DO WE REALLY NEED CONSERVATION PROGRAMS FOR THE SOUTHERN PINES?

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Abstract: --The importance of conservation programs for rare endemics like *Pinus jaliscana* in Mexico is apparent. The species has only been found at 9 locations in the state of Jalisco in the western part of the country. It often occurs near streams or along northern or western slopes of canyons where moisture deficits are not extreme. Population sizes range from only 5 to 2000 ha. Logging roads have now been placed through many of the remaining *P. jaliscana* stands and urgent conservation activities are needed at some locations to protect the genetic base of the species.

The need for conservation programs for economically important species like *Pinus elliottii* and *Pinus taeda* is less obvious. Millions of hectares of both species have been established in plantations world-wide, and long term breeding programs with clonal archives are in place in the southern United States.

Recent studies using RAPD-based phylogenetics indicate that taxa in the *Australes* subsection (that includes both *P. elliottii* and *P. taeda)* were originally derived from ancestors of Mesoamerica pines in the *Oocarpae* subsection. Gene groups from progenitor Mesoamerica *Oocarpae* may be especially useful in breeding programs for southern US pines in the next century. Strategies could be developed to use genes of progenitor species to improve disease and insect resistance, wood quality, and growth. With advancements in forest biotechnology and the future ability to identify individual genes that control the expression of important traits, conservation of genes in ancestral related species ultimately may be as important as identifying unique genes in target species. Concepts about forest gene conservation of southern pines need to be broadened to accommodate a range of new opportunities. Specifically, conservation needs to be viewed as a tool to improve productivity.

Keywords: evolutionary history, closed-cone pines

INTRODUCTION

Forest conservation issues will become more important in the southern United States in the next century as genetically modified seedlings become available to growers. The public will want to know how traditional tree breeding programs for southern pines have changed patterns of genetic diversity. Do genetic base populations of southern pines exist and are they large enough to ensure broad adaptability and disease resistance? How will cross fertilization between genetically modified southern pines and those in native stands or plantations, whether by accident or intent, alter the genetic composition of progeny? Foresters will need to have sound answers to the types of questions asked by an increasingly educated and aware public.

The conservation of southern pines like *Pinus taeda* (loblolly pine) and *P. elliottii* (slash pine) has not become a major issue in the US in the past for several reasons. First, the geographic range of the economically important southern pines is immense and these are not imminently threatened. Large areas of plantations of southern pines also exist as exotics in countries like Australia, Argentina, Brazil, China and South Africa (Bridgwater et al. 1997). Second, both species are native to the US (rather than exotic) and the local populace has accepted the need for plantation forestry and the wood and paper products that are produced. Third, clonal banks exist throughout the South that contain many of the original first generation selections made 30 years ago. With such large areas of *P. elliottii* and *P. taeda,* and the existence of archived

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genetic material, the question can reasonably be asked about the need to do anything additional for their conservation.

This paper re-evaluates the importance of conservation of loblolly and slash pine. The evolutionary history of pines *in* both *Australes* and *Oocarpae* subsections are described in terms of the beneficial genes that they might posses. A different vision about forest gene conservation of the southern pines is recommended.

BACKGROUND

Usually, the terms "biodiversity" and "genetic diversity" are misused in discussions about forest conservation. Biodiversity is defined as "the variety of life forms, the ecological role they perform, and the genetic diversity they contain" (Kemp 1993). Genetic diversity is defined as "the heritable component of variation", and therefore, is a component of biodiversity (Kemp 1993). Most often when foresters talk about the conservation of biodiversity, they really mean genetic diversity. Conservation does not imply preservation or absolute protection, but wise management of genetic resources for both present and future (human) generations (Kemp 1993).

Pinus jaliscana: A case study for conservation

Some species generate much interest for their conservation. *Pinus jaliscana* is a rare endemic native only to the mountains of western Jalisco, Mexico. Its geographic range is approximately 120 km from north to south and 50 km from east to west. It was first described in the early 1980s by Perez de la Rosa (1983) and belongs to the closed-cone pine group that includes *P. patula* and *P. oocarpa.* In 1998, the first provenance and mother tree collections were initiated by the CAMCORE Cooperative, North Carolina State University (NCSU), and collaborating institutions in Mexico for the purpose of establishing *ex situ* gene conservation plantings (Dvorak et al. 1998). Based on two years of fieldwork, 9 provenances have now been identified in the mountains of western Jalisco that range in size from 5 to 2000 ha. Ironically, more intensive explorations in the area for *P. jaliscana* populations were made possible by newly constructed logging roads financed by local sawmillers.

Pinus jaliscana is found predominantly in canyon bottoms near streams or on the northern and western slopes of mountains. Each canyon bottom has a different vegetation composition as a result of altitude and aspect differences as well a history of fire. Seeds from the *P. jaliscana* collections are being distributed to CAMCORE members in Argentina, Mexico, Brazil and South Africa for conservation plantings and molecular marker studies are underway at NCSU to better understand the species genetic structure.

THE ORIGIN OF LOBLOLLY AND SLASH PINE

Whereas foresters can easily perceive the need to conserve *P. jaliscana,* such enthusiasm does not exist for loblolly and slash pine for reasons already discussed. However, might unique genes that are useful for the future development of both loblolly and slash pine be found in their progenitors? These unique genes could impart better adaptability, disease resistance and wood properties to both species.

It has been assumed, based on fossil records, that the *Australes* subsection (that includes loblolly and slash pine) originated in refugia in the southern United States during the Eocene (Millar 1993) or Miocene (Krupkin et al. 1996, Axelrod 1980). Speciation may have been driven by drier climates in the southern US generated by mountain uplifting in western North America (Axelrod 1980).

However new research recently conducted at NCSU using RAPD molecular markers now suggests that the *Australes* group of pines originated from Mesoamerica *Oocarpae* in Mexico and Central America (Dvorak et al. unpublished data). The theory suggests that the progenitors of Mesoamerica *Oocarpae* originated in northern Mexico in the Miocene and migrated east across the United States. After millions of years of evolution, present-day *P. palustris, P. echinata,* and *P. taeda* formed. Similarly, the progenitors of Mesoamerica *Oocarpae* also migrated south into Mexico and Central America during the Miocene and eventually entered the Caribbean and Florida to form present-day *P. elliottii.* Results suggest that both loblolly and slash pines are evolutionary very young species. Genes in the progenitor Mesoamerica *Oocarpae* may be the ones to ultimately conserve to promote the future development of the target species like loblolly and slash pines.

CONSERVATION OF MEXICAN PINES TO IMPROVE SOUTHERN PINES

Disease resistance serves as a good example of how genes from progenitor species may be useful in developmental programs for US southern pines (see Table 1).

Table 1. Percent live stem for seedling inoculated with pitch canker and fusiform rust infection levels at the seedling stage (after Hodge and Dvorak 1999, Lambeth et al. 1997, and Tainter and Anderson 1993).

Species	**Pitch Canker**	**Fusiform Rust**
P. radiata	1%	90%
P. patula	25%	50%
P. greggii (S)	23%	65%
P. teocote	---	30%
P. jaliscana	99%	29%
P. oocarpa	97%	80%
P. tecunumanii (L)	93%	78%
P. caribaea hondurensis	91%	90%
P. elliottii (improved)	32%	72%
P. taeda	69%	78%

The values for pitch canker infection show that *P. elliottii* is moderately susceptible to the disease and that *P. jaliscana* is very resistant. The values for fusiform rust infection suggest that both loblolly and slash pine are moderately susceptible and *P. teocote* and *P. jaliscana* are moderately resistant. Utilization of genes in *P. jaliscana* or *P. teocote* to promote better fusiform rust resistance in loblolly or slash pines may be beneficial. Utilization of genes for pitch canker resistance in *P. jaliscana* and *P. oocarpa* may be the only way that *P. radiata* growers will be able to protect themselves against this disease problem in Chile, New Zealand or Australia. Of course, the opportunity for finding such genes rests on our ability to conserve base populations of Mexican pines.

The wood properties of several Mexican pines in the *Oocarpae* group are different than loblolly and slash pines. Some exhibit higher wood density, or lower extractive percentages than the southern pines. *Pinus tecunumanii* in south central Brazil had 12% less bark content per unit volume than did loblolly pine grown in the same region (Villela per. comm.). Can inclusion of genes from Mexican pine species into US southern pines improve their wood quality? Should efforts to change the amount of lignin in loblolly pine in the southern US through biotechnology be intensified, or do trees with those wood properties already exist in wild stands in the mountains of Mexico?

USE OF HYBRIDS

There is little doubt that pine F(1) hybrid program combined with vegetative propagation using Mesoamerican pines will be important in parts of Latin America and southern Africa. Already *P. greggii x P. patula* crosses are being made to combine the cold and drought tolerance of *P. greggii* with the good growth of *P. patula* for commercial use in South Africa. Likewise, opportunities exist from hybridization of Mexican pines with southern pines to improve growth, disease resistance and wood properties in places like southern Brazil and coastal Argentina. The CAMCORE Cooperative has initiated an experimental hybrid-crossing program that includes the southern pines and the Mexican pines. Successful crosses have been made of *P. taeda x P. tecunumanii* and *P. taeda x P. greggii* in South Africa (Dvorak et al. unpublished data) and such crosses will eventually be tried and tested in Argentina and Brazil. Hybridization may be one of the ways that organizations in the southern US can incorporate special genes of selected Mexican pine species into the genetic base. More study needs to be given to understand the inheritance patterns of important traits at the gene level in hybrid crosses. Sophisticated biotechnological approaches may also prove useful for including new sets of genes into target species.

DISCUSSION

Forest gene conservation needs to be viewed as a tool to improve productivity rather than a social obligation with little financial return. Additional conservation programs for loblolly and slash pine are now not needed in the southern United States because genetic material from hundreds of selections have already been placed in clonal banks across the south. However, these clonal banks only have value when their genetic composition is well documented and the genetic material is accessible to the users, whether they be industry or state agencies. Recent industry acquisitions and mergers will skew ownership patterns of this genetic material. Important decisions about how to manage first generation clonal banks will eventually have to be made as they grow older.

Because of the close evolutionary relationships between the Mesoamerica *Oocarpae* and *Australes*, and the potential for finding useful genes in progenitor species, foresters in the southern US should be keenly aware of conservation efforts of pine species in Middle America by organizations like the CAMCORE Cooperative. With advancements in forest biotechnology and the future ability to identify individual genes that control the expression of important traits, conservation of genes in ancestral related species ultimately may be as important as identification of unique genes in target species.

Two social/political/economic developments may hinder the use of genes from Mexican and Central American species in breeding programs in the southern US. First, the questions of intellectual property rights (ipr) must be handled in a sensitive and fair manner. Several countries in southeast Asia are now very reluctant to distribute plant germplasm internationally because of a concern that ipr will be claimed on donated material. Second, forest gene conservation is rapidly becoming the "Science for the Rich" because its development parallels advancements in biotechnology. At a time when million dollar robotic systems are being installed to streamline micro-array technologies in developed countries, organizations in developing countries are trying to secure funds to maintain electrophoresis laboratories. Most of the forest gene conservation research in developing countries is going to be done by scientists in developed countries in the next century because of access to better technology and more financial resources. This situation has the potential to adversely affect collaborative research between countries and willingness to share both genetic material and scientific ideas.

Despite the challenges, opportunities remain bright. To realize these opportunities, concepts about forest gene conservation in the southern US need to be broadened to include progenitor species from Middle America.

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