
ECOLOGICAL AND GENETIC STUDIES OF PHYTOCENOSSES



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ALLOZYME VARIATION AMONG EUROPEAN BEECH (*FAGUS SYLVATICA* L.) STANDS IN BOSNIA AND HERZEGOVINA

Abstract. From the economical and ecological point of view, beech (*Fagus sylvatica* L.) is one of the most important forest tree species in Bosnia and Herzegovina. To understand the significance of beech forests, something about the structure of forests and forest lands needs to be said. Bosnia and Herzegovina has 3.231.500 hectares of forests and forest land, which is about 60% of its surface. In the forest and forest lands structure, we can see that it has high forest occupying 51.1% of the forest area, coppice occupying 38.70%, shrubs occupying 4%, bare land and clearings occupying 5.80% and other unproductive areas occupying 0.40%. Beech can be found in mixed stands of beech and fir, as well as stands of beech, fir and spruce that occupy 46% of all high forests. Thus, the total area of forests where the beech is found is approximately 1.652.400 hectares.

The aim of the study was to carry out the analysis of genetic structures of natural beech populations in Bosnia and Herzegovina by using isoenzyme markers. Conducting a biochemical genetic structure analysis of 14 beech populations, using 10 enzyme systems with 16 isoenzyme gene loci, we found significant differences. Variability in some gene loci is large, while some populations for some gene loci showed monomorphism.

The results indicate that in order to maintain natural genetic resources of common beech in Bosnia and Herzegovina, there should be a dense network of gene reserves established. This network from one of the Balkan countries should then become a constituent part of all-European network. These gene banks need *in situ* and *ex situ* methods (seed banks, seed stands, and seed orchards) to maintain the genetic diversity of populations. Based on the research results, every ecological niche of common beech i.e. their genetic variation should be conserved regarding the appropriate number of populations and individuals to preserve the ecological and physiological features of this valuable commercial species.

Key words: European beech, isoenzymes, genetic variability and differentiation.

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АЛЛОЗИМНАЯ ВАРИАНТНОСТЬ БУКОВЫХ ДРЕВОСТОЕВ (*FAGUS SYLVATICA* L.) В БОСНИИ И ГЕРЦЕГОВИНЕ

Аннотация. В статье представлены результаты анализа генетической структуры с использованием изоферментных маркеров 14 естественных популяций бука европейского в Боснии и Герцеговине. Полученные результаты указывают на то, что для сохранения природных генетических ресурсов бука европейского в Боснии и Герцеговине должна быть создана информативная сеть генетических резерватов. Такие генетические банки требуют применения методов *in situ* и *ex situ* (семенных банков, древостоев и плантаций) с целью поддержания генетического разнообразия популяций. Поэтому каждая экологическая ниша бука европейского, то есть его генетические вариации, должны сохраняться в соответствии с количеством популяций и особей с целью сохранения экологических и физиологических особенностей этого ценного промышленного вида.

Ключевые слова: бук европейский, изоферменты, генетическая изменчивость и дифференциация.

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АЛЛОЗИМНА ВАРІАНТНІСТЬ БУКОВИХ ДЕРЕВОСТАНІВ (*FAGUS SYLVATICA* L.) У БОСНІЇ ТА ГЕРЦЕГОВИНІ

Анотація. З економічної та екологічної точок зору бук європейський (*Fagus sylvatica* L.) є одним з найбільш важливих деревних видів у Боснії та Герцеговині. Країна на 60 % вкрита лісом та лісовими угіддями. За площею ця цифра становить 3 млн 231,5 тис. га. У просторовій лісовій структурі високостовбурний насінневий ліс займає 51.1 % площі, порослевий – 38.7 %, чагарники – 4 %, пустки та галявини – 5.80 %, інші непродуктивні землі – 0.4 %. Бук європейський здебільшого зустрічається в мішаних древостанах з участю ялиці та ялини, угруповання яких займають 46 % від усіх лісів насінневого походження. Загальна площа лісів з участю бука становить приблизно 1 млн 652.4 тис. га.

Мета даного дослідження полягала в проведенні аналізу генетичної структури з використанням ізоферментних маркерів у природних популяцій бука Боснії та Герцеговини. Застосовувались 10-ферментні системи з 16-ізоферментними генетичними локусами. Результати проведення біохімічного генетичного аналізу показали суттєві відмінності в структурі 14 популяцій бука. У деяких генних локусах вона виявилась досить значною, у той час як генні локуси окремих популяцій проявили мономорфізм.

Середнє число алелів на локус коливалось від 2.19 у популяціях Бугойно і Бусовача до 2.75 у популяції Дінара. Водночас число генотипів на локус змінювалось від 2.68 у популяції

Бусовача до 3.56 у популяції Дінара. Найвищий показник гетерозиготності виявлено в популяції Бусовача ($H_o = 0.29$), а найменший – у популяції Велеш ($H_o = 0.19$). У 12 популяціях розмір очікуваної гетерозиготності виявився вищим за спостережну гетерозиготність.

Деякі фіксовані алелі (Pgi-B1) є доволі рідкісними спадковими одиницями та носіями цінної інформації для ідентифікації походження насіння та посадкового матеріалу, а також репрезентують характерні маркери деревостанів. Встановлення походження репродуктивного матеріалу має особливе значення для успішного проведення лісгосподарських заходів.

Негативні значення індексу фіксації як міри генетичної відмінності є індикаторами того, що в досліджуваних деревостанах слід проводити більш гнучкі заходи, які б сприяли збереженню генетичного потенціалу до адаптації через належну генетичну мінливість. Ці показники зафіксовані в популяціях Бусовача та Посуша. Найвищий рівень генетичної різновидності виявлено в популяції Дрвар – 185.29, у той час як найвища субпопуляційна диференціація встановлена в популяції Бігач (8.28), що вказує про високу стабільність і однорідність популяції по відношенню до інших у даному дослідженні.

Отримані результати вказують на те, що для збереження природних генетичних ресурсів бука європейського в Боснії та Герцеговині повинна бути створена щільна мережа генетичних резерватів. Такі генетичні банки потребують застосування методів *in situ* та *ex situ* (насінневих банків, деревостанів та плантацій) з метою підтримки генетичної різноманітності популяцій. Тому вважаємо, що кожна екологічна ніша бука європейського, тобто його генетичні варіації повинні зберігатися відповідно до кількості популяцій та особин з метою збереження екологічних та фізіологічних особливостей цього цінного промислового виду.

Ключові слова: бук європейський, ізоферменти, генетична мінливість і диференціація.

INTRODUCTION

European beech (*Fagus sylvatica* L.) belongs to the most significant forest tree species according to its ecological, social, and economic value. Large stands of this important hardwood cover an area totalling about 20 million hectares scattered across the countries of the Balkan Peninsula, France, Germany, Denmark, Switzerland and Italy. According to Fukarek (1970), beech also occupies the majority of the forested area of Bosnia and Herzegovina.

The First State Forest Inventory, cited by Matić et al. (1971), shows that forests in Bosnia and Herzegovina and Herzegovina occupy about 2.5 million hectares, with pure beech stands occupying about 13.3 % of the surface, mixed stands of fir and beech with spruce occupying about 22.4 %, and the coppice beech forests and shrubs occupying about 12.6 % of the surface, which means that the beech was present in Bosnia and Herzegovina in about 48.35 % of the forest area.

Common beech in Bosnia and Herzegovina occurs in a variety of mixtures with other species, arising from the lowest forest regions with sessile oak and common oak (*Fagetum submontanum*), then in upland regions, where it builds pure stands (*Fagetum montanum*), and, most importantly, in the mountain region where in the community with silver fir or silver fir and spruce, it builds our most important forest community beech-fir forests (*Abieti fagetum*) (Stefanović, 1977; Stefanović et al., 1983; Beus, 1984).

Characteristics of beech forests in Bosnia are different, but their specificity in Central Bosnia is that significant areas of pure beech forests are of secondary origin (Beus, 1997). They are made of anthropogenic forests of beech and fir, and beech, fir and spruce as a result of human activities in the Middle Ages, and as such, represent a traditional stage of vegetation. In terms of beech in Bosnia and Herzegovina, it should be noted that it represents the most important species in seven well-preserved prime forests: Ravnavala on mountain Bjelašnica (Pintarić, 1986), Janj and Lom (Maunaga et al., 2001), Mačen do (Drinić, 1956; Mešković, 2007), Trstionica (Ballian, Mikić, 2002), Plješevica (Višnjići et al., 2009), and rainforest Perućica (Fukarek 1962, 1964a, 1964b; Stefanović, 1970, 1988). When making an overview about the management of beech forests in Bosnia and Herzegovina, we must start from the basic fact that, despite the common primeval origin

(up to 90–100 years ago they were the rainforest), beech stands in Bosnia and Herzegovina do not have the similar structural constitution. Today, the composition of beech forests does not suit any of the basic forms of high forests. Thus, according to Bozalo (1991), there are large differences in the wood density and structure constitution between the stands and within the same stand. From these observations about the composition and structural constitution of beech stands, we can see that the introduction of the clear-cut and seed tree harvest as a method of forest management did not work.

While the shelterwood cutting method in beech forests was not representing an acceptable solution, although it was the most often applied method until now, there were several attempts to develop a new and more appropriate solution of forest management within one of the well-established management systems, so Pintarić (1991) advocates a combined way of natural regeneration considering these three conditions: 1) the yield should be permanently high and with high quality; 2) that machinery works get high as possible particularly during the wood extracting phase; 3) preserving and enhancing other permanent beneficial functions of beech forests. So Bozalo (1991) and Pintarić (1991, 2000) starting from the current situation and structural construction of beech forests, found the solution in the group selection system of forest management.

As for the coppice beech forests, they were treated using clear-cut harvest in terms of their conversion to conifer forests, so Pintarić (1986) was urging the use of sparse cuts to fix the structure quality of forests. In the past 5 years, according to Matić (1985), a system of forest management by using selective tree cutting for tree stands of 40–60 years old was developed (Koričić, 2004). Based on those facts, in Western Bosnia coppice forests are being converted into high forests.

As in the past 15 years beech in Bosnia and Herzegovina gained its importance, special activities related to the protection and promotion of beech populations and their genetic resources are being made. Thus, this pilot study will be the basis for all future activities to improve the use of beech forests on the principle of sustainability and preservation of the indigenous genepool of beech in Bosnia and Herzegovina.

MATERIALS AND METHODS

According to standard methods of isoenzyme analysis, our survey was conducted in fourteen indigenous populations of European beech in Bosnia and Herzegovina (table 1, fig. 1). In the winter period, we took a branch with dormant buds from each of the sampled trees, which were used for the extraction of enzymes. The buds were preserved until analysis in test tubes at a temperature of -20°C . The trees were chosen by a random sample. The sample was 50 adult trees for each population. The genetic variability of the fourteen sampled beech populations was analyzed by means of isoenzyme gene markers using starch electrophoresis as the separation method. Enzyme extraction from dormant buds, electrophoresis conditions and staining, and enzyme visualization were performed according to Konnert et al. (2004) (table 2).

Table 1

Basic data of the researched populations of beech in Bosnia and Herzegovina

Population	Weather station (for the population) and altitude (m)	Distance between weather station and population (aproxim.)	Area	Region	Locality	Altitude (m)	Longitude	Latitude
1	2	3	4	5	6	7	8	9
*Bihać (seed stand)	Bihać (246)	10 km	Cazinska krajina	–	Risovac	657	44° 43' 11"	15° 59' 01"
**Bugojno (seed stand)	Bugojno (562)	9 km	Srednjo-bosansko	Vranički	Skrta Nišan	729	43° 58' 24"	17° 30' 36"

End of table 1

1	2	3	4	5	6	7	8	9
**Busovača (seed stand)	Fojnica (584)	10 km	Srednjobosansko	Vranički	Tisovac	624	44° 03' 11"	17° 50' 59"
***Čemerno	Čemerno (1305)	1 km	Submediteransko planinsko	–	Čemerno	1290	43° 14' 49"	18° 36' 37"
****Dinara	Bosansko grahovo (861)	15 km	Submediteransko planinsko	–	Crni lug	886	44° 03' 33"	16° 33' 09"
**Drvar	Drvar (485)	8 km	Submediteransko planinsko	–	Jadovnik	926	44° 18' 04"	16° 24' 25"
**Igrište	Vlasenica (668)	4 km	Istočnobosanske visoravni	Romanijski	Igrište	1005	44° 09' 26"	18° 55' 52"
**Kakanj (seed stand)	Zenica (344)	25 km	Srednjobosansko	Sarajevsko-zenički	Brnjic	646	44° 12' 09"	18° 04' 35"
**Olovo (seed stand)	Maoča (335)	12 km	Zavidovičko-tesličko	–	Duboštica	959	44° 16' 50"	18° 18' 39"
****Posušje	Rakitno (915)	3 km	Submediteransko planinsko	–	Bosiljna	1289	43° 32' 53"	17° 28' 35"
****Prenj (seed stand)	Konjic (280)	12 km	Submediteransko planinsko	–	Rakov laz	1158	43° 32' 24"	18° 01' 09"
**Sjemeć	Sjemeć (1180)	1 km	Istočnobosanske visoravni	Romanijski	Sjemeć	1103	43° 47' 45"	19° 08' 03"
*Tešanj	Tešanj	5 km	Sjevernobosansko	–	Crni vrh	503	44° 34' 39"	17° 58' 28"
****Velež	Nevesinje (905)	4 km	Submediteransko planinsko	–	Grebak	1058	43° 44' 56"	18° 05' 32"

* – continental climate; ** – altered continental climate; *** – subalpine climate; **** – sub-Mediterranean climate (mountain)

Table 2

Enzyme systems, E.C. reference number, scored loci and number of alleles			
Enzyme systems	E.C. Number	Scored loci	Number of alleles
Phosphoglucose isomerase	5.3.1.9	<i>Pgi</i> –B,	3
Glutamate oxalacetate transaminase	2.6.1.1	<i>Got</i> –A, –B,	3, 3
Aconitase	4.2.1.3	<i>Aco</i> –A, –B,	3, 4
Phosphoglucomutase	2.7.5.1	<i>Pgm</i> –A,	4
Menadion reductase	1.6.99.2	<i>Mnr</i> –A,	5
Isocitrate dehydrogenase	1.1.1.42	<i>Idh</i> –A,	3
Malatdehydrogenase	1.1.1.37	<i>Mdh</i> –B, –C,	5, 2
6Phosphogluconate dehydrogenase	1.1.1.44	<i>6-Pgdh</i> –A, –B, –C,	3, 2, 4
Shikimate dehydrogenase	1.1.1.25	<i>Sdh</i> –A,	3
Peroxidase	1.11.1.7	<i>Per</i> –A, –B,	2, 3
Total 10	–	16	52

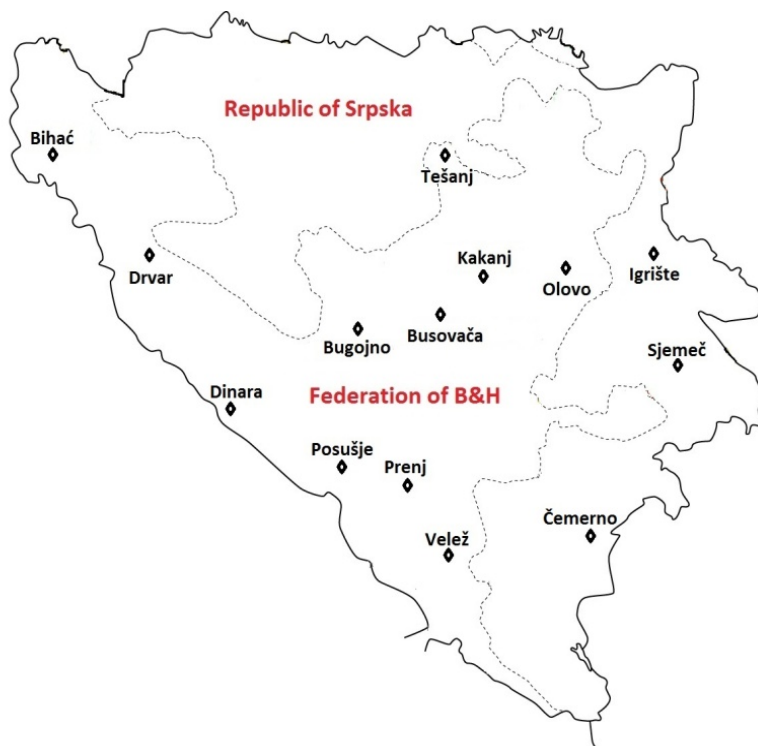


Fig. 1. Location of the researched populations

We analyzed ten enzyme systems, with 16 polymorphic gene loci (table 2). Statistical analysis of genotype and gene frequencies for all 16 gene loci investigated was performed for each of the studied populations. The degree of genetic variability within and among populations is determined by the standard genetic parameters such as:

- A / L = genetic multiplicity, computed as the average number of alleles per locus and
- G / L = average number of genotypes per locus;
- V_p = genetic diversity and V_{gam} = multilocus diversity (Gregorius, 1987);
- Heterozygosity (H_o = observed heterozygosity and H_e = expected heterozygosity based on Hardy-Weinberg proportions (Nei, 1978));
- Fixation index (a measure of population differentiation due to genetic structure);
- Subpopulation differentiation (D_j), (Gregorius, Roberds 1986).

Statistical analysis was performed by using SAS macros software (MACGEN – Stauber, Hertel, 1997); <http://www.mol.schuttle.de/wspc/genetik1.htm>.

RESULTS OF RESEARCH

Variability of alleles. Based on the obtained allele frequencies of the analyzed loci, it is evident that all 16 of the analyzed gene loci show a certain degree of polymorphism, although in certain populations gene loci (*Pgi*) show monomorphism, as it is the case with populations of Bihac, Bugojno, Busovača, Kakanj, Posušje, and Velež.

Rare alleles occur in the populations Drvar and Olovo with *Pgi-B1*, whereas *Aco-A1* allele occurs only in population Preanj and Olovo. *Aco-A3* appears in low frequencies mainly in populations of Western Bosnia near the border with the Republic of Croatia and in North Bosnian population Tešanj. In addition, there is rare allele *Mdh-B2* in population Kakanj, *6-Pgdh-A1* in the Bihac population and *Sdh-A2* in the Bugojno and Olovo population, while the *Sdh-A1* allele was not detected in this study. The gene locus *Mnr-A* is monomorphic in the Bugojno, which seems to be a specific characteristics of this region.

Our analyses show the occurrence of rare alleles at the gene locus *Idh-A*. These rare alleles and specific monomorphisms can serve to identify beech populations in Bosnia and Herzegovina. In overall population, the average number of alleles ranged from 2.19 in the Bugojno and Busovača populations to 2.75 in the Dinara population.

Genetic diversity. The resulting size of the genetic variation within the population is presented in table 3. Average number of genotypes at loci is quite high in all populations except the populations of Busovača, Bugojno, Posušje, and Velež. Average number of genotypes ranged from 2.68 (Busovača population) to 3.56 (Dinara population), which may be associated with its position and specific action selection processes and genetic drift in it, as Submediterranean population is relatively isolated from the central part of beech spreading in Bosnia and Herzegovina.

Table 3

The average number of alleles and genotypes at the locus, the observed heterozygosity (H_o) and expected heterozygosity (H_e), fixation index

Population	Average number of alleles in locus, A/L	Average number of genotypes in locus, G/L	Observed heterozygosity, H_o	Expected heterozygosity, H_e	Fixation index
Bihać	2.50	3.06	0.22	0.25	0.09
Bugojno	2.18	2.75	0.19	0.21	0.03
Busovača	2.18	2.68	0.29	0.25	-0.11
Kakanj	2.56	3.06	0.20	0.21	0.04
Olovo	2.50	3.25	0.23	0.24	0.03
Prenj	2.50	3.00	0.21	0.22	0.00
Čemerno	2.43	3.25	0.25	0.26	0.02
Dinara	2.75	3.56	0.22	0.24	0.05
Drvar	2.68	3.37	0.24	0.26	0.06
Igrište	2.50	3.37	0.21	0.23	0.06
Posušje	2.43	2.87	0.23	0.22	-0.02
Sjemeć	2.56	3.18	0.20	0.21	0.06
Tešanj	2.56	3.37	0.21	0.23	0.10
Velež	2.37	2.93	0.19	0.20	0.07

We also analyzed the observed and expected heterozygosity. Observed heterozygosity varied from 0.19 in the Bugojno and Velež populations to 0.29 in the Busovača population. In 12 populations, the size of the expected heterozygosity is bigger than the observed heterozygosity, which is indicated by positive fixation coefficient, or the occurrence of inbreeding present in the studied populations. Only in the Busovača and Posušje populations, we found a higher expected heterozygosity than the observed heterozygosity, suggesting the absence of inbreeding in this population.

Parameters of genetic variability indicate the existence of a large diversity in allele frequencies between the 14 populations of beech in Bosnia and Herzegovina (table 4). Thus, the highest diversity was found in the Drvar population, which is the easternmost ($V_{gam} = 185.29$ and $V_p = 1.36$). In the population of Velež, a very small size diversity was registered, significantly below average compared to the other studied populations ($V_{gam} = 55.26$ and $V_p = 1.20$), although given the position of the population, a greater value has been expected. This result can be linked to the specific action of genetic drift acting in that Submediterranean population. Other populations have a variety of sizes 63.27, which is registered in the population of Bugojno, to 173.87 in Čemerno population.

If we analyze the results of genetic differentiation (δT), presented in Table 4, we note that the differentiation in populations ranges from 0.21 at the population of Velež to 0.26 in the populations of Drvar and Čemerno, which is the highest range in the analyzed population.

Table 4

The diversity and size differentiation				
Population	Diversity		Differentiation	Subpopulation differentiation
	V_{gem}	V_p	δ_T	Dj (%)
Bihać	162.00	1.34	0.25	8.28
Bugojno	63.27	1.27	0.21	5.05
Busovača	158.19	1.33	0.25	5.59
Kakanj	65.63	1.27	0.21	4.36
Olovo	116.19	1.32	0.24	6.14
Prenj	82.64	1.28	0.22	5.41
Čemerno	173.87	1.35	0.26	4.49
Dinara	112.07	1.32	0.24	3.20
Drvar	185.29	1.36	0.26	5.70
Igrište	87.80	1.30	0.23	3.13
Posušje	88.54	1.29	0.23	7.58
Sjemeć	66.79	1.28	0.22	4.94
Tešanj	103.94	1.30	0.23	4.88
Velež	55.26	1.20	0.21	4.97

The largest secondary gene pool differentiation within the population (subpopulations) was shown in the population of Bihać, with 8.28 %, and the lowest one was shown in the population of Igrište with 3.20 %. The mean value of 5.26 % indicates interpopulation differentiation in this study. Results obtained in this study show that 5.26 % of the total genetic diversity can be attributed to the differentiation between populations, and the remaining 94.74 % can be attributed to allelic variation among individuals in a population.

DISCUSSION

It could be concluded that the postglacial migration is responsible for genetic variability and differences between populations, as published by several authors (Comes and Kadereit, 1998; Taberlet et al., 1998; Hewitt, 1999, 2000; Cruzan, Templeton, 2000; Willis, Whittaker, 2000; Stewart, Lister, 2001; Petit et al., 2002; Taberlet, Cheddadi, 2003; Lascoux et al., 2004; Magri et al., 2006), or perhaps the adaptability of certain genotypes in a specific habitat in which operate specific selection processes (Ballian, Kajba, 2011).

Due to very poor structures in numerous natural beech forests that are in various stages of degradation, the future depends on artificial regeneration, thus it is necessary to gather a genetic picture of all potential sources of reproductive material. High genetic variation in the reproductive material is usually considered as necessary concerning adaptiveness, at least as the adaptive potential of future generations of forest trees. This serves as a basis for good artificial reconstruction under altered environmental conditions. There is also a problem related to the production of planting materials, primarily from the complicated production in nurseries due to special ecological requirements of the species to the gene pool poorly represented in the produced material.

Although we analyzed only 14 populations, based on the given results and high genetic diversity, the main question is "how many populations can represent the genetic structure of beech in Bosnia and Herzegovina?" Given the broad distribution (Fukarek, 1970), it is not easy to answer that question, because in Bosnia and Herzegovina, beech appears in different ecological niches and many forest communities.

When performing a restoration of beech, by any method, there is also the problem of whether to include all the alleles and genotypes. Therefore, in areas such as Bosnia and Herzegovina, with very diverse environmental conditions on very small areas (Stefanovic et al., 1983), as well as with many forest communities of beech (Stefanović, 1977), a variant method of multiple breeding population should be applied (Ballian and Kajba, 2011).

The basic setting in terms of artificial reconstruction of beech populations in Bosnia and Herzegovina is that special attention needs to be paid to the local population or populations from one region, mostly because beech shows great plasticity and adaptive

potential, which in Bosnia and Herzegovina has to be proven through a series of field experiments as it is already being done through international beech provenance test in Kakanj (Ballian, Zukić, 2011).

During investigations or application works with beech and with other species, it is advisable to pay attention to the genetic structure of the population according to its age stages because during aging due to systematic effects of selection, it reduces the number of trees and changes the genetic structure. This statement is verified in the research of age stage of population of spruce by Ruetz et al. (1996). Therefore, in the reconstruction of beech, checks should be made with genetic structure directing it in the desired direction (Behm, Konner, 1999), because the genetic differences between old and young trees in one population, can be minimized by using appropriate silvicultural measures, with special care taken in the future.

CONCLUSIONS

Sixteen isozyme gene loci were analysed to determine the genetic structures of 14 beech populations, which turned out to be significantly differentiated.

Variability with some gene loci is large, while some populations have registered monomorphism for other gene loci. The average number of alleles per locus ranged from 2.19 in the Bugojno and Busovača populations to 2.75 in the Dinara population, while the average number of genotypes at the locus ranged from 2.75 to 3.56. Observed heterozygosity was highest in the population of Busovača, and the lowest one was in the population of Velež. The Busovača and Posušje populations had negative values of the fixation index, while the other populations had positive values. Negative values of the fixation index are an indicator that the studied seed stands can be maintained more flexibly. They would not lose much of their genetic potential for adaptation because they have enough genetic variability and such value was registered. Three of the alleles that are registered, represent rare alleles, such as *Pgi-B1* and *Idh-A*, which are very useful in the subsequent determination of the origin of seeds and planting materials, and represent specific markers of these stands. In addition to the importance of determining the origin of reproductive material, it is very important for the successful implementation of management measures.

The multilocus genetic diversity ranged between 55.26 and 185.29, which shows the population of Drvar and gene pool diversity between 1.26 and 1.36.

The result is a medium size differentiation for all populations, which is quite low, and $D_j = 5.26\%$. This size shows the share of total diversity, which can be estimated at about 94.74%. This is due to the genetic diversity among populations and within populations, variability and poor differentiation among populations. The population of Bihać had greatest differentiation (8.28%), indicating a high stability and homogeneity of the population in comparison to others in this study. This might refer to special adaptive processes in this particular population. The lowest values for D_j were found in Dinara and Igriste, which are therefore the most representative ones in our survey.

As this research only gave a partial genetic structure of beech in Bosnia and Herzegovina, it is necessary to continue with further research in order to do genetic zoning of this valuable species. In these studies, special attention should be paid to the demarcation of provenance (seed stands), as well as the experimental regionalization based on the provenance tests, through research of ecological and physiological characteristics.

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