

# GENETIC DIVERSITY OF *Picea orientalis* (L.) LINK POPULATIONS IN TURKEY

## GENETSKA RAZNOLIKOST POPULACIJA *Picea orientalis* (L.) LINK U TURSKOJ

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### Summary

Knowledge of genetic variation is needed to understanding the genetic structure in forest tree populations. In addition, the determination of the genetic structure in the natural distribution areas of forest trees has become easier depending on the development of the isoenzyme technique. Determining the genetic structure and variations of *Picea orientalis* (L.) Link, which is limited local natural distribution areas on the world, transfer of this genetic to the future generations with sustainable forestry is important to ensure the continuity of the species. In this study, genetic differences and similarities were determined for *P. orientalis* populations in selected regions (Artvin, Torul-Örümcek, Tirebolu-Akıl Baba, Ordu-Çambaşı, Artvin-Şavşat, Ardanuç-Ovacık, Şavşat-Sahara, Artvin-Saçınka, Ardahan-Posof and Maçka-Hamsiköy) in Turkey. In the study using 10 gene loci in different enzyme systems to determine the genetic variation, the values of heterozygosity ( $H_o$ ), number of alleles per locus ( $A_l$ ), genetic diversity ( $v$ ), intrapopulation differentiation ( $d_p$ ), multilocus diversity ( $V_{gam}$ ) and differentiation among populations ( $D_j$ ) were determined in these populations. The grand means were obtained as 0.154, 1.74 and 1.719 for the observed heterozygosity, alleles per locus and genetic diversity, respectively. Moreover, when the genetic diversity was considered, three different groups arose in terms of selected populations. Since Torul-Örümcek population had relatively higher results in contrast to other populations, this population has high importance for sustainability of gene resource of oriental spruce.

**KEY WORDS:** Genetic diversity, conservation, Isoenzyme, *Picea orientalis*,

### INTRODUCTION

#### UVOD

*Picea orientalis* (L.) Link (oriental spruce) spreads over North-East Anatolia and in adjacent region of the Caucasus. The whole area of its present distribution has a North to South extensions from 43°50' N. to 40°23'N., and East to West extensions from 44°13' E. (Greenwich) to 37°47'E., this area is horseshoe-shaped in outline and is part of the mountainous vegetation zones. The high mountain chains have a great modifying influence on the climate and on the vegetation throughout all the area. *P. orientalis* covers parts of the big Caucasus Mountains, covering the Giorgi and

Tiflis regions, the small Caucasus Mountains, and the Pontus range in North-East Anatolia. Spread to the South-East is prevented by the arid climate of the hinterland. Further limitations are evident by the Black Sea and by mountain chains, except in the West near the Melet River where *P. orientalis* is restricted westwards of the River by dense beech forest. In vertical direction, it begins at the coastal zone and continues as high as 2400 m altitude (Saatçioğlu 1976; Kayacık 1980; Atalay 1984).

Oriental spruce, paleo endemic tree species (Yahyaoğlu et al. 1991), is one of the most important tree species for Turkey. In addition, this species plays a significant role for the

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country in terms of ecological and silvicultural aspects. Natural distribution ranges of oriental spruce are between 550 and 2400 m and it is widespread in the Eastern Black Sea Region, the center of its distribution areas. On the other hand, the species is dominant at treeline and upper subalpine forest, the elevation of this zone varies between 1800 and 2400 m depending on anthropogenic pressure and local ecological conditions in its natural distribution area (Üçler et al. 2001; Üçler et al. 2018). However, a small number of studies were conducted on genetic variation of oriental spruce. In a study about morphological characters of *P. orientalis* in Turkey, it was determined that the main reason of seed, cone and wing size variation was ecological differentiation throughout gradients, especially regarding watershed parameters and altitude (Turna 2004). In another study performed in *P. orientalis*, genetic variation was attempted by using only two enzyme systems (Turna and Yahyaoglu 2002). Results of genetic monitoring in populations concerning the species were rare. Goncharenko et al. (1996) stated that heterozygosities and genetic diversities of *P. orientalis* clearly fell below the average.

For sustainable forest health, genetic diversity provides evolutionary potential against a changing environment. As trees are normally the key element of forest ecosystems, their genetic diversity has also special importance. At the same time, it is known that genetic variability is the basis for tree breeding. Thus, the genetic diversity of trees can be seen as the primary factor for forest sustainability and ecosystem stability. Allozymes and molecular markers (Avisé 1994; Ouborg 1999) based on DNA can assist in the estimation of genetic diversity, in the development of sustainable forest management practices as genetic, in the determination of genetic structure and diversity of populations (Luo et al. 2005).

Although genetic diversity has been predominantly predicted by DNA markers over the last decade, allozyme still remain a preferred marker due to a number of advantages.

These indicators, which demonstrate the genetic diversity between individuals and populations, are necessary for the development of effective strategies for sustainable management and protection (Crawford 1989; Hamrick et al. 1992; Vicario et al. 1995; Luo et al. 2005; Radu et al. 2014). In addition, the allozyme markers are useful for monitoring the genetic changes in the evolutionary process and for identifying geographic variation models that are useful in gene conservation.

Monitoring the geographical genetic variation within natural populations of *P. orientalis* in Turkey consists of the aim of the present study. In this way, it can be provided a contribution to the characterization of genetic resources and to the practical measures for in-situ conservation of genetic variation. A check on genetic erosion and inbreeding will help to detect genetic loads and thus to avoid destabilization following the use of unqualified forest reproductive material.

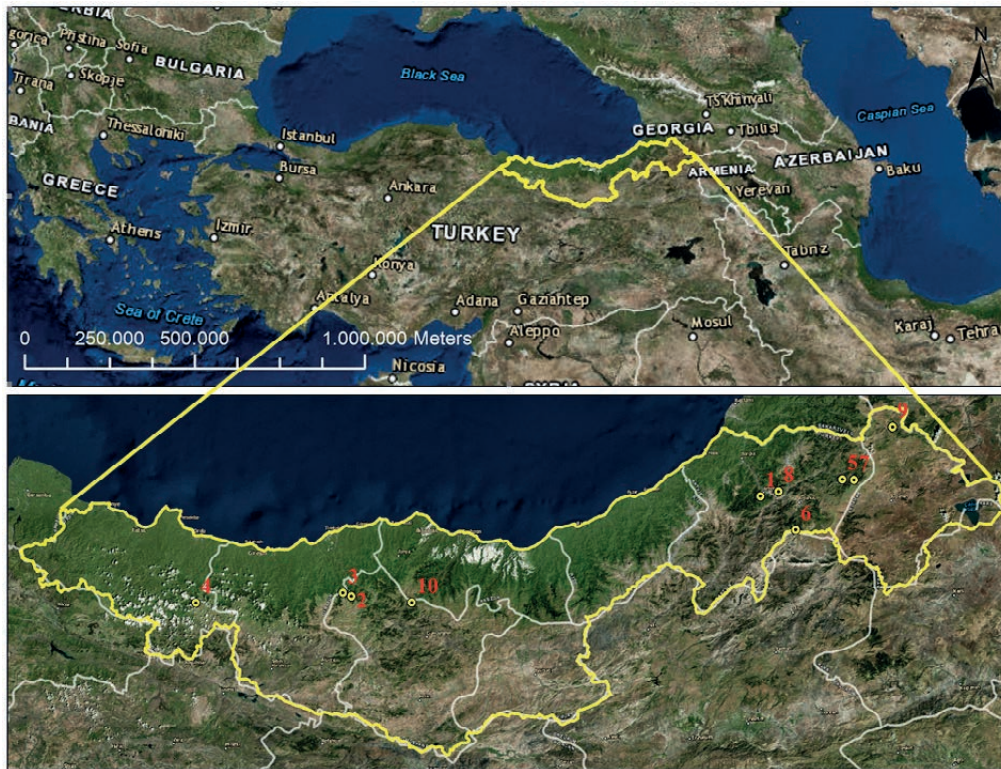
## MATERIALS AND METHODS

### MATERIJALI I METODE

In the scope of this study, seeds were collected from 10 different populations (to be at least 20 trees per population) of oriental spruce. Haploid endosperms and diploid embryos of the air-dry seeds of oriental spruce were used in isoenzyme analysis. Sampling in 10 populations of this species a smaller amount of material was available so that routinely only 60 samples per stand were genotyped, i.e. endosperm and embryo of each of 30 seeds. The geographical coordinates of selected populations of oriental spruce naturally grown in Turkey (Table 1) and distribution on the map, determined by using management plans belong to the country, (Figure 1) are given in below. The geographic distribution of sampled populations allowed an evaluation of overall genetic diversity of this species in Turkey.

**Table 1.** Elemetar data and elevations related to the populations  
**Tablica 1.** Temeljni podaci i nadmorske visine populacija

No Broj	Provenance Provenijencija	Latitude (° , ' , ") Zemljopisna širina	Longitude (° , ' , ") Zemljopisna dužina	Altitude (m) Visina
1	Artvin	41° 09' 46"	41° 47' 57"	1150
2	Torul-Örümcek	40° 40' 29"	38° 58' 01"	1700
3	Tirebolu-Akıl Baba	40° 41' 32"	38° 54' 32"	1850
4	Ordu-Çambaşı	40° 38' 08"	37° 53' 55"	1640
5	Artvin-Şavşat	41° 14' 08"	42° 22' 13"	1265
6	Ardanuç-Ovacık	40° 58' 54"	42° 02' 04"	1920
7	Şavşat-Sahara	41° 13' 49"	42° 26' 59"	1900
8	Artvin-Saçınka	41° 11' 06"	41° 55' 29"	2014
9	Ardahan-Posof	41° 29' 52"	42° 44' 00"	1370
10	Maçka-Hamsiköy	40° 38' 30"	39° 22' 54"	1810



**Figure 1.** Natural distribution areas of *Picea orientalis* in Turkey and locations of sampled populations  
**Slika 1.** Prirodno rasprostriranje *Picea orientalis* u Turskoj i lokaliteti uzorkovanih populacija

**Table 2.** Survey of enzyme system and polymorphic gene loci  
**Tablica 2.** Pregled enzimskih sustava za polimorfne genske lokuse

Enzyme system and Enzyme Commission number (EC) <i>Enzimski sustav i enzimski broj (EC)</i>	Studied gene loci <i>Istraživani genski lokusi</i>
Aspartate aminotransferase (AAT syn. GOT), EC 2.6.1.1	AAT-A
Aconitase (ACO), (ACO) EC 4.2.1.3	ACO-A
Alcohol dehydrogenase (ADH) EC 1.1.1.1	GDH-A
Glutamate dehydrogenase (GDH) EC 1.4.1.2	IDH-B
Isocitrat dehydrogenase (IDH) EC 1.1.1.42	LAP-B
Leucin aminopeptidase (LAP) EC 3.4.11.1	MDH
Malat dehydrogenase (MDH) EC 1.1.1.37	MNR
Menadion reductase (MNR) EC 1.6.99.2	6-PGDH-A
6-Phosphogluconate dehydrogenase (6-PGDH) EC 1.1.1.44	PGI-B
Phosphoglucose isomerase (PGI) EC 5.3.1.9	PGM-B
Phosphoglucomutase (PGM) EC 2.7.5.1	SKDH-A, -B
Shikimate dehydrogenase (SKDH) EC 1.1.1.25	
Number of studied loci Broj istraživanih lokusa	10

Embryo and megagametophyte were homogenized in 0.08-0.1 M Tris-HCl buffer with pH 7.5. Other compounds added were: 5 g saccharose, 150 mg DTT and 3 g PVP in 100 ml of buffer. Extracts from the megagametophyte and the embryo were positioned adjacent to each other in the gels. Horizontal starch gel electrophoresis (10.5% starch concentration plus 2.5-3.5% sucrose) was performed as described by Feret and Bergmann (1976), Conkle et al. (1982) and Liengsiri et al. (1990). The buffer system of Ashton pH 8.6 for GOT and PGM as well as Tris-Citro pH 7.3 were used as electrode and gel buffers for SKDH, MDH and 6-PGDH. In addition, used enzyme systems and 10 gene loci are listed in Table 2.

Genetic variation within populations is measured by counting the number of alleles or genotypes per gene locus ( $A_L$ ,  $G_L$ ), with the gene pool diversity in combination with the hypothetical gametic multilocus diversity ( $v$ ,  $V_{gam}$ ) (Gregorius 1978; Gregorius 1987) and the intra-populational genetic differentiation ( $d_r$ ) (Gregorius 1987). Heterozygosity is described by the observed proportion ( $H_o$ ) of heterozygotes, fixation coefficients according to Wright (1978). Differences between frequencies of genetic types are statistically tested applying the G-test of homogeneity. In the present study, GSED version 1.1 (Gillet 1998) and BIOSYS-2 (Swofford and Selander 1997) programs were used to calculate the measures.

## RESULTS REZULTATI

Differentiations among populations were evident in respect of heterozygosity, the number of alleles per locus and especially the hypothetical gametic multilocus diversities. Variation parameters including number of trees (N), mean number of alleles and genotypes per locus ( $A_L$ ,  $G_L$ ), genetic differentiation ( $d_T$ ), observed heterozygosity ( $H_o$ ), expected heterozygosity ( $H_c$ ), fixation index ( $F_{is}$ ), genetic diversity ( $v$ ), multilocus diversity ( $V_{gam}$ ) and differentiation among populations ( $D_j$ ) related to seed samples of *Picea orientalis* from 10 different locations in Turkey are examined in Table 3.

### Heterozygosity ( $H_o$ ) – Heterozigotnost ( $H_o$ )

For a particular locus, the observed heterozygosity ( $H_o$ ) is calculated by dividing the number of heterozygous trees with the overall number of the individuals surveyed (Goncharenko et al. 1996). The observed heterozygosity ( $H_o$ ) values ranged between 0.110 (Artvin-Saçınka) and 0.190 (Ordu-Çambaşı), equivalent to a ratio 1:1.72, and the grand mean of 0.154.

### Number Alleles per locus ( $A_L$ ) – Broj alela po lokusu ( $A_L$ )

Mean number of alleles per locus is computed by dividing the number of alleles revealed by the overall number of the loci analyzed (Goncharenko et al. 1996).  $A_L$  values ranged between 1.70 (Provenance No. 1, 2, 3, 4, 7, 9 and 10) and 1.90 (Provenance No. 6), equivalent to a ratio 1:1.12. In addition, the grand mean was obtained as 1.74 alleles. In the studies on other tree species, this value ranged between 1.60–4.30 for *Picea abies* (L.) Karst., 1.70–4.70 for *Abies alba* Mill., 1.50–1.90 for *Pinus cembra* L., 1.20–2.10 for *Pinus halepensis* Mill., 1.40–1.60 for *Pinus leucodermis* Ait., 2.40–3.00 for *Pinus nigra* Arnold., 2.60–4.30 for *Pinus sylvestris* L., 1.70–3.20 for *Castanea sativa* Mill., 2.20–4.00 for *Fagus syl-*

*vatica* L. and 3.10–3.20 for *Quercus petraea* Liebl. Moreover, this was determined as 1.90, 2.30, 1.60, 2.70, 2.80 and 3.20 for *Larix decidua* Mill., *Pinus pumila* (Pall.) Regel, *Pinus sibirica* Du Tour, *Ficus carica* L., *Quercus ilex* L. and *Quercus robur* L., respectively (Müller-Starck et al. 1992; Müller-Starck 1995).

### Genetic diversity ( $v$ ) – Genetički diverzitet ( $v$ )

Differences were indicated in terms of the genetic diversity  $v$ -values ranges 1.555 (Ordu-Çambaşı) and 1.990 (Ardu-Çambaşı), equivalent to a ratio 1:1.279, and the grand mean of 1.719. For each population, the comparison of  $A_L$  and  $v$ -values allow to infer tentatively on the mode of frequency distribution of alleles. Samples with similar or identical  $A_L$  values (e.g.  $A_L=1.70$  for Provenance No. 1, 2, 3, 4, 7, 9 and 10) can show distinct deviations with respect to the corresponding diversities ( $v=1.738$ ,  $v=1.768$ ,  $v=1.709$ ,  $v=1.555$ ,  $v=1.600$ ,  $v=1.811$  and  $v=1.730$ , respectively). This demonstrates the greater evenness of the allelic frequency distributions of Provenance No. 9 as compared to Provenance No. 1, 2, 3, 4, 7 and 10. In addition, Provenance No. 6 revealed the largest  $v$ -value (1.990). On the other hand, it was determined that the second largest  $A_L$  value (1.80) occurred by Provenance No. 5 and 8, but the corresponding low  $v$ -values (1.700 and 1.586, respectively) suggests a larger proportion of rare alleles due to greater deviations from even frequency distribution of alleles (Müller-Starck 1995).

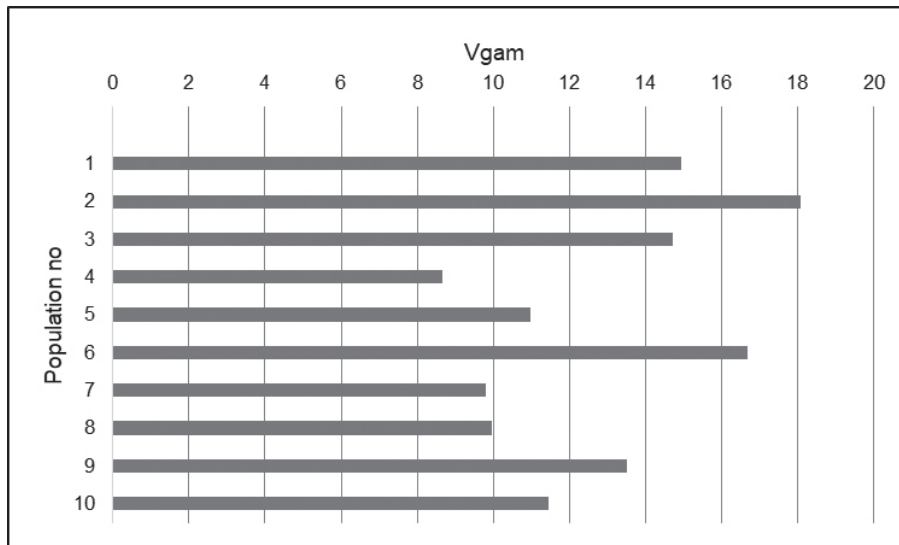
### Intrapopulational differentiation ( $d_T$ ) – Intrapopulacijska diferencijacija ( $d_T$ )

The trends with respect to the gene diversities were also evident for the gene (allelic) differentiation. Accordingly, while Tirebolu-Akıl Baba population gave the largest value ( $d_T=0.326$ ), Ordu-Çambaşı population had the smallest value ( $d_T=0.255$ ). These deviations were equivalent to a ratio of 1:1.278. This ratio was very close with genic diversity

**Table 3.** Variation parameters in seed samples of the populations

**Tablica 3.** Parametri varijabilnosti u uzorcima sjemena populacija

Populations Populacije	Number Broj		Diversity Diverzitet		$d_T$	$H_o$	$H_c$	$F_{is}$	Div.V	$V_{gam}$	$D_j$	
	N	$A_L$	$G_L$	Alleles v								
Artvin	30	1.70	2.50	1.359	1.738	0.306	0.157	1.251	0.234	1.267	14.942	0.104
T. Öürümcek	30	1.70	2.40	1.398	1.768	0.301	0.114	4.960	0.443	1.280	18.077	0.058
T. Akıl Baba	30	1.70	2.50	1.343	1.709	0.326	0.153	1.533	0.270	1.274	14.710	0.086
O. Çambaşı	30	1.70	2.30	1.279	1.555	0.255	0.190	5.160	-0.044	1.207	8.656	0.136
A. Şavşat	30	1.80	2.60	1.326	1.700	0.275	0.153	1.836	0.111	1.224	10.971	0.067
A. Ovacık	30	1.90	2.80	1.388	1.990	0.319	0.190	5.573	0.250	1.270	16.674	0.106
Ş. Sahara	30	1.70	2.50	1.297	1.600	0.264	0.147	2.073	0.244	1.220	9.816	0.075
A. Saçınka	30	1.80	2.40	1.304	1.586	0.264	0.110	5.683	0.268	1.221	9.964	0.071
A. Posof	30	1.70	2.40	1.349	1.811	0.310	0.163	2.390	0.222	1.250	13.501	0.092
M. Hamsiköy	30	1.70	2.50	1.326	1.730	0.300	0.160	5.964	0.067	1.234	11.459	0.080
Mean	30	1.74	2.49	1.337	1.719	0.292	0.154	3.642	0.207	1.245	12.877	0.088



**Figure 2.** Hypothetical gametic multilocus diversity related to the populations  
**Slika 2.** Hipotetska gametska multilokusna raznolikost populacija

(1:1.279). Thus, it can be understood that discriminative function of the gene differentiation and gene diversity is similar.

#### Multilocus diversity ( $V_{gam}$ ) – Multilokusna raznolikost ( $V_{gam}$ )

$V_{gam}$  attributes to differences among samples with respect to the genetic diversity. This shows the potential of a set of trees in order to produce genetically different gametes. Thus, genetic variation can submit to the next generation. For autochthonous tree populations, genetic variability is a basic precondition for adaptation and survival in heterogeneous environments (Müller-Starck 1995). This measure is suggested to quantify the ability of forest tree populations to create genetic variation and thus to facilitate adaptation to changing environmental conditions (Gregorius et al. 1986).

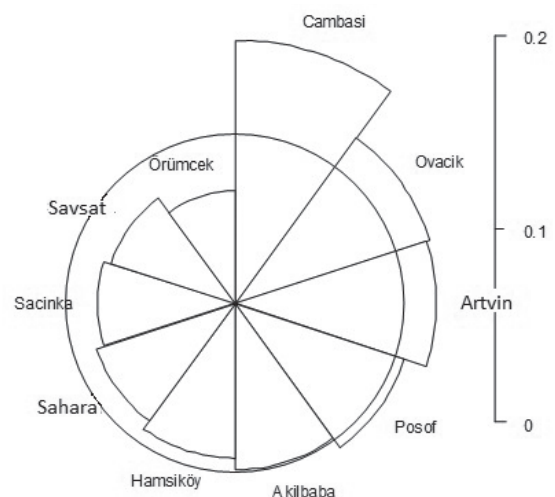
As can be seen from Figure 2, there were significant differences among populations. Whereas the maximum  $V_{gam}$  was obtained as 18.077 in Torul-Örümcek population, the minimum  $V_{gam}$  was determined as 8.656 in Ordu-Çambaşı population. This was equivalent to a ratio of 1:2.09.

#### Differentiation among populations ( $D_j$ ) – Diferencijacija među populacijama ( $D_j$ )

Genetic differentiation among subpopulations is based on genetic distances. Frequencies of genetic types of one population are contrasted with the weighted averages of the frequencies of the remaining populations. Each population is considered as a subpopulation and differentiation is quantified via the genetic distances between one sample and the remaining ones that are pooled as the respective complement population. As a conclusion, genetic differentiation is quantified as a whole (Müller-Starck 1995).

As can be seen from the last column in Table 3,  $D_j$  values differentiated considerably from each other: the maximum value occurred in Ordu-Çambaşı population (0.136), the minimum value revealed in Torul-Örümcek population (0.058). This was equivalent to a ratio of 1:2.34. In Figure 3, the genetic differentiation was illustrated.

Three different groups depending on the gene pool occurred according to the snail diagram used among 10 populations. Ordu-Çambaşı population differentiating from other regions as genetic structure was in a group by itself. Ardanuç-Ovacık and Artvin populations, being genetically close to each other and separating from the other regions, took place in the same group. Another group was formed by Torul-Örümcek, Tirebolu-Akıl Baba, Artvin-Şavşat, Şavşat-Sahara, Artvin-Saçınka, Ardahan-Posof and Maçka-Hamsiköy populations.



**Figure 3.** Genetic differentiation related to the populations  
**Slika 3.** Genetska diferencijacija populacija

## DISCUSSION AND CONCLUSION RASPRAVA I ZAKLJUČCI

Earlier studies on variation in morphological and genetic characters have revealed the existence of considerable variation in oriental spruce (Atalay 1984; Goncharenko et al. 1996; Turna and Yahyaoğlu 2002; Turna 2004; Temel 2010). However, there is not much study showing genetic variation by using different enzyme systems to represent the natural distribution areas of this species.

Expected and observed heterozygosities allow the most accurate estimation of the genetic variation level within populations. According to the results of the present study, it was determined that the mean observed heterozygosity ( $H_o$ ) value was 0.154. In a study conducted in 12 populations using two enzyme system for *P. orientalis* in Turkey, mean expected heterozygosity per population varied from 0.128 to 0.463, with an average of 0.280 (Turna and Yahyaoğlu 2002). Serbian spruce (*Picea omorika* (Panc.) Purk.), having isolated distribution range like *Picea orientalis*, exhibited considerable variation in terms of both heterozygosity and gene diversity among populations. Observed heterozygosities ranged from 0.018 to 0.132, whereas expected heterozygosities varied from 0.017 to 0.096 (Ballian et al. 2006). In a research made in the populations of *Picea abies*, observed heterozygosity ranged from 0.136 to 0.173, with the mean of 0.158 in Carpathian region (Korshikov and Privalikhin 2007). Another study was conducted for Norway spruce distributed in Romania. According to this, expected heterozygosity ( $H_e=0.115$ ) was similar to the average value obtained in 70 populations from Europe natural range of the species (Lagercrantz and Ryman, 1990; Radu et al. 2014). While expected heterozygosity was 0.156 in a study conducted in the same species in Poland, expected and observed heterozygosity were determined as 0.186 and 0.185, respectively, in a study conducted in Latvia (Goncharenko et al. 1995; Lewandowski and Burczyk 2002). Ballian et al. (2009) stated that observed heterozygosity in the populations of *P. abies* ranged from 0.19 to 0.22 in Slovenia and Bosnia and Herzegovina, on the extreme sites (for realistic data from Bosnia and Herzegovina, the author should consult the proposed literature). It is clearly understandable that there are similarities between the previous researches related to *Picea* genus and the present study. Unlike this situation, Gömöry (1992), in the study for *P. abies* in Poland, reported that expected and observed heterozygosity were 0.306 and 0.275, respectively. In this study for oriental spruce, the grand mean of  $H_o=0.154$  showed the smaller average heterozygosity than the reported studies for Norway spruce including  $H_o=22.6\%$  (Müller-Starck 1995),  $H_o=25.2\%$  (Konnert and Franke 1990; Konnert 1991),  $H_o=22.2\%$  (Löchelt and Franke 1993). In addition, observed heterozygosity was found as 14.7% in a study in Austria (Geburek 1999).

The number of alleles per locus ( $A_L=1.74$ ) obtained from the present study conducted for *Picea orientalis* was higher than other Norway spruce populations studied in Romanian Carpathians region ( $A_L=1.21$ ) (Radu et al. 2014). While  $A_L$  value (1.58) obtained for *Picea abies* in another study (Lagercrantz and Ryman 1990) was close to the value that we obtained in our study,  $A_L=1.45$  value obtained for *Picea asperata* was lower (Luo et al. 2005). Krutovskii and Bergmann (1995) found that this value occurred as 2.4 for *Picea obovata* in Kazakhstan and Siberia. In different studies made for *P. abies*, the number of alleles per locus was determined as 2.17 in Poland (Lewandowski and Burczyk 2002), as 2.2 in Austria (Geburek 1999), as 2.26 in Latvia (Goncharenko et al. 1995), as 2.50, 2.80, 2.90, 2.90 and 2.80 in Germany, Sweden, Byelorussia, Ukraine and Russia, respectively (Krutovskii and Bergmann 1995), as 2.59–2.71 in the Mountain of Igman (Ballian et al. 2007a), as 2.06 and 3.38 in Slovenia and Bosnia and Herzegovina, respectively (Ballian et al. 2009), and as 3.55 in Ukrainian Carpathians (Korshikov and Privalikhin 2007). As can be seen from the results, these values are higher than the number of alleles per locus obtained for *P. orientalis* in this study.

According to results of a study conducted for *P. asperata* in China, the sampled populations were characterized by low genetic diversity (mean  $H_e=0.096$ ) and a low level of inbreeding (mean  $F_{is}=0.005$ ). In addition, the expected heterozygosities ( $H_e$ ) and observed heterozygosities ( $H_o$ ) were relatively low and ranged from 0.066 to 0.131, and from 0.059 to 0.141, with an average of 0.096 and 0.094, respectively (Luo et al. 2005). In a study carried out for *P. abies* in Poland, a relatively low allozyme differentiation was determined among populations from north-eastern and southern Poland (mean genetic distance  $D=0.005$ ). According to the results, historical events and extensive gene flow played a significant role in the distribution of the observed allozyme differentiation of the species in Poland (Lewandowski and Burczyk 2002). In another study conducted by Geburek (1999) regarding *P. abies*, while the genetic diversity was 1.18 in Austria, this varied from 1.23 to 1.28 in Slovenia and Bosnia and Herzegovina, on the extreme sites. (for realistic data from Bosnia and Herzegovina, the author should consult the proposed literature) In the study conducted in Latvia, the genetic distance among the populations ranged between 0.003 and 0.012. When the results of the study were evaluated, there were a very low differentiation and a close genetic relationship among the populations in Latvian (Goncharenko et al. 1995).

While the highest value in terms of  $V_{gam}$  (18.077) was determined in Provenance No. 2 (Torul-Örümcek), the lowest one was obtained as 8.656 in Provenance No. 4 (Ordu-Çambaşı). The arithmetic grand mean related to this value was 12.877. Oriental spruce has a local and limited natural distribution for both Turkey and the world. Therefore, ge-

netic variation of this species is of great importance. In this study, Torul-Örümcek population having the highest  $V_{gam}$  value is located in backward section of Eastern Black Sea Region in Turkey. In the genetic diversity studies concerning oriental spruce and the other species, this area is presented as a region with high variation (Temel 2010; Velioglu et al. 2012). Ordu-Çambaşı population having the lowest  $V_{gam}$  value is located in Central Black Sea Region in Turkey. In the scope of the study, three different groups revealed among the populations. Similarly to this study, Turna (2004) found that Ordu-Çambaşı region was located in a group being different from the other regions. It should be added that Torul-Örümcek population stands out with its genetic variation. In-situ and ex-situ conservation of these populations, located in natural distribution area of oriental spruce and having high genetic variation, is important. In Turkey, rough geographical structure, different climate types and soil characteristics encourage to create local breeds even in short distances (Işık 1988; Kaya 1989). Optimal protection of a species and its genes can take place in its natural habitat.

At the beginning of breeding programs, genetic diversity and variation studies are emphasized within species. If there is not enough genetic diversity between trees and populations in terms of desirable characters in tree species, and the inheritance values of tree characters are too low, the expected benefits from breeding will not occur (Işık 1994; Güney 2005).

In terms of climate change, genetic diversity is one of the most important factors that can contribute to the adaptation of species (Thompson et al. 2009; Radu et al. 2014). Characterization and conservation of genetic variation is significant for tree populations exposed to a wide range of abiotic and biotic stress factors in time and space. Since future environmental stress factors together with the global warming will increase, the adaptability of tree populations becomes even more important. The situation of genetic variation in present and future generations will determine this adaptation (Müller 1995).

The great number of rare alleles being evident in forest tree populations and having a large potential to create genetic diversity should be preserved. Rare alleles considerably increase the genetic variability and thus the ability of adaptation and survival of long lived carrier species of complex forest ecosystems under highly variable environmental conditions. Local populations which are reserves against genetic erosion and genetic pollution should be protected to be used as genetic sources in future (Müller 1995). On the other hand, Ballian et al. (2007b) stated that it would be necessary to establish a dense network of gene banks in situ and ex situ, and to preserve the genetic diversity within populations in order to preserve the natural genetic resources of spruce in Bosnia and Herzegovina.

The diversity of gene, species and ecosystem levels for sustainable development should be protected and maintained. Genetic diversity provides wide adaptability and evolutionary potential to the species carrying those genes in order to adapt changing conditions and environments. Therefore, the components of biodiversity must first be protected, then researched and learned, and finally, they should be used in accordance with the principles of sustainability within the framework of the knowledge and understanding derived from them.

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## SAŽETAK

Za razumijevanje genetske strukture populacija šumskog drveća potrebno je poznavati genetsku varijabilnost. Razvoj izoenzimske tehnike olakšao je određivanje genetske strukture populacija u području rasprostranjenja vrsta. Određivanjem genetske strukture i varijabilnosti *Picea orientalis* (L.) Link, koja je u svijetu ograničena na manje područje, transfer trenutne genetske strukture na buduće generacije putem održivog gospodarenja šumama važan je za osiguravanje kontinuiteta vrste. U ovom istraživanju određene su genetske različitosti i sličnosti za populacije *P. orientalis* u odabranim populacijama (Artvin, Torul-Örümcek, Tirebolu-Akılbaşa, Ordu-Çambaşı, Artvin-Şavşat, Ardanuç-Ovacık, Şavşat-Sahara, Artvin-Saçinka, Ardahan-Posof an Maçka-Hamsiköy) Turske. Korišteno je 10 genskih lokusa u različitim enzimskim sustavima, a određena je genetska varijabilnost, vrijednost heterozigotnost ( $H_o$ ), broj alela po lokusu ( $A_L$ ), genetski diverzitet ( $v$ ), intrapopulacijska diferencijacija ( $d_r$ ), multi-lokusna raznolikost ( $V_{gam}$ ) te diferencijacija među populacijama ( $D_j$ ). Za promatranu heterozigotnost, broj alela po lokusu i genetski diverzitet dobivena je središnja vrijednost od 0.154, 1.74 i 1.719. Nadalje, kod razmatranja genetskog diverziteta, pojavile su se tri različite skupine u smislu odabranih populacija. S obzirom da je populacija Torul-Örümcek pokazala relativno više vrijednosti u odnosu na ostale populacije, ova populacija je vrlo važna za održivost genetskih izvora kavkaske smreke.

**KLJUČNE RIJEČI:** genetski diverzitet, očuvanje, izoenzimi, *Picea orientalis*