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Final address

Genetics of oak species and the spectre of global climate change

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Summary — Information on the population genetics of oaks is important in designing conservation strategies. If the threat of global warming materializes as projected, it will be necessary to actively intervene to conserve the genetic resources of oaks and other wildland plants. What has been learned about the genetic structure of oak species and gene flow within and among species will guide sampling efforts and the management of *in situ* reserves. However, it will be necessary to provide a backup for natural reserves by propagating oaks *ex situ* in provenance tests, clone banks or tissue culture.

climate change / population genetics / conservation

Résumé — Génétique des chênes et le spectre du changement climatique. *L'information relative à la génétique des populations des chênes est un préalable nécessaire à l'adoption d'une stratégie de conservation de ces espèces. Si la menace du réchauffement global se concrétise, des mesures concrètes devront être prises pour sauvegarder les ressources génétiques des chênes et d'autres espèces sauvages. Les connaissances acquises à propos de la structure génétique des chênes et des flux géniques à l'intérieur et entre espèces seront valorisées dans l'échantillonnage et la gestion* in situ *des réserves. En outre il sera sans doute nécessaire d'attribuer des moyens complémentaires à cette conservation en multipliant* ex situ *les chênes en tests de provenances, banques de clones ou par la culture* in vitro.

changement climatique / génétique des populations / conservation

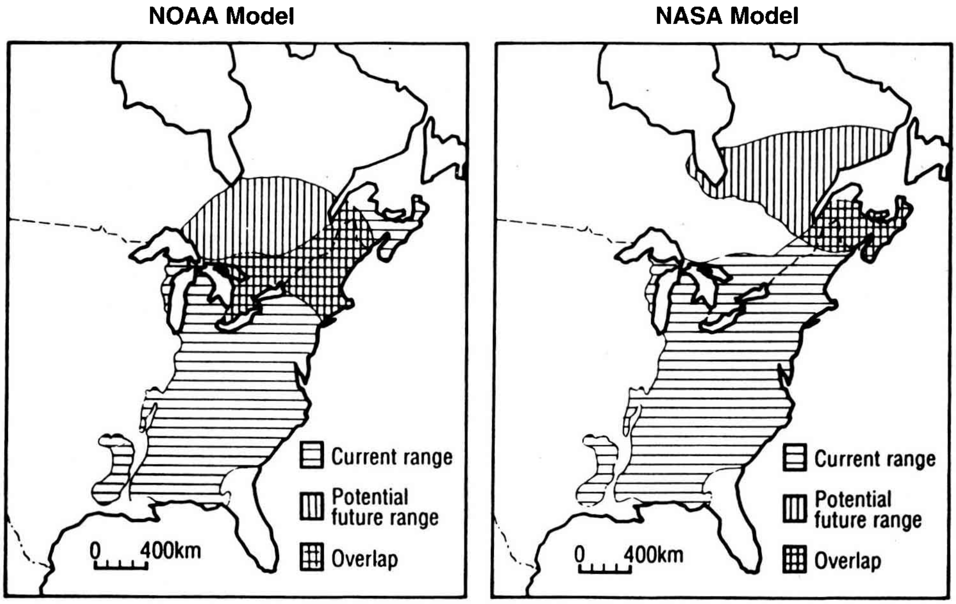
In closing the IUFRO Symposium on the Genetics of Oak Species, I would like to draw a connection between what we have learned about the population biology of oaks and the dilemma of conservation in the face of global warming.

In his welcoming address, B Chevalier, Sous-Directeur des Forêts au Ministère de l'Agriculture, introduced the topic of global warming in his reference to the Strasbourg Conference of 1990. He stressed the importance of genetic resources in an era of environmental change. However, we generally failed to follow Mr Chevalier's lead and largely neglected the implications of our research to the management of genetic resources threatened by global warming.

Recently, two groups (Davis and Zabinski, 1992; Botkin, 1991) modeled the effect of a 2.5 °C change on the ranges of some North American forest trees. Though no oaks were included in their simulations, Davis and Zabinski (1992) did model the effect of climate change on the range of another Fagaceae, American beech (*Fagus grandifolia* Ehrh). An increase in mean annual temperature of 2.5 °C will eliminate beech from most of its range in the southern and central United States (fig 1). Changes in forest composition will occur very rapidly, in less than 50 years, as projected by Botkin *et al* (1991) forest growth simulator.

Where will the genetic resources come from to replace the species lost as a result of climate change? Perhaps, southern species can be moved north. Mark Coggleshall may no longer have to worry about winter injury to his southern red oak (*Quercus falcata* Michx) in Indiana. And the rich genetic resources that Kevin Nixon described in Mexico may find a place in the southern United States or Europe, if Mexican species can adjust to the longer, northern photoperiods.

However, the situation may be even worse than the ecologists have projected. None of them has taken genetic variation into account. Their models suggest that beech and other species can survive in the northern United States and Canada after the projected changes, but they assume that every individual throughout the present range has identical environmental tolerances and limitations. As geneticists, we know that is not so. What might survive in the northern United States after global warming of 2.5 °C are not beech trees adapted to the current environment, but beech that presently grow at the southern limit of their range. Therefore, I expect widespread forest decline throughout the range.


NOAA Model

NASA Model

Fig 1. Actual and future potential ranges of *Fagus grandifolia*. Future ranges were modeled according to mean annual temperature increase of 2.5 °C (Davis and Zabinski, in press).

It is likely that some trees will survive. The great genic diversity of most of our forest species argues for the existence of variants preadapted to the new conditions. A wealth of experience has demonstrated that, on any reasonable test site, even the most maladapted provenance will harbor a few tolerant individuals. Nevertheless, a severe reduction in numbers is to be expected and, coupled with demographic chance, is likely to lead to local extirpations. Alexis Ducousso pointed out that oaks are strongly outcrossing. A drastic reduction in numbers is likely to increase inbreeding, reducing seed set and increasing the probability of reproductive failure.

In the Holocene and in earlier postglacial eras, oaks contended with change by migration to new habitat. That is not possible in today's world. Migration corridors are closed by human-imposed barriers; *ie,* agricultural fields and urban development. Furthermore, the projected changes in the next century will be much too rapid to be accommodated by migration. The clustered pattern of chloroplast genomes found by Alexis Ducousso and his colleagues underscores the limited dispersal capacity of acorns.

Therefore, we must be prepared to move provenances as well as import new species if worst-case projections are realized. If we are to move materials, we need to provide for the conservation of genetic resources now. Genetic resources for breeding are not my main concern. I am more concerned about conservation of the genetic diversity necessary to restore healthy ecosystems. *In situ* conservation is the best strategy because it allows for the evolutionary dynamics necessary to maintain viable communities. But what do we do in case of catastrophic loss of the reserves or an environment that changes too rapidly to permit evolutionary adaptation? We have no back up to our present national systems of *in situ* reserves; *ie*, no system of *ex situ* conservation. In the United States, as Kim Steiner told us, very few improvement programs have adequately integrated gene conservation into their operations.

No institutional mechanism exists for the maintenance of seedbanks and provenance tests past the tenure of the scientists who initiated them. Howard Kriebel provided cases in point. With the exception of his provenance test of red oak (*Quercus rubra* L), there were only 2 other old, oak provenance tests in the United States; Scott Pauley established a test of northern red oak and Roland Schoenike established a test of southern red oak. Both were lost when Pauley and Schoenike died. When a scientist in the United States installs ambitious tests, there is no provision for its continuity or even for archiving the records. Therefore, it was encouraging to hear Jochen Kleinschmitt emphasize the need to provide for continuity when he told us about his extensive tests of pedunculate (*Q robur* L) and sessile (*Q petraea* (Matt) Liebl) oaks.

Storage of seed is not a viable long-term option for *ex situ* conservation of oaks. However, the success in clonal propagation and tissue culture reported by Vladimir Chalupa, Jorg Jorgensen, and others offered hope that genetic resources can be preserved in clone banks.

With that as preamble, let's turn our attention to population genetics. Why do we, as forest geneticists, establish provenance trials, uniform garden studies, reciprocal transplant experiments? So we can map patterns of variation — clinal or ecotypic. If the patterns are regular, we interpolate to pinpoint the area of desirable seed sources. Or we identify distinct populations which it may be prudent to conserve, either *in situ* or *ex situ.* We seek patterns because we cannot test every population. A pattern emerging from isozyme studies in conifers is a north–south trend of increasing heterozygosity (Ledig, 1987). Does a pattern like that exist in oaks? Antoine Kremer suggested that it might. However, in species not forced south by glaciation, such as the California oaks (*Q agrifolia* Nee, *Q douglasii* Hook and Arn and *Q garryana* Dougl ex Hook) that Larry Riggs described, no such patterns should exist. In Europe also, although affected by glaciation, patterns may be especially difficult to define because of the impacts of ancient cultures.

What else does population genetics tell us? It tells us how to manage species to reduce inbreeding, the appropriate size for reserves, and the most efficient sampling scheme for conservation or breeding. From Victoria Sork we learned that white oak (*Q alba* L) and northern red oak from the midwestern United States may grow in patches of related trees. This may suggest how we should thin a stand to reduce inbreeding or how to sample for conservation or testing purposes.

Others who spoke at the symposium used isozyme studies to measure gene flow between taxa. Roberto Bacilieri found that gene flow between intraspecific populations of European oaks was 100 times higher than gene flow between Europe's 2 problem taxa, sessile and pedunculate oak. However, Rémy Petit found that rDNA gave estimates of gene flow 10 times greater than that indicated by isozymes. This is disturbing, and we need more work with DNA markers, as Kornel Berg told us. We must develop probes for restriction fragment length polymorphisms, which will certainly be a more random set of markers than isozymes. And we need comparisons using the RAPD technology.

Studies of hybridization may be especially valuable. Do the oaks provide a model for management of forest genetic resources? Do they suggest that long-term evolutionary success is favored by diversity and an open recombination system? I believe that is what Gerhard Muller-Starck implied.

Of course, many questions still remain about the population genetics of oaks, as well as other forest trees. For example, we have not obtained a good consensus on the importance of selection in the short-term. Antoine Kremer invoked selection to explain an increase in heterozygosity with age of northern red oak naturalized in France. Oak decline may provide an even better opportunity to document selection. Studies of oak decline in the United States have revealed that both white and red oak populations are divided into 2 groups: those that suffered drastic decline after 1951 and those that did not. Are these groups genetically different? Is selection occurring?

To conclude, change is inevitable, whether it is decline resulting from introduced disease, global warming induced by human activities, or part of a natural cycle beyond our making or control. Can we preserve the present genetic structure of our oak forests? No! But we are changing the environment so rapidly that oak forests are certain to suffer genetic erosion — biotype depletion — compounding the threats to productivity and forest health... unless we are prepared to learn more about the genetics of forest populations and then manage them to maintain diversity. We must prepare to move genetic materials and track changing environments.

I have doubts that genetic improvement of oaks is a sound economic investment in the United States, but an oak insurance policy is! Studies of population biology may tell us how to build a lifeboat– an ark, if you wish. And for that, society is usually willing to pay.

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