African Journal of Biotechnology Vol. 11(23), pp. 6389-6395, 20 March, 2012
Available online at http://www.academicjournals.org/AJB
DOI: 10.5897/AJB11.3340
ISSN 1684–5315 © 2012 Academic Journals

Full Length Research Paper

Variation in seedling morphology of Turkish fir (*Abies nordmanniana* subsp. *bornmulleriana* Mattf)

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Accepted 3 February, 2012

In this study, the genetic variation of some seedling characteristics of Turkish fir was investigated. A total of 303 trees were selected from 17 plots and 10 seedlings from each tree were used. Fifteen morphological characteristics were determined, including root collar diameter, seedling height, total needle, bud length and width, epycotyl length, needle length and width of 1 year seedlings and root collar diameter, shoot height and diameter, needle length and width, bud length and width of 2 years seedlings. Data were analyzed by using SPSS and SAS programs. The results show that there were significant differences among the populations in terms of morphological characteristics. In addition, 12.51% of the total variation is distributed among populations. The results of this research could be used for breeding studies in Turkish fir and *in-situ*/*ex-situ* conservation strategies, silvicultural purpose and breeding strategies.

Key words: Genetic variation, *Abies nordmanniana* subsp. *bornmulleriana* Mattf, Turkish Fir.

INTRODUCTION

The success of any sustainable reforestation program, among other things, depends on the quality of seeds (Hampton, 2002). Several factors affect the quality of seed and seedling production, example, insect infestation (El Atta, 1993; Dajoz, 2000), pollination failure and post-zygotic degeneration (Owens et al., 1990), infection by seed borne pathogens (Pritam and Singh, 1997), environmental conditions during seed and seedling development (Gutterman, 2000) as well as the genetic constitution (Bazzaz et al., 2000).

Genetic diversity is the richness of the hereditary information in the gene pole of one species (Şevik et al., 2010). Over a long term, the ability of a species to respond adaptively to environmental changes depends on the level of its genetic variability (Ayala and Kiger, 1984). As a process, genetic differentiation by natural selection to facilitate reproductive isolation involves the presupposition of the origin of geographic races, subspecies and species (Stebbins, 1999). A species without an appropriate amount of genetic diversity is thought to be unable to cope with changing environments or evolving competitors and parasites. Therefore, the investigations regarding genetic structures of populations within a species may not only help the evolutionary process and mechanism but also provide information useful for biological conservation (Schaal et al., 1991).

Up till now, in Turkey, studies about genetic diversity of the main forest trees have been concentrated on pine species. There are no enough studies on the other species.

Turkish fir (*Abies nordmannianan* subsp. *bornmülleriana*) has a special importance to Turkey due to its increasing economic value in the market and decorative characteristic in landscape architecture. For this reason, the species, endemic to Turkey, is mostly preferred to as Noel tree in the world. Turkish fir is distributed from Kizilirmak River to Mount Uludağ in Western Black Sea region, particularly in Ayancik, Ilgaz and Bolu Seben Mountains, Boyabat-Göktepe forests, Abant and Mount Uludağ. Stands of fir species occupy about 600.000 ha in Turkey (Anonymous, 2006).

The objective of this study was to investigate the genetic diversity between and within Turkish fir populations in Turkey, using 15 different morphological characters of species seedlings.

MATERIALS AND METHODS

Seed collection and sowing

Open pollinated seed materials were collected from seventeen

Figure 1. Locations of the populations.

different natural populations of Turkish fir in Western Black Sea region. Location and description of the studied populations are presented in Figure 1 and Table 1, while seeds were sown at seed beds of 0.5 cm depth in February. Seeds were sown in river sand (10%), forest soil (30%) and peat (60%), respectively and covered with perlite and snow. At the end of the vegetation period, morphological features were measured for 1 year old seedlings. After 1 year, morphological features were measured again for 2 years old seedlings.

Seedling morphological variables studied and data collection

In this study, root collar diameter (RCD1), seedling height (SH1), total needle (TN1), bud length (BL1), bud width (BW1), epycothyl length (EL1), needle length (NL1), needle width (NW1) of 1 year seedlings and root collar diameter (RCD2), shoot height (SH2), shoot diameter (SD2), needle length (NL2), needle width (NW2), bud length (BL2) and bud width (BW2) of 2 years seedlings were determined. All the length and width measurements were done by digital microcompas (0.01 mm) of 10 seedlings from 303 sample trees.

Statistical analysis

Data were standardized before the calculations and the morphological distance among populations were estimated as:

$$Z_{i,k} = \frac{(X_{i,k} - \bar{x}_k)^2}{S_k}$$

Where, $Z_{i,k}$ is the standardized values of the k^{th} characteristics of the i^{th} population; $X_{i,k}$ is the original average of the k^{th} characteristics of the i^{th} populations for the k^{th} characteristics and S_k is the standard deviation of the studied populations for the k^{th} characteristics (Yahyaoğlu et al., 2001).

$$D_{i,j} = \sum_{k=1}^{p} \frac{(\mu_{ki} - \mu_{kj})^2}{p.V_k}$$

Where, D_{ij} is the morphological distance between the i^{th} population and the j^{th} populations; n is the number of studied characteristics; μ_{kj} is the standardized values of the k^{th} of the l^{th} population; μ_{kj} is the standardized values of the k^{th} characteristics of the j^{th} population; V_k is the variance of standardized averages of the k^{th} characteristics (Yahyaoğlu et al., 2001). This was applied by standardized values in SPSS program (Şevik, 2010).

Table 1. Description of the studied populations.

Population number	Population name	City	Number of sample trees	Altitude (m)	Longitude (E)	Latitude (N)
1	Bafra1	Samsun	10	828	35°21'18"	41°34'01"
2	Bafra2	Samsun	10	1012	35°21'33"	41°33'28"
3	İskilip1	Amasya	20	1673	33°46'11"	41°22'36"
4	İskilip2	Amasya	20	1852	34°13'34"	40°49'01"
5	Türkeli	Sinop	13	1348	34°16'15"	41°44'58"
6	Ilgaz1	Kastamonu	20	1430	33°49'17"	41°09'27"
7	Ilgaz2	Kastamonu	20	1624	33°49'11"	41°08'60"
8	Ilgaz3	Kastamonu	20	1995	33°50'58"	41°07'47"
9	Ballıdağ1	Kastamonu	20	1056	33°29'02"	41°37'11"
10	Ballıdağ2	Kastamonu	20	1374	33°25'29"	41°34'12"
11	Ballıdağ3	Kastamonu	20	1640	33°22'37"	41°31'58"
12	Samatlar	Kastamonu	20	1497	33°15'32"	41°22'06"
13	Eflani	Karabük	20	1102	32°51'45"	41°29'02"
14	Aladağ	Bolu	10	968	31°37'15"	40°40'21"
15	Kıbrıscık2	Bolu	20	1499	32°00'42"	40°25'46"
16	Kıbrıscık1	Bolu	20	1791	32°02'22"	41°28'43"
17	Göynük	Bolu	20	1270	30°41'27"	40°30'08"

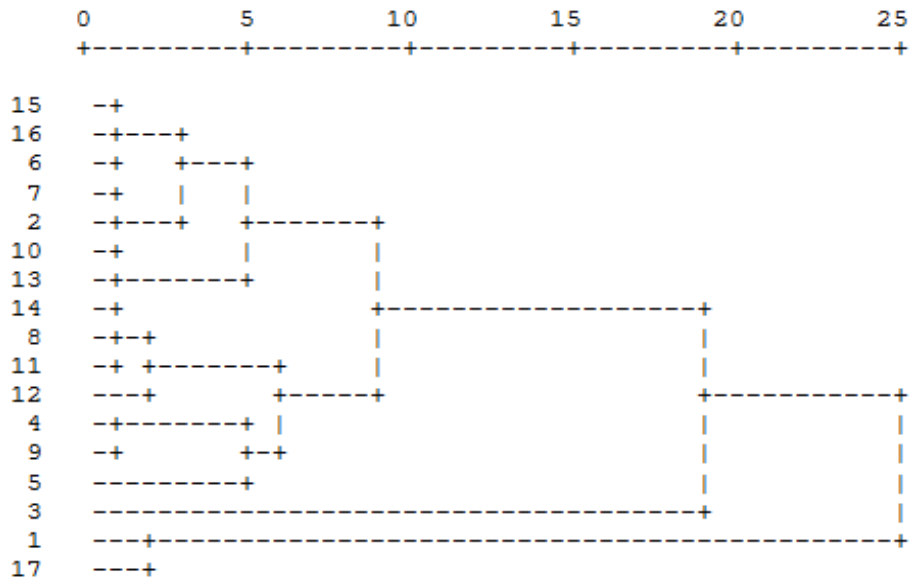

Figure 2. Dendrogram of 17 population of Turkish fir based on 15 morphological seedling traits.

Evaluating quantitative genetic traits

Data analyses were conducted using the SAS program (SAS Institute Inc. 1987). All traits were subjected to analysis of variance (ANOVA), first for each individual test and then with the data sets combined over field sites in each population. Since error variances were consistent for each trait from site to site in each population, there was no adjustment necessary to combine the data over sites. Because of differences in statistical designs used in the seedlings, different random models were employed. The linear model for the combined data over the seedlings was:

$$y_{ij} = \mu + \alpha_i + \beta_{j(i)} + e_{ij} \; (i=1,\ldots,a \; j=1,\ldots,b \; k=1,\ldots,n)$$

Where, y_{ij} is the observation on the jth tree of the ith population; μ is the overall mean; α_i is the effect of the ith population; $\beta_{j(i)}$ is the effect of the jth tree at the ith population and e_{ij} is the random error.

RESULTS AND DISCUSSION

According to the results of cluster analysis (Figure 2), two

Table 2. Morphological distance among populations according to Penrose formula.

	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	Total
1	2.57	1.72	2.62	2.14	2.45	2.95	0.65	2.84	3.33	1.96	3.79	2.6	1.99	2.72	3.01	0.88	**38.22**
2		1.94	1.21	2.35	1.12	1.65	1.98	1.10	1.61	3.19	**4.43**	1.50	3.95	1.67	1.71	1.97	**33.95**
3			1.20	1.80	1.14	1.96	1.35	0.89	2.00	1.96	**4.13**	1.12	2.88	0.84	1.18	1.27	**27.38**
4				1.28	0.81	1.76	1.44	0.89	1.00	1.25	3.98	**0.36**	2.75	**0.54**	0.92	1.99	**24.00**
5					2.11	2.39	1.29	1.54	1.51	0.79	2.52	1.81	2.76	1.64	1.57	2.21	**29.71**
6						0.91	1.58	0.74	1.3	2.21	**4.46**	0.63	2.82	**0.47**	0.71	2.22	**25.68**
7							2.02	0.69	1.13	2.5	2.76	1.46	3.86	1.10	1.38	1.96	**30.48**
8								2.07	2.56	1.29	3.24	1.58	1.65	1.72	2.21	0.88	**27.51**
9									**0.55**	1.98	3.17	0.81	3.71	0.62	0.63	1.85	**24.08**
10										1.87	3.89	1.36	4.09	1.06	0.86	2.15	**30.27**
11											2.37	1.29	2.73	1.59	1.97	2.34	**31.29**
12												3.71	**4.16**	3.98	**4.88**	4.06	**59.53**
13													3.09	0.61	0.88	2.38	**25.19**
14														3.02	4.12	2.91	**50.49**
15															**0.42**	2.02	**24.02**
16																2.40	**28.85**
17																	**33.49**

distinct groups can be noticed: The first is pop1 (Bafra1) and pop17 (Göynük) and the others. The second group can distinguish between two groups, pop3 (İskilip1) and the others. Accordingly, it can be said that there are three main groups. Morphological distance and grouping according to Penrose formula are shown in Table 2.

The highest 5 values were calculated between pop12 (Samatlar) and the other populations. A maximum of 5 values are between the pop12 and pop16 (4.88), pop6 (4.46), pop2 (4.43), pop14 (4.16) and pop3 (4.13). The lowest 5 values are 0.36 (pop4 and pop13), 0.42 (pop15 and pop16), 0.47 (pop6 and pop15), 0.54 (pop4 and pop15) and 0.55 (pop9 and pop10). Maximum total morphological distance values are shown by pop12 (59.53), pop14 (50.49) and pop1 (38.22), whereas minimum total morphological distance values are 24.00 (pop4), 24.02 (pop15) and 24.08 (pop9).Source of variation from SAS is shown in Figure 3. The results show that genetic variance among population were much lower than that within population. The ratio of genetic variation among the populations is 21% for RCD1, 23.2% for SH1, 16.2% for TN1, 5.5% for BW1, 8.2 for EL1, 12.7 for BL1, 19.8 for NL1, 24.6 for NW1, 7.6 for RCD2, 10.5 for SD2, 16.7 for SH2, 4.8 for NW2, 8.1 for BW2 and 4% for BL2. It ranged from 4 (BL2) to 24.6% (NW1).

According to the results of the cluster analysis, Bafra1 and Göynük populations are very close to each other but very different from the others. This situation can be as a result of geographical conditions. These populations are the eastern and the western populations according to geographical positions. Some populations are geographically and genetically close to each other such as, Kibriscik1 (pop15) and Kibriscik2 (pop16) populations. Some of them are geographically close to each other even though they are genetically different from each other, example, Bafra1 (pop1) and Bafra2 (pop2) populations. On the contrary, some populations are genetically close to each other even though they are geographically different from each other, for example, Bafra2 (pop2) and Ballıdağ2 (pop10) populations.

Morphological distance values range from 0.36 to 4.88 according to the results of Penrose formula. Similar to the results of cluster analysis, some populations are geographically and genetically close to each other, example, Kibriscik1 (pop15) and Kibriscik2 (pop16) populations. Some of them are geographically close to each other though genetically different from each other. For example, Ilgaz1 (pop6) and Kibriscik1 (pop16) populations and some populations are genetically close to each other even though they are geographically different from each other, for example, Bafra1 (pop1) and Göynük (pop17) populations.

These results could be used in preparation of gene map, seed transfer zones, determination of breeding populations, gene conservation areas, geographic variation and they result to provenance trials of the species in a short period. Preparation of forest gene maps and determination of seed transfer zones and geographical

Figure 3. Source of variation (y-axis is in %).

variation by morphological distance were also suggested by Yahyaoğlu et al. (2001).

According to the results of SAS, the variation among the populations is averaged at 12.51%. This result is in accordance with other studies. Yücedağ et al. (2010) stated that the variation among populations was less than 30% for 75 days seedlings of Crimean juniper. Shea (1990) reported that the variation among the populations is small (1.3%) but significant in *Abies Lasiocarpa*. Sorensen and Franklin (1977) reported that year effect including interactions with places and trees in places made up an estimated 45% of the variance in seed weight and 25% of the variance in cotyledon number. Among population, genetic variance was much lower than within population variance, ranging from 6.6 to 6.8% for drought resistance traits to 7.8–14.0% for bud-break dates and a maximum of 10.0 to 17.9% for height growth traits of *Abies alba*. Therefore, genetic variance was predominantly within population (Sagnard et al., 2002).

The average genetic distance for all pair-wise comparisons between the ten populations of *A. alba* in Italy was 0.014 (Parducci and Szmidt, 1997). 7.3% of the total genetic variation was due to the differences among populations for gymnosperms (Hamrick et al., 1992) and 10% for eight Abies species (Shea and Furnier, 2002). 13.3% of the total diversity is distributed among populations in *A. alba* (Vendramin et al., 1999). Great variation was observed in the heterozygosity among the populations studied and ranged from 0.010 (*Abies pinsapo*) to 0.328 (*Abies cephalonica*). The inter population genetic diversity was about 26% of the total genetic diversity. The average coefficient of gene differentiation (Gst) was 0.255, which means that approximately 26% of the total diversity of the Mediterranean firs exist among the populations. In particular, the geographical Area III (Turkey) has scored the highest value of Gst (25.8%), (Scaltsoyianne et al., 1999). The proportion of genetic diversity among the populations of *Abies sachalinensis* is 1.5% (El-Kassaby, 1992), populations of *Abies mariesii* is 2.6% (Suyama et al., 1992) and populations of *A. cephalonica* is 4.8% (Fady and Conkle, 1993).

Conte (2004) reported that most of the genetic variation resides within subsets (84%) by ANOVA done for *Abies nebrodensis*. More than 10% of the total genetic diversity was due to differences among populations of *A. nebrodensis* (Vicario et al., 1995).

Total percentage of genetic variation present in the population shown by interplot or among subpopulation differences is 0.35% of *Abies fraseri*. Thus, more than 99% of the genetic variation is due to within plot (that is tree to tree) variation (Diebel and Feret, 1991). Most of the genetic diversity lies within populations of *A. cephalonica* (Fady and Conkle, 1993). Less than 10% of the total observed variation appeared among populations of *A. cephalonica* (Hamrick, 1989) and the variation among the populations is 11% in *A. alba* (Vicario et al., 1995). Vendramin et al. (1999) reported that 13.3% of the total diversity is distributed among populations in *A. alba*. On the average, the genetic diversity among populations of *Abies* species has been found to be 6.3% (Hamrick et al., 1992).

The high within-population genetic diversity and low among-population differentiation observed in conifers

have been attributed to common lifehistory traits, such as longevity and extensive gene flow (Hamrick et al., 1992; Streiff et al., 1998). The biogeographic history of a species should also contribute significantly to current patterns of genetic variation (Planter et al., 2000).Despite the comparatively low levels of allozyme variation and the small genetic distances between populations, geographical differentiation among silver fir populations at different spatial scales could be demonstrated with markers (Konnert and Bergmann, 1995). Ecological and geographical differentiations are important factors that influence the breeding and sampling strategies of tree crops. It is also essential to consider the relationship between population structure in natural and domesticated populations (Chalmers et al., 1992; Şevik, 2010). Results of this study could be taken into consideration in silvicultural purpose (afforestation and artificial regeneration) and breeding strategies (that is determination of breeding populations, gene conservation areas, seed transfer zones, seed sources and geographic variation, resulting to provenance trial; establishment of seed orchard) of this species. Until now a few studies have been conducted about Turkish fir (Kaya et al., 2008; Şimşek, 1991; Velioğlu et al., 1999; Kaya and Raynal, 2000; Nielsen and Chastagner, 2005). But there is no comprehensive study disclosing the spatial distribution of Turkish fir and providing background information for future studies. In the near future, the studies done with the morphological characters of genetical variations should also be analyzed with DNA markers and isosymes analysis.

REFERENCES

Anonymous (2006). Orman Varlığımız, T.C. Çevre ve Orman Bakanlığı Orman Genel Müdürlüğü, Orman İdaresi ve Planlama Dairesi Başkanlığı, Ankara, p. 160.

Ayala FJ, Kiger JA (1984). Modern genetics, 2nd (edn) Benjamin-Cumings, Menlo Park, US.

Bazzaz FA, Ackerly DD, Reekie EG (2000). Reproductive allocation in plants. In Seeds: the Ecology of Regeneration in Plant Communities (ed. Fenner M), 2nd ed., pp. 1-29. CABI Publishing, Wallingford, UK and New York, USA.

Chalmers KJ, Waugh R, Sprent JI, Simons AJ, Powell W (1992). Detection of genetic variation between and within populations of Gliricidia Sepium and G. maculata using RAPD markers, Heredity, 69: 465-472.

Conte L, Cotti C, Schicchi R, Raimondo FM, Cristofolini G (2004). Detection of ephemeral genetic sub-structure in the narrow endemic *Abies nebrodensis* (Lojac.) Mattei (Pinaceae) using RAPD markers, Plant Biosystems, 138(3): 279-289.

Dajoz R (2000). Insects and Forests: The role and diversity of insects in the forest environment. Intercept Ltd, London-Paris-New York. p. 668.

Diebel KE, Feret PP (1991). Isozyme variation within the Fraser fir (*Abies fraseri* (Pursh) Poir.) population on Mount Rogers, Virginia: lack of microgeographic differentiation. Silvae Genet. 40: 79-85.

El Atta HA (1993). The effect of *Caryedon serratus* Oliver (Col., Bruchidae) on viability and germination of seeds of *Acacia nilotica* (L. Willd. Ex Del.) in the Sudan. Forest Ecol. Manage. 57: 169-177.

El-Kassaby YA, Edwards DGW, Taylor DW (1992). Genetic control of germination parameters in douglas-fir and its importance for domestication, Silvae Genet. 41(1): 49-53

Fady B, Conkle MT (1993). Allozyme variation and possible phylogenetic implications in *Abies cephalonica* Loudon and some related eastern Mediterranean firs. Silvae Gent. 42: 351-359.

Gutterman Y (2000). Maternal effects on seeds during development. In Seeds: the Ecology of Regeneration in Plant Communities (ed. Fenner M). 2nd ed. CABI Publishing, Wallingford New York. pp. 59-84.

Hampton JG (2002). What is seed quality? Seed Sci. Technol. 30: 1-10.

Hamrick JL (1989). Isozymes and the analysis of genetic structure in plant populations. In Soltis DE and Solits PS (Eds): Isozymes in plant biology 87-105. Portland, Oregon: Dioscorides Press.

Hamrick JL, Godt MJW, Sherman-Broyles SL (1992). Factors influencing levels of genetic diversity in woody plant species. New Forests 6: 95-124

Kaya Z, Raynal D (2000). Biodiversity and conservation of Turkish forests, Biological Conservation 97 (2001) 131-141

Kaya Z, Skaggs A, Neale DB (2008). Genetic Differentiation of Abies equi-trojani (Asch. & Sint. ex Boiss) Mattf. populations from Kazdağı, Turkey and the genetic relationship between Turkish Firs belonging to the *Abies nordmanniana* Spach Complex, Turk J. Bot. 32: 1-10

Konnert M, Bergmann F (1995). The geographical distribution of genetic variation of silver fir (*Abies alba*, Pinaceae) in relation to its migration history. Plant Syst. Evol. 196: 1-2, 19-30.

Nielsen UB, Chastagner GA (2005). Genetic variation in postharvest needle retention among Nordmann fir families and grafted clones, Scandinavian J. Forest Res. 20: 304-312

Owens JN, Colangeli AM, Morris SJ (1990). The effect of self-cross, and no pollination on ovule, embryo, seed, and cone development in western red cedar (*Thuja plicata*). Can. J. Forest Res. 20: 66-75.

Parducci L, Szmidt AE (1997). Genetic variation among nine Mediterranean *Abies* species based on PCR-RFLP analysis of chloroplast DNA. Proceedings, International Conference on Biodiversity and Bioresources: Conservation and Utilization; Phuket, Thailand, p. 87.

Planter EA, Furnier GR, Eguiarte LE (2000). Low levels of genetic variation within and high levels of genetic differentiation among populations of species of *Abies* from southern Mexico and Guatemala, Am. J. Bot. 87(3): 362-371.

Pritam S, Singh P (1997). Forest tree seed pathogens and their management in sustainable forestry. J. Mycol. Plant Pathol. 27: 138-147.

Sagnard F, Barberot C, Fady B (2002). Structure of genetic diversity in *Abies alba* Mill. from southwestern Alps: multivariate analysis of adaptive and non-adaptive traits for conservation in France, Forest Ecol. Manage. 157: 175-189.

SAS Institute (1987). SAS User's Guide. Release 6.03 Edition. Cary, North Caroline.

Scaltsoyiannes A, Tsaktsira M, Drouzas AD (1999). Allozyme differentiation in the Mediterranean firs *(Abies, Pinaceae).* A first comparative study with phylogenetic implications, P1. Syst. Evol. 216: 289-307

Schaal BA, Leverich WJ, Rogstad SH (1991). Comparison of methods for assessing genetic variation in plant conservation biology. In: Falk DA, Holsinger KE (eds). Genetics and conservation of rare plants. Oxford University Press, New York, 123-134.

Shea KL (1990). Genetic variation between and within populations of Engelmann spruce and subalpine fir. Genome, 33: 1-8.

Shea LS, Furnier GR (2002) Genetic variation and population structure in central and isolated populations of balsam fir, A*bies balsamea* (Pinaceae), Am. J. Bot. 89(5): 783-791.

Stebbins GL (1999) A brief summary of my ideas on evolution. Am. J. Bot. 86: 1207-1208

Streiff R, Labbe T, Bacilieri R, Steinkellner H, Glossl J and Kremer A (1998). Within-population genetic structure in *Quercus robur* L. and *Quercus petraea* (Matt.) Liebl. assesed with isozymes and microsatellites. Mol. Ecol. 7: 317-328

Suyama Y, Tsumura Y, Ohba K (1992). Inheritance of isozyme variants and allozyme diversity of *Abies mariesii* in three isolated natural populations. J. Japanese Forest. Soc. 74: 65-73.

Şevik H (2010) Structure of genetic diversity in the populations of Turkish fir (*Abies nordmanniana* subsp. *bornmülleriana* Mattf.), Karadeniz Technical University, Graduate School of Natural and

Applied Sciences, Doctorate Thesis, p. 150.
Şevik H, Ayan S, Turna I, Yahyaoğlu Z (2010). Genetic diversity among populations in Scotch pine (*Pinus silvestris* L.) seed stands of Western Black Sea Region in Turkey, Afr. J. Biotechnol. 9(43): 7266-7272
Şimşek Y (1991) Türkiye orijinli goknar türlerinin (*Abies nordmanniana, Abies bornmuellariana, Abies equi-trojani*) genetik yapıları üzerine araştırmalar. OAE Yayınları, Teknik Bulteni 221.
Velioğlu E, Çiçek FF, Kaya Z, Çengel B (1999). Kaz dağlarındaki doğal Kazdağı göknarı (*Abies equi-trojani* Aschers. Et. Sint.) populasyonlarında genetik çeşitliliğin yapılanması, Orman Ağaçları ve Tohumları Islah Araştırma Müdürlüğü, 3, 74, 10, 31, Ankara.
Vendramin GG, Degen B, Petit JR, Anzidei M, Madaghiele A and Ziegenhagen B (1999). High level of variation at *Abies alba* chloroplast microsatellite loci in Europe. Molecular Biol. 8: 1117-1126.
Vicario F, Vendramin GG, Rossi P, Liò P, Giannini R (1995) Allozyme, chloroplast DNA and RAPD markers for determining relationships between *Abies alba* and the relic population of *Abies nebrodensis*, Theor. Appl. Genet. 90: 1012-1018.
Yahyaoğlu Z, Demirci A, Bilir N and Genç M (2001). Comparison of 22 taurus cedar (*Cedrus libani* A. Rich.) origins by seedling morphological distance, Turkish J. Biol. 25, Ankara, pp. 221-224.