Gene conservation in European beech (*Fagus sylvatica* L.)

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Abstract

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The European beech is one of the most important broadleaved forest tree species in Europe occurring in various ecological conditions. After the establishment of numerous provenance experiments in this species (the last one containing 188 provenances and 23 trials), extensive genetic inventories in most part of Europe has been carried out. *In situ* and *ex situ* gene conservation in European beech is outlined.

Introduction

The European beech (*Fagus sylvatica* L.) is considered at present as the most common economically important broadleaved tree species in Europe. The extent of beech forests (*Fagus sylvatica* and *F. orientalis* together) in Europe and Asia Minor is estimated to be between 17 and 20 million ha (e.g. Milescu & al. 1967 estimate 16.8 million ha) and represents approximately 10 % of European forests. The proportions of beech forests in individual regions represent frequently up to 30% of the total forest area (e.g the former Yugoslavia, Slovakia, Romania etc.)

Both *Fagus sylvatica* and *F. orientalis* belong to the forest tree species with the widest natural range in the western part of Eurasia (Fig. 1). *F. sylvatica* is distributed in western, central and southern Europe with individual occurrences in southern England and southern Scandinavia. *F. orientalis* is distributed in Asia Minor, in Caucasus, in the Amanus mountains (Syria), and in the Elburz mountains (Iran).

Contact zone between the natural ranges of both species runs in northern Greece and Bulgaria. Isolated occurrences of *F. orientalis* outside the natural range were recorded in eastern Serbia (Glišič 1973), in Macedonia (Cernavski ex Milescu & al. 1967), in Banate and Moldova (Milescu & al. 1967), and in Dobrudja and Central Bulgaria (Czeczott 1932).

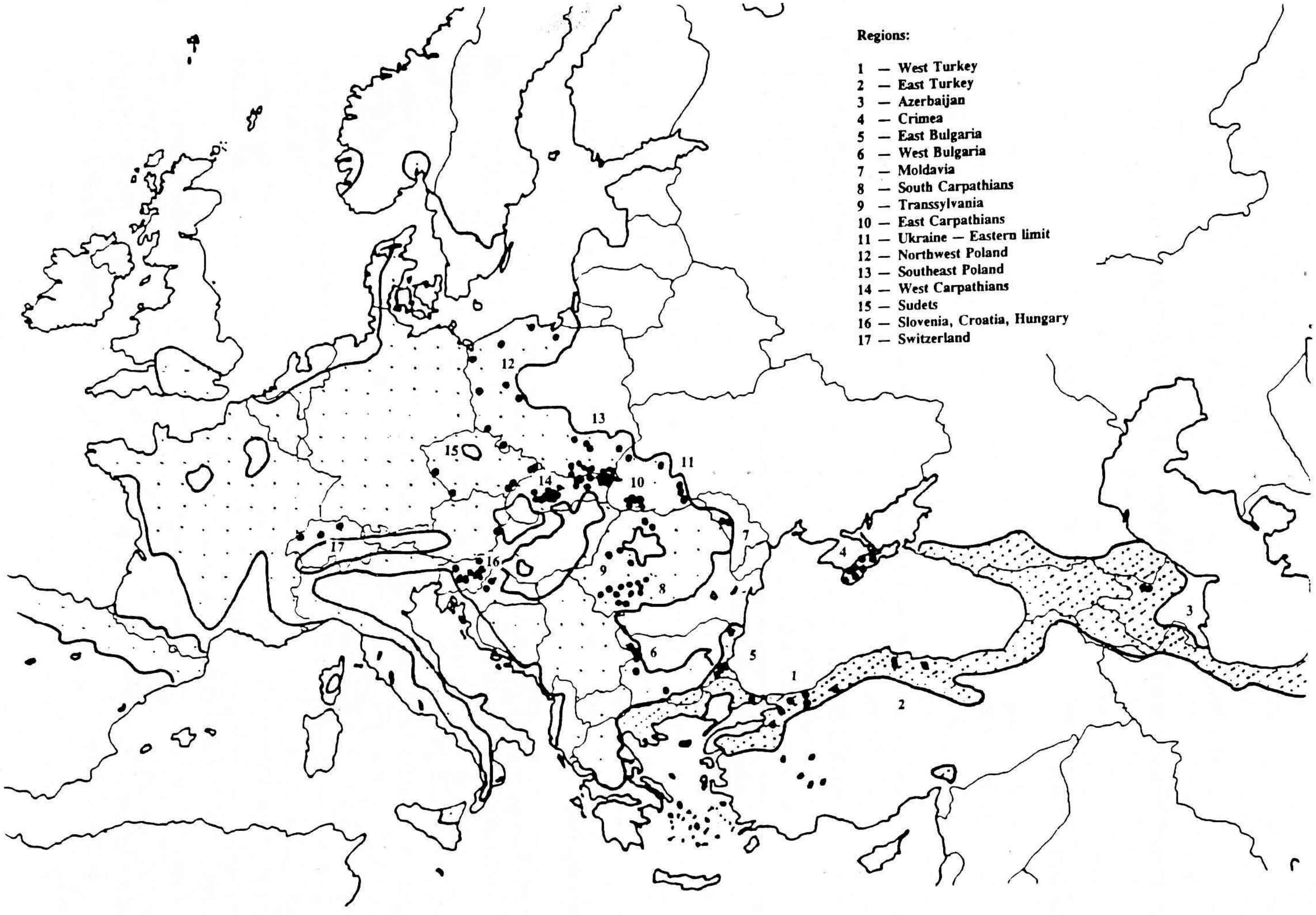

Fig. 1. Natural range of *Fagus sylvatica* (sparsely dotted) and *Fagus orientalis* (densely dotted). Bold dots represent investigated populations within the genetic inventory carried out in Zvolen laboratory (Paule & al. 1995).

The taxonomic identity of the beech trees growing in Crimea is problematic. Poplavskaja (1928) described the beech in the Crimean peninsula as an independent species – *F. taurica*. Beech occurs in Crimea in two altitudinally separated zones. The lower zone was more frequently described as *F. orientalis* and the upper one as *F. taurica* (Molotkov 1966, Milescu & al. 1967), but Wulff (1932) describes it as *F. sylvatica*.

Another dubious taxon unit is *F. moesiaca* known mainly from the Balkans. Miši (ex Glišič 1973) considers it an independent species of Tertiary origin but most botanists regard it as a subspecies or variety of *F. sylvatica*.

From the above statements it is obvious that taxonomic status of the beech populations in several areas is unclear.

The original description of these taxa (*F. moesiaca* and *F. taurica*) was based mainly on the morphological traits of leaves, and rarely do these taxa occur in comparative provenance trials together with *F. sylvatica*. The aim of recent investigations carried out in Slovakia, France and other countries is to characterize both species – *F. sylvatica* and *F. orientalis* – using gene markers, to define the zone of introgressive hybridization and the limits or the direction of the gene exchange between both species, and to characterize the structure of diversity within the genus *Fagus* in Europe and western Asia (e.g. Demesure & al. 1996, Paule & al. 1995).

Natural range and present distribution of *Fagus sylvatica*

The European beech (*F. sylvatica)* is a tree species of oceanic and suboceanic climate. Its eastern limit runs on the limit of continentality (Stanescu 1979). Except the continentality, the eastern limit is defined by the air humidity and late frost (Pukacki 1990). Although the European beech is resistant to fairly low winter temperatures, and grows also at relatively high altitudes, it is sensitive to late spring frost – a limiting factor for lower altitudes with greater accumulation of cold air (Becker 1981). This is one reason why the European beech does not occur in the frost-prone valleys or in regions with a more continental climate (e.g. the valley of Ebro, Languedoc, Provence, the central Alps, the Hungarian and Vienna lowlands and the Hungarian plain as well as the inner part of Transsylvania (Svoboda 1955).

Fagus sylvatica requires a humid and moderate climate during the summer period, the total precipitation has to be higher than the total evaporation. Optimal sites for beech require at least a five-month growth period, a mean annual temperature of 10° C, a mean July temperature about 18° C, and precipitation optimum of 800 to 1 000 mm. It is indifferent to soil substrata, except sandy, wet, and otherwise poor soils. When climatic conditions are optimal it grows best, however, on rich soils.

Eastern Europe and Carpathians

In eastern Europe, the European beech probably originated from the principal Balkan glacial refugium, from where it started to spread 13 000 years ago. Since the late Atlantic period, i.e. since approx. 3 000 years, it has become dominant in practically the whole of its present distribution range (Huntley & Birks in Horvat-Marolt 1992). Postglacial migration ways can be, besides refugia, other factors, which modelled the genetic differentiation patterns. In some parts of the distribution range of the European beech the allelic structure may be affected by gene flow from adjacent populations of the other beech species (*Fagus orientalis* in European Turkey and eastern Bulgaria, and *F. taurica* in Crimea).

The forests of the Carpathians cover in total approximately 8 million ha, and the beech share in these forests is 3.4 million ha. The proportion of beech in the Carpathians is approximately 32 %. It covers along the Carpathians the altitudes from 250-300 m up to the upper tree limit. In Slovakia and Poland, the upper tree limit is formed by Norway spruce and the mountain pine belt, while in the western Ukraine the upper tree limit is formed by beech in altitudes of 1 250 - 1 380 m. In the eastern part of the Ukrainian Carpathians and in Romania, the upper tree limit is formed by spruce. Within the Carpathians European beech is besides Norway spruce and silver fir one of the most important tree species which form, in mountainous regions, the single-species as well as mixed forest stands.

Geographical variation

The number of provenance experiments with European beech is much lower than with any conifer species of economical importance. Within the last forty years numerous provenance trials were established in Germany, Slovenia, Czech Republic, Slovakia, France, Denmark and Poland (for review see Giertych 1990). They are characterized by a small numbers of used provenances and replications under different ecological conditions.

Due to the lack of provenance experiments with higher number of provenances which were established in more replications, there has not been the possibility to make any broader statements on geographic variation of growth traits.

Apart of growth traits (height, diameter and volume) and some qualitative traits (forking), the variation in flushing is one of the adaptive traits of importance. It reflects the existing possibilities of the utilization of individual, suitable performing provenances in afforestation or reforestation programmes.

In one older provenance experiment Brinar (1962) investigated the growth of 29 provenances of beech from Slovenia occurring along the altitudinal gradient and originated from the altitudes 310 to 1 360 m. He found that the delay in flushing by one day corresponds to an altitude difference of 122 m, and a delay by one day in autumn colouring corresponds to 113 m in altitude.

Von Wuehlish & al. (1995) found significant differences and a pronounced east-west trend. Eastern and southeastern provenances started to flush in German, French and Belgian provenance trials earlier than in western ones, while the high correlations among flushing ranks in individual trials showed high stability with respect to this adaptive trait.

Genetic resources

In most parts of the natural range of the European beech, such as the Carpathians, or the Balkans, the prevailing forest management practice in beech stands was natural regeneration. Due to this fact, that natural composition of mixed forests with participation of beech has been preserved in many parts of the European natural range, and the genetic structure of beech populations can be expected not to deviate significantly from the 'natural' one.

This is, however, not true in the western part of Europe, where a large proportion of indigenous beech forests were converted during the last two centuries into coniferous stands. This is true in Germany, the Czech Republic, the western part of Poland etc., where beech stands were frequently replaced by Scots pine and Norway spruce.

This is the basic situation which we have to take into account when evaluating the genetic resources of beech in Europe. The natural range of the European beech in central, eastern and the southeastern Europe includes a large proportion of primary and well preserved secondary genetic resources of beech (virgin and natural forests) with original genetic structure. In the Carpathians remnants of beech virgin forests from several hundreds to several thousands of hectares occur (e.g. Uholka, Carpatho-Ukraine with 11000 ha).

Genetic markers

Unlike the variation of phenotypic traits, marker gene loci in European beech have only recently become available for research. This was made possible through experiments conducted by earlier research workers. Forty years ago, Nielsen and Schaffalitzky de Muckadell (1954) crossed several beeches in the Arboretum Hørsholm and out-planted their progenies. This enabled Kim (1979) to identify the first enzyme gene locus by studying the zymograms of parent trees and their offspring. Later Thiébaut & al. (1982) also used the Hørsholm material for his investigation.

Paule (1992) and Hattemer & al. (1993) published reviews of the isozyme systems, their biochemical analyses and controlling gene loci which were applied in genetic inventories of beech. They listed the following 17 isozyme systems controlled by 27 gene loci: *aco* – 2 gene loci, *acp* – 2, *dia* – 1, *gdh* – 1, *got* – 2, *idh* – 2, *lap* – 2, *mdh*– 3, *mnr* – 1, *ndh* – 1, *pepca* – 1, 6*pgdh* – 3, *pgi* – 1, *pgm* –1, *per* – 2, *skdh* – 1, and *sod* – 1.

Müller-Starck & Starke (1993) and Merzeau & al. (1989) studied the inheritance patterns of the enzyme systems in progenies from controlled crossings and single trees, respectively.

Recently, SDS-PAGE was applied to find species-specific differences in the seed protein content of *F. sylvatica* and *F. orientalis* populations from Bulgaria. The comparative analysis of the their patterns showed more similarity than dissimilarity between these species Busov (1995).

Finally, the polymorphism in the chloroplast DNA have been detected by resolutive restriction site studies of PCR-amplified fragments. Eleven haplotypes, which could be phylogenetically ordered, were detected in a large survey (399 individuals in 85 populations) encompassing most of the natural range of the species (Demesure & al. 1996).

Genetic diversity and differentiation of beech populations

Extensive studies on the geographical geneticvariation of the European beech based on isozymes were started in France. The first investigations used only a small number of isozyme markers (3–6) (Comps & al. 1987, 1990. In later studies the number of polymorphic isozyme loci increased to 10–16 (Müller-Starck & Ziehe 1991, Gömöry & al. 1992, Hattemer & al. 1993, Turok 1993, 1996, Leonardi & Menozzi 1995, Tröber, 1995, Larsen 1995).

In general, the genetic differences between stands in the same geographic region were found to be low. The variation is reported to be greater in the southern parts of the distribution range. With the exception of gene loci coding for peroxidases, the differences in allele frequencies do not indicate correlations with the climate of the place of origin (Barrière & al. 1984, Comps & al. 1987, 1990). Allele frequencies at other loci such as *Got-1* seem to be related to geographic gradients of unknown selective pressure (Barrière & al. 1984, Comps & al. 1991). If similar correlations of the type mentioned were detected independently in various parts of the distribution range, selection would have been considered as the causal agent for differentiation between populations at these loci (Paule 1992).

Western Europe

In Europe there have been several groups investigating the genetic diversity and differentiation of beech populations. The first one was the French group (Thiébaut, Compa etc.) that started to investigate the genetic variation of west European populations. They have applied from the beginning, only a few enzyme systems (*px*, *got*, *idh*, *mdh*, *pgi*). Later the number of isozyme systems was increased (*acp*, *got*, *mdh*, *mnr*, *6-pgd*, *pgi*, *pgm*, *pxc*, *sod*). The German group (Müller-Starck) has independently developed procedures for staining and interpretation of numerous isozyme systems on strach gels that could be utilized for *Fagus sylvatica* as well as for *F. orientalis* (Müller-Starck 1985, Müller-Starck & Starcke 1993).

Beech occurs in the larger part of western Europe except in southern parts with a drier climate. In the southeastern part of France beech is growing in higher altitudes with more humid climate, but it can occur also in the lower altitudes with drier climate. In one of the first papers the French group investigated populations from the two types of plant associations: *Fagetum* and *Quercion pubescenti* with the help of isozyme markers. For comparison, peroxidases (isozyme systems sensitive to ecological conditions) were tested and the allelic the allelic frequencies found showed correlation with the environmental factors.

In another paper, Comps & al. (1987) investigated 104 stands from the Atlantic region using four polymorphic loci (*Px–1*, *Px–2*, *Pgi–1* and *Got–1*). They found, that populations with the highest diversity occurred in southern regions – Spain, the Pyrenees, and Aquitaine. In contrast to the previous paper the allelic frequencies in the Mediterranean populations are independent from the ecological parameters. The selection effect seems to be revealed only at one single locus (*Px–1*).

The genetic variation of beech stands depends on the ecological conditions. In the central part of the natural range it is continuous. In the marginal populations the variation is discontinuous being influenced by small effective population sizes and, besides that, a small gene flow occurs with regard to the distances and phenological differences.

Based on the French investigations, it could be concluded that as regards allelic frequencies there are no wide differences between individual regions. An exception are the two gene loci (*Px–1* and *Got–1*). In *Px–1*, the frequency of the most common allele increases from the 54 % in Scandinavia and in the Mediterranean region to over 72% and the Pyrenees, 83 % in the Atlantic populations and up to 94 % in central Europe.

The frequency of the most common allele at *Got–1* increases from 49 % in the south European populations to over 75 % in the Mediterranean region and in Atlantic stands and up to 86–96 % in the remaining stands. The genetic diversity in peroxidases is smaller in populations growing under optimal ecological conditions.

Gömöry & al. (1992) investigated the genetic structures of 48 French beech populations which were selected in the gene pool conservation project. They used multilocus records based on 12 gene loci. The results have shown that the allelic frequencies of several loci correspond with the geographical longitude, or with the mean temperature or precipitations. The biggest difference were found between individual populations and regions in the following loci: *Px–2, Acp–1, Got–1* and *Idh–1*. The results have shown that the populations from northwest and northeast France are best separated from those originating from the Pyrenees, and the remaining populations have been characterized by the intermediate position. This fact can be considered to prove that these two population groups originated from two different refugia and were distributed by two different migration ways.

The German investigations focused on three different aspects of genetic studies:

- comparison of sensitive and tolerant sets of beech individuals within populations and of initial population and survivors (Müller-Starck 1993)
- genetic inventories of beech populations for gene conservation purposes (Turok 1996)
- population genetic studies and reproduction processes (comparison of different ontogenetic stages) (Müller-Starck, Starke).

Müller-Starck (1985, 1989, 1993) studied the impact of environmental stress on demes of 'tolerant' and 'sensitive' beeches. He found that genetic structures deviate significantly between tolerant and sensitive demes in adult stands, and between initial populations and juvenile survivors. Tolerant subsets were characterized by greater heterozygosity and greater gene pool diversity. Losses of subsets were evident in surviving subsets.

Turok (1993, 1996) found in Nordrhein-Westfalia and Rheinland-Pflaz high values of diversity as well as genetic differentiation within the populations. Genetic differentiation between populations revealed only modest geographic and/or ecological patterns. A group of indigenous populations from altitudes ranging between 300 and 600 m showed a higher degree of genetic similarity. Non-indigenous populations have rather heterogeneous genetic structures. Significant contribution to gene conservation are genetic investigations of reproductive processes in beech stands (Hattemer & al. 1993, Gregorius & al. 1986, Gregorius & Degen 1994).

In the last few years several other studies were published which aimed at genetic diversity and differentiation of indigenous beech stands included in the gene conservation programs. Konnert (1996) investigated the differentiation of beech populations in Bavaria by use of on 16 isozyme loci. His study revealed that a very high proportion of variation occurs within individual stands (98 %). In a similar study, Tröber (1996) analyzed the remnants of indigenous Saxon beech populations (five stands). Using 10 isozyme loci, she compared the diversity of parent stands with progenies grown in different nursery conditions (greenhouse and open nursery beds). Löchelt (1993) initiated genetic inventory in Baden-Württenbergian beech populations. She also found that the differences between the individual stands were smaller that the variation within stands.

Leonardi & Menozzi (1995) compared Italian populations and found higher levels of genetic variation in southern parts of peninsular Italy. This provides evidence for a southern origin of beech and its northward recolonization.

Central and Eastern Europe

The study of Comps & al. (1990) covered 140 populations and tested populations originating from a transect starting from Poland through Slovakia and Croatia and ending in Sicily and Corsica. This study was based on 6 common isozyme loci. It revealed a strong differentiation of Corsican and Italian populations from those of Balkans and Central Europe. Surprisingly, Polish populations seemed to be also quite different, whereas those from Czecho-Slovakia, Bulgaria, Romania and Serbia formed a relatively homogeneous group. The distribution of genetic diversity was similar as found in the western Europe: higher diversity values were found in the southern populations.

Further studies by Comps & al. (1991) used the same set of loci and focused on Croatia. Thirty-five populations originated from different climatic regions, soils and plant associations were tested. Theyrevealed only quite few significant differences in allelic frequencies and gene diversities between the Mediterranean and continental regions in Croatia, but many more differences between highland and lowland populations within the Mediterranean region as well as between populations belonging to the association *Seslerio-Fagetum* (on carbonate soils) and other associations.

The studies of Gömöry & al. (1992) and Vyšný & al. (1994) were based on the material from Czecho-Slovakia. In 10 of the 12 isozyme gene markers used by them, a significant heterogeneity of allelic frequencies was found among populations. However, the variation among pooled Czech and Slovak populations was significant only at 4 loci. Clinal variation along the latitudinal, longitudinal, and altitudinal gradients was revealed for some alleles among the Czech populations. At the same time, significant correlations of frequencies of several alleles with indicators of air pollution were found.

In 1993, larger investigation of gene diversity and genetic differentiation of beech populations in eastern Europe and in the transition zone between *Fagus sylvatica* and *F. orientalis*, started in Zvolen (Slovakia). The results discussed here originated from the genetic inventory of 110 European beech populations and from 30 populations of *Fagus orientalis*, including the transition zone between these two species. Among the twelve isozyme loci studied only *Mdh–1* proved to be completely monomorphic in most populations. Five other loci (*Mnr–1*, *Mdh–2*, *Pgi–2*, *Pgm–1* and *Skdh–1*) exhibited generally a low degree of polymorphism as well. In total, 42 allelic variants were identified, but some of them with an extremely low frequency, thus contributed little to the allelic diversity. The overall mean number of alleles was 2.21, with slight differences among individual geographic regions. A slight marginal effect can be observed in the mean number of alleles. The Polish and Ukrainian populations situated on the range limit are poorer in alleles than the central ones. For most loci, there are significant differences in allelic frequencies among investigated regions at least at 95 % probability level. However, the differences among populations proved to be significant only in six loci, probably due to the reduced sample size. Some alleles (*Got–2(A)*, *Mdh–1(D, E, F)*, *Mdh–2(E)*, *Mdh–*

3(C), *Skdh–1(D)* were specific for a single or several adjacent regions, but always on a very small frequency (Paule & al. 1995).

Genetic differentiation pattern based on genetic distances revealed that Slovenia and Croatia are rather deviating regions, probably due to a different postglacial origin of *F. sylvatica* from the Apennine glacial refugium (Paule & al. 1995). This is also indicated by a continuous area with a high beech pollen occurrence from northern Italy to Slovenia and northern Croatia in Preboreal and Boreal periods (Huntley & Birks in Horvat-Marolt 1992).

The remaining east European regions exhibit a more or less continuous trend from the Sudets through to the Carpathian arc. This trend may be again the result of postglacial migration paths. However, the effect of selection along the longitudinal gradient (i.e., the gradient of continentality) can be expected.

Transition zone of *Fagus sylvatica* and *F. orientalis*

The Zvolen genetic studies also revealed that beech samples from Bulgaria and adjacent Jugoslavia were differentiated from the rest of the European samples. They also belonged to the taxonomically problematic *Fagus moesiaca* that is considered by many botanists as intermediate between *F. sylvatica* and *F. orientalis*. Another quite deviating region is Moldova on the eastern limit of the distribution range.

In order to distinguish the allelic frequency patterns of both main *Fagus* species, several *F. orientalis* populations originating from Turkey and Caucasus were analyzed. Isozyme loci *Got–2* and *Mdh–3* are almost or completely monomorphic in *F. orientalis*, while in *F. sylvatica* there occur two alleles with almost equal proportions.

In opposite, major polymorphisms were found in *Pgi–1*, *Mdh–1*, *Skdh–1* in *F. orientalis*, in contrast to *F. sylvatica*.

The species specific alleles (*e.g.*, *Mdh–1(A)*, *Mdh–2(D)*, *Mdh–2(E)*) have generally rather low frequencies, and the differences in the proportions of common alleles are not big enough to distinguish both species unambiguously.

However, in Bulgaria, where the contact of natural ranges of both species occur, the difference between them is quite clear – the genetic structure of the population from the Strandja, that can be morphologically classified as *F. orientalis*, is most similar to the west Turkish populations, while the beech in western Bulgaria (Rodopi, Rila) is genetically more similar to *F. sylvatica*.

The alleles typical for *F. orientalis* (*Skdh–1 (D)*, *Pgi–2(A*,C*)*, *Mdh–1(B, D)* etc.) occur in western Bulgaria in higher frequencies. Also the allele representation in some loci (*Lap–1*, *Idh–1*, *Mdh–3*) is slightly shifted towards the structure of *F. orientalis* in Strandja and western Turkey (cf. Paule & al., in prep.).

Introgression between both species in southern Europe seems to be limited to western Bulgaria and probably Macedonia, northern Greece, and a part of southern Serbia. Admixture of genes of *F. orientalis* is also characteristic for populations from Moldova. However, their the migration is from the eastern direction. Alleles characteristic of the Eastern beech occur sporadically also in Romanian populations from the Southern Carpathians.

It is difficult to define the limits of the gene flow, and we have not analyzed the populations from eastern Romania. Based on the allelic frequencies, it is possible to conclude that the main direction of the gene flow prevails from *F. orientalis* to *F. sylvatica*, rather than in the opposite direction.

Forest management practices and gene pool conservation

In situ *gene conservation*

The longest proved method for conservation of genetic diversity in beech stands is natural regeneration. The large scale application of natural regeneration was possible due to shade tolerance of this species. Prolongation of the regeneration period by means of phytotechnical measures might probably compensate for temporal differences in the seed production structure (Hattemer & al. 1995).

In general it has been found that it is more worth while to designate larger units for conservation than many smaller units in *in situ* gene conservation practice. In a programme of *in situ* gene conservation in Poland 13 selected seed stands were established with size 10–150 ha (Janson & Sulkowska 1993). The same attempt has been applied in Slovakia and in the Czech Republic where the size of the gene bases as the principal tool of *in situ* conservation covers 100–500 ha (Paule & al. 1993, Hynek & al. 1993). Within the French gene conservation program of the European beech 20 regions of provenances were defined and within them selected stands of different size were delimited (185 stands belonging to 20 regions of provenances and representing more than 11,400 ha) (Teissier du Cros & Bilger 1995). In Germany both representativeness of stands and their overall performance are being used as criteria for the selection for gene conservation purposes.

Ex situ *gene conservation*

Due to environmental pollution in many parts of Europe it appears to be insufficient to rely on *in situ* conservation alone. The following two principal possibilities for saving population resources *ex situ* are available: static preservation in gene bank and dynamic conservation in plantations. For static conservation the long-term storage of beech nuts has been recently developed (Suszka 1996).

In both *in situ* and *ex situ* conservation, the limiting factor is design of gene sampling. For *ex situ* conservation, seed collection should be carried out only after heavy seed crop in a large continuous stand of unreduced density. *Ex situ* conservation plantations have to be established in one year and thus represent a large sample size of parent trees.

In general, the minimum sample size for preservation of gene resources for *in situ* conservation is not a significant problem for entire stands are usually a subject of natural regeneration. In the application of conservation practices *ex situ* the sample size should be based on estimation of frequencies of rare alleles.

Natural regeneration

The European beech is in a favorable situation in contrast to other tree species of economical importance. Due to its ecological peculiarities the most common sylvicultural practice has always been natural regeneration. Sampling for the previous investigations was easy because in all cases we were dealing with naturally regenerated indigenous beech populations. There are, however, in the eastern Europe traces of improper forest management of beech stands. Coppiced stands, mainly in mixtures with oak, are characteristic for contact zones with agricultural land in lower altitudes or in regions poor in wood, for example in the Balkans. In western Europe, however, there were more cases than in eastern Europe of previous deforestation and replacement of beech stands by more productive coniferous ones. Many cases of beech stands artificially regenerated in the last two centuries are also known. One of the best examples of the introduction of non-indigenous provenances is in Danish forestry. Since the beginning of the 20th century the import of beech seed of foreign provenances was recorded, and it continues up to the present time (Larsen 1995).

The purpose of gene conservation is straightforward and its significance is supported by the prognosis of changes in the climate. If, in the case of climatic changes the necessity of the replacement of the local populations by the southern ones occurs, it is very important to make sure that genetic resources will be available.

A European network for the Evaluation of Genetic Resources of Beech has been established and its main objectives are the following (Muhs & von Wuehlisch 1996):

(1) Tree improvement
  - testing suitability of provenances for different sites,
  - selection of basic material,
  - setting up recommendations for trade and use of provenances at national and international level;

(2) Gene conservation
  - assessment of genetic and phenotypic variation,
  - development of conservation strategies,
  - evaluation methods and ecodistances;

(3) evolution biology
  - adaptedness, adaptability,
  - natural selection forces and their significance;

(4) research on impacts of global climate change; and

(5) stimulation of European co-operation in forest research.

Within this network 15 provenance experiments were established in 1986, 1987, and 1988 containing a total of 188 provenances. In 1995, 23 field trials followed, and they include usually 49, some 100 or more provenances, and the nursery trial with 161 provenances. The field trials were established in spring of 1995 and are located in altogether 17 European countries throughout the range of distribution of beech and in one case even outside its range. The collected data will be managed centrally at a data base at Grosshansdorf (Muhs & al. 1996). Another provenance trial is prepared for sowing in 1996 which will include regions less represented in the previous experiments.

The main aim of these provenance experiments is to test the adaptation potential of individual provenances to changing environmental condition in reply to partially predictable climatic changes.

Artificial regeneration

Establishment of provenance experiments is the best way to answer the questions of whether an intentional seed transfer could be a safe enough for the establishment of beech forest stands in conditions under environmental stress, or on abandoned agricultural lands outside or even inside the beech natural range.

Artificial regeneration will be a more common method of regeneration of beech stands mainly in the future. There are vast areas in western Europe which were converted from mixed or broadleaved stands to coniferous monocultures. It is a common case that these stands were established at non-appropriate sites and that their ecological stability is uncertain. Mainly in the air polluted areas of Germany, Czech Republic and Poland the consequences are visible. It is expected to reconvert these stands to mixed or broadleaved with higher resistance potential.

The second potential application of artificial reforestation is abandoned agricultural land where the selected material could be used, to establish mixed stands or broadleaved stands and to increase the potential of these newly established forest lands to adapt to environmental changes.

The act of sowing or planting stands outside the region of origin of a population is expected to induce a process of adaptation to the new local environment through viability selection. Adaptive processes will be facilitated in case of genetically highly diverse reproductive material.

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