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PROTECTION OF GENETIC VARIABILITY IN FOREST TREES

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PREFACE

In Europe, most of the tree populations are part of long-lived and heterogenous forest ecosystems. Within these systems, trees are ecological significant carrier species. Generally, forest ecosystems are considered to be an indispensable part of nature and to provide substantial benefits for the human society (protection forests, social functions, economics).

Particularly in Central Europe, numerous forest ecosystems are increasingly threatened by decline following air pollution and other environmental impacts. In addition, forest ecosystems are subjected considerably to forest management and modifications of land use. Global warming can be expected to increase the complexity of environmental stress conditions.

The deterioration to which forest ecosystems are exposed, severely challenge the potential of forest tree populations to adapt to and to survive under changing environmental conditions. Genetic variability determines the adaptive potential of species and is an essential component of the stability of ecosystems (*e.g.*, LEDIG 1986, SCHOLZ *et al.* 1989, HAMRICK & GODT 1990, MÜLLER–STARCK & ZIEHE 1991). Consequently, preservation of genetic variability *in situ* is crucial in order to maintain adaptability and thus to contribute to the ecological stability of species and ecosystems.

PECULIARITIES OF FOREST TREE POPULATIONS

Among many tree specific characteristics, the following major peculiarities are evident with respect to environmental conditions and to parameters of genetic variation:

Complex environmental situation

In contrast to most of the agricultural crops, forest tree populations usually are subjected to the following major environmental challenges:

- Tree populations are exposed to a great heterogeneity of environmental conditions in time and space: trees are outstandingly long-lived (*e.g.*, rotation times up to 300 years or more in oak stands) and grow in natural environments which reveal complex and highly variable site conditions. Generation cycles of trees and parasites deviate extremely.
- The complexity of environmental stress conditions cannot efficiently be controlled: prophylactic pest control like in agriculture is not possible, fertilization and other measures to improve site conditions are strictly limited in their efficiency, and impacts of stress components like frost events cannot be avoided.
- Future environmental stress can deviate substantially from the present conditions because of long term complexity of environmental stress, of interactions among stress components, and because of its non predictable dynamics. Global warming will interfere abiotic and biotic stress conditions and possibly further increase environmental variability and dynamics.

Large genetic heterogeneity within tree populations

Tree populations usually reveal outstandingly large genetic variation within populations. In Table 1, results from genetic inventories are compiled which refer to populations of European tree species in contrast to various dicotyledonous and monocotyledonous species.

In the interpretation of these data, it has to be taken into account that the given survey can only illustrate trends. The summarized results refer to studies which include different gene loci, number of loci, sample sizes, materials and ontogenetic stages. Furthermore, mode of geographical and mating systems vary considerably among species. For instance, obligatory self-fertilized species like certain monocots and dicots will reveal much lower heterozygosities than facultative self-fertilized or obligatory cross-fertilized species such as trees.

Table 1 demonstrates significant deviations between genetic parameters of trees and non tree species (reference species). The average proportion of heterozygotes (multilocus mean of the ratio of heterozygotes within the population is equivalent to the average individual degree of heterozygosity, which measures the individual genetic variation. Observed average heterozygosities in trees exceed the corresponding values for the reference

Table 1 Observed proportion of heterozygotes and number of alleles per locus (isoenzyme gene markers) for European coniferous and deciduous tree species in contrast to various dicotyledonous and monocotyledonous species ([1] Mitton 1983, [2] Hamrick & Godt 1989, [3] Müller-Starck 1991)

	Number of studied species	Average proportion of heterozygotes	Average number of alleles per locus
Tree species (genera):			
Abies, Larix, Picea, Pinus	10	25.1 %[3]	2.2[3]
Castanea, Fagus, Quercus	5	23.4 %[3]	2.7[3]
Dicotyledonous species*	74[1], 338[2]	11.3 %[1]	1.4[2]
Monocotyledonous species	28[1], 80[2]	16.5 %[1]	1.4[2]

* Tree species excluded

species by 74 % (see previous comments on inferences by the mating system).

In the case of genetic variation at the population level, the average number of alleles per locus in trees exceeds the corresponding value of the reference species by 58 %. This surplus indicates an important difference between trees and other plant species: large numbers of genes per population are equivalent to a great potential to form genetically different multilocus-genotypes in the next generation and thus to respond to environmental challenges by means of genetically variable offspring populations.

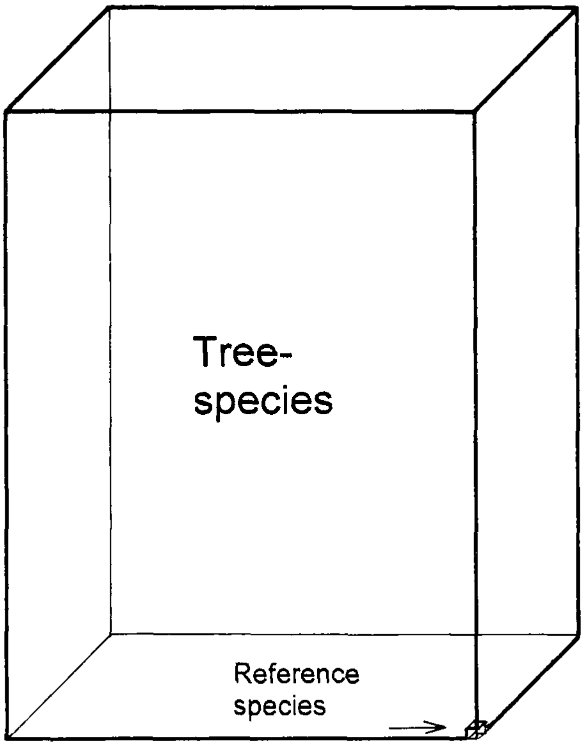

Figure 1 Maximum potential genotypic multiplicity (18-locus-genotypes) for tree populations (big cube) in contrast to non-tree reference populations (small cube)

In order to demonstrate the resulting peculiarities of forest tree species, the largest number of genetically different 18–locus–genotypes was calculated which can be formed by a population with an average number of alleles per locus of 2.45 and 1.55 respectively (maximum potential genotypic multiplicity). In the case of even frequency distribution of alleles per locus, the number of different individuals is 9.9x10^{10} for tree species and 5.9x10^{4} for the reference species. The relation is illustrated in Figure 1 by two cubes. Deviations from even frequency distribution will reduce the values but not essentially change the proportions.

Preservation of genetic variability is crucial for adaptation and survival of species and entire ecosystems under changing environmental conditions. Environmental dynamics and anthropogenic impacts can alter genetic variability to such an extent that the adaptive potential of species and ecosystems could seriously be impaired. Measures to increase genetic variability will increase chances of survival and will contribute to ecological stability and thus to sustainable development.

Any conservation practices have to take into account the large genetic heterogeneity of tree populations under natural conditions. In forest management, silvicultural practices are required, which maintain genetic variability in any long–lived forest ecosystems (*e.g.*, mode of regeneration, choice of reproductive material, mode of thinning), which systematically protect genetic resources and which increase genetic variability in case of genetic erosion ("sustainable silviculture").

Generally, peculiarities of trees with respect to environmental situation and genetic variability suggest the following hypotheses:

- Forest environments severely challenge the adaptive abilities of forest tree populations;
- Preservation of adaptability of forest ecosystems requires maintenance of genetic variability in any forest tree population;
- In genetic impoverished populations, increase of genetic variability will help to contribute to sustainable ecological development;
- Additional measures of gene conservation (gene reserve areas *in situ* and *ex situ*, or conservation via "gene banks") will help to preserve extremely rare alleles.

INITIATIVES AND PERSPECTIVES

Preservation of genetic variability in forest tree populations is a new challenging task. It requires appropriate methods for the assessment of genetic variation (genetic markers, methods for quantification) with inclusion of gene flow and hybridization, the definition of criteria for conservation of genetic resources (genetic and environmental variables), and of management regimes in order to realize genetically sustainable development thus contributing to the preservation of adaptability of complex forest ecosystems.

In many cases, genetic resources of forest tree populations became part of research programmes which originally refer to agricultural crops. During last six years, various initiatives have been started in order to combine efforts in the conservation and management of environment and natural habitats. In 1989, the "Colloquium on the Conservation of Wild Progenitors of Cultivated Plants" was held in Strassbourg 27–29 November. It was decided that attention should be paid to conservation problems of wild relatives of cultivated plants in Europe.

In June 1990, Recommendation No. R (90) 16 of the Committee of Ministers of the Council of Europe of the member states regarding the conservation of wild progenitors of cultivated plants was adopted. Furthermore, the "Group of Specialists on Biodiversity and Biosubsistence" was established on behalf of the Council of Europe. Based on suggestions of the last named group, three workshops were initiated on "Conservation of the Wild Relatives of European Cultivated Plants: Developing Integrated Strategies".

The first workshop was held at Faro, Portugal, at the Ria Formosa Nature Reserve, November 8–12, 1992. Three major themes were addressed: (1) Ecogeographical Surveys, (2) Demography, and (3) Reproductive Biology. Agricultural crops were on focus. The necessity was pointed out to bring together the specialists from different disciplines and to combine scientific approaches with practical and management skills needed for effective conservation of plants. In particular, taxonomists, ecologists, physiologists, conservationists and land use planners are concerned. There is a need for long-term studies on systematics, ecology, conservation biology and genetics in order to provide the basis for establishing effective conservation strategies for target species. Furthermore, the establishment of university centers for research and training in plant genetic resources, evolution and conservation was considered to be essential. Generally, conservation of wild relatives in their natural habitats is preferable. In many cases, an integrated conservation strategy which involves both *in situ* and *ex situ* approaches is required.

During the second workshop which was held at Neuchâtel, Switzerland, October 14–17, 1993, four themes were discussed: (1) Interactions among organisms and between organisms and ecosystems, (2) Gene flow in wide ranging species – spatial problems, (3) Environmental stress and survival strategies, and (4) Synthesis: managing the populations. In particular, threats by regional and global environmental changes were on focus and corresponding problems of preservation of adaptability of plant populations. Generally, conclusion from the first workshop in 1992 were confirmed. It was for the first time that forest tree species were taken into account. Four pilot conservation networks were established which concern Norway spruce, cork oak, black poplar, and selected rare hardwoods (gene conservation projects developed by the European Forest Genetic Resources Programme in cooperation with IBPGR and FAO).

The third workshop was held at Gibilmana–Palermo, Italy, September 21–27, 1994. The following four themes were discussed: (1) Principles and practice of management and monitoring, (2) Protection of genetic variability in forest trees, (3) Role of genetic resources managers, and (4) Case studies: *Brassica, Capparis, Abies, Olea* and rosaceous fruit trees. During this meeting, forest tree species were integrated into joint efforts in the conservation and management of natural habitats. A "Catalogue of Wild Relatives of the Cultivated Plants of Europe" will be compiled which enumerates and briefly characterizes various species which are cultivated for food, forage, herbs, ornaments, timber and other purposes. Economically and/or ecologically significant indigenous tree species will be part of this initiative and be integrated in conservation programmes which take peculiarities of tree populations and environments into account.

Within these fields, subsequent contributions will address important topics: H. H. HATTEMER (Göttingen, Germany) will survey concepts and requirements in the conservation of forest genetic resources from the point of view of a population geneticist. V. KOSKI*) (Vantaa, Finland) reviewed experiences and perspectives of the "Spruce Gene Conservation Advisory Group" which is the first European initiative in the preservation of gene resources of forest tree species.

A case study with respect to the protection of genetic variability in polluted stands is presented by B. ZIEGENHAGEN and F. SCHOLZ (Großhansdorf, Germany) This contribution addresses silver fir (*Abies alba* Mill.) which is considered as endangered species in certain parts of its geographical range of distribution. G. G. VENDRAMIN and co-authors (Firenze, Italy) analyzed genetic resources of the Sicilian relic tree species *Abies nebrodensis* which is highly endangerend. Gene conservation in European pine species is surveyed by S. PUGLISI (Bari, Italy). In addition to the previous contributions, conservation *in situ* is on focus.

A. ZANETTO and A. KREMER*) (Pierroton, France) presented results of a large genetic inventory in European oak species which are significant model species due to their carrier function in extremely long-lived forest ecosystems. Conservation of species which are subject to intensive forest tree breeding, is demonstrated by L. CAGELLI (Casale Monferrato, Italy) and F. LEFÈVRE (Ardon, France). In the last contribution, genetic resour-ces of a predominant tree species, *i.e.* European beech, are surveyed and measures of conservation are outlined by L. PAULE (Zvolen, Slovakia).

These contributions will help to better understand peculiarities with respect to forest tree populations and may facilitate interdisciplinary efforts in the conservation and management of natural habitats. An essential part of such efforts is the assessment of genetic variation and its dynamics under changing environmental conditions and the utilization of genetic criteria for gene conservation in forest tree populations.

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*) The presentations of V. Koski and A. Zanetto and A. Kremer are not published in this issue.