha.² The Bureau of Land Management has 326 more, but these are not as well documented or protected.

One problem with RNAs is their small average size. First, species extinction is likely in small reserves. Second, if surrounded by plantation forest, pollen contamination may be a problem for the tree component; i.e., the native genetic resources may be modified or swamped by gene migration from surrounding plantations. Third, some foresters have opposed establishment of RNAs. Many of the national forests are under administrative pressure to increase timber harvest, and RNAs reduce the land base for timber production. Therefore, forest supervisors are reluctant to designate RNAs in areas of prime timber types, and this reluctance has slowed establishment (Henson and Nelson 1986). The record of other agencies, such as the Bureau of Land Management, has been no better. I single out my own agency because it is most familiar to me, but in fact it is generally responsive to criticism.

Botanical areas are another category of reserve. However, few of these

¹Edward R. Haberlin, 1986. Personal communication. National Park Service, San Francisco, CA.

²Russell M. Burns, 1986. Personal communication. Research Natural Areas Program, USDA Forest Service, Washington, DC.

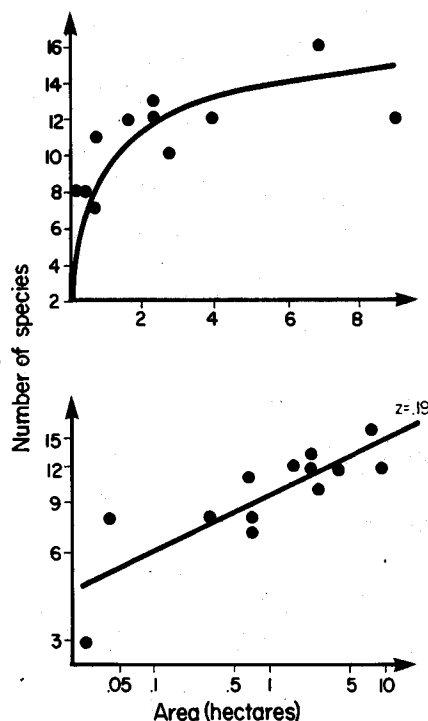


Figure 3. Species-area relationship for arctic-alpine plant species (after Riebesell 1982): numbers of species and the areas of the alpine ecosystem in the Adirondack Mountains, New York (top—arithmetic scale; bottom—logarithmic scale).

are established on federal land, and they can be extremely small, perhaps only a few square meters in area. The Ancient Bristlecone Pine Forest in the White Mountains of the Inyo National Forest is a large botanical area that is an exception to the rule; it includes 11,732 ha (of which 42 ha are private land). Other species are protected in state parks and forests, in wildlife refuges, and in private natural areas, such as those of The Nature Conservancy. Finally, some wildland plants exist in roadside and streamside leave-strips, mandated under various state and national forest regulations, and on railroad right-of-ways.

While many types of set-asides preserve natural forest-, shrub-, desert-, and wet-lands and their associated species, the major question regarding *in situ* preserves is: Are they really adequate? Probably not. Gaps are likely in the distribution of reserves. Furthermore, the theory of island biogeography indicates that small habitat fragments are susceptible to loss of species and, of course, genes (Harris 1984). As the size of reserves decreases,

so do the number of species (Figure 3). This relationship is linear when transformed to a logarithmic scale. Also, the adequacy of a reserve depends on surrounding land use (see Schonewald-Cox, page 480 this issue). If there is no adjacent source of immigrants, species collapse will be rapid and continue to erode the resource (Wilcox 1980).

To offset some of these problems, I argue for a new category of management unit, a large unit to be called a Genetic Resource Management Unit (GRMU) (suggested by Krugman 1984). A GRMU would have as a primary function the protection of genetic resources, either single species or an entire community, but could be used for other economic benefits, such as grazing or timber harvest, as long as the other uses did not threaten the primary function.

Timber harvest is not necessarily incompatible with conservation of genetic resources. If gene conservation was established as the primary function of a unit, timber could still be harvested in a way that assured adequate regeneration with seed from the *in situ* populations, including the entire diversity of woody and herbaceous species present. Preferably, natural regeneration would be used, but planting with seedlings from the native stand might be acceptable if done at high density, providing an opportunity for natural selection. Timber production would be less than that under intense culture with "improved" seed orchard stock, but not reduced so much that it would generate the type of opposition that has characterized the establishment of RNAs on some national forests. Conservation efforts will be more successful if conservation and development go forward together (see Dasmann, page 487 this issue).

Since GRMUs would not be removed from production, they could be large enough to reduce the impact of pollen contamination from artificially regenerated sites. Conservationists should inventory and evaluate the present network of natural areas to determine where it is inadequate and persuade federal and state land management agencies to establish GRMUs to fill the gaps. The California Forest Genetic Sources Catalog prepared for the University of Califor-

nia's Wildland Resources Center represents a first step in this direction (Genetic Resources Consultants [GENREC] 1987).

A global outlook. Most of the preceding discussion applied to the United States, which has a tremendous genetic resource in its forest species. These US resources are important to the economy of many other countries. The United States is a great exporter of genes. Monterey pine (*Pinus radiata* D. Don.), loblolly pine, slash pine (*Pinus elliottii* Engelm.), and Douglas-fir (*Pseudotsuga menziesii* [Mirb.] Franco) from the United States are grown around the world. More than 350,000 ha are planted to Douglas-fir in Europe (Hermann 1987); 2,800,000 ha are planted to loblolly and slash pines in Asia, Africa, and Latin America (McDonald and Krugman 1986); and more than 3,000,000 ha are planted to Monterey pine alone, mainly in Chile, New Zealand, Australia, and Spain.³ This dependence confers a tremendous responsibility on us: the responsibility to protect the genetic resources upon which the wealth of other nations, as well as our own, may depend.

But deforestation is a global problem. How does the situation in other countries compare, particularly developing countries? Our nearest neighbor, Mexico, can be taken as an example. According to the most recent authoritative account (Martinez 1948), Mexico has 107 species of conifers (when varieties are included, there are 143 named taxa). Some of these are the major tropical pines, such as Caribbean pine (*Pinus caribaea* Morelet), Ocote pine (*Pinus oocarpa* Schiede), and Mexican weeping pine (*Pinus patula* Schiede and Deppe), which have been exported to Asia, Africa, and Australia and become important in plantation forestry.

New species and populations of rare species are still being discovered, although it has been nearly a half millennium since the Conquest and the exploration of Mexico by Spain. The Institute of Forest Genetics is working with Chihuahua spruce (*Picea chihuahuana* Martinez), discovered in the Sierra Madre Occidental

³A. R. Griffin, 1988. Personal communication. CSIRO, Canberra, A.C.T., Australia.

only in 1942 (Martinez 1948). Other spruces have been found even more recently (Figure 4). As little as 20 years ago, only nine populations of Chihuahua spruce were known (Gordon 1968). Today there are 27, and in the last few years the species has been found in the Sierra Madre Oriental. Taxonomic status of the Mexican spruces, and Mexican conifers in general, is uncertain. And the oaks seem to be even more numerous, more variable, less studied, and more difficult to classify. Botanical exploration and taxonomic investigations are sorely needed. In contrast to Mexico, the United States is well explored and has only 96 species of conifers (Little 1981), although we have five times the land area (925.5 million ha vs. 197.2 million ha).

Mexico trails the United States in protecting its genetic resources. *In situ* reserves are one measure of comparison. The United States has 39.9 million ha in national parks and wilderness areas, or four percent of its total area. Mexico has only 0.8 million ha, or 0.4% its total area, in *in situ* reserves. Proportionally, it has put aside only one-tenth as much land to protect even greater botanical riches than those of the United States (OTA 1984).

In most other developing countries, the situation is worse—a particularly tragic fact because developing countries are the centers of the world's genetic resources. Tropical moist forest covers only 7% of the land area, but it is the habitat for 40% of all species (Myers 1984). Species are being eliminated before they are even discovered.

Kenya is one of the few developing countries that has set aside major areas for conservation. It has put six percent of its land into national parks. But it is extremely difficult to protect parks against population pressures. In Kenya, population growth averages seven children per woman. This population growth, if unchecked, means that parks in Kenya and elsewhere could turn out, in Norman Myer's (1984) words, to be merely "paper parks." Single-use preserves that lock people out are in jeopardy, so the GRMU concept may be of value in developing countries as well as in the United States. As Dasmann (page 487 this issue) notes, local communities

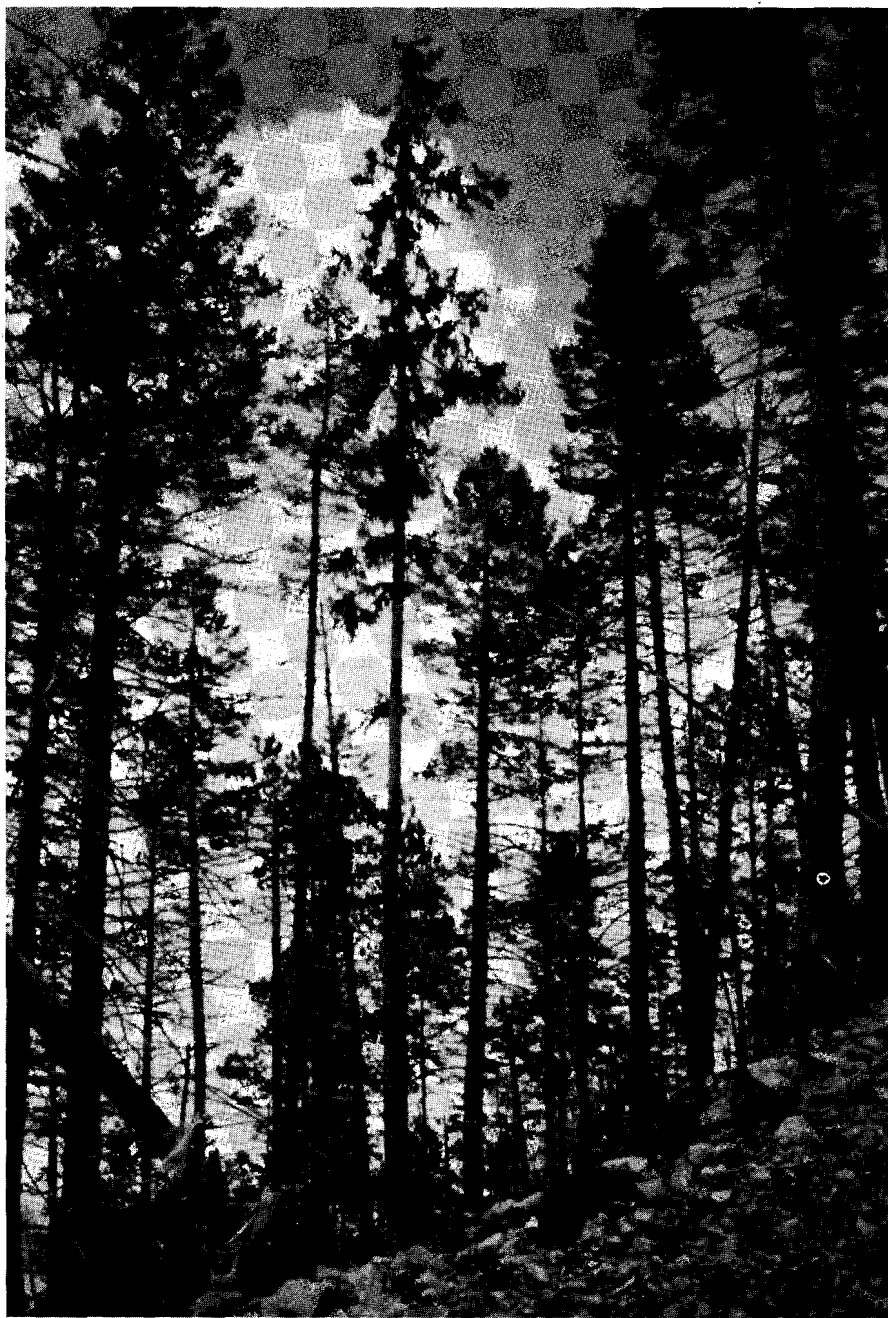


Figure 4. Mexican spruce (*Picea mexicana* Martinez) discovered in 1961 in the Sierra Madre Oriental, Nuevo Leon, Mexico.

must support reserves, not be displaced by them, if reserves are to fulfill their function efficiently. In the United States, as in developing countries, conservation must be integrated with other land-use practices.

As for *ex situ* conservation, only two organizations are dedicated to conservation of tropical trees in Mexico. The Central America and Mexico Coniferous Resources Cooperative (CAMCORE) is headquartered at North Carolina State University. The

Oxford Forestry Institute is a division of Oxford University in England. Both concentrate primarily on conifers. In addition to these organizations, the Institute of Forest Genetics (with aid from USDA Office of International Cooperation and Development) has begun a cooperative program with the Mexican Centro de Genetica Forestal to map genetic resources using isozyme electrophoresis. But this effort is pitifully small, and it leaves the tropical hardwoods, a much larger

group than the conifers, almost totally unprotected. The need is clear, but the task is enormous, and time is running out.

Conclusions

Nevertheless, there is still time to save the majority of the world's forest species, even in the tropics. With active intervention to maintain viable populations, perhaps even controlled breeding and restocking, small areas of a few hundred hectares could function as preserves. However, a few hundred hectares is too small, in isolation, to prevent associated fauna, especially large carnivores, from going extinct. Some other solutions to deforestation are to be found in plantation culture, habitat restoration, and integration of conservation with nondestructive use. Plantation culture of fast-growing timber, pulp, and fuelwood species has already helped to meet local needs and reduce the rate of deforestation (Rocca Calienes 1985); Janzen (1988) is demonstrating the feasibility of forest restoration in Costa Rica; and GRMUs may provide a mechanism for conserving genetic resources and simultaneously providing economic benefits. Certainly, exploitation without conservation leads to a situation in which no one benefits for long (Gentry and Vasquez 1988). Measures that both conserve resources and provide economic benefits can forestall the collapse of our natural ecosystems and buy the world precious time to attack the root of the conservation problem—population growth and concomitant poverty.

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