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Evaluation of Turkish oat landraces based on morphological and phenological traits

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Abstract

In a two-year study, 196 Turkish oat landraces and 3 standard cultivars ('Checota', 'Faikbey' and 'Seydişehir') were evaluated for morphological traits: germination rate, stem diameter, upper inter-node length, plant height, flag leaf width, flag leaf length, single plant biomass, lodging severity and barley yellow dwarf virus, and for phenological traits: vegetative period, grain filling period and, days to maturity.

According to two years' data, all traits differed for years except germination rate. Genotypes varied for upper inter-node length, stem diameter, plant height, flag leaf width, vegetative period, grain filling period and days to maturity. In addition, year × genotype interaction was significant for stem diameter, flag leaf width, vegetative period, grain filling period and days to maturity.

Traits such as flag leaf length, flag leaf width, days to maturity, vegetative period, single plant biomass and germination rate were more promising ones as selection criteria. However, lodging severity, plant height, barley yellow dwarf virus, upper inter-node length and grain filling period were more important for negative selection.

Results indicate that, E1, A56, E7, E55, A17, E38, A40, A63, A25, A69, A26, A83, A1, A2, K11, K9, K3, K53, K30, K1, K2, K7, K5, K8, K48 and K4 were some of the genotypes in the right quadrants of the biplot with vegetative period, days to maturity, flag leaf width, flag leaf length, germination rate, single plant biomass and stem diameter traits.

Key words: oat, landraces, lodging, plant height, phenological traits.

Introduction

Cultivated oat consists of two groups, white oats (*Avena sativa* L.) and red oats (*Avena byzantina* C. Koch) which are differentiated primarily by their rachilla fracturing pattern (Stanton, 1955) and preponderance of common oat (*A. sativa* L.) accessions contained T7C-17 in contrast to the absence of the translocation in most of red oat (*A. byzantina* C. Koch) accessions (Jellen, Beard, 2000). These two species of oat are used as dual purpose crop as grain and forage. The grain is also used as supplementary feed for livestock as well as horses.

Agricultural production in semiarid areas of the world is limited by extreme climatic conditions with reduced rainfall, which is usually unevenly distributed by season (Martinez et al., 2010). The major oat growing areas are between latitudes of 40° and 60° N (Asia, Europe and North America), whereas a small proportion of production

originates from southern hemisphere (South America, Australia and New Zealand) (Forsberg, Reeves, 1992).

In recent years, oat production has continuously decreased (Buerstmayr et al., 2007), whereas the demand for oat for human food has increased because of dietary benefits of whole grain and β-glucan (Buerstmayr et al., 2007; Achleitner et al., 2008).

Improvement of agronomic traits has been primary objective of the oat breeders. Besides grain yield, yield components and quality traits, morphological, biological and phenological traits are also important for breeding programs. Since oat acreage is much lower than that of most cereals, commercial effort in oat breeding is also lower (Buerstmayr et al., 2007).

Landraces are populations that have been formed by natural selection processes under the effects of

climate, soil type and agronomic conditions of a particular region, and have suffered artificial selection pressures from the deliberate manipulation of farmers. They contain important genetic variability, which determines their ability to adapt to changes in their environment (Frankel, Brown, 1995). In addition, landraces provide an important source of useful variability for breeding activities (Frankel, Brown, 1995; Allard, 1997) provided that they are accompanied by information on characterization and agronomic evaluation. This information is essential for the correct conservation of genetic variability and for the accessions to be of use in breeding programs (Vilaro et al., 2004).

In this study, we aimed to evaluate 196 Turkish oat landraces and 3 commercial cultivars based on morphological and phenological traits.

Materials and methods

Plant material. The seeds of 196 oat (*Avena sativa* L.) landraces were obtained from Institute of Plant Genetics and Crop Plant Research Gatersleben, Germany (81) are coded "A", from Aegean Agricultural Research Institute Plant Gene Resources Department Izmir, Turkey (60) are coded "E" and from Bahri Dağdaş Agricultural

Research Institute Konya, Turkey (55) are coded "K". In addition, 3 commercial oat cultivars ('Checota', 'Faikbey' and 'Seydişehir'), which are commonly planted in the region, were used in the study. The entry names and the pedigrees of the oat landraces are given in Dumluşinar et al. (2011).

Field trials. Field trials were carried out consecutively for two cropping years (2007–2008 and 2008–2009) at Kahramanmaraş province, located between 37° 53' N and 36° 58' E in East Mediterranean region of Turkey. The experiment was arranged in an augmented split block experiment design with six replications of standard cultivars (Federer, 2005). The seeds were planted in two row plots, each row was 1 m. The experiments were planted on the dates of 18 November 2007 and 18 November 2009. The experiments were carried out in rainfed conditions. The planted rows were harvested individually based on their maturity and threshed with a bundle thresher. The Mediterranean climate is typical of the region and some climatic data are given in Table 1. Fertilizers were applied at planting (50 kg ha⁻¹ N and 50 kg ha⁻¹ P₂O₅) and at tillering as topdressing (100 kg ha⁻¹ N). Herbicide (Tribenuron-methyl 75% (DF)) was used for weed control. However, there was no application of chemicals to control pests and diseases.

Table 1. Average climatic data from Kahramanmaraş province

Months	Rainfall mm			Temperature °C			Relative humidity %		
	2007–2008	2008–2009	Long-term (1930–2009)	2007–2008	2008–2009	Long-term (1930–2009)	2007–2008	2008–2009	Long-term (1930–2009)
November	105.9	105.9	90.2	13.2	13.2	11.4	64.1	64	64.0
December	96.2	96.2	128.1	6.1	6.1	6.6	65.5	66	71.0
January	78.6	107.5	122.6	3.3	4.5	4.9	55.0	69.0	70.0
February	121.5	221.2	110.1	5.5	7.2	6.3	61.4	78.8	65.0
March	69.5	158.0	95.0	14.4	9.4	10.4	59.6	67.2	60.0
April	54.7	82.5	76.3	18.1	15.1	15.3	55.5	59.4	58.0
May	23.7	43.4	39.9	20.2	20.5	20.4	56.5	51.9	54.0
June	0.0	3.7	6.2	27.3	26.8	25.1	49.8	48.2	50.0
Total	550.1	818.4	668.4						
Mean				13.5	12.8	12.6	58.4	63.0	61.5

Investigated traits. In the experiment, morphological and phenological traits were measured. Morphological traits: germination rate, stem diameter, upper internode length, plant height, flag leaf width, flag leaf length, and single plant biomass were determined as previously described (Bares et al., 1985) lodging severity and barley yellow dwarf virus were scored according to a linear 1–9 scale (1 – no severity and 9 – severe). Phenological traits: vegetative period was calculated as days from planting to flowering, grain filling period was determined as days from flowering to maturity and, days to maturity was determined as days from planting to maturity.

Statistical analysis. The data across the two years was analyzed as an augmented split block design by ANOVA. The mean values of the 199 genotypes for investigated traits were subjected to genotype-by-trait, principal components (PC) factor analysis and biplot analysis of PC1 and PC2 and, Spearman correlation coefficients between mean

values of the investigated traits were calculated (JMP User Guide, 2007). Lodging severity and yellow dwarf virus were not subjected to variance analysis. However, biplot analysis was applied to those traits.

Results

Morphological and phenological traits. According to two years' data, all traits were found different for experimental years ($P < 0.01$) except germination rate (GR). Genotypes varied for upper inter-node length (UINL) ($P < 0.05$), stem diameter (SD), plant height (PH), flag leaf length (FLW), vegetative period (VP), grain filling period (GFP) and days to maturity (DM) ($P < 0.01$). In addition, year \times genotype interaction was significant for SD, FLW ($P < 0.05$), VP, GFP and DM ($P < 0.01$) (Tables 2 and 3).

Table 2. Mean squares according to years, genotypes and year \times genotype interactions for morphological traits

	DF	GR	SD	UINL	PH	FLW	FLL
Years	1	237.482	214.378**	1047.5**	1000007.3**	2.353099**	1371.745**
Genotypes	198	165.0083	0.58957**	45.13528*	214.0218**	0.07692**	11.14915
Year \times genotype	198	160.5325	0.33830*	29.07724	54.95722	0.045295*	10.32531

Notes. Explanations of abbreviations under Table 4. * – $P < 0.05$, ** – $P < 0.01$.

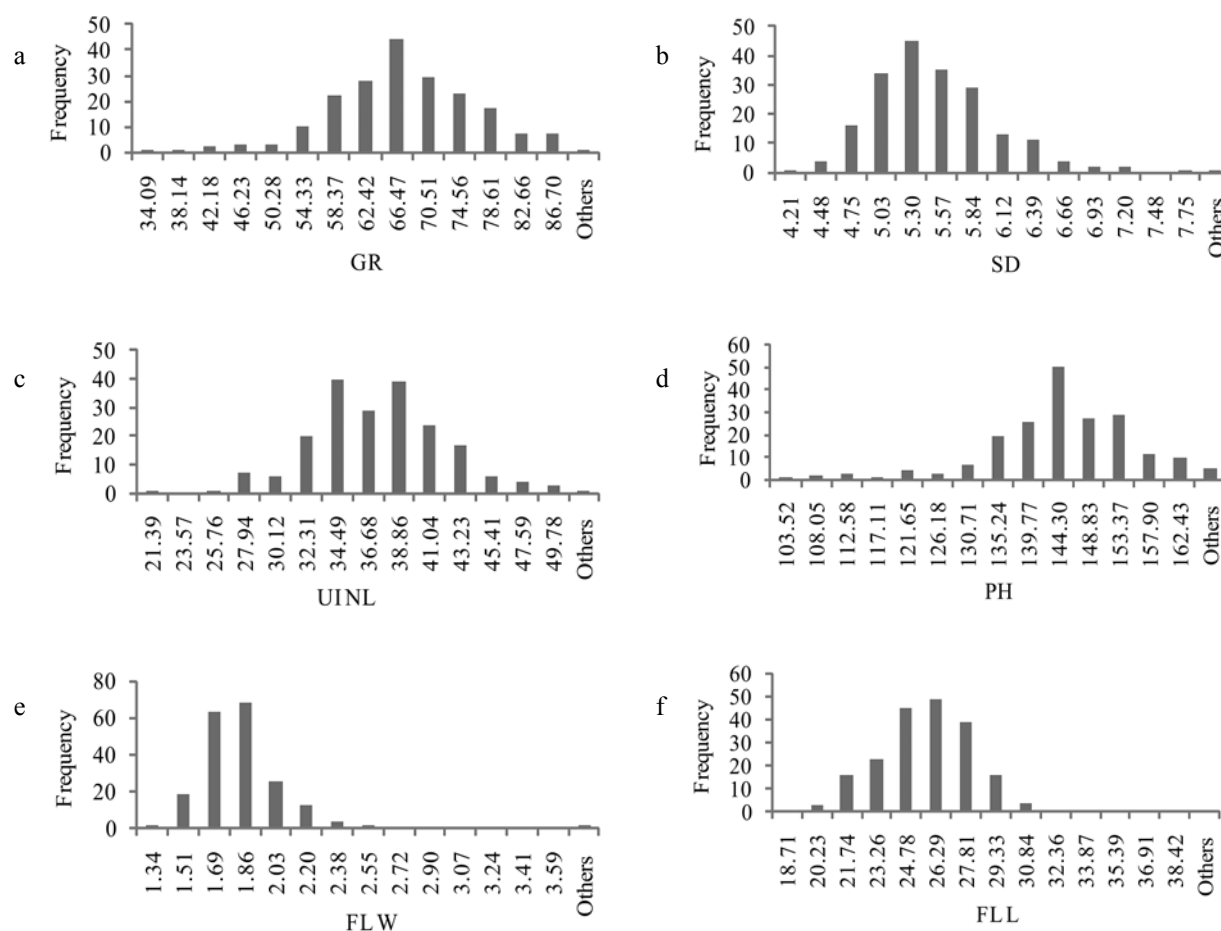
Table 3. Mean squares according to years, genotypes and year \times genotype interactions for morphological and phenological traits

	DF	B	LO	BYDW	VP	GFP	DM
Years	1	33.94214**	§	§	4669.521**	826.7176**	1566.671**
Genotypes	198	1.473546	§	§	37.76326**	16.49646**	22.70891**
Year \times genotype	198	1.187125	§	§	12.89869**	14.4975**	17.35545**

Notes. Explanations of abbreviations under Table 4. * – $P < 0.05$, ** – $P < 0.01$; § – data are not subjected to statistical analysis.

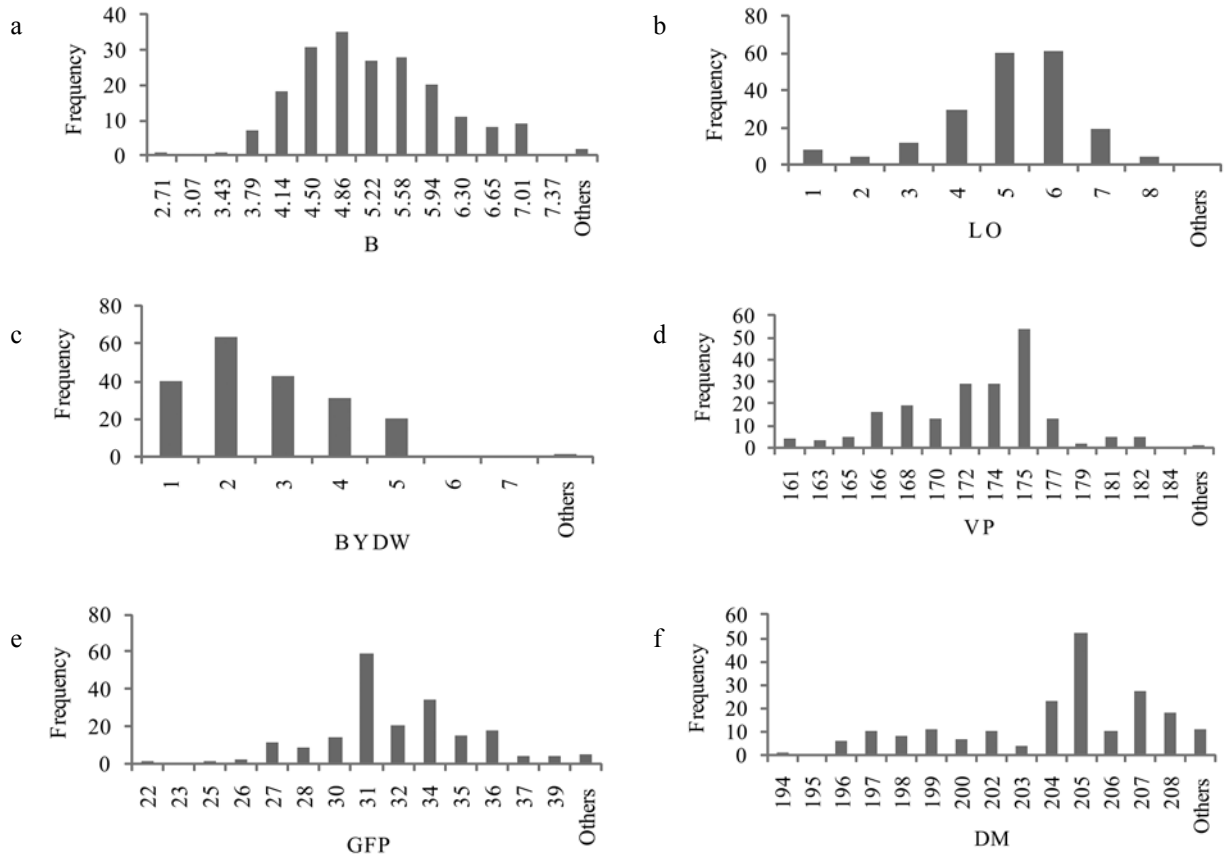
The data belonging to the genotypes for investigated traits are given in the text, and a huge table and his-

tograms were constructed to show the distribution of the investigated traits across oat genotypes (Figs 1 and 2).



Note. Explanations of abbreviations under Table 4.

Figure 1. The histogram shows the distribution of data across 199 oat lines for morphological traits evaluated for two years



Note. Explanations of abbreviations under Table 4.

Figure 2. The histogram shows the distribution of data across 199 oat lines for morphological and phenological traits evaluated for two years

Germination rate of the genotypes was different for the first year, but second year and mean germination rate (GR) values for two years were not significantly different. According to two years' data, K35, E20, E51, A39 and K15 genotypes (90.75, 86.50, 85.42, 84.42 and 84.09 %, respectively) had the higher GR, while lower rates were obtained from E2, E43, A15 and E1 genotypes (34.09, 37.92, 40.25 and 42.09 %, respectively). However, standard cultivars had average GR ('Checota' 74.17%, 'Faikbey' 66.67% and 'Seydişehir' 65.42%). Stem diameter (SD) was found different across experimental years ($P < 0.01$), genotype ($P < 0.01$), and year \times genotype interaction ($P < 0.05$) (Table 2). K48, K4, K6, K3 and K5 genotypes (8.02, 7.64, 7.09, 6.99 and 6.84 mm, respectively) were high in SD, while E49, E40, A20, E46 and K14 genotypes (4.21, 4.24, 4.24, 4.38 and 4.44 mm, respectively) were low. However, 'Checota', 'Faikbey' and 'Seydişehir' had average SD values (5.43, 5.23 and 4.77 mm).

A measure of upper inter-node length (UINL) varied for year ($P < 0.01$) and genotype ($P < 0.05$). Higher values were obtained from A50, A19, A65, A70 and K54 genotypes (51.96, 49.32, 49.16, 48.99 and 47.46 cm, respectively), while lower values were obtained from E40, E3, K20, A63 and E27 genotypes (21.39, 25.39, 25.99, 27.06 and 27.19 cm, respectively). In addition, standard cultivars had similar UINL values ('Checota' 39.93 cm, 'Faikbey' 37.52 cm and 'Seydişehir' 38.79

cm). Plant height (PH) was variable for year ($P < 0.01$) and genotype ($P < 0.01$). E2, K36, A69, K39 and A35 genotypes were taller (166.96, 165.99, 163.96, 163.19 and 162.46 cm, respectively), while K1, K2, K5, K8, K6 and K7 genotypes (103.52, 107.72, 108.02, 110.52, 110.82 and 110.92 cm, respectively) were shorter. 'Faikbey' cultivar was taller (145.90 cm) when compared to 'Checota' and 'Seydişehir' (133.72 and 137.27 cm).

Flag leaf width (FLW) was significant for year ($P < 0.01$), genotype ($P < 0.01$) and year \times genotype interaction ($P < 0.05$) (Table 2). A65, K55, K48 and A25 genotypes (3.76, 3.59, 2.44 and 2.40 cm, respectively) had higher FLW values, while K34 and K22 genotypes had the lowest FLW value (1.34 cm). 'Checota' had 1.74 cm FLW, while 'Faikbey' and 'Seydişehir' had 1.82 and 1.64 cm FLW. However, flag leaf length (FLL) was variable for only year. Higher FLL values were obtained from E30, K46, E38 and K45 genotypes (39.94, 31.12, 30.82 and 30.78 cm, respectively), while shorter FLL values were obtained from K29, A72, A13 and A10 genotypes (18.71, 19.50, 19.85 and 20.22 cm, respectively). 'Checota', 'Faikbey' and 'Seydişehir' cultivars had similar FLL values (24.98, 26.70 and 25.49 cm, respectively).

Single plant biomass (B) was found variable only for year ($P < 0.01$). E13, A7, E34 and K46 genotypes (7.73, 7.46, 6.99 and 6.94 g, respectively) had higher B values, while the lower B values were obtained from A77, A66, K41 and A45 genotypes (2.71, 3.08, 3.44 and

3.49 g, respectively). ‘Seydişehir’ cultivar had the lowest B value (3.77 g) compared to ‘Checota’ and ‘Faikbey’ standard cultivars (4.71 and 4.84 g).

In respect to two years’ data, E45 (9) was the most susceptible genotype to lodging severity (LO), while A70, K15, K46 and K49 genotypes (8) followed it. The most resistant genotypes to LO were K1, K2, K4, K5, K7, K8, K9 and K48 (1). However, according to the two years’ data, barley yellow dwarf virus (BYDV) score of A39 genotype was 5 in year one and 9 in year two and it was the most susceptible genotype to BYDV in year two. Vegetative period (VP) was found variable for year ($P < 0.01$), genotype ($P < 0.01$) and year \times genotype interaction ($P < 0.01$). The longest VP was obtained from A83 genotype (183 days), while A40, A56 and A69 genotypes followed this genotype with 182 days. The shortest VP was obtained from K35, E49, E46 and E20 genotypes with 161 days. In addition, ‘Checota’, ‘Faikbey’ and ‘Seydişehir’ cultivars had average VP (168, 173 and 166 days, respectively). Grain filling period (GFP) varied for year ($P < 0.01$), genotype ($P < 0.01$) and year \times genotype interaction ($P < 0.01$). The longest GFP was obtained from A1, A18, E35 and K35 genotypes with 40 days, while the shortest GFP was obtained from A83 and A69 (22 and 24 days) and A56 and A45 genotypes followed this genotype with 25 days. In addition, ‘Checota’, ‘Faikbey’ and ‘Seydişehir’ cultivars (33, 31 and 35 days) had average GFP values. Days to maturity (DM) was also varied for year ($P < 0.01$), genotype ($P < 0.01$) and year

\times genotype interaction ($P < 0.01$). A1 genotype had the longest DM with 218 days. A17, A49, A50, E48 and E50 genotypes followed this genotype with 209 days. The shortest DM was obtained from E49 genotype with 194 days. E46, E30, E20, A9, A27 and A22 genotypes followed this genotype with 196 days. In addition, ‘Checota’ and ‘Seydişehir’ had 200 days DM, while ‘Faikbey’ had 204 days.

Trait correlations and biplot analysis. Based on mean values of 12 traits, some of the traits were found highly correlated to each other. Also, genotypes grouped into related traits according to biplot of PC1 and PC2. According to PC factor analysis, variation proportions, accounting for 12 components (C) were: C1 22.13%, C2 15.83%, C3 13.37%, C4 10.18%, C5 8.79%, C6 7.34%, C7 6.16%, C8 5.33%, C9 4.38%, C10 3.74%, C11 2.71%, and C12 0.00%. Correlations between the selected traits (Figs 3 and 4) and biplot of PC1 and PC2 of 199 oat genotypes based on 12 traits are shown in Figure 5. In addition, Spearman correlation coefficients of the 12 traits are shown in Table 4.

Relations between BYDV \times B, BYDV \times SD and LO \times FLW were negatively correlated ($r = -0.25^{**}$, $r = -0.19^{**}$ and $r = -0.17^{**}$) (Figs 3A, 3B, 3D and Table 4), while LO \times PH, SD \times FLW, FLW \times FLL, B \times FLL and B \times FLW were significantly correlated ($r = 0.31^{**}$, $r = 0.48^{**}$, $r = 0.24^{**}$, $r = 0.17^*$ and $r = 0.14^*$, respectively) (Figs 3D, 4A, 4B, 4C, 4D and Table 4).

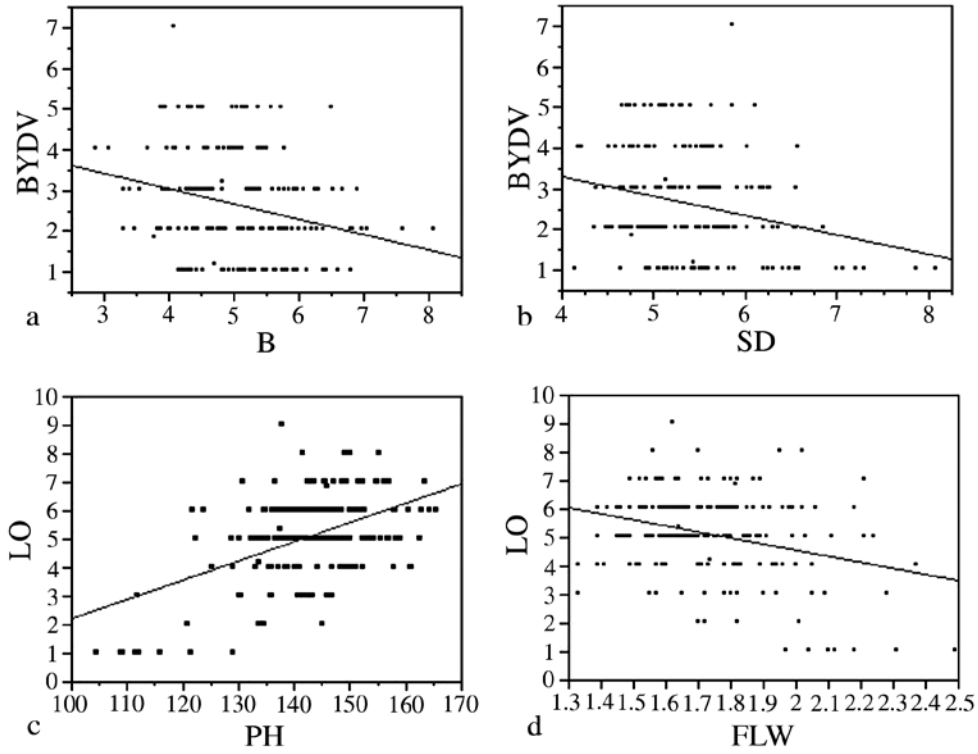
Table 4. Spearman correlation coefficients based on mean values of 12 traits

	GR	SD	UINL	PH	FLW	FLL	B	LO	BYDV	VP	GFP	DM
GR	–											
SD	0.14*	–										
UINL	0.02	–0.06	–									
PH	0.00	0.14*	0.30**	–								
FLW	0.08	0.48**	–0.02	0.11	–							
FLL	–0.14*	0.11	0.02	0.09	0.24**	–						
B	0.10	0.19**	–0.08	0.16	0.14*	0.17*	–					
LO	–0.008	–0.08	0.09	0.31**	–0.17**	0.02	–0.08	–				
BYDV	–0.33**	–0.19**	–0.10	–0.04	–0.11	–0.03	–0.25**	0.12	–			
VP	0.01	0.31**	–0.24**	0.13*	0.34**	0.14*	–0.01	0.02	0.13	–		
GFP	–0.12	–0.10	0.23**	0.05	–0.15*	–0.02	–0.02	0.09	–0.11	–0.63**	–	
DM	–0.07	0.28**	–0.14*	0.24**	0.31**	0.12	0.005	0.12	0.05	0.68**	0.03	–

Notes. GR – germination rate, SD – stem diameter, UINL – upper inter-node length, PH – plant height, FLW – flag leaf width, FLL – flag leaf length, B – single plant biomass, LO – lodging severity, BYDV – barley yellow dwarf virus, VP – vegetative period, GFP – grain filling period, DM – days to maturity. * – $P < 0.05$, ** – $P < 0.01$.

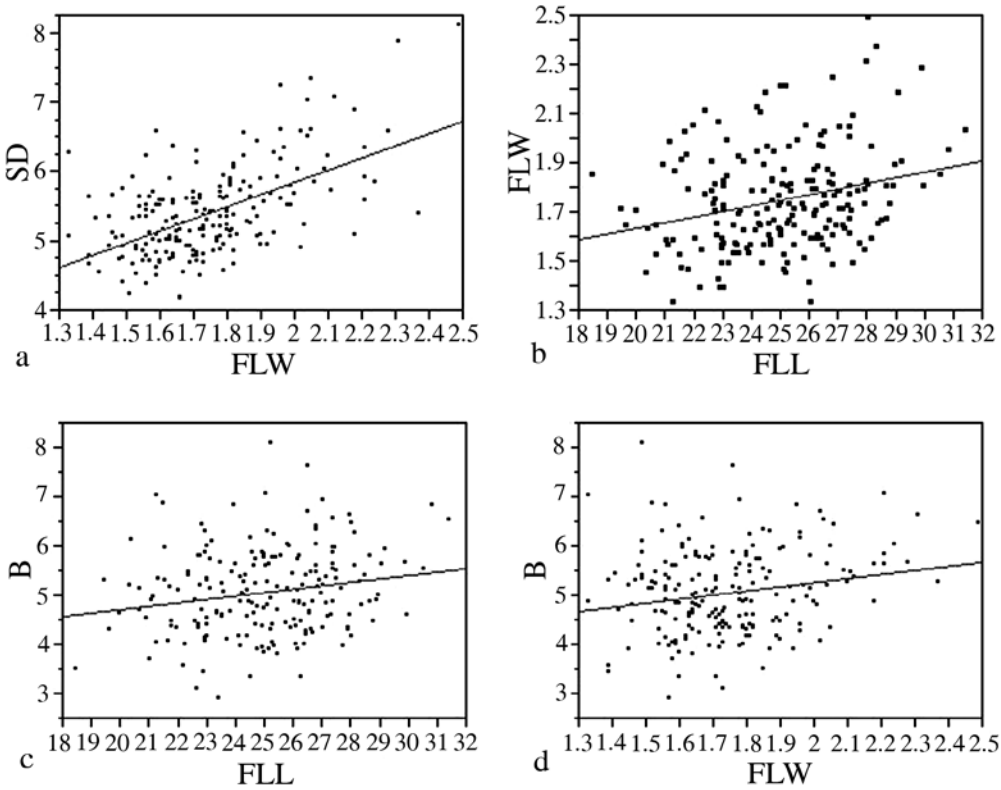
However, correlations between SD \times B, SD \times GR, SD \times DM, UINL \times PH, GFP \times UINL, FLW \times VP, VP \times DM, PH \times VP and FLL \times VP ($r = 0.19^{**}$, $r = 0.14^*$, $r = 0.28^{**}$, $r = 0.30^{**}$, $r = 0.23^{**}$, $r = 0.34^{**}$, $r = 0.68^{**}$, $r = 0.13^*$ and $r = 0.14^*$, respectively) were significantly correlated, while GR \times BYDV, VP \times UINL, GFP \times VP, DM \times UINL and FLW \times GFP ($r = -0.33^{**}$, $r = -0.24^{**}$, $r = -0.63^{**}$, $r = -0.14^*$ and $r = -0.15^*$, respectively) were negatively correlated (Table 4).

Biplot of PC1 and PC2 for 199 oat genotypes illustrates a clear separation of genotypes and investigated traits. E1, A56, E7, E55, A17, E38, A40, A63, A25, A69, A26, A83, A1, A2, K11, K9, K3, K53, K30, K1, K2, K7, K5, K8, K48 and K4 were some of the genotypes in the right quadrants with VP, DM, FLW, FLL GR, B and SD traits. However, E9, E49, E20, E46, K35, A34, A22, A9, A68, ‘Checota’, E2, E6 and E45 were some of the genotypes in the left quadrants with PH, UINL, GFP, LO and BYDV (Figs 5A and 5B).



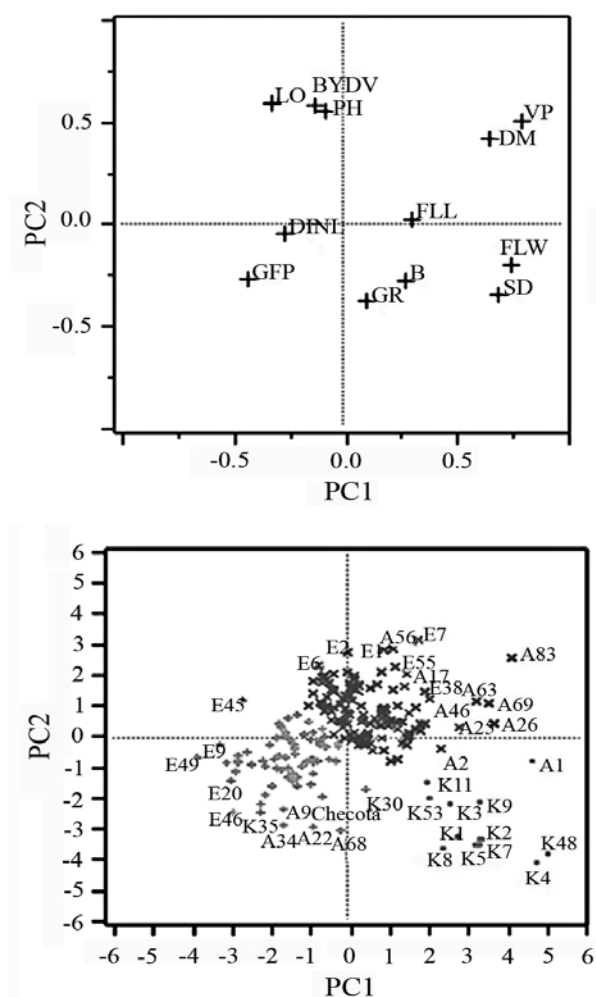
Note. Explanations of abbreviations under Table 4.

Figure 3. The correlation between selected traits based on mean values of 199 oat genotypes for BYDV × B, BYDV × SD, LOY × PH and LO × FLW



Note. Explanations of abbreviations under Table 4.

Figure 4. The correlation between selected traits based on mean values of 199 oat genotypes for SD × FLW, FLW × FLL, B × FLL and B × FLW



Note. Explanations of abbreviations under Table 4.

Figure 5. Biplot of principal components 1 and 2 of 199 oat genotypes based on mean values of 12 traits

Nevertheless, the upper right quarter of the biplot (positive PC1 and positive PC2) is mainly associated with FLL, DM and VP, the lower right quarter of the biplot (positive PC1 and negative PC2) is mainly associated with GR, SD, B and FLW, the upper left quarter of the biplot (negative PC1 and positive PC2) is mainly associated with PH, LO and BYDV, and the lower left quarter of the biplot (negative PC1 and negative PC2) is mainly associated with UINL and GFP. Thus, oat genotypes with high FLW, FLL, SD, B, GR and shorter phenological durations are located along the right quadrants of the biplot. Oat genotypes with higher LO, BYDV, PH and GFP are located along the left quadrants of the biplot (Fig. 5B).

Discussion

Morphological and phenological traits. Germination rate (GR) of genotypes was lower in year one, while there were no significant differences among genotypes in year two. The lower germination rate for the first

year might be due to different seed storage durations in gene banks. Stem diameter (SD) was found highly variable for year, genotype and year \times genotype interaction. Ahmad et al. (2008) reported high SD variation among the genotypes, which is in agreement with our findings. Upper inter-node length (UINL) is one of the components of the final plant height. In our study UINL varied for year and genotype. In previous works, Gautam et al. (2006) reported environmental effect for UINL and Peltonen-Sainio and Rajala (2007) determined that UINL was influenced by genetics. Plant height (PH) is one of the important traits for oat plant which has a lodging problem. PH was found highly variable for year and genotype. Corville Baltenerger and Frey (1987) reported genetic influence for plant height, as well as Matiello et al. (1999) who determined genetic influence inter-specific and intra-specific. Nawaz et al. (2004) also observed high variation among cultivars. In addition, our findings were in agreement with Gautam et al. (2006), Ma et al. (2006), Zaman et al. (2006), Buerstmayr et al. (2007) and Ahmad et al. (2008). Flag leaf width (FLW) varied for year, genotype and year \times genotype interaction, while flag leaf length (FLL) varied only in year. Semchenko and Zobel (2005) indicated significant FLW and FLL variations among oat cultivars, which is in agreement with our results. Different FLL values between years were due to higher rainfall in year two. Also, Gautam et al. (2006) reported environmental influence on FLL. Single plant biomass (B) was not found variable for genotypes, but it was found variable for years. Robertson and Frey (1987) reported that biomass and grain yield are important selection criteria and selection for biomass is more valuable for selection for grain yield. However, Chernyshova et al. (2007) found that genotypes with the higher β -glucan had lower grain yield and biomass. Lodging is one of the critical traits for oat and most of the landraces have lodging problems. In our study, some of the genotypes had severe lodging problems, while there were some genotypes which did not. Lodging severity (LO) is also affected by environment and some cultural treatments such as irrigation. In previous works, Tamn (2003) reported environmental influence, while Buerstmayr et al. (2007) found genetic influence and heritability, which are in agreement with our findings. Barley yellow dwarf virus (BYDV) was severe in year one while it did not appear in the second year except one genotype. This may be due to cool growing season in the second year, which delayed pest and insect occurrences and limited infection of the genotypes. Vegetative period (VP), grain filling period (GFP) and days to maturity (DM) were found variable for year, genotype and year \times genotype interaction. This may be due to genetic influence and climatic conditions. Matiello et al. (1999), Nawaz et al. (2004), Buerstmayr et al. (2007) and Locatelli et al. (2008) also reported variation and genetic influence for vegetative period and earliness. In

addition, Gautam et al. (2006) determined environmental influence for vegetative period. Also, Wych et al. (1982) and Peltonen-Sainio and Rajala (2007) reported genetic influence for GFP. In addition, Nawaz et al. (2004) stated that DM was influenced by genetics.

Trait correlations and biplot analysis. BYDV disease was negatively correlated with B, GR and SD. The severity of the disease decreased the biomass yield and SD. Interestingly, low germination rate caused severe BYDV disease. This may be due to high tillering rate of the genotypes which allows diseases to spread easily. SD positively correlated with FLW, B, GR and DM. Higher SD values resulted in high biomass yield and FLW. Also, high GR with the low tiller number resulted in high SD which was expected, while higher SD caused long DM. Lodging severity was negatively correlated with FLW, while highly correlated with PH. Higher PH increased the LO, which was expected. Buerstmayr et al. (2007) found high correlation between PH \times LO and indicated that selection for reduced PH will improve lodging resistance indirectly. Upper inter-node length was positively correlated with PH, VP and GFP. UINL is critical for final PH and higher UINL increased the PH. Also, long VP increased the UINL which was expected. Nevertheless, higher UINL resulted in long GFP which was unexpected. This may be due to lodging of higher plants. Flag leaf width (FLW) was highly correlated with FLL which was expected. Also, FLW increased the VP and DM durations, while increasing the biomass yield as well. However, a negative correlation was determined between FLW \times GFP. Flag leaf width (FLW) caused shorter GFP durations which can be explained by high photosynthesis capacity of wider flag leaves that might cause early maturing. In addition, VP was highly correlated with DM, while negatively correlated with GFP. Longer vegetative durations resulted in longer DM and decreased the GFP which was not desired.

Results of biplot analysis indicated the most promising traits as selection criteria for genotypes used in this study. Germination rate (GR), SD, DM, VP, FLL, FLW and B traits that fell into the two right quadrants of the biplot, might be more promising than LO, BYDV, PH, UINL and GFP traits that fell into the two left quadrants of the biplot. Peterson et al. (2005) reported that biplot analysis can be used to select genotypes that may have favourable combinations of traits for use in breeding programs.

Conclusion

Oat production in the world is gradually decreasing, while its valuable nutritional benefits are being more important. Especially, health claims of the oats add value to this cereal crop.

Genetic resources are one of the crop development sources for stress tolerance and desired traits. Tur-

key is one of the centers of origin of the oat, thus the genotypes used in this study are very important for future studies.

Our results indicate that stem diameter, flag leaf length and width, days to maturity, vegetative period, biomass and, germination rate are more promising traits for use in breeding programs. However, traits such as lodging, plant height, barley yellow dwarf virus, upper internode length and grain filling period are more important for negative selection. Also, some genotypes with higher performance in respect to those traits are determined, which may be important for oat breeding programs.

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Senujų turkiškų avižų veislių įvertinimas, remiantis morfologiniais ir fenologiniais požymiais

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Santrauka

Dvejus metus vykdytų bandymų metu tirtos 196 senųjų turkiškų ir 3 standartinių ('Checota', 'Faikbey' bei 'Seydişehir') avižų veislių morfologinės (sudygimo greitis, stiebo skersmuo, viršutinio tarpubamblio ilgis, augalo aukštis, viršūninio lapo plotis bei ilgis, vieno augalo biomasė, augalų išgulimas ir miežių geltonosios žemaūgės virusas) ir fenologinės (vegetacijos laikotarpis, grūdų pildymosi periodas bei dienos iki brandos) savybės.

Dvejų metų tyrimų duomenys parodė, kad šios savybės skyrėsi tarp metų, išskyrus sudygimo greitį. Genotipai skyrėsi viršutinio tarpubamblio ilgiu, stiebo skersmeniu, augalų aukščiu, viršūninio lapo pločiu, vegetacijos laikotarpiu, grūdų pildymosi periodu ir dienomis iki brandos. Be to, metų ir genotipo sąveika buvo esminė stiebo skersmeniui, viršūninio lapo pločiui, vegetacijos laikotarpiui, grūdų pildymosi periodui ir dienoms iki brandos.

Svarbesni atrankos kriterijai buvo šie požymiai: viršūninio lapo ilgis bei plotis, dienos iki brandos, vegetacijos laikotarpis, vieno augalo biomasė ir sudygimo greitis. Neigiamai atrankai buvo svarbesni augalų išgulimas, aukštis, miežių geltonosios žemaūgės virusas, viršutinio tarpubamblio ilgis ir grūdų pildymosi periodas.

Tyrimų rezultatai parodė, kad E1, A56, E7, E55, A17, E38, A40, A63, A25, A69, A26, A83, A1, A2, K11, K9, K3, K53, K30, K1, K2, K7, K5, K8, K48 ir K4 buvo genotipai, išsidėstę dešiniajame binarinės diagramos kvadrante su neigiamais vegetacijos laikotarpio, dienų iki brandos, viršūninio lapo pločio bei ilgio, sudygimo greičio, vieno augalo biomasės ir stiebo skersmens požymiais.

Reikšminiai žodžiai: avižos, senosios veislės, pasėlio išgulimas, augalo aukštis, fenologiniai požymiai.