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IDENTIFICATION OF TURKISH OAT LANDRACES (*Avena sativa* L.) BASED ON AVENİN PROTEINS BY SDS-PAGE TECHNIQUE

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ABSTRACT

Oat genotypes exhibit valuable and reproducible polymorphism in the avenin pattern which is important to identify genotypes and to use in breeding programs. Therefore, in this study, 196 Turkish oat landraces (*Avena sativa* L.) and three commercial cultivars (Checota, Faikbey and Seydişehir) were identified using the SDS-PAGE technique based on oat avenin protein band numbers and molecular weights. Results indicate that genotypes varied in avenin protein band numbers and molecular weights. Avenin protein band numbers and molecular weights ranged from 4 to 16, and 8.8 to 45 kDa, respectively. The bands having the highest molecular weight (45 kDA) was obtained from E19 and E45 genotypes, while the bands having the lowest molecular weights were obtained from A76, A81, A79, E20 and A29 genotypes (8.8, 9.2, 9.5, 9.6 and 9.8 kDa, respectively). A18, A34 and K3 genotypes had the lowest avenin bands (4), while E20 and A54 genotypes had the highest avenin bands (15 and 16, respectively).According to genetic similarity analysis based on avenin protein band numbers and molecular weights, oat genotypes clustered in two major groups at 0.240 genetic similarities. The first major group consisted of A53, E37, E59, A23, A34, and A41 genotypes. In this group, A23-A41 and A53-E37 genotypes were similar with 0.801 and 0.767 coefficients respectively. The second group consisted of three large groups and several small groups. The genotypes clustered in many groups with a large number of genetic similarity coefficients. A2-E57 and K13-K35 genotypes were the most similar with 0.920 genetic similarity coefficients.

Keywords: Avenin, genetic similarity, landraces, oat, SDS-PAGE

INTRODUCTION

Cultivated oat (*Avena sativa* L.) consists of polyploidy series of wild, weedy, and cultivated species which are spread worldwide (Baum, 1997; Dvoracek et al., 2003). Turkey is one of the centers of origin of oat (*Avena sativa* L.) with a large number of landraces. Oat research has lagged behind other cereals such as wheat, maize and barley due to lack of high yielding, non-shattering, and non-lodging cultivars in Turkey. Landraces are a good source for expanding genetic variations which allows developing new cultivars with high quality traits. Identification of genetic variation levels and similarities within landraces is also important to prevent duplicate accessions in gene banks (Leisova et al., 2007).

Oat synthesizes and stores proteins during the seed development stage, which are used by young seedlings as a nutrient source in germination period. Most of these proteins, called seed storage proteins are saline soluble proteins; globulins and alcohol soluble proteins; prolamines (Chesnut et al., 1989). The storage proteins generally occur in the endosperm in an insoluble form. During germination, their components are hydrolyzed and transported to the embryo to be used by seedlings (Bewley and Black, 1994).

Oat seed storage proteins show some characteristics as compared to other cereals. The proportion of avenins is quite low compared to wheat gliadins, barley hordeins, or maize zeins (Mosse 1966; Pernollet et al., 1982). In oat, globulins represent 50 to 80% of the seed proteins whereas the prolamines (avenins) account for 10 to 20% of the total protein (Frey, 1951; Peterson and Smith 1976; Chesnut et al., 1989).

Oat genotypes exhibit valuable and reproducible polymorphism in the avenin pattern. Polymorphism in the avenin pattern is more heterogeneous than in the globulin pattern (Robert et al., 1983; Dvoracek et al., 2003). The avenin patterns differ among species of *Avena* and among cultivars of *Avena sativa* L. Therefore, the avenin proteins have been investigated as a tool for cultivar identification (Hansen et al., 1988; Peterson et al., 1988).

Avenins belong to the alcohol soluble protein group. However, all polypeptide chain extracted by ethanol solutions; differ from the typical prolamines (Pernollet et al., 1982). Identification of avenins needs further characterization by electrophoresis and amino acid analysis (Kim et al., 1978; Pernollet et al., 1982).

Identification of proteins is based on; a) gel electrophoresis via sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE), isoelectric focusing (IEF), (Hansen et al., 1988; Peterson et al., 1988; Yano et al., 1998) and two-dimensional polyacrylamide gel electrophoresis (2D PAGE). In the first dimension, native proteins are separated based on their original charge by isoelectric focusing. In the second dimension, SDS-PAGE is used to separate denatured proteins based on their molecular weight (Gevaert and Vandekerckhove 2000; Larsen and Roepstorff 2000; Clark, 2005), b) and the western blot method which allows detection of single proteins within a sample. The sampled proteins are separated by size, using SDS-PAGE or 2D-SDSPAGE and then electrophoretically transferred to a solid membrane (Clark, 2005).

In this study, 196 Turkish oat landraces and three commercial cultivars were examined based on avenin protein band numbers and molecular weights using SDS-PAGE, which might be useful to construct core collections representing the maximum genetic diversity, and to use in future breeding programs.

MATERIALS AND METHODS

Plant Material

The seeds of 196 Turkish oat landraces (*Avena sativa* L.) were obtained from Institute of Plant Genetics and Crop Plant Research Gatersleben, Germany (81), Aegean Agricultural Research Institute Plant Gene Resources Department Izmir, Turkey (60) and Bahri Dağdaş Agricultural Research Institute Konya, Turkey (55) and, three commercial oat cultivars (Checota, Faikbey and Seydişehir) were used in the study (Table 1).

Table 1 Entry names, gene bank accession numbers and origin of 199 Turkish oat genotypes.

Entry Name[#]	Accession Number	Origin	Entry Name[#]	Accession Number	Origin
A1	AVE 1900/84	N/A	E20	TR26393	İzmir
A2	AVE 4336/88 No: 4651	N/A	E21	TR26468	İzmir
A3	AVE 4349/89 No:4650	N/A	E22	TR26550	Balıkesir
A4	AVE 3564/98	N/A	E23	TR26552	Balıkesir
A5	AVE 3465/98	N/A	E24	TR26575	İzmir
A6	AVE 4348/88 No:4693	N/A	E25	TR26611	Çanakkale
A7	AVE 3464/98	N/A	E26	TR26648	Çanakkale
A8	AVE 3462	N/A	E27	TR26674	Çanakkale
A9	AVE 4109/98 463/62.	N/A	E28	TR26681	Balıkesir
A10	AVE 120/89	N/A	E29	TR26736	Bilecik
A11	AVE 3490/98 No:5325.	N/A	E30	TR12106	Muğla
A12	AVE 4217/77	N/A	E31	TR12198	Aydın
A13	AVE 442/84	N/A	E32	TR12454	Burdur
A14	AVE 3228	N/A	E33	TR12471	Antalya
A15	AVE 3474	N/A	E34	TR39400	Aydın
A16	AVE 3426	N/A	E35	TR4649	Aydın
A17	AVE 4344	N/A	E36	TR4656	Muğla
A18	AVE 1303/84	N/A	E37	TR4657	Aydın
A19	AVE 3460/98	N/A	E38	TR12755	Balıkesir
A20	AVE 3233 No: 10283	N/A	E39	TR40651	Muğla
A21	AVE 3456/98	N/A	E40	TR40660	Muğla
A22	AVE 1416/93	N/A	E41	TR40673	Muğla
A23	AVE 4358/90 No: 4657	N/A	E42	TR40707	Antalya
A24	AVE 3372	N/A	E43	TR40758	Hatay
A25	AVE 1310/99	N/A	E44	TR40775	Hatay
A26	AVE 1312/78	N/A	E45	TR12250	Antalya
A27	AVE 3230/98	N/A	E46	TR12269	Antalya
A28	AVE 4545/89 No: 5440	N/A	E47	TR26541	Balıkesir
A29	AVE 4110/89 P.No:59/639 Kütük No: 9885/1	N/A	E48	TR40667	Muğla
A30	AVE 3448/99	N/A	E49	TR40688	Antalya
A31	AVE 4113/89 No: 5739	N/A	E50	TR40730	Mersin
A32	AVE 4107/89 No: 5951	N/A	E51	TR46568	Antalya

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Table 1 continue

Entry Name[#]	Accession Number	Origin	Entry Name[#]	Accession Number	Origin
A33	AVE 2834/99	N/A	E52	TR63288	Çanakkale
A34	AVE 463/92	N/A	E53	TR63294	Çanakkale
A35	AVE 1304	N/A	E54	TR63295	Bartın
A36	AVE 4841/98	N/A	E55	TR63357	Balıkesir
A37	AVE 4381/89 No: 4691	N/A	E56	TR63368	İzmir
A38	AVE 3642/98	N/A	E57	TR63449	Balıkesir
A39	AVE 216/91	N/A	E58	TR63529	Antalya
A40	AVE 1119/75	N/A	E59	TR63777	Adana
A41	AVE 4402/90 No:4665	N/A	E60	TR68745	Bilecik
A42	AVE 4344/88 No:5441	N/A	K1	N/A	Konya-Bozkır-Bademli-
A43	AVE 1311/84	N/A	K2	N/A	Konya-Bozkır-Bademli-
A44	AVE 3454/98	N/A	K3	N/A	Konya-Bozkır-Bademli-
A45	AVE 3485/98 No: 4678	N/A	K4	N/A	Konya-Bozkır-Bademli-
A48	AVE 441/84	N/A	K5	N/A	Konya-Bozkır-Bademli
A49	AVE 4340/88 No: 5829	N/A	K6	N/A	Konya-Bozkır-Bademli
A50	AVE 4396/99	N/A	K7	N/A	Konya-Bozkır-Bademli
A51	AVE 3453/99	N/A	K8	N/A	Konya-Bozkır-Bademli
A52	AVE 289/86	N/A	K9	N/A	Konya-Seydişehir-Oğlakç
A53	AVE 4186/77	N/A	K10	N/A	Faikbey
A54	AVE 4426/99	N/A	K11	N/A	Konya-Akşehir-Yaylabelen
A55	AVE 3455/98	N/A	K12	N/A	Konya-Derebucak-Durak
A56	AVE 4346/99	N/A	K13	N/A	Konya-Derebucak-Durak
A57	AVE 1386/85	N/A	K14	N/A	Konya-Akşehir-Yaylabelen
A58	AVE 3818/89	N/A	K15	N/A	Konya-Seydişehir-Dikilitaş
A59	AVE 4112/91 120/62	N/A	K16	N/A	Konya-Seydişehir-Dikilitaş
A60	AVE 4359/88 No:4661	N/A	K17	N/A	Konya-Seydişehir-Dikilitaş
A61	AVE 4105/89 No:5910	N/A	K18	N/A	Konya-Seydişehir-Dikilitaş
A62	AVE 4343/89 No:4690	N/A	K19	N/A	Konya-Bozkır-Karacaardıç
A63	AVE 4785/99	N/A	K20	N/A	Seydişehir
A64	AVE 4360/88 No: 5439	N/A	K21	N/A	Konya-Seydişehir-Oğlakçı
A65	AVE 3198 Ankara 84	N/A	K22	N/A	Konya-Seydişehir-Bostandere
A66	AVE 130/82	N/A	K23	N/A	Konya-Seydişehir-Bostandere
A67	AVE 4554 No: 4675	N/A	K24	N/A	Konya-Seydişehir-Dikilitaş
A68	AVE 1387/82	N/A	K25	N/A	Konya-Bozkır-Karacaardıç
A69	AVE 3532 KN 325	N/A	K26	N/A	Konya-Hüyük-Başlamış
A70	AVE 4354/88 No:4647	N/A	K27	N/A	Konya-Bozkır-Karacaardıç
A71	AVE 4395/88 No:4692	N/A	K28	N/A	Konya-Bozkır-Karacaardıç
A72	AVE 1118/75	N/A	K29	N/A	Konya-Derebucak-Durak
A73	AVE 4575/98 No: 4652	N/A	K30	N/A	Karaman-Kazımkarabekir
A74	AVE 4559/88 No: 5438	N/A	K31	N/A	Konya-Seydişehir-Bostandere
A75	AVE 4345/88 No: 4689	N/A	K32	N/A	Konya-Derebucak-Durak
A76	AVE 4127/88 No: 5459	N/A	K33	N/A	Konya-Hüyük-Başlamış
A77	AVE 4338/89 No: 4688	N/A	K34	N/A	Konya-Hüyük-Başlamış
A78	AVE 4443/89	N/A	K35	N/A	Konya-Hüyük-Başlamış
A79	AVE 4434/88 No:5320	N/A	K36	N/A	Konya-Seydişehir-Bostandere
A80	AVE 4561/89 No: 5442	N/A	K37	N/A	Konya-Derebucak-Durak
A81	AVE 4537/88 No: 5550	N/A	K38	N/A	Konya-Derebucak-Durak
A82	AVE 3512	N/A	K39	N/A	Konya-Derebucak-Durak
A83	AVE 3498 No: 4653	N/A	K41	N/A	Konya-Akşehir-Yaylabelen
E1	TR33296	Edirne	K42	N/A	Konya-Bozkır-Karacaardıç

Table 1 continue in next page

Table 1 continue

Entry Name[#]	Entry Name[#]	Entry Name[#]	Entry Name[#]	Entry Name[#]	Entry Name[#]
E2	TR35074	Adapazarı	K43	N/A	Konya-Derebucak-Durak
E3	TR35165	Nevşehir	K44	N/A	Konya-Akşehir-Yaylabelen
E4	TR35457	Burdur	K45	N/A	Konya-Seydişehir-Bostandere
E5	TR35498	Burdur	K46	N/A	Konya-Bozkır-Karacaardıç
E6	TR36925	Çanakkale	K47	N/A	Konya-Bozkır-Karacaardıç
E7	TR37371	Çorum	K48	N/A	Konya-Bozkır-Bademli
E8	TR37440	İzmir	K49	N/A	Konya-Bozkır-Karacaardıç
E9	TR37450	İzmir	K50	N/A	YGB-36ANTALYA
E10	TR37477	İzmir	K51	N/A	Konya-Bozkır-Karacaardıç
E11	TR39068	Muğla	K52	N/A	Konya-Bozkır-Karacaardıç
E12	TR26229	Mersin	K53	N/A	Konya-Bozkır-Karacaardıç
E13	TR26241	Adana	K54	N/A	Konya-Derebucak-Durak
E14	TR26252	Adana	K55	N/A	Konya-Derebucak-Durak
E15	TR26256	Hatay	K56	N/A	Konya-Seydişehir-Bostandere
E16	TR26295	Muğla	Checota	N/A	Cultivar
E17	TR26303	Muğla	Faikbey	N/A	Cultivar
E18	TR26318	Muğla	Seydişehir	N/A	Cultivar
E19	TR26324	Muğla			

N/A: Not available

[#] Turkish oat genotypes were obtained from different gene banks, which are coded 'A' for Institute of Plant Genetics and Crop Plant Research Gatersleben, Germany, 'E' for Aegean Agricultural Research Institute Plant Gene Resources Department İzmir, Turkey and, 'K' for Bahri Dağdaş Agricultural Research Institute Konya, Turkey.

Sample Preparation

Sample preparation was performed according to Örçen et al. (1995). Five dry seeds from a single panicle of each genotype were hand-hulled and ground using a mortar and pestle. The samples were weighed and placed in 2 mL microcentrifuge tubes and a 52% ethanol solution was added (24 µL mg^{-1} sample). The tubes were vortexed in 10 minute intervals for an hour and centrifuged at 13,000 x g for 10 minutes. The supernatant was transferred into a new microcentrifuge tube and 50 µL of 10% TCA (Trichloroacetic acid) was added. Samples were then centrifuged at 13,000 x g for 10 minutes to precipitate avenins. The supernatant was removed; the pellet rinsed twice with 70% ethanol, and allowed to dry. After drying, the pellet was suspended in 40 µL of 1 M NaOH, for use in the research. Equal amount of sample buffer (40 µL sodium dodecyl sulfate, 5% 2-mercaptoethanol, 10 mM Tris-HCl pH 8.0, 1 mM ethylenediaminetetraacetic acid) were added to avenin extractions (40 µL) and boiled (100 °C) for 3 minutes in a water bath. Loading dye (20 µL) (25% of 0.25 M Tris-HCl pH 6.8, 25% glycerol, 0.1% bromophenol blue and 50% ddH_2O) was then added. Aliquots of the extracts (4 µL) were used in the research. The remaining avenin extracts were stored at -20 °C until further analysis.

SDS-PAGE

Electrophoresis analysis was performed using a modified discontinuous SDS-PAGE system (Leammli, 1970) as described by Örçen et al. (1995). The SDS-PAGE was performed using "AE 6200 Atto Maxi-Slab Gel Chamber" with 15x15x0.1 cm glass plates. 20 µL of 15% separating gel consisted of 10 mL Acyrl-bisacryl (N,N'-Methylenebisacrylamide 29:1), 5 mL separating gel buffer (1.5 M tris pH 8.8), 200 µL SDS, 4.8 mL ddH_2O, 100 µL of 10% APS (Ammonium per sulfate) and 20 µL TEMED (Tetramethylethylenediamine) and 10 µL of 3% stacking gel consisted of 1.33 mL Acyrl-bisacryl (N,N'-Methylenebisacrylamide 29:1), 2.5 mL stacking gel buffer (0.5 M tris pH 6.8), 100 µL SDS, 6 mL ddH_2O, 50 µL of 10% APS (Ammonium per sulfate) and 20 µL TEMED (Tetramethylethylenediamine) with a running buffer (25 mM tris, 250 mM glycine, 0.1% SDS). 4 µL of each sample and 2 µL of standard protein mixtures; BSA (Bovine serum albumin, mw 66,000 Da), Ovalbumin (mw 45,000 Da), Glyceraldyde 3-phosphate dehydrogenase (mw 36,000 Da), Carbonic anhydrase (mw 29,000 Da), Trypsinogen (mw 24,000 Da), Trypsin inhibitor (mw 20,100 Da), ά-lactalbumin (mw 14,200 Da) (Sigma, #M3913-1VL), were loaded to the wells and used to estimate protein bands. The electrophoresis was performed approximately for 2.5 hours at 250 V and 30 mA. The gels were stained overnight on an orbital shaker at 50 rpm with comassie brilliant blue R-250 staining solution (0.5 g of 0.025% comassie brilliant blue R-250, 800 mL of 40% methanol, 140 mL of 7% acetic acid, and completed to 2 liters with ddH_2O) and destained for half an hour with destain solution-I (400 mL of 40% methanol, 70 mL of 7% acetic acid, and completed to 1 liter with ddH_2O) and destain solution-II (50 mL of 5% methanol, 70 mL of 7% acetic acid, and completed to 1 liter with ddH_2O). Destaining with solution-II was repeated until protein bands were clearly visual. Images were captured by HP Color 3600 Scanner.

Data analysis

The relative mobility of avenin bands were calculated by the formula; R_f (retention factor) = distance traveled by the

band / distance traveled by the dye, where the R_f is; in a gel of uniform density the relative migration distance of a protein is negatively proportional to the log of its mass (Örçen et al., 1995). The molecular weights were determined by molecular mass standard curve of avenin protein band's relative mobility, compared to standard protein mixtures (Figure 1).

Genetic similarities based on avenin protein band numbers and molecular weights were estimated for the 199 oat genotypes using Dice's index (Dice, 1945) with NTSYSpc ver. 2.20q (Rohlf, 2005). Prior to analysis, presence or absence of each protein band generated with each genotype was coded as one or zero to produce a binary data matrix. From the similarity matrix, a dendrogram was constructed using unweighted pair group method arithmetic average (UPGMA).

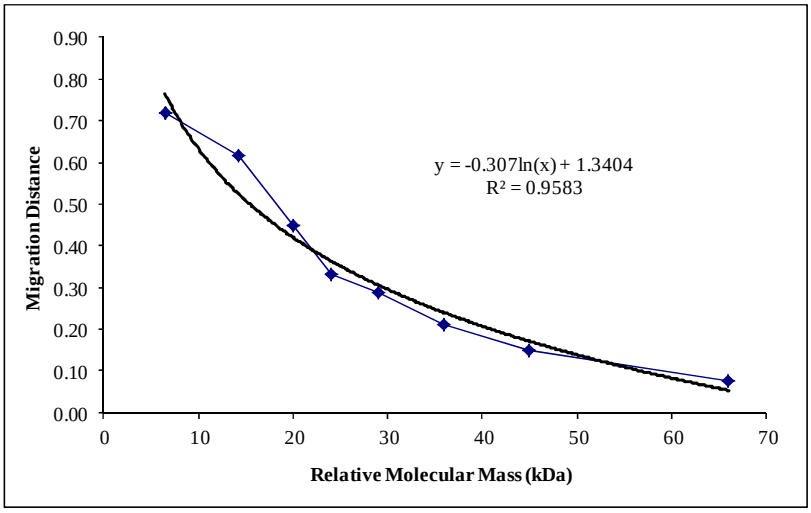

Figure. 1 Molecular mass standard curve, avenin protein bands. Avenin molecular weights of the oat genotypes were determined by comparing relative mobility with standard reference protein mixtures.

RESULTS

Molecular Weights and Avenin Bands

The identification of avenin protein bands in respect to electrophoresis analysis of the oat genotypes were performed using the SDS-PAGE technique. Genotypes varied in avenin protein band numbers and molecular weights. Detailed avenin protein band numbers and molecular weights of the genotypes are indicated in Dumlupınar (2010). Avenin protein band numbers ranged from 4 to 16, while their molecular weights ranged from 8.8 to 45 kDa. The highest molecular weight (45 kDA) was obtained from E19 and E45 genotypes, while the lowest molecular weights were obtained from A76, A81, A79, E20 and A29 genotypes (8.8, 9.2, 9.5, 9.6 and 9.8 kDa, respectively). A18, A34 and K3 genotypes had the lowest avenin bands (4), while the E20 and A54 genotypes had the highest ones (15 and 16, respectively). Avenin protein bands of some genotypes with the reference standard protein mixtures are shown in Figure 2.

The molecular weights of the commercial cultivars; Checota ranged from 15.8 to 41 kDa and had eight avenin protein bands, while Faikbey had nine avenin protein bands with molecular weights between 14.2 and 34 kDa. However, Seydişehir cultivar had 11 protein bands with molecular weights ranged from 15.4 to 33.8 kDa.

Genetic Similarities

A dendogram was constructed using UPGMA. According to the dendogram oat genotypes clustered in two major groups with 0.240 genetic similarities. First major group was small while the second major group was large. The first major group consisted of A53, E37, E59, A23, A34, and A41 genotypes. In this cluster, A23-A41, and A53-E37 genotypes were similar to each other with 0.801 and 0.767 coefficients, respectively (Figure 3).

On the other hand, the second group consisted of three large sub-groups and several small sub-groups. The genotypes clustered in many small and large sub-groups with a large number of different genetic similarities. A2-E57 and K13-K35 genotypes were the most similar with 0.920 genetic similarity coefficients. Also, A36-E56, A65-A66, K19-K31 and A37-A61 genotypes were similar with 0.909 coefficients, while E33-K41 and A4-A51 genotypes were similar at 0.906 (Figure 3).

The commercial cultivars Checota, Faikbey and Seydişehir were not found to be similar; each cultivar was clustered with the other landraces. However, Checota and Faikbey were found similar with 0.512 coefficients, while Seydişehir, Checota and Faikbey were similar at 0.376.

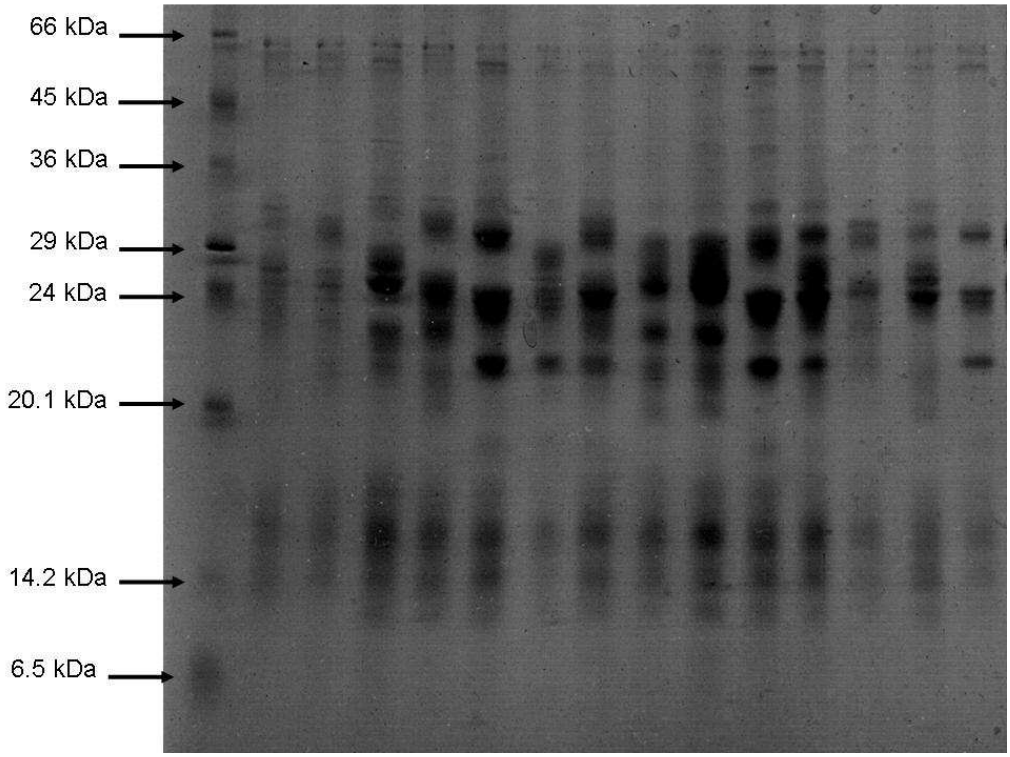

Fig. 2 Figure shows the standard reference protein mixture bands and avenin protein bands of the oat genotypes, K44, K47, K8, E12, K4, E46, E52, E45, K50, A77, E60, K56, K55 and K1 (left to right).

DISCUSSION

These results indicate that Turkish oat genotypes varied in avenin protein bands and molecular weights. This shows the genetic diversity of oats in Turkey which are derived from different regions. Landraces consisted of spring, winter and facultative type genotypes. Most of the genotypes were clustered together with similar origin of centers as expected. However, some of the genotypes which clustered together were not expected. This may be due to genotype transfers among the regions.

Molecular Weights and Avenin Bands

In previous studies, molecular weights of the oat genotypes were reported to be between 20 to 36 kDa (Dvoracek et al., 2003), 21 to 68 kDa (Luthe, 1987), 22 to 43 kDa (Peterson et al., 1988) in *Avena sativa* and 14.2 to 34 kDa in *Avena fatua* (Mirza et al., 2007) while the avenin bands were found 7 to 11 (Portyanko et al., 1998), 7 to 14 (Jussila et al., 1992) in *Avena sativa* and 24 to 34 in *Avena fatua* (Mirza et al., 2007) with different methods. The differences among the reported molecular weight ranges and the avenin band numbers might be due to cultivars investigated, geographical distributions of the genotypes and the techniques used to identify the avenin proteins. In our study, a large number of genotypes which are geographically distributed within Turkey identified by SDS-PAGE systems.

Genetic Similarities

Genetic similarities of the genotypes were calculated with Dice's index. Genetic similarity of the oat landraces was different. A2-E57 and K13-K35 genotypes were found to be the most similar with 0.920 coefficients. E57 genotype derived from Balıkesir province, while there is no available information about origin of center for A2 genotype. However, A2 genotype is likely related to E57 genotype. K13 and K35 genotypes had the same origin of centers and they derived from Konya province. They are also known as winter type genotypes. A36-E56, A65-A66, K19-K31 and A37-A61 (0.909), E33-K41 and A4-A51 (0.906), A32-Faikbey, E5-(E35-E41), A5-A1 and A7-A63 (0.886), and E29-K18, E24-E31 and E15-K47 (0.875) genotypes were found to be similar (Fig. 3). Lookhart (1985) reported that protein band differences among 23 oat cultivars and 10 of them were different while the other 13 segregated into three groups. Members of the each group had small groups with similar pedigrees. Many researchers reported avenin band polymorphisms and genetic similarities among oat landraces and cultivars with high coefficients. (Luthe, 1987; Peterson et al., 1988; Jussila et al., 1992; Portyanko et al., 1998; Ahokas, 2000; Dvoracek et al., 2003).

However, some of the genotypes were found non-similar, which are important in breeding programs with efforts to improve efficiency by emphasizing crosses between parents

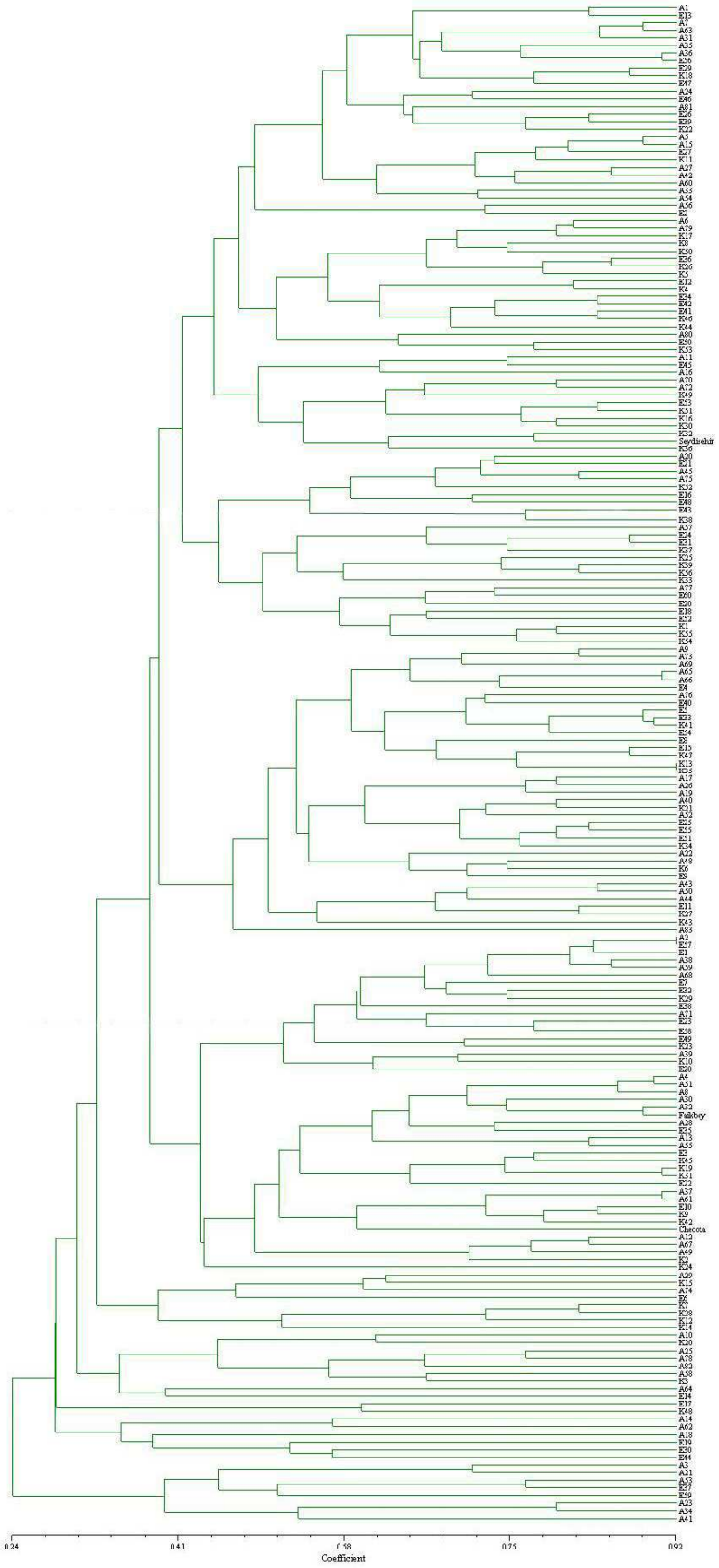

Figure 3 Dendrogram showing relationship among 199 oat genotypes constructed using Dice's similarity coefficients and unweighted pair group method arithmetic average (UPGMA).

with diverse protein bands (Lookhart, 1985). Ahokas et al. (2005) indicated that polymorphism between protein patterns would allow breeding of oat cultivars showing further lowering of protein putatively toxic to celiac patients assuming oats contain these toxic proteins. Ahokas et al. (2005) also reported that the protein bands extracted with alcoholic solutions possibly contain proteins, which are toxic to celiac patients.

CONCLUSION

The current study presents SDS-PAGE systems identifies oat landraces based on avenin protein bands and molecular weights. Further goal of this study is to develop new oat cultivars with high yielding, non-shattering, synchronous maturity features as well as reasonable grain quality by using those genotypes in oat crossing programs.

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