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Agronomical Screening of OGLE1040/TAM O-301 Oat Genetic Mapping Population

(Penyaringan Agronomi Pemetaan Populasi Genetik Oat OGLE1040/TAM O-301)

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ABSTRACT

In recent years, mapping populations have provided improvements for oat genomic researches. A two-year study was conducted in East-Mediterranean conditions using Ogle1040/TAM O-301 pure-line mapping population including 136 individuals and parents. Stem diameter (SD), plant height (PH), panicle length (PL), vegetative period (VP), grain filling period (GFP), days to maturity (DM), grain number per panicle (GNP), grain weight per panicle (GWP), thousand kernel weight (TKW) and grain yield (GY) were investigated in 2014 and 2015 cropping seasons in Kahramanmaras. All the investigated traits were significantly different for years ($p<0.01$*) and genotypes (*$p<0.05$ *and* $p<0.01$*) except SD and GNP. Genotype x year (G x Y) interaction was significant for PL, VP, GFP, DM and GY (*$p<0.01$*). In the first year, the average GY per row was 227.6 g, whilst it was 184.5 g in the second year. In terms of GY, the parents Ogle 1040 and TAM O-301 showed lower performance (154.5 and 111.5 g/row, respectively) compared to Ogle1040/TAM O-301 (OT) population average (206 g/row). OT129 genotype had the highest GY with 360 g/row. Principal component (PC) factor analysis yielded 10 PC explaining 100% of total variance in the data and the chi-square values of the PC1 to PC9 were found significant. According to PC biplot analysis, genotypes with high GY, TKW, GNP, GWP, PL and GFP were located throughout the right quadrants whereas the genotypes with high VP, DM and SD were located throughout the left quadrants. The relationships between PH × GY, GWP × GNP and GWP × TKW were positive and significant.*

Keywords: Agronomic traits; biplot; mapping population; oat

ABSTRAK

Dalam tahun-tahun kebelakangan ini, pemetaan populasi telah memberikan penambahbaikan bagi penyelidikan genom oat. Kajian dua tahun telah dijalankan di kawasan Timur Mediterranean menggunakan pemetaan populasi Ogle1040/TAM O-301 termasuk 136 individu dan induk. Diameter batang (SD), tinggi tumbuhan (PH), panjang penikel (PL), tempoh vegetatif (VP), tempoh pengisian bijirin (GFP), hari kepada kematangan (DM), bilangan bijirin setiap panikel (GNP), berat bijirin setiap panikel (GWP), berat seribu kernel (TKW) dan hasil bijirin (GY) telah dikaji pada musim penanaman tahun 2014 dan 2015 di Kahramanmaras. Semua trait yang dikaji adalah berbeza secara signifikan daripada segi tahun ($p<0.01$*) dan genotip (*$p<0.05$ *dan* $p<0.01$*) kecuali SD dan GNP. Interaksi genotip x tahun (G x Y) adalah signifikan bagi PL, VP, GFP, DM dan GY (*$p<0.01$*). Pada tahun pertama, purata GY setiap baris adalah 227.6 g, manakala 184.5 g pada tahun kedua. Daripada segi GY, induk Ogle 1040 dan TAM O-301 menunjukkan prestasi yang lebih rendah (masing-masing 154.5 dan 111.5 g) berbanding purata penduduk Ogle1040/TAM O-301 (OT) (206 g/row). Genotip OT129 mempunyai GY tertinggi dengan 360 g/baris. Analisis faktor komponen utama (PC) menghasilkan 10 PC menerangkan 100% daripada jumlah varians dalam data dan nilai khi kuasa dua PC1 hingga PC9 didapati signifikan. Menurut analisis biplot PC, genotip dengan GY tinggi, TKW, GNP, GWP, PL dan GFP terletak di seluruh kuadran kanan manakala genotip yang mempunyai VP, DM dan SD yang tinggi terletak di sepanjang kuadran kiri. Hubungan antara PH × GY, GWP × GNP dan GWP × TKW adalah positif dan signifikan.*

Kata kunci: Biplot; oat; pemetaan populasi; trait agronomi

INTRODUCTION

Oat (*Avena* spp.) is a cereal crop used for human food and livestock feed worldwide (Achleitner et al. 2008; Peterson et al. 2005). Cultivated oats, *A. sativa* L. and *A. byzantina* Coch., are hexaploid (2n = 6x = 42) and have been broadly adapted to marginal environments with cool-wet, low fertility soils and low rainfall climates (Buerstmayr et al. 2007; Hoffman 1995; Ren et al. 2007). In recent years, health benefit claims of oat grains and products with high fiber and antioxidant content have made oat popular for human consumption (Hoffmann 1995). However, less effort has been given to oat research compared to other cereals such as wheat, rice and maize. One of the important reasons for the limitation of oat production is lack of well adapted cultivars for the different environments. Oat breeders put high effort to develop cultivars with the superior traits such as high yielding, non-lodging and non-shattering cultivars with high quality (high protein and β-glucan content).

Genetic and environmental factors affect all these morpho-agronomical traits (Doehlert et al. 2001; Peterson et al. 2005). The important developments have been made in biotechnology and the model mapping populations have been developed to investigate quantitative trait loci (QTLs) in the plant genomes. Ogle1040/TAM O-301 is one of the model mapping populations in oat, developed by Portyanko et al. (2001). The pure-line population consists of 136 individuals and parents, developed as a genetic mapping population and provided very early linkage maps for oats. There have been many studies with Ogle1040/TAM O-301 genetic mapping population so far and high resolution linkage maps were constructed with high marker coverage (Jackson et al. 2010; Oliver et al. 2011a; Portyanko et al. 2001). Health claims of oat in the human diet including high fat and protein content, cholesterol lowering and hearth healthy soluble fiber (Braaten et al. 1994; Eggum et al. 1989; Oliver et al. 2011b) had increased the demand for the oat products.

Even though Turkey is a center of origin for oat and there are plenty of landraces in Turkey, limited number of cultivars has been developed from cross breeding. Most of the commercial cultivars are developed by selection and introduction methods. This study has been the first study on oat genetic mapping population in Turkey. It was aimed to determine agronomic performance of Ogle1040/TAM O-301 genetic mapping population under East-Mediterranean conditions for two years.

Materials and Methods

The field trials were carried out in 2014 and 2015 cropping years under Kahramanmaraş conditions (East-Mediterranean region of Turkey) located between 37° 53¹ N, 36° 58¹ E. Ogle1040/TAM O-301 genetic mapping population including 136 individuals and parents developed at USDA ARS Aberdeen, Idaho USA (Portyanko et al. 2001) were used as plant materials.

The seeds of parents and the mapping population were planted as two-rows in 1 m length and the experiment was arranged in an augmented experimental design with six replications. Four control genotypes namely Kırklar, Kahraman, Checota and Faikbey were used in this study. Fertilizers were applied as 60 kg/ha N and 60 kg/ha P_2O_5 at planting and, topdressing was applied as 80 kg/ha N at tillering. Herbicide (Tribenuron-Methyl 75%) was used for weed control and there was no pesticide application.

Stem diameter (SD), plant height (PH), panicle length (PL), vegetative period (VP) (calculated as the total days between planting and 75% flowering of the plants), grain filling period (GFP) (determined as the total days between flowering to maturity), days to maturity (DM), grain number per panicle (GNP), grain weight per panicle (GWP), thousand kernel weight (TKW) and grain yield (GY) were investigated for two consecutive years as described previously (Dumlupinar et al. 2012a, 2011).

The data over the two years were analysed by the augmented design using JMP software. Biplot of principal component, eigenvalues and correlation analysis were performed using JMP software. Histograms of MS Excel software were used to visualise the mean values of the 136 individuals and the parents. The z-scores were calculated by the formula shown (Iverson 2011) and converted to P-values by a web-based application (https://goodcalculators.com/p-value-calculator/?pinpt=-7&tpval=2).

$$z-score=\frac{x-\mu}{\sigma}$$

where z is the standard score; x is the mean of the parents in the data set; μ is the mean of all values in the data set; and σ is the standard deviation of a sample.

TABLE 1. The mean squares and F values of genotype, year and GY interaction for yield components subset of 138 lines and two years

Source of Variation	SD	PH	PL	VP	GFP	DM	GNP	GWP	TKW	GY
					Mean Squares					
Genotype (G)	2.09	321.67	24.29	85.943	24.76	69.28	2062.89	2.82	68.03	5720.0
Year (Y)	152.13	5942.0	209.2	92752.5	5138.2	54229.2	29072.7	21.60	1950.7	151479.1
GY Interaction	1.0007	1.3931	20.24	76.241	24.03	56.65	177.31	0.048	16.68	4214.9
					F Values					
Genotype (G)	0.53^{ns}	4.51*	15.53**	11.72**	14.25**	13.28**	1.64^{ns}	8.57**	2.88*	4.85**
Year (Y)	38.49**	83.34**	133.8**	12648**	2956**	10400**	23.15**	65.64**	82.59**	128.6**
GY Interaction	0.25^{ns}	1.95^{ns}	12.94**	10.39**	13.83**	10.86**	0.141^{ns}	0.147^{ns}	0.84^{ns}	3.57**
CV (%)	27.9	8.7	4.7	1.5	3.4	1.1	27.4	17.5	14.4	16.6

SD: stem diameter (mm), PH: plant height (cm), PL: panicle length (cm), VP: vegetative period (days), GFP: grain filling period (days), DM: days to maturity (days), GNP: grain number per panicle (grains), GWP: grain weight per panicle (g), TKW: thousand kernel weight (g), GY: grain yield (g/row), CV: Coefficient of variation
Significance: ** P < 0.01, * P < 0.05, and ns: not significant

Results

Investigated traits

From the data collected during the two years, all traits were significantly different for years ($p<0.01$). Genotypes were significantly varied for all traits ($p<0.05$ and $p<0.01$) except SD and GNP. Genotype x Year (G x Y) interaction was significant for PL, VP, GFP, DM and GY ($p<0.01$) (Table 1). Histograms were made to show the distribution of the data across oat genotypes for each investigated traits (Figure 1).

In an ideal QTL mapping study, a normal distribution of phenotypes is expected. The deviations from the normal distribution may affect the accuracy of QTL detection and lead to false QTLs. Histograms were made to evaluate the distribution of phenotypes for later QTL mapping studies. The standard deviations were 0.88, 12.46, 3.53, 5.44, 3.58, 50.1, 29.1, 1.14, 5.17 and 51.84 for SD, PH, PL, VP, GFP, DM, GNP, GWP, TKW and GY, respectively. Significant differences were measured for the parents in PH, PL, VP, GNP, GWP, TKW and GY. A significant normal distribution was obtained from GY with 0.0069 P-value (Figure 1).

Stem diameter was found variable for years, while was not significant for genotypes and GY Interaction. Ogle 1040 and TAM O-301 had very close values (6.59 and 6.22 mm) of stem diameter. The highest SD value was obtained from OT7 with 9.8 mm and the lowest from OT129 with 3.4 mm. In the first year, the mean SD of the genotypes was 6.16 mm, while it was 7.54 mm in the second year (Figure 1A).

A measure of PH was different for years ($p<0.01$) and genotypes ($p<0.05$), while not for GY interaction. Ogle 1040 had a 98.5 cm PH, while TAM O-301 had an 84.25 cm PH. The average PH was 95.93 and the tallest one was OT9 with 119.4 cm and the shortest one was OT133 with 46 cm PH. In the first year experiment, average PH was 100.2 cm and in the second year was 91.67 cm (Figure 1B).

Panicle length was significantly different for years, genotypes and GY interaction. In the first year, PL of the genotypes was 27.22 cm, while it was 25.5 cm in the second year. Ogle 1040 had 25.7 cm PL, while TAM O-301 had 23.9 cm PL and the average PL was 26.36 cm. The highest PL was obtained from OT67 with 34.8 cm PL and the shortest PL was obtained from OT44 with 14.6 cm (Figure 1C).

Vegetative period of the genotypes was varied between years, genotypes and GY interaction ($p<0.01$) (Table 1). The average VP of the first year experiment was 187 days, while it was 153 days for the second year. The parents had different VP values and TAM O-301 was earlier than Ogle 1040 (170 and 176 days, respectively). The earliest genotype was OT133 with 160 days and the latest one was OT44 with 188 days. The average VP was 170 days for the OT mapping population (Figure 1D).

Grain filling period significantly varied for genotypes, years and GY interaction ($p<0.01$) (Table 1). In the first year, the average GFP of the genotypes was 33 days, while 41 days in the second year. Ogle 1040 and TAM O-301 had close GFP with 32 and 35 days, respectively, while the average GFP of the OT mapping population was 37 days. The earliest genotype was OT84 with 29 days, while OT69 was the latest genotype with 47 days (Figure 1E).

Days to maturity was found significant among genotypes, years and GY interaction ($p<0.01$). In the first experimental year, the average DM was 221 days, while it was 195 days in the second year. The DM values of the parents were 208 days for Ogle 1040 and 205 days for TAM O-301 and the average DM of the OT mapping population was 208 days. OT133 genotype was the earliest and the OT17 genotype was the latest one (192 and 225 days, respectively) (Figure 1F).

Grain number per panicle of the genotypes significantly varied for years ($p<0.01$), while it was non-significant for genotypes and GY interaction (Table 1). In the first year, the average GNP was 123 grains, while it was 103 grains in the second year. Ogle 1040 had 85 GNP, while TAM O-301 had 140 GNP and the average GNP value of the population was 112.5 grains. The lowest GNP was obtained from OT75 genotype with 65 grains and the highest GNP was obtained from OT80 with 184 grains (Figure 1G).

Grain weight per panicle was found significantly variable according to the years and genotypes ($p<0.01$), but not for GY interaction (Table 1). In the first and second years, the average GWP were 3.51 g and 2.96 g, respectively. TAM O-301 had 4.4 g GWP which was more than the average of the population (3.23 g), while Ogle 1040 had 2.7 g GWP. The lowest GWP was 1.4 g obtained from OT79 and the highest was 6.3 g obtained from OT3 (Figure 1H).

Thousand kernel weight (TKW) significantly varied among genotypes ($p<0.05$) and between years ($p<0.01$), nevertheless, GY interaction was not significant (Table 1). In the first and second years of the experiment, the average TKW were 36 g and 30.9 g, respectively. The parents had higher TKW (Ogle 1040 and TAM O-301, 34.6 and 39.4, respectively) compared to the mean of the OT population (33.4 g). The highest TKW was obtained from OT30 with 44.1 g, while the lowest was obtained from OT107 with 21.5 g (Figure 1I).

Grain yield was found significant for years, genotypes and GY interaction ($p<0.01$) (Table 1). In the first experimental year, the average GY was 227.6 g/row, while the value was 184.5 g in the second year. In terms of GY, the parents Ogle 1040 and TAM O-301 showed lower performance (154.5 and 111.5 g/row, respectively) compared to OT population average (206 g/row). OT129 genotype had the highest GY with 360 g/row, while OT20 genotype had the lowest GY with 105.5 g /row (Figure 1J).

Relationship among traits

In order to determine the relationships among traits, biplot analysis (Figure 2) and correlation coefficients were performed (Table 2). According to the biplot of principal components 1 and 2 for OT mapping population, Ogle 1040 was placed in the left quadrant, while TAM O-301 in the right quadrant (Figure 2). OT1, OT6, OT14, OT17, OT18, OT26, OT37, OT39, OT40, OT41, OT46, OT51, OT54, OT55, OT61, OT62, OT63, OT69, OT72, OT74, OT75, OT76,

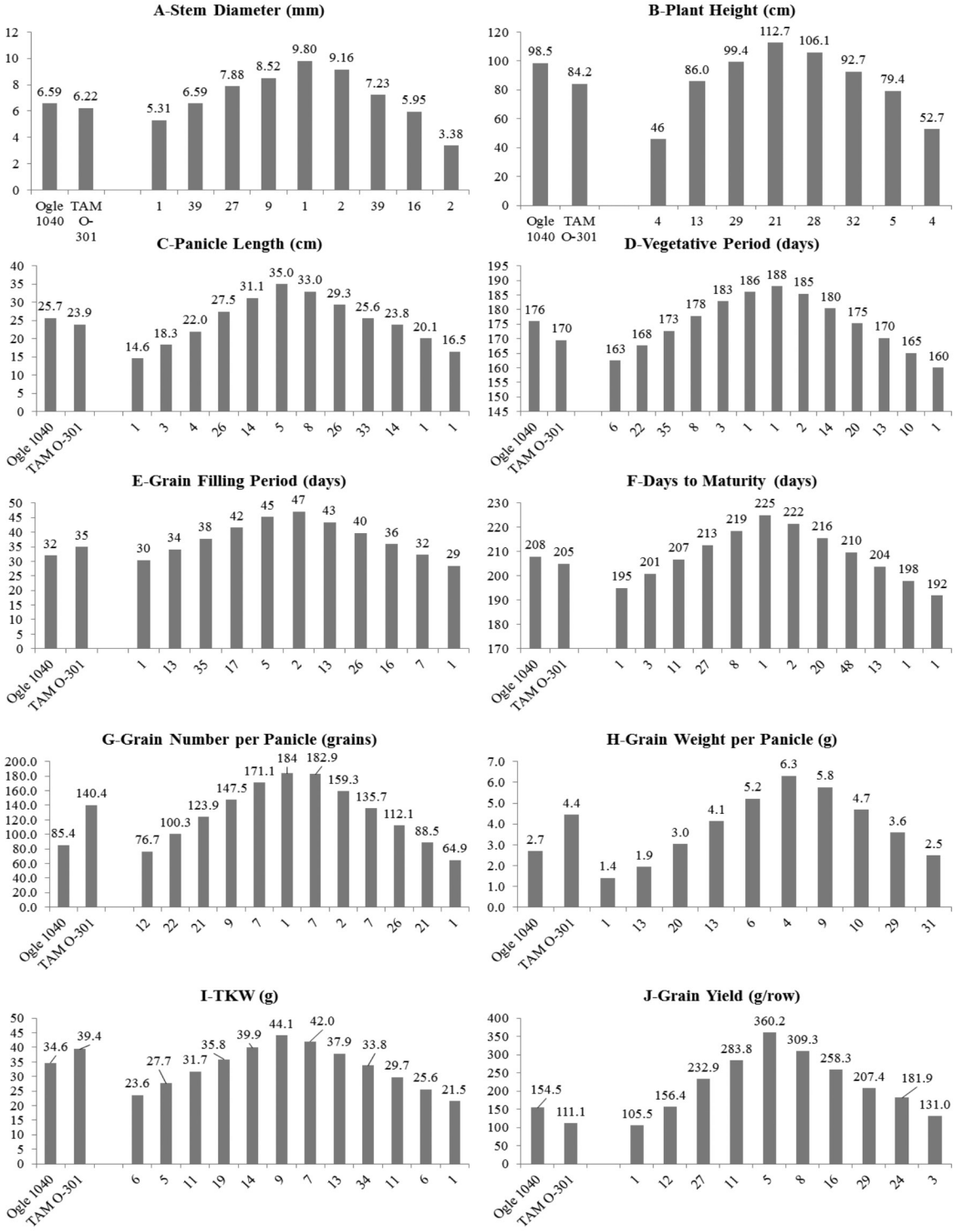

FIGURE 1. The histogram shows the distribution of data across 138 oat genotypes for agronomic traits evaluated for two years

OT80, OT85, OT94, OT122, OT124 and OT131 were some of the genotypes in the right quadrants with PL, PH, GFP, GNP, GWP, TKW and GY. On the other hand, OT5, OT21, OT25, OT27, OT42, OT44, OT47, OT48, OT73, OT77, OT86, OT89, OT97, OT98, OT103, OT107, OT108, OT111, OT114, OT118, OT121, OT129, OT130, OT133, OT135 and OT136 were some of the genotypes in the left quadrants with the traits for VP, DM and SD. Oat genotypes with high GY, TKW, GNP and GWP, long PL and long GFP were located throughout the right quadrants of the biplot. On the other hand, the genotypes with longer VP, longer DM and thick stems have been located throughout the left quadrants of the biplot (Figure 2).

In addition, the upper right quarter of the biplot (positive PC1 and positive PC2) was mainly related with PL, PH, GFP, GNP, GWP and TKW, the lower right quarter

TABLE 2. Pearson correlation analysis of investigated traits

	SD	PH	PL	VP	GFP	DM	GNP	GWP	TKW	GY
SD	--									
PH	0.0962	--								
PL	0.2347**	0.5858**	--							
VP	0.1375	-0.1778*	0.0522	--						
GFP	0.1554	0.1181	0.0743	-0.3899**	--					
DM	0.2466**	-0.1175	0.0957	0.8314**	0.1836*	--				
GNP	-0.1138	0.1882*	0.0567	-0.1020	-0.1335	-0.1897*	--			
GWP	-0.0037	0.2257**	0.0814	-0.0581	-0.0285	-0.0830	0.5989**	--		
TKW	-0.0491	0.1881*	0.0172	-0.0498	0.0518	-0.0251	0.0259	0.4634**	--	
GY	-0.0998	0.1551*	-0.0006	-0.1103	-0.0176	-0.1325	0.0256	0.0924	-0.0156	--

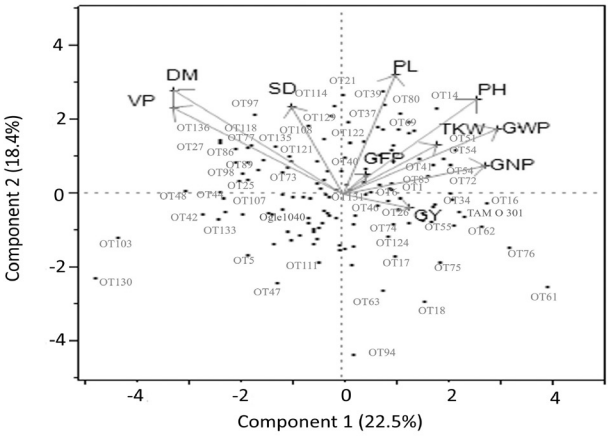

FIGURE 2. Biplot presentation of principal component analysis 1 and 2

of the biplot (positive PC1 and negative PC2) was mainly associated with GY, the upper left quarter of the biplot (negative PC1 and positive PC2) was mainly associated with VP, DM and SD, and there was no association with the investigated traits in the lower left quarter of the biplot (negative PC1 and negative PC2).

Relationships between SD × PL, SD × DM, PH × PL, PH × GNP, PH × GWP, PH × TKW and PH × GY were positive and significant (r= 0.2347** and r= 0.2466**, r= 0.5858**, r= 0.1882*, r= 0.2257** r= 0.1881* and r= 0.1551*, respectively), while PH × VP was negatively correlated (r= -0.1778*). The relationship between VP × GFP was significantly negative (r= -0.3899**), while VP × DM was significantly positive (r=.0.8314**). Days to maturity (DM) was highly correlated with GFP (r=0.1836*), while negatively significantly correlated with GNP (r= -0.1897*). The relationships between GWP × GNP and GWP × TKW were positive and significant (r= 0.5989** and r= 0.4634**).

DISCUSSION

All the traits investigated in Ogle 1040/TAM O-301 mapping population had a normal distribution which is very important for QTL analysis as phenotyping. The stem diameter of the OT mapping population was widely changed between 3.38 and 9.8 mm and the genotypes had mostly 5.95 to 7.88 mm SD. Ahmad et al. (2008) and Dumlupinar et al. (2012a) similarly reported variations for SD among the genotypes and years. In the OT mapping population, there were rather short (around 46 cm) and tall plants (around 112 cm). The plant height values of the population mostly ranged from 92.7 to 112 cm. Baltenberger and Frey (1987), Dumlupinar et al. (2012a) and Matiello et al. (1999) also reported genetic influence for PH. Many reports in the literature indicated that there were high variations among cultivars and years (Ahmad et al. 2008; Buerstmayr et al. 2007; Dumlupinar et al. 2012a; Gautam et al. 2006; Ma et al. 2006; Nawaz et al. 2004; Zaman et al. 2006). Panicle length was found variable for OT mapping population. The panicle length distribution of the population mostly ranked in 23 to 31 cm. Dumlupinar et al. (2012a) and Yanming et al. (2006) also reported genetic influence for PL and high variation among the oat genotypes. The phenological traits including VP, GFP and DM significantly varied for genotype, year and GxY interaction. The OT population had a wide range of VP (160 to 188 days), GFP (29 to 47 days) and DM (192 to 225 days). Similarly, Buerstmayr et al. (2007), Dumlupinar et

al. (2012a), Locatelli et al. (2008), Matiello et al. (1999) and Nawaz et al. (2004) determined genetic influence for VP and earliness. It was also indicated that VP was influenced by environmental conditions (Gautam et al. 2006). Grain filling period was influenced by genotype (Dumlupinar et al. 2012a; Peltonen-Sainio & Rajala 2007; Wych et al. 1982). Variation among the genotypes for the DM was due to influence of genetics (Nawaz et al. 2004). Grain numbers and weights of the oat genotypes also widely changed (64.9 to 184 grains and 1.4 to 6.3 g, respectively). In previous work, Dumlupinar et al. (2012a) reported genetic and environmental influence for GNP and GWP of oat landraces which are in agreement with our findings. Thousand kernel weight (TKW) influenced by genetic and environmental conditions is one of the most important criteria for quality traits and there was an important variation (21.5 to 44.1 g) in OT population for TKW. Similar with our findings, Buerstmayr et al. (2007), Dumlupinar et al. (2011) and Yanming et al. (2006) indicated significant genotypic influence for TKW.

There was significant variation for year and G × Y interaction. Grain yields of some OT population individuals were higher than their parents. The grain yield of the OT mapping population varied between 105.5 and 360.2 g/row and most of the genotypes were in the range of 181 to 258 g/row. Previously, Baltenberger and Frey (1987) had indicated genetic influence for GY where Robertson and Frey (1987) determined GY as important selection criteria whereas Doehlert et al. (2001) reported higher environmental influence than genetic influence. In addition, Ahmad et al. (2008), Buerstmayr et al. (2007), Gautam et al. (2006) and Nawaz et al. (2004), also reported that GY was influenced by genetics, while Dumlupinar et al. (2012a) and Tamn (2003) indicated both genetic and environmental influences on GY for oat genotypes.

According to the biplot of principal component analysis, PL, PH, GFP, GNP, GWP, TKW and GY traits fell into the two right quadrants of the biplot and could be more promising than VP, DM and SD that fell into the left quadrants. Previous work by Peterson et al. (2005) indicated that biplots can be used to select genotypes that may have favorable combinations of traits for use in breeding programs. The average PH of the OT mapping population was 95.93 cm and GY was significantly correlated with only PH (r=0.1551*). The longer plant heights especially in oat causes grain yield losses due to lodging (Buerstmayr et al. 2007; Dumlupinar et al. 2012b). The OT mapping population had moderate plant heights and correlated positively with grain yield. Krishna et al. (2014) also reported positive correlation between GY and PH. There were also positive and significant correlations between PH x PL (r=0.5858**), GNP × GWP (r=0.5989**) and, GWP × TKW (0.4634**) and grain weight had the most important role to determine TKW. In previous works, positive correlations were found between PH and PL (Krishna et al. 2014), GWP and GNP and, GWP and TKW (Dumlupinar et al. 2012b).

Conclusion

In this study, OT mapping population consisting of 136 genotypes and parents were investigated based on some agronomical traits. According to the results, all investigated traits in the study showed a normal distribution along the OT mapping population which is very important in QTL analysis. The GY of parents (Ogle 1040 and TAM O-301) showed lower performance compared to OT population average and the highest GY was obtained from OT129. According to the biplot of PC1 and PC2, Ogle 1040 was placed in the lower left quadrant, while TAM O-301 in the lower right quadrant. The traits PL, PH, GFP, GNP, GWP and TKW were mainly placed in the upper right quadrant of the biplot, while GY was in the lower right quadrant of the biplot. The traits such as PL, PH, GFP, GNP, GWP and GY might be assumed as positive selection criteria for oat under East-Mediterranean and the genotypes OT30, OT84, OT67, OT129 and OT133 the most promising ones.

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