GENETIC STRUCTURES OF BEECH *(FAGUS SYLVATICA)* IN MOUNTANEOUS REGIONS: CONSEQUENCES FOR CONSERVATION OF GENETIC RESOURCES

Doris Krabel[1], Tanja Freytag[2], Roland Hartz[1], Sven Herzog[2]

Abstract:--Whereas beech *(Fagus sylvatica)* forms in most parts of its natural range more or less dense pure or mixed stands, this is not the case in mountaneous regions. At the upper limit of its natural range, beech normally forms scattered stands with only few individuals per hectare.

We based our studies on the hypothesis that this different structure of beech stands, *i.e.* their occurrence as small groups of trees or even single trees, will have impact on the mating system of this normally outcrossing species. As a consequence, influences on the genetic structures were assumed.

For the assessment of the genetic structures, beech stands from the Harz Mountains (Germany) were studied by methods of isoenzyme analysis. Significant deviations from previously observed patterns of genetic variation have been found. This has been explained by the phenomenon of genetic drift rather than by selective forces.

No significant excess of homozygotes, indicating a tendency to self-fertilization, has been observed. However, this phenomenon may be explained by the observed high proportion of empty seeds, meaning a strong viability selection against homozygotes in early ontogenetic stages and thus prohibiting them to be detected by genetic methods.

The consequences of genetic drift as well as increased self-fertilization rates are discussed in the context of genetic conservation in mountaneous regions.

INTRODUCTION

Whereas beech *(Fagus sylvatica)* forms in most parts of its natural range more or less dense pure or mixed stands, the situation in mountaneous regions is quite different. Especially at the upper limit of its natural range, beech forms only scattered stands with only few individuals per hectare.

We based our studies on the hypothesis that this different structure of beech stands, *i.e.* their occurrence in mixed stands, as small groups of trees or even single trees, will have an impact on the mating system of this normally outcrossing species. As a consequence, influences on the genetic structures, especially an increase of phenomena like selfing or preferential mating of closely related individuals, was assumed. The efficiency of a pollen cloud depends on several factors of pollen distribution. Local effects, as for example the position of an individual to its next neighbor, isolation effects caused by mixture with other tree species, and microclimatic or microtopographic effects may influence the mating system or at least the mating success by reduction of the density of the pollen cloud.

In this context, the question as to the amount of selfing or mating of closely related individuals arises. This may be the consequence of a reduced number of individuals of each species in mixed stands as well as of inhibition of pollen dispersion by neighboring trees of other species. Additionally, reproductive

Institut für Forstbotanik und Forstzoologie, Technische Universität Dresden, Pienner Strasse 7, D-01737 Tharandt, Germany

[2] Institut für Forstgenetik und Forstpflanzenzüchtung, Georg-August-Universität, Büsgenweg 2, D-37077 Gottingen, Germany

'Institut für Waldbau und Forstschutz, Technische Universität Dresden, Pienner Strasse 8, D-01737 Tharandt, Germany isolation may not only be due to low population density and filter effects of other species but may be reinforced by different flowering periods of neighboring trees.

The present paper deals with the question as to the rate of selfing of *Fagus sylvatica* in mixed stands of different structure from submountaneous to mountaneous regions.

MATERIALS AND METHODS

The present study covers altogether 11 mixed stands of beech *(Fagus sylvatica)* and several other tree species as *e.g* oak *(Quercus sp.)*, spruce *(Picea abies)* or Douglas fir *(Pseudotsoga menziesii)* from altitudes between 251 meters and 820 meters above sea level of the Harz Mountains (state of Niedersachsen, Germany). The highest locations are covered with scattered rests of formerly more dense beech or mixed stands.

In all stands, amount and quality of beechnuts from the 1995 mast have been evaluated. For this purpose, we selected nine different mother trees and sampled the beechnuts from the 1995 mast by random.

The influence of a the mixture with sessile oak *(Quercus petraea)* on genetic structures of a naturally regenerated adult beech stand and its offspring was studied in one of the above mentioned stands, located between 251 and 350 m above sea level. The forest stocking is a mixed forest around 134 years old consisting of beech, sessile oak *(Quercus petraea)*, and maple *(Acer pseudoplatanus* and *Acer platanoides)* and a few individuals of European larch *(Larix decidua)* and spruce *(Picea abies)*. Moreover, the genetic structures of three stands from altitudes of 700 meters, 740 meters and 820 meters above sea level were studied by methods of isoenzyme analysis using ten different gene loci. Genetic variation was found at all loci. The polymorphic loci are thus appropriate for the investigated stand as marker gene loci. The genetic control of the applied enzyme systems was verified previously using the offspring of controlled crosses (see Kim 1979, Thiebaut *et al.* 1982, Müller-Starck 1985, 1989, Müller-Starck and Starck 1993).

RESULTS

Based on the comparison between specific mother trees and their offspring, their degree of self-fertilization and the composition of the pollen-cloud was estimated.

For this mixed stand the calculated maximal selfing rate of beech was about 36% and thus relatively high compared to the results of previous studies with the same set of isoenzyme gene markers. Additionally, the proportion of seeds were the hypothesis of origin from self fertilization could not be rejected, was compared with the degree of empty seeds and showed the same tendencies. The results indicate a rather inhomogenous pattern of pollen (outcrossing pollen) distributed within the stand and also within the crown of a single tree.

Beech stands or groups of trees from more mountaneous regions, located between 400 m and 820 m above sea level have also been studied with respect to isolating effects of the increasing distances between trees, groups of trees or stands with increasing altitude. In these cases, the geographic distances rather than the presence of other tree species are assumed to be the main isolating factor.

Significant deviations from previously observed patterns of genetic variation have been found. This has been explained by the phenomenon of genetic drift rather than by selective forces. No significant excess of homozygotes, indicating a tendency to self-fertilization, has been observed. However, this phenomenon may be explained by the observed high proportion of empty seeds, meaning a strong viability selection against homozygotes in early ontogenetic stages and thus prohibiting them to be detected by genetic methods.

The consequences of genetic drift as well as increased self-fertilization rates are of importance in the context of genetic conservation in mountaneous regions. The stands may be differentiated not primarily by selective forces but more by random effects. Thus, we cannot assume that we will find one or few stands representing the genetic structure of a whole region and, as a consequence, genetic conservation becomes more difficult in these regions. On the other hand, adaptations to certain ecological conditions may have led to unique genetic structures justifying the declaration as a gene resources. This dilemma may be at least partially solved by a clear concept of genetic conservation, including a definition as well as a ranking of the goals that have to be reached by the conservation efforts.

LITERATURE CITED

Kim, Z.S. 1979. Inheritance of leucine aminopeptidasae and acid phosphatase isozymes in beech *(Fagus sylvatica L.).* Silvae Genetica 28, 68-71.

Müller-Starck, G. 1985. Genetic differences between "tolerant" and "sensitive" beeches *(Fagus sylvatica* L.) in an environmentally stressed adult forest stand. Silvae Genetica 34, 241-247.

Müller-Starck, G. 1989. Genetic implications of environmental stress in adult forest stands of Fagus sylvatica L. In: Scholz, F.: Gregorius, H.-R.; Rudin, D. (editors): Genetic Aspects of Air Pollutants in Forest Tree Populations. Springer-Verlag: Berlin, Heidelberg, New-York, 127-142.

Müller-Starck, G. and R. Starke. 1993. Genetic control and inheritance of isoenzymes in beech *(Fagus sylvatica L.).* Journal of Heredity 84, 291-296.

distinction and analysis of polymorphism in several French populations. Silvae Genetica 31, **51-60.**