RETENTION OF OLD FOREST STANDS AND INDIVIDUAL OLD TREES

Raffaello Giannini
University of Florence, Italy

Giovanni Giuseppe Vendramin
National Research Council, IGV Florence, Italy

Federico Sebastiani
University of Florence, Italy

Giovanni Emiliani
University of Florence, Italy

Ladislav Paule
Technical University, Zvolen, Slovakia

Keywords: old-growth forest, biodiversity, conservation biology, old trees

Contents

Summary

The importance of old growth forests in conservation biology is outlined. Old growth forests are habitats for a variety of animal, plant, and insect species and can provide long-term biological records of climate. Socially, they are valued for the economic value of some large-diameter trees, for recreation, and as part of our natural heritage.

1. A Perspective on Forest Tree Biodiversity Conservation

Most of the tree forest populations are part of long-lived and heterogeneous forest ecosystems. Within these systems, trees are ecologically significant carrier species. Generally, forest ecosystems are considered to be an indispensable part of nature and provide substantial benefits for human society (recreation and economic activities such as logging). In addition to the irreplaceable asset of trees, the following major peculiarities are evident with respect to environmental conditions and to parameters of genetic variation: (a) tree populations are exposed to a great heterogeneity of environmental conditions in time and space; trees are outstandingly long-lived and grow in natural environments that reveal complex and highly variable site conditions; (b) the complexity of environmental stress conditions cannot efficiently be controlled; (c) future environmental stress conditions can deviate substantially from present conditions. Global warming will introduce abiotic and biotic stress conditions and possibly further increase environmental variability and dynamics.

Tree populations usually reveal large genetic variation within populations. Many tree populations possess an efficient system of gene flow through pollen and/or seeds. The combination of high genetic variation and prevailing cross-fertilization is responsible for the fact that degrees of heterozygosity in trees exceed those of other organisms surveyed. Only a few species of forest trees are cultivated. Therefore, in conserving genetic variation of forest trees, the focus is on the multiplicity of species, composed by several populations and occupying a range of heterogeneous environments. Many factors may explain the need for gene conservation. The presence of humans has multiple impacts on the genetics of the species. Human has eliminated well-adapted tree populations or species, often considerably reducing also their natural distribution. Decreased size of tree populations generally leads to changes in allelic structure including the loss of allelic variants. Decreased density of tree populations has an impact on their mating systems. The fragmentation of the habitats of tree populations by forest exploitation, by conversion of former forest areas to food production, by traffic networks, and by human settlements may result in an obstacle to gene flow. A common practice in tree cultivation is the mass growing of only few genotypes. This may induce or accelerate adaptive processes in parasites and herbivores. The transfer of provenience and of species as exotics between continents creates mating contacts among allopatric species, thus favoring the process of hybridization and introgression.

Both ethical and aesthetic perspectives call for conserving biological diversity. Forests are increasingly important and valuable not only as renewable natural resources but also as reservoirs of biological diversity and environments for recreation. The few native European conifers deserve respect, because they must have a specific genetic composition that allowed them to survive through changing climatic conditions. It is evident that the genetic diversity must be preserved: the loss of genetic diversity is an irreversible process that leads to a decrease of the adaptability of a population. In forestry, three major objectives of gene conservation can be identified: (a) yield potential (i.e., the genetic potential for expression of desirable phenotypic characters (managing diversity)); (b) genetic adaptability (i.e., the ability of the populations to survive and reproduce even in a changing environment); and (c) conservation of as much variation as possible (maximizing diversity).

Conservation and management of genetic diversity is not based on a single mode of action. First, we have to separate the conservation of genetic diversity of natural populations from the maintenance of adequate genetic variation in breeding populations. Conservation of representative samples of the genetic diversity of autochthonous populations is the primary goal. Samples of natural populations are most suitable for *in situ* gene conservation (dynamic conservation). Taking advantage of existing nature protection areas, the selection and maintenance of special gene reserve forests are relatively inexpensive. Dynamic conservation does not preclude evolutionary processes, but allows for adaptive and other changes in a changing environment. Standard procedure is the maintenance of populations *in situ*. In contrast to resource conservation in crop plants, this method of conservation is most important in forest trees and range species. The objective of the static conservation is to fixate the status quo. The *in situ* conservation approach is usually achieved by preservation *ex situ* when the population is endangered in its natural habitat. However, at least slight genetic changes due to manipulation are inevitable.

Species that are only marginally represented, but hold the promise of high future value, may be targeted if the risk of losing potentially valuable alleles and variation is high. Species or populations at the margin of their ranges of adaptability represent good targets for special interest, even though they may be of little present value. Such populations may be targeted for maintenance in some reserve status in case their future value increases. For populations or species of unknown value, genetic surveys may be useful only to confirm that they will be able to exist in future environment. In this context, old forest stands and old trees may represent a very important reservoir of genetic variation and useful genes for future adaptation to new environmental conditions in the light of dramatic global change, and their conservation represents an important step for the maintenance of evolutionary potential.

-
-
-

Bibliography

Everett R., Hessburg P., Lehmkuhl J., Jensen M., and Bourgeron P. (1994). Old forests in dynamic landscapes. *Journal of Forestry* **92**(1), 22–25. [This research paper presents data on distribution of old forests in eastern Oregon and Washington.]

Frankel O.H., Brown A.H.D., and Burdon J.J. (1995). *The Conservation of Plant Biodiversity*, 113 pp. Cambridge, UK: Cambridge University Press. [This book takes an evolutionary perspective to the conservation of plant biodiversity.]

Hayward G.D. (1991). Using population biology to define old-growth forests. *Wildlife Society Bulletin* **19**, 111–116. [This article provides criteria to define "old-growth" forests.]

Hunter M.L., Jr., ed. (1990). *Wildlife, Forests and Forestry*, 400 pp. Englewood Cliffs, NJ: Prentice Hall. [This book provides basic concepts of managing forests for biological diversity.]

Morgan P. (1994). Dynamics of ponderosa and Jeffrey pine forests. *Flammulated, Boreal, and Great Gray Owls in the United States: A Technical Conservation Assessment*, (ed. Hayward G.D. and Verner J.). Gen. Tech. Rep. RM-253. Fort Collins, CO: U.S. Department of Agriculture, Forest Service, Rocky Mountain Forest and Range Experiment Station. [This chapter documents the importance of old-growth stands in a forest succession.]

Myers N., Mittermeier R.A., Mittermeier C.G., da Fonseca G.A.B., and Kent J. (2000). Biodiversity hotspots for conservation priorities. *Nature* **403**(24), 853–958. [This article provides detailed data on biodiversity hot spots for conservation planning.]

Biographical Sketches

Raffaello Giannini, full professor of forest tree breeding at the University of Florence and director of the Forest Tree Breeding Institute of the CNR (Consiglio Nazionale delle Ricerche). He has extensive experience in forest genetics, forest tree breeding, and silviculture. He is involved in research dealing with population genetics of forest trees with emphasis on aspects related to the introgressive hybridization and phylogeny, to conservation of forest genetic resources, and to functional genomics.

Giovanni G. Vendramin, senior researcher of the Forest Tree Breeding Institute. His experience is in forest genetics and population genetics. He has extensive experience in molecular genetics of forest trees, and has worked on several aspects of population genetics of forest trees, mainly focused on the analysis of natural forest genetic resources and reconstruction of postglacial pathways of recolonization.

Federico Sebastiani, PhD student at the University of Florence. His experience is in yeast genetics and population genetics; he is involved in research focused on chloroplast genome organization and evolution.

Giovanni Emiliani, PhD student at the University of Florence. His experience is in population and forest genetics; he is mainly involved in functional genomics of forest trees.

Paule Ladislav, full professor of forest genetics and tree breeding and head of the Department of Phytology at the Technical University of Zvolen. He has extensive experience in genetic structure of forest population and genecology, in breeding programs, and progeny testing of forest trees.