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EVALUATION OF YIELD AND SOME QUALITY CHARACTERS OF WINTER BARLEY (*Hordeum vulgare* L.) GENOTYPES USING BILOT ANALYSIS

SUMMARY

In this study, it was used 19 winter barley advanced lines which are selected from regional yield trials and 5 cultivars (TARM-92, Aydanhanım, Sladoran, Karatay-94 and Kalaycı-97) in order to determine grain yield and some quality traits under ecological condition of Diyarbakır. The experiment was conducted in 2004-2005 growing seasons in Diyarbakır under rainfed conditions, with randomized complete block design with 3 replications. Grain yield and different quality traits were considered: test weight (HLT), thousand kernel weight (TKW), grain protein content (PC), starch value (STR) and 2.5-2.8 mm sieve ratio (SV). According to the results; the highest grain yield obtained from G16 (5269 kg ha⁻¹), G17 (4930 kg ha⁻¹) and Karatay-94 (4868 kg ha⁻¹) genotypes, the lowest grain yield obtained from G6 (2625 kg ha⁻¹), G21 (3186 kg ha⁻¹) and G11 (3428 kg ha⁻¹) genotypes. According to biplot analysis that based on the visual correlation between traits, HLT, SV, GY and STR were involved in the same group, while TKW and PC were involved individually in separate groups genotypes located in corner of the polygon, G11 and G21 had highest values or desirable traits for protein content, G8 was the best for TKW while G7, Kalaycı-97 and Sladoran were the best for HLT and SV. The results also showed that genotypes with appropriate combination in terms of examined traits were selected for national winter wheat breeding programs.

Key words: Biplot, grain yield, quality, winter barley.

INTRODUCTION

Barley is classified as a long-day plant, which means that it will flower earlier when exposed to increasing day lengths (Casao et al, 2011). Barley (*Hordeum vulgare* L.), a member of the grass family, is one of the eight founder crops (einkorn wheat, emmer wheat, barley, lentil, pea, chick pea, bitter vetch, and flax) (Kant and Babu 2016). Barley was first domesticated in the Fertile Crescent in the Near East which spans present-day Palestina-Israel, Northern Syria, Southern Turkey, Eastern Irak and Western Iran (Harlan 1979). The total

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area covered by barley is about 2.74 million hectares with total production of 6.7 million tons and the yield of the crop is low with national average of 2.48 t ha^{-1} in Turkey (TMO, 2016). It is the second important cereal crop of Turkey and accounts for about 25% of the total cereal production (Oralet al., 2018).

In Southeastern Anatolia region, the total area covered by barley is about 0.327 million hectares with total production of 1.035 million tons and the yield of the crop is low with regional average of 3.04 t ha^{-1} (Gaputaem, 2013). In Southeastern Anatolia, barley is sown in late autumn, after the occurrence of the first rains in the arid environments. Kılıç et al, (2010) reported that barley has been cultivated for many years and has significant role in dry areas of Eastern Transitional Zone, Turkey and barley grain yield and quality are exposed to different factors varying on a large scale. The Northern part of southern region's climate is sufficiently humid (annual precipitation rate 500 mm) with mild-hard winter weather which enable winter barley to perform well. Because the interaction between environmental stress and barley genotypes has not been sufficiently investigated (Ceccarelli et al. 2010; Alemayehu et al., 2014;), this target should be involved in breeding strategies. Mohammadi et al. (2013) reported that some barley varieties require certain times expose to cold temperatures to initiate flowering, while others initiate flowering without any obligation for vernalization.

Thus, learning more about genetic variation of winter and spring types in barley breeding genotypes is useful for developing and adaptation new varieties for worked environments. The aim of this study was to evaluate the yield performances of various winter barley varieties and advanced lines for the Diyarbakır region in terms of adaptability.

MATERIAL AND METHODS

The study was carried out on the experimental area of GAP International Agricultural Research and Training Center, Turkey, ($37^{\circ}56' \text{ N}$; $40^{\circ}15' \text{ E}$; 599 m altitude) during the growing seasons of 2004 to 2005 (Fig 1).

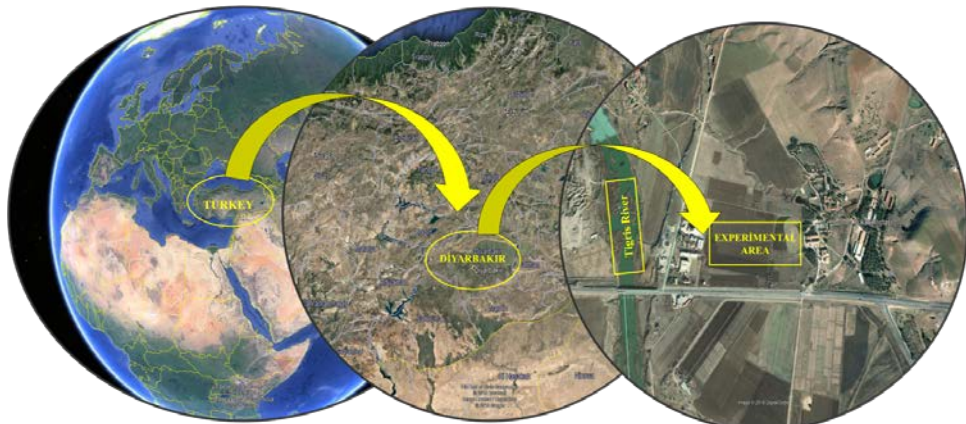


Fig. 1. Experimental Area (US Dep of State Geography © 2018 Google image landset/Copernics)

The 25 two row-barley genotypes were tested under dryland conditions of Northern part of southern Anatolia (Diyarbakır) (Table 1).

Table 1. Name and origin of barley genotypes used in experiment.

Code	Name	Year of release	Origin
G1	Eskişehir-18	Advanced line	Anadolu Agricultural Research Inst
G2	Eskişehir-14	Advanced line	Anadolu Agricultural Research Inst
G3	Eskişehir-13	Advanced line	Anadolu Agricultural Research Inst
G4	Eskişehir-8	Advanced line	Anadolu Agricultural Research Inst
G5	TARM-92	1992	Central Res Inst. for Field Crops
G6	Eskişehir-2	Advanced line	Anadolu Agricultural Research Inst
G7	Edirne-11	Advanced line	Thrace Agricultural Research Inst.
G8	Edirne-10	Advanced line	Thrace Agricultural Research Inst.
G9	Edirne-9	Advanced line	Thrace Agricultural Research Inst.
G10	Aydanhanım	2002	Central Res Inst. for Field Crops
G11	Ankara-4	Advanced line	Central Res Inst. for Field Crops
G12	Ankara-13	Advanced line	Central Res Inst. for Field Crops
G13	Ankara-14	Advanced line	Central Res Inst. for Field Crops
G14	Ankara-16	Advanced line	Central Res Inst. for Field Crops
G15	Sladoran	1998	Thrace Agricultural Research Inst.
G16	Ankara-21	Advanced line	Central Res Inst. for Field Crops
G17	Ankara-59	Advanced line	Central Res Inst. for Field Crops
G18	Ankara-62	Advanced line	Central Res Inst. for Field Crops
G19	Ankara-64	Advanced line	Central Res Inst. for Field Crops
G20	Karatay-94	1994	Bahri Dagdas Intern. Agr.Res. Inst.
G21	Ankara-416	Advanced line	Anadolu Agricultural Research Inst
G22	Ankara-107	Advanced line	Anadolu Agricultural Research Inst
G23	Ankara-116	Advanced line	Anadolu Agricultural Research Inst
G24	Ankara-148	Advanced line	Anadolu Agricultural Research Inst
G25	Kalaycı 97	1997	Anadolu Agricultural Research Inst

The soil of the experimental field was silty loam with pH of 7.87, the organic matter was 1.16%, phosphorus (P_2O_5) 32 kg ha⁻¹, potassium (K_2O) 950 kg ha⁻¹, saturation 68% and lime ($CaCO_3$) 10.2%. The weather conditions during the crop cycles are presented in Table 2. Sowing was done by a Wintersteiger drill on 15 November in 2004.

The experiment was conducted in a Randomized Block Design with three replications. Seeding rates were 400 seeds m⁻². Plot size was 7.2 m⁻² (1.2 × 6 m). The plots were fertilized with 60 kg N ha⁻¹ and 60 kg P_2O_5 ha⁻¹ at the sowing and 40 kg N ha⁻¹ in spring at stem elongation for drought conditions. Harvest was done using Hege 140 harvester in 6 m⁻². Grain yield was recorded in kg per hectare (kg ha⁻¹) after combine harvesting. Thousand grain weights (TGW) and hectoliter (HL) were determined according to the ICC standard method. The

barley samples were graded by size fractionation with sieving fractions with three slotted sieves of different widths (2.8, 2.5 and 2.2 mm).

Table 2. Monthly and long term averages of the climatic data in the experimental area.

Months	Precipitation mm ⁻¹		Mean air temperature °C	
	Long-term	2004-2005	Long-term	2004-2005
September	2.7	0.0	24.8	25.0
October	31.1	1.3	17.0	18.2
November	54.0	123.1	9.6	8.2
December	71.5	4.7	4.1	1.4
January	73.5	58.7	1.6	2.3
Ferbruary	67.1	46.8	3.6	3.0
March	67.9	58.4	8.1	8.4
April	70.5	36.8	13.8	14.1
May	42.1	26.5	19.3	19.6
Jun	7.0	33.1	25.9	25.8
July	0.7	0	31.0	32.0
August	0.5	0	30.3	31.8
Total	488.6	389.4		

A sample of 100 g of grain was placed onto the top sieve and shaken for 5 min (Magliano *et al.*, 2014). Protein and starch content are analyzed by **Whole Grain Analyzer (NIT)** instrument that principles described by Maghirang *et al* (2006) and Dowell *et al.* (2006).

Analysis of variance (ANOVA) was used to determine the effects of genotype on yield and quality traits. Tukey test was performed to determine the significant differences between individual means. All statistical analyses were performed using the SAS program (SAS Institute, 1999) and GenStat 14 software. GGE biplot analyses were carried out using GGE biplot software to assess traits (Yan and Thinker, 2006, Dogan *et al*, 2016). In multi-traits (MT) for genotypes, biplots were constructed by plotting the first two principal components (PC1 and PC2) derived from centered quality criteria data to singular value separation. Also, with the GGE biplot analysis graphs in the study: It was aimed at revealing relation among examined traits and genotypes means by scatter plot (Fig. 2), and grouped traits and performance of each genotype at each trait (Fig. 3), Which-Won-Where based on traits and genotypes (Fig. 4), compare the desirable genotypes to ideal center on traits by comparison model (Fig. 5).

RESULTS AND DISCUSSION

Grain yield

Grain yield is ultimate component, which is not only genetically determined but also related to the growing conditions or environment (Popović et al., 2011; Mladenović et al., 2009; Đekić et al., 2012.a) Sabaghnia et al., 2013; Chamurliyski et al., 2015). The analyses of variance revealed that grain yield had significant differences between genotypes (Table 3).

Table 3. Means of Test weight, TGW, coarse grain, protein, starch and grain yield of winter barley genotypes

Deneme Adı	Test Weight kg m ⁻³	TKW g	Coarse grain % >2.5 mm (%)	Protein %	% Starch	Grain yield kg ha ⁻¹
G1	59.6	34.8	37.08	12.9	62.3	4258 abc
G2	53.2	33.0	25.81	15.1	60.1	3564 bcd
G3	60.1	34.5	42.35	14.7	61.2	4042 a-d
G4	60.8	37.3	52.66	13.5	62.0	4233 a-d
G5 TARM-92	60.9	33.6	41.35	15.1	62.0	4275 abc
G6	49.6	23.7	15.18	14.8	58.9	2625 d
G7	62.7	35.4	46.68	15.3	61.2	3822 a-d
G8	66.5	34.6	67.88	14.2	61.5	3758 a-d
G9	66.5	37.0	67.85	12.8	62.9	4011 a-d
G10	62.3	31.1	73.43	13.7	62.4	
Aydanhanım						4672 abc
G11	59.1	36.7	38.58	16.1	60.1	3428 bcd
G12	61.5	35.4	57.55	14.3	61.8	3978 a-d
G13	62.6	36.5	47.83	15.3	62.0	4000 a-d
G14	61.8	33.9	63.61	15.2	61.5	4156 a-d
G15 Sladoran	62.3	37.1	67.27	12.8	62.2	3542 bcd
G16	64.1	37.5	60.87	13.1	63.5	5269 a
G17	65.6	36.5	66.50	13.7	62.2	4931 ab
G18	59.8	34.9	48.81	13.7	61.8	4511 abc
G19	62.0	36.4	60.01	13.5	62.4	3828 a-d
G20 Karatay-94	63.4	32.4	56.02	13.8	62.6	4858 ab
G21	62.0	36.4	60.00	13.5	62.4	3186 cd
G22	55.6	36.4	52.35	15.5	59.9	4000 a-d
G23	65.7	34.6	51.59	14.8	61.4	3947 a-d
G24	60.5	37.0	52.67	12.7	62.6	4458 abc
G25 Kalaycı 97	62.8	37.1	57.09	13.6	62.5	4258 abc
Min.value	53.2	23.7	15.18	12.7	58.9	2625
Max. value	66.5	37.3	67.88	16.1	63.5	5269
CV%						12.6

According to the results; the highest grain yield obtained from G16 (5269 kg ha⁻¹), G17 (4931 kg ha⁻¹) and Karatay-94 (4858 kg ha⁻¹) genotypes, the lowest grain yield obtained from G6 (2625 kg ha⁻¹), G21 (3186 kg ha⁻¹) and G11 (3428 kg ha⁻¹) varieties. The results are consistent with those of Kılıç et al. (2010) and

Bayram et al. (2017) while the results are lower than those of Öztürk et al. (2007); Sirat and Sezer (2017); in these, higher yields can be obtained in a warmer climate only by means of better adapted genotypes. Moreover, Akıncı and Yildirim (2009), who studied barley accessions from South East region of Turkey, reported that the decreasing of grain yield at high rainfall environment depend on lodging.

Biplot analysis

Principal component analysis was used to show the distribution of genotypes based on traits. The two dimensional PCA score plot for the 25 genotypes data, derived from multi-traits and explained 78.86% (64.57% and 14.29% by PC1 and PC2, respectively) of the total variation (Figs. 1-4). This view of the biplot explains understanding of the interrelationships among the traits (Yan, Rajcan, 2002; Segherloo et al., 2016). GT biplot analysis graphs revealed significant results that there is high relation among examined traits and genotypes means by scatter plot (Fig. 2), and grouped traits and performance of each genotype at each trait (Fig. 3), which-won-where based on traits and genotypes (Fig. 4), compare the desirable genotypes to ideal center on traits by comparison model (Fig. 5).

The relationship each genotype by each trait: Both the genotypes vectors and the traits vectors are drawn in Fig. 1, so that the specific interactions between a genotype and a trait (i.e., the performance of each genotype in each trait) can be visualized. Therefore this figure can be used (1) to rank the genotypes based on performance in any trait, and (2) to rank traits on the relative performance of any genotype. The interpretation of performance a genotype in a trait is better than average if the angle between its vector and the trait's vector is $<90^\circ$; it is poorer than average if the angle is $>90^\circ$; and it is near average if the angle is about 90° (Yan and Tinker, 2006). The results of traits showed that there is high variation among genotypes. According to results, there was high correlation among GY-STR, SV-HLT-TKW and while negative correlations among these Traits and PC. Moreover the effect of each trait generally was the same because the long of each trait vector was the same. On the other hand; some genotypes related with special trait; G16 for GY-STR, G17 for SV-HLT-TKW, G11 and G21 for PC. The genotypes are far from center of biplot graphs, are specific genotypes (G16, G11 and G21) for specific trait. While G6 located opposite of traits, so this genotype did not related with any genotypes. Therefore, there is major contribution of trait to traits; because of they have opposite direction, so they can make up different genetic contribution (Jalata 2011). The GT biplot mainly allows the visualization of any crossover GT interaction, which is very important for the breeding program (Atnaf et al., 2017). The GT (genotype-trait) biplot provides an excellent tool for visualizing genotype $\times$ trait data (Adjabi et al., 2014).

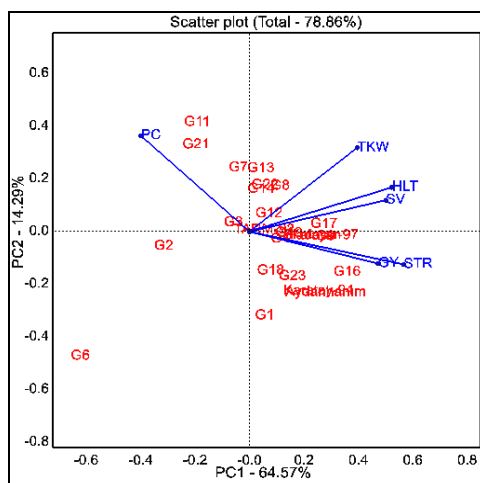


Figure 2. Relation of traits and genotypes based GT Biplot

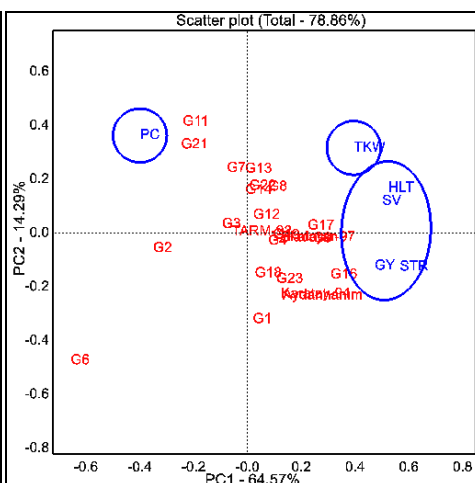


Figure 3. Group of traits based on genotypes by GT Biplot.

Group of traits based on genotypes by GT Biplot: The GGE biplot visualize the correlation amongs traits and grouping them also to visualize the interaction patterns between genotypes and traits (Yan and Tinker 2006). The partitioning of GT interaction divided into three groups (Fig. 3). The traits (GY, STR, SV and HLT) took place in first group; TKW in second group; and PC in third group. The majority of genotypes showed general adaptability for traits. On the other hand, there was correlation among traits which took places in same group. These genotypes took places near group of trait can be select for this group traits (G2 for PC) or some of them is poorest genotypes (G6) for all of traits because they were farthest from the origin of the biplot. GT biplots were found to be effective to reveal important relationships among genotypes and traits of winter barley for ease multi-variety selection (Yan and Kang 2003). The Genotype by Trait (GT) biplot can be used to compare cultivars on the basis of multiple traits and to identify cultivars that are particularly good in certain traits and therefore can be candidates for parents in plant breeding program (Dolatabad et al., 2010). Mega traits "which-won-where" pattern to identify the best genotypes in each environment: Discriminating the target environment into meaningful mega-traits and deploying different genotypes for different mega-traits is the only way to utilize positive GT and avoid negative GT and the sole purpose for genotype by environment interaction analysis (Yan and Tinker 2006; Yan and Rajcan 2002). This definition explains the following biplot based on the multi-traits trials (MT) data of barley yield illustrates two points: 1) A mega-traits may have more than one winning genotypes (sector 2), and 2) even if there exists a universal winner (G16, G17), it is still possible and beneficial, to divide the target traits into meaningful mega-traits (Fig. 4). Mainly, the six lines of biplot graph divide the biplot into six sectors. The traits located in three separate sectors; this means that the traits can be used in the selection special genotypes. On the other hand, second sector consist of all controls variety with some

genotypes and related with GY, STR, SV, HLT, and G16 represented of vertex this sector. While TKW took places in third sector and did not related with any genotype and PC consists of consists of took places in fifth sector and related with G11, G21. The result of this study showed that G16, G11 is suitable to recommend to high potential for special traits. Kendal and Sayar (2016) reported that there is a strong correlations between traits, which located in same sector. Mohammadi et al. (2011), the large variation due to traits indicated strong influence of trait and existence of mega-traits among trial conducting traits; this suggests the usefulness of GT biplot technique for identifying mega- traits among barley genotypes. According to Yan and Rajcan (2002), multiple trait data illustrated that GT biplots graphically displayed the interrelationships among traits.

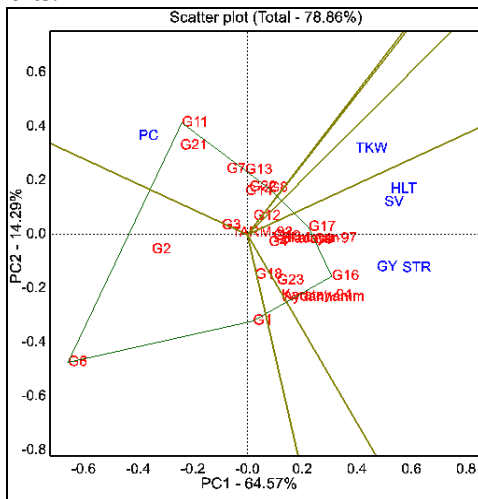


Figure 4. Which-Won-Where based on traits and genotypes by GT Biplot.

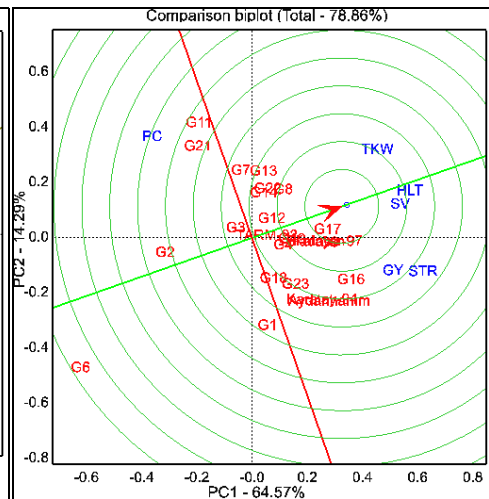


Figure 5. Comparison genotypes based on traits by GT Biplot.

Comparison of genotypes based on traits by ideal genotype: The genotype has both high traits mean and high stability is called an ideal genotype (Fig. 5). The center of the concentric circles is a point on the AEA ("absolutely ideal") in the positive direction and has a vector length equal to the longest vectors of the traits on the positive side of AEA (highest mean performance). So, genotypes located closer to the ideal circle are meaning that it is ideal genotype than others (Yan and Tinker, 2006). In the study, G17 located in center of AEA (absolutely stable), but; G16 took place of near center of AEA. On the other hand; G1, G2 and G6, G11 and G21 were undesirable for all traits except PC, because they took places under mean of trait s values. So, G17 is ideal than other genotypes. Consequently, G17 can be recommended for release in terms of all traits. Ngozi (2011), genotype evaluation and selection of parents for traits are facilitated by GT biplot. The genotype with both high mean performance and high stability for all of the traits was called an ideal genotype (Akinwale et al., 2014). Therefore the center of the concentric circles (i.e., ideal genotype) was the

AEA in the positive direction. Genotypes located closer to the ideal genotype were more desirable than others.

CONCLUSIONS

In the study, the GT Biplot results indicated that yield performance and quality performances of barley genotypes were highly influenced by growing season conditions (rainfall). The genotype G17, demonstrated best performance among genotypes tested growing seasons, while G21 and G11 had good result for PC, while G16 for STV, GY, SV, and HLW. Therefore, G17 was desirable in terms of majority of traits; while the specific genotypes were appropriate for specific traits (G 11 for PC, G16 for GY). As a result indicated that G17 and G16 are suitable to recommend for release, while G21 and G11 valuable source for PC to use in barley breeding program. The result showed that GT Biplot analysis permitted a meaningful and useful summary of GT interaction data and assisted in examining the natural relationships and variations in genotype performance on traits.

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