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ASSESSMENT OF GRAIN YIELD AND QUALITY TRAITS OF DIVERSE OAT (*AVENA SATIVA* L.) GENOTYPES

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Abstract - Oat (*Avena sativa* L.) is used as an important source of essential nutrients for both humans and animals. There is an increasing demand in the world due to the high nutritional content and adaptability to low fertility conditions. This study was carried out to determine important yield and quality traits in 347 oat lines and 12 oat cultivars selected from a large number of pure line oats between 2012-2013 and 2013-2014. Grain yield, test weigh, groat percentage, along with crude protein, starch, β-glucan, fat, palmitic, stearic, oleic and linolenic acids, ash, potassium, phosphorus, magnesium, acid detergent fiber and neutral detergent fiber contents were determined. Significant differences were found between the genotypes in terms of the studied traits. Principal component analysis indicated that the first six axes accounted for 84% of the variability. The results indicate which genotypes that is hopeful for use in breeding programs.

Keywords: oat; genotype; yield; biplot; quality.

Introduction

Oat belonging to the Poaceae family and the genus *Avena* is a low input cereal crop that is used worldwide for human food consumption and animal feed. The genus comprises about 70 species including diploid, tetraploid and hexaploid species (Kaur & Kapoor, 2017). *Avena sativa* is the most widely cultivated species due to its multifunctional traits and nutritional value. *Avena byzantina*, and *Avena nuda* are other important oat species cultivated (Webster, 2012).

Compared to other cereal crops, oat production is reputed to be better in low fertility environments. Oat ranks the sixth in world cereal production, following wheat, maize, rice, barley and sorghum (FAO, 2018). Oat production decreased in many Countries in recent years because of the decline in oat production for on-farm feed. In addition, the decline in production is linked to the higher monetary returns per hectare of other crops like maize, soybean, and wheat (Buerstmayr et al., 2007).

Although oat has been widely used in animal nutrition in the past years, it has become more popular for human nutrition in the world since its significant health benefits have been unfolded recently in the field of food science (Jing & Hu, 2012). Oat grains with high fiber content and quality is known for reducing the risk of several chronic diseases such as cholesterol, blood glucose levels, cardiovascular diseases, cancer, obesity and diabetes (Redaelli et al., 2015).Oat that was traditionally used as breakfast cereal and porridge in some Countries, after the recognition as a healthy food has started to be used in other products like pasta, muffins, biscuits, cakes, bread, snack food, infant food, probiotic drinks (Andersson & Börjesdottir, 2011).

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Grain quality of oat has been subject to several researches due to unique chemical and traits. Oat is rich of β-glucan, protein, vitamin, minerals, digestible fibre, fat, unsaturated fatty acids, and some anti-oxidants (Finnan et al., 2019). The protein content of oat, which contains between 12.4 and 24.4% protein in grains, is higher than other cereals. Test weight, groat percentage, protein, β-glucan, fat and fatty acids, etc. traits are some of the widely used properties to identify oat quality (Doehlert et al., 2001). Fat composition in oats is reported to be useful and is rich in linoleic acid, which is necessary for human health (Redaelli et al., 2015).

Plant breeders generally develop cultivar from local populations that are adapted to the region and they commonly change lines and varieties among themselves. This change occurs within a limited region. The exchange of breeding lines among Countries is not widespread. Therefore, oat breeding may have comparatively low genetic diversity for agronomic and quality features (Buerstmayr et al., 2007).

The objective of this study was to assess the yield and quality traits of different 359 oat genotypes cultivate in two different years.

Materials and Methods

Plant material and location

In this study, 347 oat lines selected from Quaker International Oat Nursery and 12 oat cultivars (Seydişehir, Yeşilköy 330, Yeşilköy 1779, Faikbey, Milton, Simpson, Radar, Hifi, Maida, Beach, Souris, Morton) widely grown in different parts of the world were tested. Field trials were performed during the 2012-2013 and 2013-2014 cropping seasons at the Department of Field Crops, Faculty of Agriculture, Ondokuz Mayıs University (altitude 195 m, latitude 41°21′ N, longitude 36°15′ E), Turkey. In both years, the experimental design consisted of 17 blocks containing 25 genotypes in each with 21 test genotypes and four checks (Seydişehir, Faikbey, Milton, Radar). Each plot was consisted 4 rows of 4 m length with 20 cm between the rows. The seeding density was 450 seeds m^2. Sowing dates were 16 October 2013 and 23 October 2014, respectively. A dose as 60 kg ha^{-1} N and 60 kg ha^{-1} P_2O_5 (di-ammonium phosphate) were applied at sowing. During plant tillering, the plots were fertilized with 60 kg ha^{-1} N (urea). Herbicide (Tribenuran-metil (DF) %75) was used in the tillering stage in both years for weed control. Samples of all the plots were hand harvested close to the ground by hand using with a sickle on July 21 in the first year and on July 15 in the second year. Then these samples were threshed by plot threshing machine.

The trials were performed in clay soil with the following characteristics: 0.8 and 0.16 dSm^{-1} non-salty, 6.26 and 6.88 pH, 683.5 and 740.0 kg ha^{-1} exchangeable potassium (K_2O) content, 20.2 and 25.4 kg ha^{-1} available phosphorus content (P_2O_5), 0.18 and 0.20% nitrogen content, 2.81 and 2.85% organic matter (2012-2013 and 2013-2014, respectively). The following soil analysis were performed according to Soil Survey Laboratory: salinity, pH and potassium (SSL 1992); phosphorus content (Olsen & Sommers 1982); nitrogen content by Micro Kjeldahl method (Concon & Soltess, 1973), organic matter content by a modified form of the Walkley-Black method (Jackson, 1958).

The climatic data for the vegetation period are given in Table 1. During the growing seasons (October-July), the average temperature and total rainfall were 9.7 °C and 609.4 mm, and 11.8 °C and 415.6 mm respectively for 2012-2013, 2013-2014. Climate data were obtained from the Turkish State Meteorological Service in the period (Anonymous, 2015).

Table 1. Meteorological conditions during the 2012-2013 and 2013-2014 in the experimental areas.

	Rainfall (mm)		**Relative Humidity (%)**		**Temperature (ºC)**	
	2012-2013	2013-2014	2012-2013	2013-2014	2012-2013	2013-2014
October	36.7	51.3	69.4	65.1	12.6	16.3
November	163.6	37.8	71.5	68.4	5.6	11.9
December	102.9	56.8	66.7	53.9	7.2	7.3
January	61.3	5.1	60.0	63.2	3.7	6.2
February	30.8	34.0	70.3	69.4	1.3	7.0
March	92.8	40.8	65.5	71.4	3.3	6.8
April	57.8	24.4	72.2	75.6	8.9	9.6
May	29.6	48.1	72.2	74.4	14.9	14.8
June	33.9	62.3	67.5	66.3	18.2	17.9
July	10.6	55.0	63.2	64.5	21.1	20.1
Total/Mean	**609.4**	**415.6**	**67.9**	**67.2**	**9.7**	**11.8**

Grain yield, physical and chemical analyses

Following the harvest and threshing, grains of each plot were weighed and resultant values were converted into grain yield (GY) per hectare (ton). Test weight was measured by

using a 0.5 litre measuring instrument (AACC, 2005). In order to determine the groat percentage, the husked oats (10 g) were de-hulled by hand before the analysis and then de-hulled groats were weighed and the ratios of groat were calculated. For chemical analyses, dry seeds from each genotype were ground with a hammer mill having a 0.5 mm screen. The samples were stored for later analyses at + 4 °C. Samples were analyzed within three months after harvest in both years.

The grain samples were analyzed to determine the crude protein content [(PC), Micro Kjeldhal method of Concon & Soltess (1973)], fat content [(FC), Soxhlet method of Welch (1977) and (Rauf et al. (2019)], starch content [(SC), Ewers Polarimetric Method of AACC (2005)], b-glucan content [(bC), enzymatic method of AACC (AACC, 2005) and Motilva et al. (2014)]. These analyses were performed according to the standard Official Methods of Analysis of the Association of Official Analytical Chemists. The ADF and NDF content (Van Soest et al., 1991) were determined by using an ANKOM 220 Fiber Analyzer.

The fatty acid profile was determined with a direct method of extraction and methylation according to O'Fallon et al. (2007) to obtain fatty acid methyl esters (FAME). The methyl esters of the fatty acids (0.5 mL) were analysed in a Shimadzu GC 2010 equipped with a flame ionizing detector, a fused silica capillary column (MN FFAP, 60 m x/0.32 mm i.d.; film thickness, 0.25 μm). It was operated under the following conditions: oven temperature programme, 120 °C for 1 min raised to 240 °C at a rate of 6 °C/min and then kept at 240 °C for 15 min); injector and detector temperatures, 250 and 260 °C, respectively; carrier gas, helium at flow rate of 40 mL/min; and split ratio, 1/20 mL/min. The fatty acid composition [palmitic (16:0), stearic (18:0), oleic (18:1) and linolenic (18:2) acids] was determined by computing integrator. In this study, palmitic, stearic, oleic and linolenic acids accounted approximately 98% of total fatty acids. The K, Ca and Mg contents were determined by Atomic Absorption Spectroscopy (Kaçar, 1994), and the P content was determined by the "Olsen" method (Olsen & Sommers 1982).

Statistical analysis

The data collected genotypes in the two years were analyzed by using an augmented design (Federer, 1956). The mean values of the 359 genotypes for investigated traits were subjected to genotype-by-trait, principal components (PC) factor analysis and biplot analysis of PC1 and PC2 and, Pearson's correlation coefficients between mean values of the investigated traits was calculated (JMP, 2007).

Results and Discussion

Total rainfall was higher in the first year (609.4 mm) than the second year (415.6 mm).The average relative humidity was higher in the second year (67.2%) than the first year (67.9%) while the average temperature was higher in the first year (9.7 °C) than the second year (11.8 °C) (Table 1). The descriptive data (mean, standard deviation (SD), standard error of the mean (SEM) minimum, maximum) of the 16 quality traits are reported in Table 2.

Table 2. The mean values and ranges of the grain yield and 16 quality traits of the 359 genotypes in the combined data of the years. **(**SEM: Standard error of mean; SD: Standard deviation).

Nutrient content	Mean	SEM	SD	Range		P value
				Min.	Max.	
Grain yield (ton ha^{-1})	3.60	0.05	0.97	1.85	6.87	<0.001
Ash (%)	2.24	0.01	0.22	1.73	2.90	<0.001
Protein (%)	10.36	0.04	0.83	8.18	12.91	<0.001
Starch (%)	45.20	0.20	3.70	33.83	53.61	<0.001
β-glucan (%)	2.47	0.02	0.31	1.27	3.48	<0.001
Acid detergent fiber (%)	15.25	0.08	1.44	10.11	19.02	0.026
Neutral detergent fiber (%)	32.60	0.09	1.75	23.20	36.70	0.015
Potassium (g kg^{-1})	5.05	0.03	0.55	2.78	6.73	0.019
Phosphorus (g kg^{-1})	4.19	0.01	0.25	3.44	5.47	0.038
Magnesium (g kg^{-1})	1.48	0.01	0.11	1.16	1.90	0.014
Groat percentage (%)	73.01	0.16	3.06	63.44	80.89	<0.001
Test weight (%)	47.85	0.13	2.40	41.35	56.75	<0.001
Fat (%)	4.99	0.04	0.81	2.71	7.16	<0.001
Palmitic (16:0) (%)	19.02	0.03	0.54	17.50	20.93	0.011
Stearic (18:0) (%)	1.75	0.01	0.10	1.37	2.00	0.009
Oleic (18:1) (%)	40.41	0.14	2.74	33.66	52.99	<0.001
Linoleic (18:2) (%)	36.80	0.11	2.01	23.63	41.38	<0.001

Among the agronomic traits, grain yield has the most complex heritability and it is quite hard to achieve genetic progress in this issue. To measure the yield potential of a genotype, it should be experimented in more than one location with different climate and soil characteristics and/or in more than one year. Genotype yields varied between 1.85 (G337) to 6.87 (G341) t ha^{-1} with an average value of 3.60 t ha^{-1} (Table 2).

The G341, G324, G45, G57, G266, and G105 genotypes (6.87, 6.86, 6.45, 6.41, 6.23 and 6.06 t ha^{-1}, respectively) were higher in grain yield. However, average grain yield of standard cultivars had lower than lines (Seydişehir 4.67 t ha^{-1}, Faikbey 3.73 t ha^{-1}, Milton 2.23 t ha^{-1} and Radar 3.80 t ha^{-1}). As sees Figure 1, grain yield in the first year (4.12 t ha^{-1}) was higher than that of second year (3.08 t ha^{-1}). This may result from the fact that the total rainfall was much higher in the first year compared with the second year. Besides genetic factors, biotic and abiotic stress factors also result in different reactions of the genotypes to different environments. Low or high precipitations, high or low temperatures also influence interactions. Previous studies attributed the differences in genotype yields to differences in genotypes (Peterson et al., 2005; Mut et al., 2018), environmental factors (Doehlert et al., 2001), both genotypes and environmental factors (Mut et al., 2018) or agronomic practices (Finnan et al., 2019). Mut et al. (2018) conducted a study between the years 2010-11 and 2011-12 with 25 oat genotypes and reported grain yields of the genotypes as between 2.15- 5.81 t ha^{-1}.

Ash shows total minerals accumulated in the seeds. The ash content of the genotypes ranged from 1.73 (G298) to 2.90% (G217) (Table 2). Ash content of the genotypes was higher in the first year, in more humid conditions (Fig. 1). Doehlert et al. (2001) reported that the ash content is more affected by environmental factors than genetic diversity. Previous studies have reported that the ash content of oat genotypes ranged from 1.87 to 4.33% (Usman et al., 2010).

Protein is an important quality trait for oat grains. The protein content of the genotypes ranged from 8.18 (G298) to 12.91% (G220), mean 10.36% (Table 2). The G220, G183, G291, G219, G146, G180, G354, G273 and G172 genotypes (12.91, 12.85, 12.50, 12.31, 12.25, 12.24, 12.21, 2.11 and 12.01%, respectively) were higher than 12.0% protein content. However, cultivars of Seydişehir, Faikbey, Milton and Radar had 11.51%, 9.81%, 10.66% and 12.13% protein content, respectively. Protein content depends on environmental factors as well as genotypic factors (Stone & Savin, 1999). The average protein content was lower in the 2013-2014 growing season (Fig. 1). The protein content of cereals grown in more rainy or irrigated conditions is low. Precipitations of growing sites, monthly distribution of precipitations, temperatures and cultural practices influence protein content and quality of cereal grains (Gooding, 2010). Peterson et al. (2005), Yanming et al. (2006) and Mut et al. (2018) reported significant differences between genotypes in terms of protein content. Protein contents were previously reported between 12.1 and 12.7% by Rodehutscord et al. (2016), between 10.76 and 14.70% by Sabandüzen & Akçura (2017) and between 11.55 and 15.06% by Mut et al. (2018).

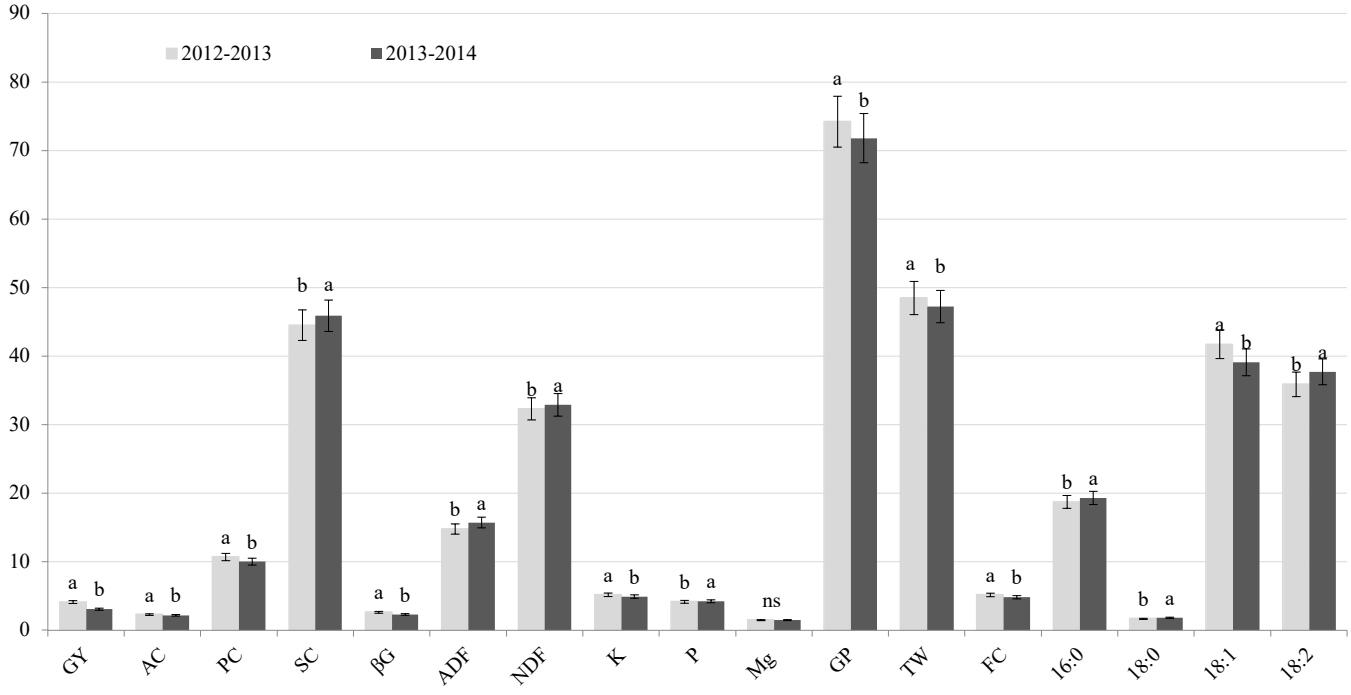

Figure 1. Mean values and standard deviation (n = 3) for grain yield and quality traits of oat genotypes in 2012-2013 and 2013-2014. Bars not accompanied by the same letter are significantly different at $P < 0.05$, using Tukey HSD test (GY = grain yield (t ha^{-1}), AC = ash content (%), PC = protein content (%), SC = starch content (%), βG = beta-glucan content (%), ADF = acid detergent fiber (%), NDF = neutral detergent fiber (%), K = potassium (g kg^{-1}), P = phosphorus (g kg^{-1}), Mg = magnesium (g kg^{-1}), GP = groat percent (%), TW = test weigh (kg hL^{-1}), FC = fat content (%), 16:0 = palmitic acid (%), 18:0 = stearic acid (%), 18:1 = oleic acid (%), 18:2 = linolenic acid (%), ns = non significant).

Punia et al. (2020) reported that starch is the primary digestible carbohydrate of the plants, thus offers important source energy in human nutrition and animal feeding. In this study, the range between oat genotypes in terms of starch content was 33.83 (G330)-53.61% (G320) with a mean value of 45.20% (Table 2). G11, G59, G63, G104, G127, G129, G130, G143, G292, G307, G318, G320 and G354 numbered genotypes were higher than 52.00% starch content. The starch content of the first year (44.52%) was higher than the second year (45.89%) in genotypes, respectively (Fig. 1). Doehlert et al. (2001) reported that starch content was more affected by environmental factors than by genetics. We thought that the starch content was high due to the high rainfall and low temperature during the first year. A wide range of starch content has been reported: 45.7-46.3% (Brunava et al., 2014) and 42.7-49.6 (Mut et al., 2018).

The β-glucan found so much in oat grains is an important naturally dissolving dietary fiber. Concerning the average of years, the β-glucan content of oat genotypes ranged from 1.27 (G123) to 3.48% (G283), mean 2.47% (Table 2). G3, G11, G27, G80, G122, G128, G133, G148, G180, G183, G185, G190, G243, G267, G283, G312 and G330 numbered genotypes were higher than 3.00% β-glucan content. The β-glucan of the first year was higher than the second year on genotypes, respectively (Fig. 1). Doehlert et al. (2001) reported that β-glucan content was equally affected by both environmental and genetic factors. In addition to genetic and environmental factors, β-glucan content can also be affected by factors such as sowing time, soil, temperature, rainfall, fertilizer and harvest date (Peterson et al., 2005, Mut et al., 2016a). High β-glucan contents are desired in oat grains to be used in human nutrition and animal feeding (Peterson et al., 2005). Webster (2002) determined β-glucan in oat seeds 2 to 7%. The β-glucan content was previously reported between between 1.98 and 6.24% by Silveria et al. (2016), between 2.9 and 3.6% by Sterna et al. (2018), between 2.93 and 3.56% by Mut et al. (2018) and between 1.02 and 6.33% by Rauf et al. (2019).

The average ADF and NDF contents of oat genotypes ranged from 10.11 (G220) to 19.02% (G280) and from 23.20 (G220) to 36.70% (G330), respectively. The ADF and NDF contents showed significant variations among the oat genotypes. The average ADF and NDF contents were 15.25 and 32.60% in the genotypes (Table 2). The G9, G11, G31, G59, G120, G128, G138, G143, G179, G180, G185, G186, G190, G198, G206, G220, G241, G306 and G307 numbered genotypes were lower than 13.00% ADF content, while the G9, G11, G57, G59, G84, G92, 106, G120, G128, G129, G143, G172, G180, G185, G186, G198, G199, G206, G219 and G220 numbered genotypes were lower than 30.00% ADF content. In terms of the mean of ADF and NDF contents, genotypes showed close values in both years (Fig. 1). The ADF and NDF protect animals against metabolic diseases by increasing rumen pH. It also plays a role in obtaining milk with a higher fat ratio by maintaining the acetic acid / propionic acid ratio. In addition, ADF and NDF increase the production of quality protein by protecting the bacterial micro-flora in rumen (Tekce & Gul, 2014). Biel et al. (2020) reported that ADF and NDF contents of hulled oat genotypes ranged from 15.6 to 18.4% and ranged from 29.7 to 38.0%. The same researcher reported that the average ADF and NDF contents of hulled oats were higher than the other examined cereals. In another study achieved with different oat cultivars, average ADF and NDF contents were reported as 15.0% and 33.0% (Mut et al., 2018).

In developing countries, cereals that are good source of minerals are used as staple foods. Mineral compounds are elements necessary in human nutrition. The human organism is incapable of producing mineral compounds, hence minerals must be supplied with food (Biel et al. 2020). The K, P and Mg contents of oat genotypes ranged from 2.78 (G306) to 6.73 (G180) g kg^{-1}, 3.44 (G286) to 5.47 (G219) g kg^{-1} and 1.16 (G286) to 1.91 (G219) g kg^{-1}, respectively. The average K, P and Mg contents were 5.05, 4.19 and 1.48% in the genotypes (Table 2). G150, G180 and G183 numbered genotypes were higher than 6.50% K content while 219 and 220 numbered genotypes were higher than 5.00% P content. The G44, G204, G219, G220, G268, G273 and G291 numbered genotypes were higher than 1.70% Mg content. In terms of the mean of K, P and Mg contents, genotypes showed close values in both years (Fig. 1). The mineral compounds are important for nutritional and technological reasons. Cereals are provide significant amounts of phosphorus, potassium, calcium and magnesium Mut et al. (2017) reported that oat genotypes showed 4.99%, 3.66% and 1.50% of K, P and Mg contents, respectively. Boila et al. (1993) indicated that K, P and Ca contents of oats were 4.83%, 3.91% and 1.44, respectively.

Groats percentage is calculated as the ratio of dehulled section of oat grain to entire grain. Groat percentage of oat genotypes varied between 63.44 (274) and 80.89% (G186) with an average value of 73.01% (Table 2). G186, G130, G180, G9, G181, G9, G155, G30, G181, G84 and G353 numbered genotypes were higher than 80.00% groat percentage, respectively. The groat percentage of the first year (74.21%) was higher than the second year (71.80%) in the genotypes, respectively (Fig. 1). Doehlert et al. (2001) reported groat percentage was equally affected by both environmental and genetic factors. Groats percentage is an important quality indicator of oat grains. It represents economic yields for millers and digestible portion of the grain for animal growers. Both in the food industry and in animal feeding are preferred oats with low hull ratio. And also, food industry is preferred oat grains high efficiency and easy-to-dehull (Doehlert et al., 2001). Welch et al. (2000) reported that there was a great variation within species and between species in terms of groat percentage of oats.

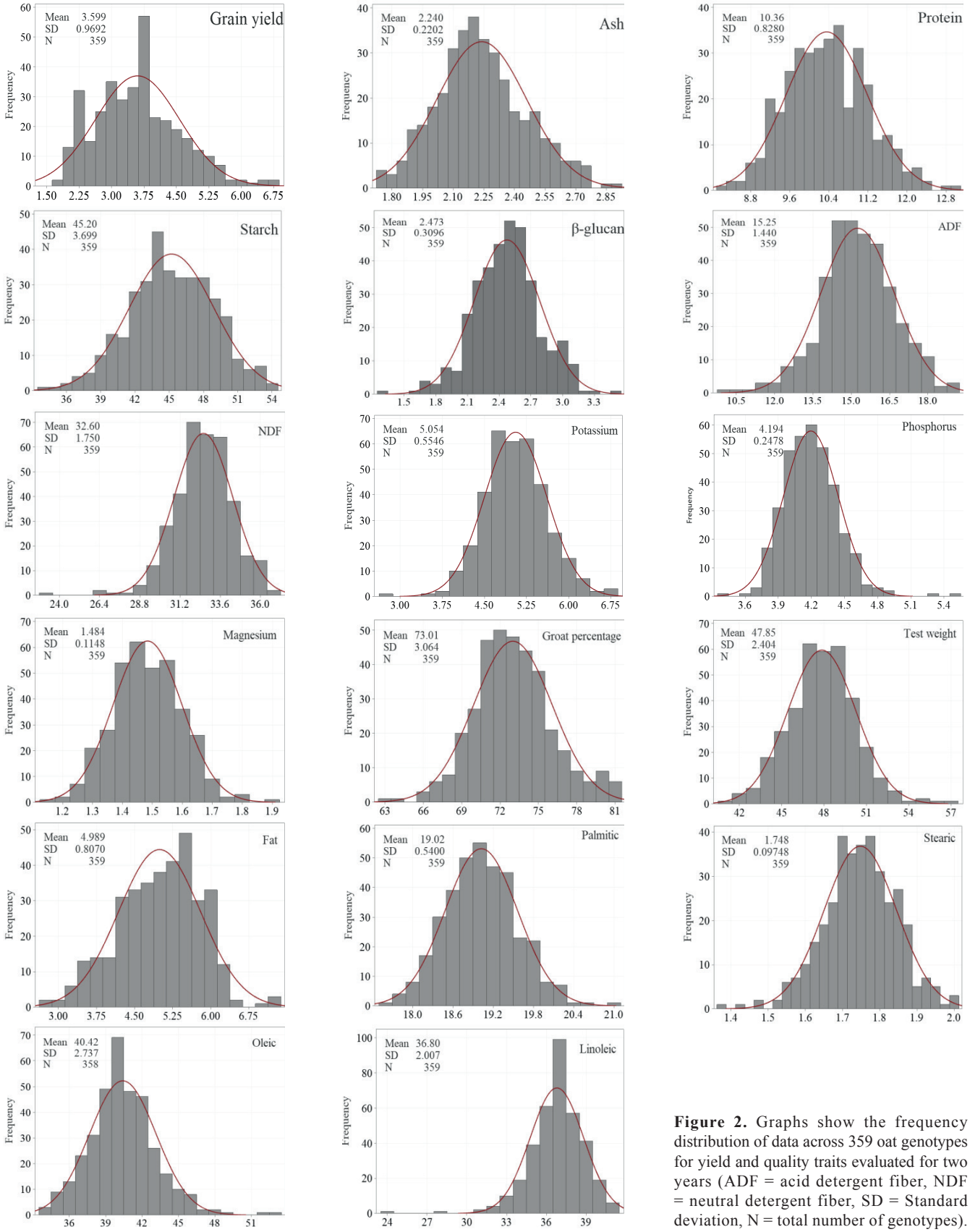

Figure 2. Graphs show the frequency distribution of data across 359 oat genotypes for yield and quality traits evaluated for two years (ADF = acid detergent fiber, NDF = neutral detergent fiber, SD = Standard deviation, N = total number of genotypes).

Doehlert et al. (2006) reported that a positive relationship between groat percentage and test weight. Previous studies have reported that the groat percentage of oat genotypes range from 56.30 to 81.1% (Buerstmayr et al., 2007; Erbaş and Mut, 2013; Mut et al., 2018).

The mean test weight in oat genotypes was found as 47.85 kg hL^{-1} and the minimum and maximum values ranged between 41.35 (G65) kg hL^{-1} and 56.75 (G220) kg hL^{-1} (Table 2). G220, G186, G59, G41, G185, G180, G19, G148 and G353 numbered genotypes were higher than 53.00 kg hL^{-1} test weight, respectively. The test weight of the first year (48.45 kg hL^{-1}) was higher than the second year (47.23 kg hL^{-1}) in the genotypes, respectively (Fig. 1). It was thought that the test weight was lower in the second year because of the higher temperature and the less rainfall. Test weight is a good indication of flour yield and is use the determination of damaged grains. It is generally enounced as kilograms per hectolitre. Test weight designates the quality of oat grains, thus designate market price of oat. Since greater test weights indicate less hull ratios, breeders generally try to select the genotypes with high test weights (Doehlert, 2002). In previous studies on oat, a wide range of test weights has been reported: 34.5-51.0 kg hL^{-1} (Erbaş & Mut, 2013), 41.5-52.3 kg hL^{-1} (Mut et al., 2016b) and 40.8-46.7 kg hL^{-1} (Mut et al., 2018).

In this study, the fat content, linolenic, oleic, palmitic and stearic acid contents of oat genotypes varied from 2.71 (G226) and 7.16% (G107), 23.63 (G220) and 41.38% (G174), 33.66 (G174) and 52.99% (G219), 17.50 (G14) and 20.93% (G132), 1.37 (G46) and 2.00% (G136), respectively (Table 2). The highest fat content (>7) was determined in the G107, G196 and G346 genotypes, while the lowest fat content (<3%) was determined in the G95, G226, G228 genotypes. While the fat content and oleic acid content were higher in the first year, linolenic, palmitic and stearic acid contents were higher in the second year (Fig. 1). The fat content of oat depends on genetic and environmental factors. Saastamoinen et al. (1989) reported that low growth temperature in oat lines and cultivars can increase the fat synthesis and most of the variation in fat content can be explained by average temperature during the growth period. Welch (1995) reported that environmental conditions might influence the fatty acid composition of oats. In the present study, the temperature of the experimental area was lower in the first year than the second year and values were measured as 9.7 °C and 11.8 °C, respectively. Martinez et al. (2010) reported that oat genotypes, fat content were reported between 3.1 to 11.6%. Oat has quite high nutritional values, because of fatty acid composition of the fat. Breeders generally prefer low-fat ratio genotypes for oats to be used in human nutrition (Mut et al., 2018).

Histograms were constructed to show the distribution of the investigated traits across oat genotypes (Fig. 2). In the present study, most of the genotypes had ash content in the range of 2.10-2.25%, protein content in the range of 10.4-10.8%, starch content in the range of 43.0-45.0%, β-glucan content in the range of 2.4-2.7%, ADF content in the range of 14.0-15.5%, NDF content in the range of 31.8-34.2%, K content in the range of 4.50-5.5 g kg^{-1}, P content in the range of 4.1-4.3 g kg^{-1}, Mg content in the range of 1.4-1.5 g kg^{-1}, groat percentage in the range of 71.5-73.5%. Also, test weight in the range of 46.5-49.5 kg hL^{-1}, fat content in the range of 5.25-5.75%, palmitic (16:0) acid contents in the range of 18.6-19.2%, stearic (18:0) acid content in the range of 1.65-1.75%, oleic (18:1) acid content in the range of 39.0-41.0% and linoleic (18:2) acid content in the range of 36.5-37.7%. To define the smallest variables that can explain the maximum ratio of the total variation is the essential purpose of Principle Component Analysis (PCA). The PCA was applied to identify the traits which were the main source of the variability and to explain the genetic diversity among genotypes. The cumulative percentages of the eigenvalues, variations percentage and load coefficient of first six components for quality traits through the application of PCA based on the correlation matrix were also showed Table 3.

Table 3. PCA value, eigenvalues and % variance values for traits of oat genotypes.

Variable	PC1	PC2	PC3	PC4	PC5	PC6
Grain yield	0.055	0.053	0.131	-0.068	-0.665	-0.562
Ash	0.398	-0.078	-0.157	0.101	0.167	0.034
Protein	0.039	0.279	-0.434	0.221	-0.037	-0.173
Starch	-0.291	0.242	0.019	-0.370	-0.206	0.122
β-glucan	-0.188	0.040	0.024	0.459	-0.427	0.540
Acid detergent fiber	0.246	-0.388	0.046	0.015	-0.066	0.179
Neutral detergent fiber	0.085	-0.452	-0.035	0.153	-0.075	0.116
Potassium	-0.038	-0.091	-0.518	0.036	-0.013	-0.030
Phosphorus	0.241	0.345	-0.154	0.045	-0.252	0.148
Magnesium	0.315	0.220	-0.280	0.122	-0.192	0.101
Groat percentage	-0.223	0.260	0.027	0.289	0.180	0.157
Test weight	0.335	0.217	0.183	-0.179	-0.011	0.163
Fat	-0.186	0.217	0.064	0.444	0.307	-0.369
Palmitic (16:0)	0.067	-0.032	-0.494	-0.295	0.127	-0.031
Stearic (18:0)	-0.186	0.266	-0.034	-0.378	0.127	0.281
Oleic (18:1)	0.342	0.218	0.276	0.067	0.105	0.010
Linoleic (18:2)	-0.372	-0.204	-0.186	-0.006	-0.148	-0.004
Eigenvalue	4.532	3.582	2.845	1.287	1.110	0.936
Variance (%)	26.7	21.1	16.7	7.5	6.5	5.5

PC1 showed 26.7% variability with eigenvalue 4.532 and PC2 showed 21.1% variability with eigenvalue 3.582. Sum of PC 1 and PC 2 explained 47.8% of the total variance (Fig. 3). PC 3, PC 4, PC 6 and PC 6 values were found as 16.7, 7.5, 6.5 and 5.5, respectively. The first six principal components accounted for 84% of the total variation (Table 3). Fig. 3 vector was drawn from the biplot origin to each of the traits. The vectors for PC, P, GY, Mg, FC and 18:1 traits extended along the same direction. The 18:2 and K which were negatively correlated with these parameters had vectors extending along the same direction. While the βG, SC, GP, TW and 18:0 vectors extended along the same direction, ADF, NDF, 16:0 and AC vectors extended along in the opposite direction with these parameters (Fig. 3). Oat genotypes with the high SC, GP, TW, BG and 18:0 were located in the upper left of the quadrant of the biplot while oat genotypes with the high PC, GY, FC, TW, BG and 18:0 were located in the upper right of the quadrant of the biplot.

If the objective is to increase the traits of GY, PC, SC, GP, TW, and FC of genotypes that are in the upper quadrants of biplots, are more important than the ones located in the lower quadrants of biplots. Lannucci et al. (2011) screened 109 oat genotypes in the 2008-2009 and 2009-2010 growing seasons. The PCA indicated that the first six principal components contributed 87% of the total variability among the genotypes. Doehlert et al. (2001) reported that there was a high relationship between yield and groat percentage. Buerstmayr et al. (2007) that there was a high relationship between yield

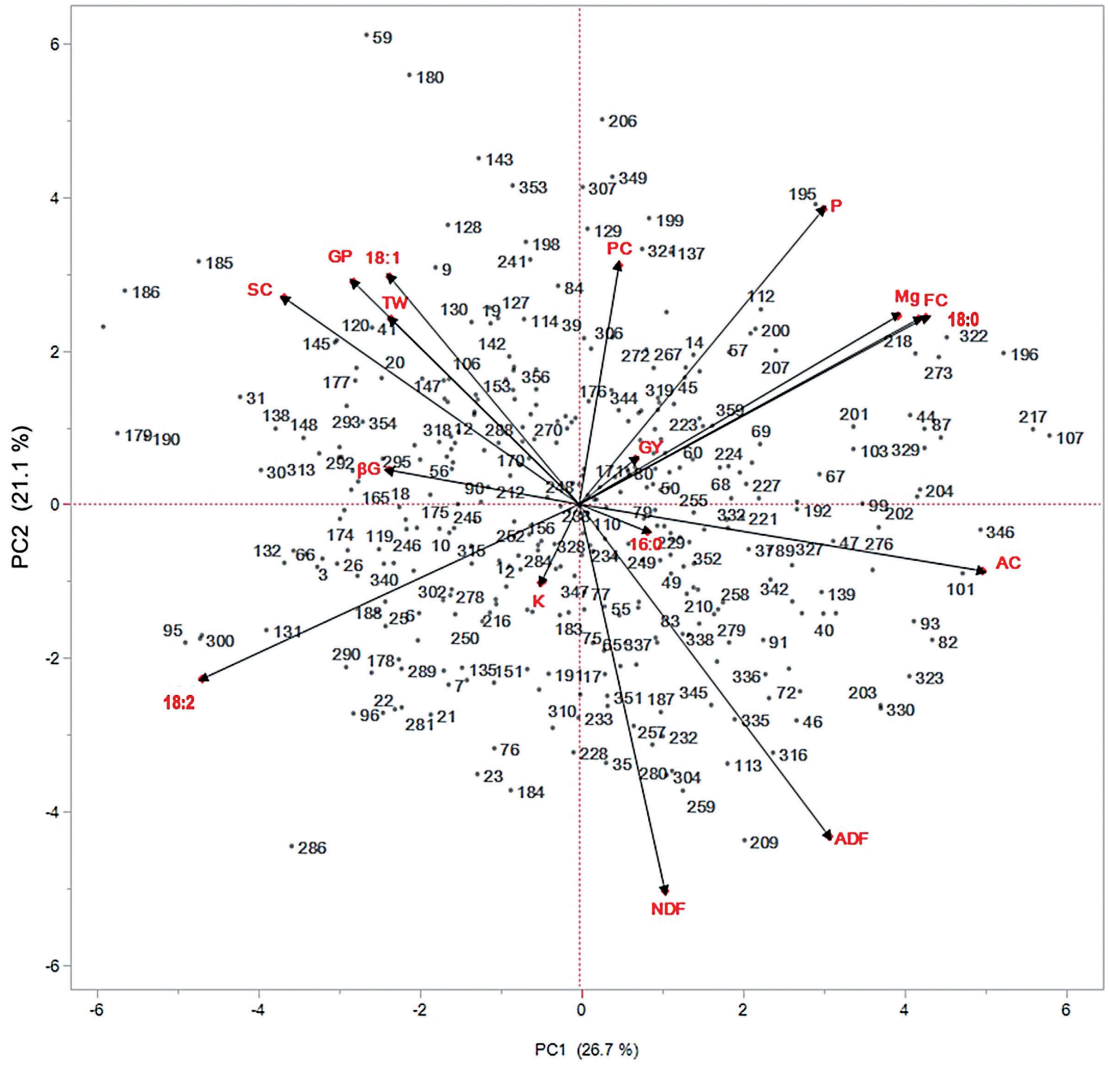

Figure 3. The grouping of the studied features by biplot analysis method and the relation of genotypes with the investigated traits (GY = grain yield, AC = ash content, PC = protein content, SC = starch content, βG = beta-glucan content, ADF= acid detergent fiber, NDF = neutral detergent fiber, K = potassium, P = phosphorus, Mg = magnesium, GP = groat percent , TW = test weight, FC = fat content, 16:0 = palmitic acid, 18:0 = stearic acid, 18:1 = oleic acid, 18:2 = linolenic acid).

and thousand kernel weight, test weight, groat percentage. Peterson et al. (2005) and reported that there was a high relationship between groat percentage and test weight. Mut et al. (2016b) reported that there was positively correlation between groat percentage and test weight. In addition, they reported that there was positively correlation between grain yield and thousand kernel weights. Similar results were reported by Doehlert & McMullen (2000). Mut et al. (2016a) determined that the oleic acid content increased and the linoleic acid content decreased as the fat content increased in the grain. Peterson et al. (2005) determined relationships between oat grain traits and some chemical traits concluding that knowledge of some relationships between grain traits could help breeders to optimize some traits at the same time.

Conclusions

The results of this study indicate that grain yield and quality traits of many oat cultivars and pure lines exhibit significant differences, thereby showing the importance of selecting suitable genotypes for specific end-uses. The genotype-trait biplot is an excellent tool used to visualize correlations between yield and quality traits and is recommended for the reliable identification of oat lines able to present high grain yield and quality traits. For all traits, many of lines had higher values than standard cultivars. Also, the results indicate which genotypes that is hopeful for use in breeding programs.

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