

ANALYSIS OF PROMISING BARLEY (*Hordeum vulgare* L.) LINES PERFORMANCE BY AMMI AND GGE BILOT IN MULTIPLE TRAITS AND ENVIRONMENT

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Abstract. The development of stable and adaptable new cultivars are based only on positive results obtained from the interaction between the genotype and the environment. Therefore, the study aimed to test the stability and general adaptability of promising barley lines in terms of grain yield and traits in multi-environments. For this purpose, twelve barley genotypes were used in the study. The trials were carried out with four replications in a random design at seven environments in years 2012-13 and 2013-14. The superior and stable genotypes were identified with GGE biplot and AMMI (Additive main effects and multiplicative interaction) models. The AMMI analysis showed that the major treatment sum of squares was affected by environments (80.6%), GE (14.0%) and genotypes (5.4%), respectively. On the other hand, the first two principal component axes (PCA 1 and PCA 2) contributed to the complete interaction with 88.1%, whereas, PCA 3 and PCA 4 axes only with 12.0%. The GGE biplot indicated that G4 is adaptable for all environments, while Altikat, G2 and G3 showed specific adaptation to E1, E3 and E5, G6, G7 and G8 to E6, respectively. According to both techniques, G2, G3, G6, G7, G8 and Altikat were the best genotypes with high yield, whereas G4 was the best with high yield, and stable and general adaptation. The results of biplot indicated that G4 (ARUPO /K8755//MORA/3/CERISE/SHYRI//ALEL I/4/CANELA/5/HART-BAR) was recommended for release and it was released as HEVSEL in 2017. On the other hand; G7 and G6 were protected as genetic material to use as parent in breeding programs for yield stability and quality respectively.

Keywords: breeding, barley, stability, GEI, grain yield

Abbreviations: AMMI, Additive main effects and multiplicative interaction; AEA, average-environment axis; AEC, average-environment coordination; GE, genotype by environment interaction; GGE, G + GE; MET, multi-environment trials; PC, principal component; PCA, principal component analysis; E, environment; G, genotype; TGW, thousand grain yield; HW, hectoliter weight; PC, protein content; HT, time of heading; PH, Plant height

Introduction

Barley (*Hordeum vulgare* L.) is the fourth most commonly used crop after wheat, rice and corn worldwide and this crop is more durable than other grains for stress conditions (drought, salinity, temperature stress), which is important in arid and semi-arid regions based on rainfall grows (Vaezi et al., 2017). The grains of barley are used as animal feed, food and biodiesel as well as raw material in malt industries to obtain

malt. Approximately 65-70% of the produced barley in the world is used as animal feed, 33-35% as malt in beer, whiskey and biodiesel production and 2-3% as human food in food production. The consumption of barley in Turkey 90-92% is used as animal feed and the rest of it as malting in brewing and food industry (Anonymous, 2019).

The potential of a genotype in any environment is determined by the effect of environmental (E), genotype (G) or interaction (GE or GEI) factors. Because the breeders need quite stable cultivars in different environmental conditions and main some traits for agronomic, new varieties must have reliable results in a wide range of environments (Solonechnyi et al., 2015). The reason for the basic differences in the performance of genotypes in wide environments is due to the interaction of the genotype with the environment (Kendal and Aktas, 2016; Neisse et al., 2018). Genotype environmental interaction (GEI) analysis is of primary importance, as is the case for other crops in barley breeding and many other intermediate studies (Kilic, 2014).

The most effective method to predict G, GE and GEI effects is multiple environmental trials (METs). METs are the most appropriate method to select the best genotypes for any environment and to identify genotypes that keep their genetic potential in many different environments (Farshadfar et al., 2012). Since the data obtained from METs are quite high, it is difficult to interpret these data without graphs. Therefore, different models have been used recently by many investigators to evaluate the data obtained from studies conducted in different environments. At the beginning of these methods, AMMI and GGE biplot methods are used and the shapes obtained from these methods visually provide the breeders with very important facilities in terms of the performance of the genotypes (Mortazavian et al., 2014; Solonechnyi et al., 2018). The AMMI model provides more information to researchers about the stability of genotypes in terms of grain yield, while GGE biplot on the relationships between genotypes and properties (Mohammadi et al., 2016).

The aim of this study was to evaluate the multiple traits data obtained from the studies conducted with advanced barley lines in multiple environmental conditions with AMMI and GGE biplot models and to determine the most stable genotypes as registration candidates and to present the benefits of these models to the breeders.

Materials and methods

Material

Ten spring barley promising lines and two checks were evaluated in seven locations across 2012-2013 and 2013-2014 years. The introductory information of genotypes presented in *Table 1* and the introductory information about locations presented in *Table 2*. **Altık** cultivar used in the study as control; because this cultivar was released in 2011 in research area. So, it is very stable among cultivars which used in research on grain yield. Because it is regional and majority barley growers prefer the 6 rows cultivar in this area. **Şahin 91** cultivar used in the study as control; because this cultivar is national a cultivar, and it is facultative type and used in common in north part of region, because it is resistant to cold damage which is sometime happening in spring time. Therefore the genotypes compared with this cultivars for grain yield and other properties of traits).

Method

The trials was carry out in a randomized block design with four replications and planting density was used 450 seeds in per m⁻². Plot size was 7.2 m⁻² in sowing time (6 m long × 1.2 m wide) planted at 20 cm spaced and composed of a total of 6 rows. Sowing of trials were done in October month and Harvest were done in June in both of season and across locations. The sowing dates and harvest dates in all locations are not very effective, because the harvesting time is dry usually and sowing were done after rainfall. The fertilizing percentages were used 60 kg N ha⁻¹ and 60 kg P ha⁻¹ with planting and 60 kg N ha⁻¹ was used to each plots at tillering time for all plots. The chemical struggle was done against weeds in the period of 2-4 leaves in all locations and seasons. Harvesting was done using a Hege 140 harvester in an area of 6 m² in each plot.

Table 1. The information's about genotypes, used in experiment

Genotypes	Pedigree of genotypes	Spike rows
G1	NK1272/Moroc 9-75/6/ VICTORIA/4/GL/COPAL/TERAN 78/5/ SHYRI/7/ CUNH./3/.. SEA01 04-OS-0SD-0SD-0SD-0SD-0SD-0SD	2 row
G2	ROBUST//GLORIA-BAR/COBAL/3/KASOTA CBSS00M00027S.0S-0SD-0SD-1SD-0SD--0SD-0SD-0SD	6 row
G3	CABUYA/JUGL CBSS00M00060S.0S-0SD-0SD-01SD-0SD-0SD-0SD-0SD	6 row
G4	ARUPO/K8755//MORA/3/CERISE/SHYRI//ALELI/4/ CANELA/5/HART-BAR CBSS00M00098S.0S-0SD-0SD-1SD-0SD-0SD-0SD-0SD	2 row
Altikat	Arta/4/Arta/3/Hml-02//Esp/1808-4L (ICB96-0601-0AP-10AP-0AP)	6 row
G6	ARUPO/K8755//MORA/3/CERISE/SHYRI//ALELI/4/ CANELA /5/HART-BAR CBSS00M00098S.0S-0SD-0SD-2SD-0SD-0SD-0SD-0SD	2 row
G7	ARUPO/K8755//MORA/3/CERISE/SHYRI//ALELI/4/ CANELA/5/HART-BAR CBSS00M00098S.0S-0SD-0SD-4SD-0SD-0SD-0SD-0SD	2 row
G8	RECLA 78/SHYRI 2000 CBSS00M00122S.0S-0SD-0SD-4SD-0SD-0SD-0SD-0SD	2 row
G9	CUCAPAH/PUEBLA/7/ROBUST//GLORIA-BAR/COPAL/3/ TOCTE /6/GLOR/... CBSS00M00206S.0S--0SD-0SD-5SD-0SD-0SD-0SD-0SD	6 row
Şahin 91	YEA 1553-1/Eskişehir.	2 row
G11	TAPIR-BAR/PETUNIA 1 CBWS00WM00056S.0S-0SD-0SD-1SD-0SD-0SD-0SD-0SD	6 row
G12	ROBUR-BAR/142-B//ASTRIX/SUTTER334.3/3/CABUYA CBSS00M00053S.0S- 0SD-0SD-2SD-0SD-0SD	6 row

Table 2. Years, sites, codes, coordinate status of environment long term of precipitation

Years	Sites	Code of sites	Altitude (m)	Latitude	Longitude	Annual rainfall (mm)
2012/13	Diyarbakir	E1	496	36° 97' N	38°42' E	680.6
	Adiyaman	E3	483	37° 46' N	40° 56' E	592.0
	Hazro	E2	895	38° 15' N	40° 49' E	743.9
2013/14	Diyarbakir	E4	496	36° 97' N	38°42' E	356.7
	Adiyaman	E6	685	37° 46' N	40° 56' E	592.0
	Hazro	E5	895	38° 15' N	40° 49' E	743.9
	Ceylanpinar	E7	363	36° 51' N	40° 20' E	260.3

The described growing seasons 2012-2013

After exiting the plants, the barley was developed with the cool weather and cold damage occurred in extreme winter days. Seasonal conditions were favorable for barley cultivation in the development period, but in March and April, partly due to arid history, the expected high yield was not obtained. Adiyaman location during the spring period to partially heat stress, Hazro location was exposed to frost damage in late spring. In Diyarbakir location, conditions were more favorable than other locations.

The described growing seasons 2013-2014

Seasonal conditions were negative in terms of barley cultivation in the development period and snowfall occurred on March 31, 2014, especially when the barley was in the period of stalking. Genotypes were exposed to drought in Ceylanpinar location. In the Adiyaman location, it was partially exposed to temperature stress and cold damage. In the Hazro location, frost damage occurred during the period of erasing. In Diyarbakir, cold stress were effective in March and heat stress after heading period. Therefore the grain yield of 2012-2013 season was suitable than 2013-14 growing season. The conditions of Ceylanpinar location is usually hard than other location, because the the total of rainfall of seasons usually is low (*Table 2*).

The protein content was measured in the NIT (Near-infrared transmittance) instrument.

Statistical analysis

The AMMI analysis was used to ranking of the genotypes based on grain yield and GGE biplot was used to see the relation hip between genotypes and tarits across seven environment and two years The AMMI model used as recommended by Verma et al. (2016), and GGE biplot were used as recommended by Yan and Thinker (2005), to identify the mega- environments and superior genotypes. Statistical analyzes of data were performed using JMP and GenStat 12 analysis programs.

The graph (1) introduced by AMMI analysis based on grain yield of across years, and other graphs (2-6) generated by GGE biplot, (2) the ranks genotypes based on stability in aceoss environments, (3) which-won-where/what of GT biplot based on across years, (4) the ranks genotypes based on ideal genotype, (5) the relationship between genotype by trait, (6) the relationship between environment by trait.

Results

The AMMI analysis showed that the major treatment sum of squares were effected by environments (80.6%), GE (14.0%) and genotypes (5.4%), respectively (*Tables 3 and 4*). The major variation of yield explained by the circles showed that the environments varied and the majority of the variation in yield was due to environmental changes. On the other hand, the first two principal component axes (PCA 1 and PCA 2) distributed to the complete interaction 88.1%, whereas, PCA 3 and PCA 4 axes only 12.0% (*Table 5*). The majority percent of multiplicative variance of the sum of the squares based interaction influenced by the first two PCA scores.

Table 3. The average yield performance at each E and over environments (kg ha⁻¹)

Genotype	E1	E2	E3	E4	E5	E6	E7	Mean of E.
1	5268 bc	4042 bd	4810 b	3675 be	4299 ac	3535 bd	1751 d	3911 CD
2	6310 a	4604 ac	4969 b	3467 cf	4109 ac	3056 de	1715 de	4033 BC
3	6399 a	4494 ad	5163 ab	3150 df	4385 ab	3321 ce	2033 c	4135 BC
4	6360 a	4775 ab	5008 ab	4617 a	4732 a	3967 bc	2695 a	4593 A
Altikat	5748 ab	4925 a	5925 a	3860 ad	4220 ac	3977 bc	1159 f	4259 B
6	4806 c	3746 d	3721 c	4288 ab	5147 a	4867 a	2354 b	4133 BC
7	5650 ac	3896 cd	5035 ab	4171 ac	4295 ac	3925 bc	2847 a	4260 B
8	5008 bc	4021 bd	4710 b	4066 ac	4571 a	4893 a	1891 cd	4166 BC
9	5494 ac	4525 ad	5071 ab	2705 f	3488 bc	2545 e	1518 e	3621 DE
Şahin 91	4877 bc	4167 ad	4988 ab	2995 ef	3478 bc	4216 ab	1255 f	3711 DE
11	5692 ac	4092 bd	4646 bc	3170 df	3292 c	3474 bd	834 g	3600 E
12	5313 bc	3746 d	5188 ab	3689 be	4100 ac	3264 ce	1760 d	3866 CE
Mean	5577 A	4253 C	4936 C	3654 F	4176 CD	3753 DE	1818 E	
CV(%)	11.4	12.8	13.4	14.6	17.5	14.6	19.6	14.2
LSD	92.1*	78.6*	94.8*	77.5**	104.8*	78.8**	19.7**	

Table 4. The variance of AMMI analysis on grain yield of barley

Source of Variance	DF	Sum of square	Mean of squares	F Ratio	Explained (%)
Treatments	83	500019991	6024337	18.48	
Genotypes	11	26817395	2437945	7.48**	5.4
Environments	6	403068142	67178024	61.74**	80.6
Block	21	22849272	1088061	3.34	
G x E	66	70134454	1062643	3.26**	14.0
Interaction PCA 1	16	43155999	2697250	8.27**	65.0
Interaction PCA 2	14	15320921	1094352	3.36**	23.0
Interaction PCA 3	12	4841983	403499	1.24	7.3
Interaction PCA 4	10	3093078	309308	0.95	4.7
Residuals	14	3722472	265891	0.82	
Error	231	75323191	326074		
Total	253	598192454	1785649		

Table 5. AMMI selections the first four genotypes for per environment and PCA scores

Sites	Mean (kg/ha ⁻¹)	Score	1	2	3	4	PCA [1]	PCA [2]	PCA [3]	PCA [4]
E1	5577	-25.89	G4	G2	G3	Altikat	-25.90	13.36	15.60	1.13
E2	4253	-20.52	Altikat	G3	G4	G2	-20.52	-9.37	11.20	-4.94
E3	4936	-26.34	Altikat	G12	G9	G4	-26.34	-16.11	-21.93	2.20
E4	3654	16.59	G4	G6	G8	G7	16.59	4.24	-3.67	22.48
E5	4176	15.53	G6	G4	G7	G8	15.53	8.48	5.73	3.97
E6	3753	29.19	G6	G8	Şahin 91	Altikat	29.19	-26.21	6.03	-9.28
E7	1818	11.43	G7	G4	G6	G3	11.44	25.59	-12.96	-15.56

The AMMI model showing Genotype x Environment means

The AMMI method is interpreted as bi-directional, the genotypes and environment main effect indicate by x axis and the effects of interaction indicate by y axis (Fig. 1).

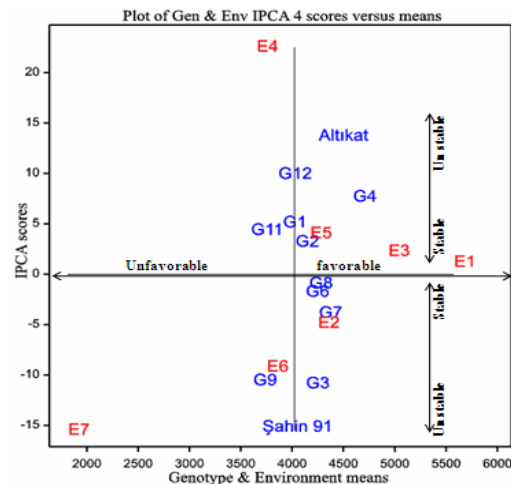


Figure 1. The AMMI model based on grain yield (kg/ha^{-1}) of genotypes(G) in 7 environments(E)

The main effects of genotype and environment are seen along the x-axis while the interaction effects are seen along the y-axis. On this figure; genotypes and environments are evaluated according to the mean (y axis) with stability (x axis). If the genotypes are close to the x axis, they are interpreted as stable, if they located the far from x axis it means that they are unstable. According to the AMMI analysis model, the genotypes showed a high variation and were found in different regions on the graph and the performance of the circles could be clearly seen. According to AMMI, E1, E2, E3 and E5 looking as high yielding environments, because these environments located upper on y axis, while E4, E6 and E7 looking as low yielding environments, because they located below of y axis. On the other hand, G2, G3, G4, G6, G7, G8 and G5 (Altikat variety) showed good performance, because of they located above on y axis (mean yield axis). It is believed that these genotypes were high yielding. But, G1, G9, G11, G12, G10 (Sahin 91) showed low performance, due to they located under on y axis (mean yield axis). Moreover, G4 is looking as high yielding genotype, but moderate stable because it was locate the far from x axis (stable line), while G8 is looking as stable, but this genotype is looking low yield potential than G4 genotype. The IPCA scores indicated that E1 could be recommended to tested genotypes, because of high yield potential of it (Table 5). According to Mirosavljevic et al (2014), the genotypes have small IPCA1 values are more stable, and similar outputs were recorded by Mohammadi et al (2013), in barley.

The recommendation of genotype for environment

The average grain yield of spring barley genotypes ranged from 3600 kg/ha to 4593 kg/ha in seven environments (Table 6). The genotype G4 was existence in the top of four environments. On the other hand, some genotypes estimated for special environments. For example; the genotype G6 dawn in the top genotype for E6, Altikat for E1, E3 and E5. Also, G4 can advise in the first to E1, E4 and the second to E5 and E7. The results of Table 5 and Table 6, showed that AMMI is an effective method to evaluate the perfect genotype for all environments or specific genotype for desirable environments. Moreover, the AMMI analysis is describe recommendations of correct genotype for special environment (Bantayehu, 2013).

The recommendation of environment

The average yield of seven environments was changed from 1818 kg/ha to 5577 kg/ha of spring barley genotypes (Table 5). The AMMI analysis indicated that E1 is the best among test environments, followed E3 and E2. On the other hand, E7 is looking very poor among test environments, because the rainfall of this environment is very low. According to results of AMMI analysis showed that we can recommend the E1 to describe the top yield of genotypes, while E7 for describe the genotypes on drought conditions (Figure 1). Xu et al. (2014) reported that the GGE biplot is the best way to determine the best environment to tested genotypes.

Table 6. The traits value of average for twelve genotypes

Genotypes	Heading time (date)	Plant Height (cm)	Thousand grain weight(g)	Hectoliter weight(g/l)	Protein content (%)
G1	98	83	38.1	74.2	13.2
G2	96	89	33.7	71.4	11.1
G3	97	83	40.1	72.2	12.1
G4	96	84	39.1	74.3	12.0
Altıkat	99	86	34.9	68.5	11.0
G6	97	82	42.9	74.8	13.0
G7	95	85	39.1	72.6	11.6
G8	95	82	40.5	73.4	12.4
G9	98	85	39.0	65.0	12.1
Şahin 91	107	79	42.6	70.9	13.0
G11	97	85	37.2	72.9	12.2
G12	96	87	39.0	71.2	12.3
Mean	97	84	38.9	71.8	12.2

Ranking genotypes based on stability and environment

The ranking genotypes indicate the ideal and stable genotype in across environments, as showed in Figure 2.

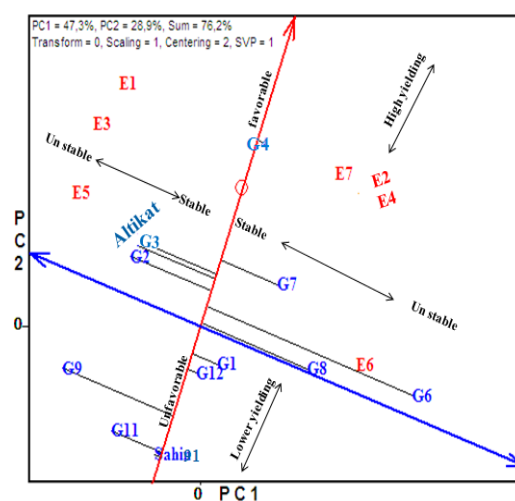


Figure 2. The rank genotypes based on stability

The horizontal line with double arrow pointed the average of environment the upper of arrow points to higher mean yield through the environments, the vertical line with one arrow is ordinate the points the stability of genotypes across environments (Yan and Tinker, 2006). Thus, the genotype G4 with short genotype vector had both the highest mean yield and stability values, while Sahin 91 had low mean yield through across environment, but stable. On the other hand, G6 had above average yield, but unstable because of long genotype vector. The genotypes have large PC1 values mean that this genotype is high yielding and stable. The results of this study showed that G4 had wide adaptability for across environments, while G1, G9, G11, G12 and Sahin 91 for none environments. Some genotypes (G2, G3 and Altikat) showed special adaptability to special environments (E1, E3 and E5), G6, G7 and G8 to E6 (Fig. 2). Therefore, the ranking of genotypes are depend on their stability performance in across environments. Taheripourfard et al. (2017) reported that the GGE is good method to tested genotypes for multi-environment.

Which-won-where/what of GE biplot based on across environments

The GE biplot based on across season data is visualize the polygon of which-won-where/what. The figure divided by thick axis from center figure, and each zone separated by two thick lines is referred to as the “sector” and is indicated by numbers 1, 2, 3 etc., starting from the lower right part of the graph, and if the genotypes and traits located in the same sector it means that are closely related each other (Yan and Tinker, 2006; Dogan et al., 2016). Considering the Fig. 3 with this prediction; thick axis from center figure divide the biplot into five sectors. The environments (E1, E2, E5, E6, E7) with G4 down in the sector 2; G2 and Altikat with E3 in sector3; G1, G6 and G8 with E6 in sector1; while other genotypes did not relation with any environment. Consequently, G4 had high yielding at five environments (E1, E2, E5, E6 and E7), while G6 at E6. Therefore, the best genotype is definete by the best performance in mega-environments.

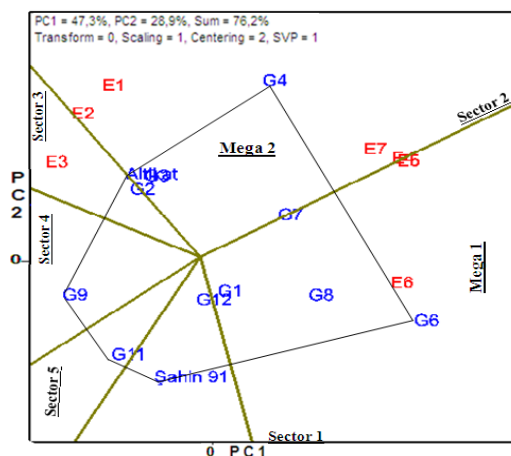


Figure 3. Which-won-where/what of GE biplot based on across season data

The ranks genotypes based on ideal genotype

The discriminating and representativeness of genotypes based traits are visualize the “ideal center” over the mean values of the environments and offers the opportunity to evaluate genotypes according to their proximity or distance to this center(Yan and Tinker, 2005; Oral, 2018). If the genotypes are located in the center, they are the most ideal, if they

are located above the average vertical axis, but far from the center, it means that they are ideal, if they are located below vertical axis, it means that they are undesirable. Considering on this prediction the Fig. 4 explained that the G4 located center of AEA, and so, it is more desirable than other genotypes, while Sahin 91 is the poorest genotype, because it is located under mean axis. The term “ideal genotype” is meaningful only when associated with mean performance. According to Fig. 4, the G4 is highly “ideal”, other genotypes (G2, G3, G7, G6, G8 and G5 (Altikat)) are desirable genotypes, and because of G4 took places in center of AEA and other genotypes took places on above averages yield axis, and so it means that they are just yielding for specific environments. On the other hand, G1, G9, G11, G12 and Sahin 91 are very poorest for average yield, so they are undesirable genotypes across environment. From this example, we can say that the ideal genotype (G4) is the best among genotypes for across environments.

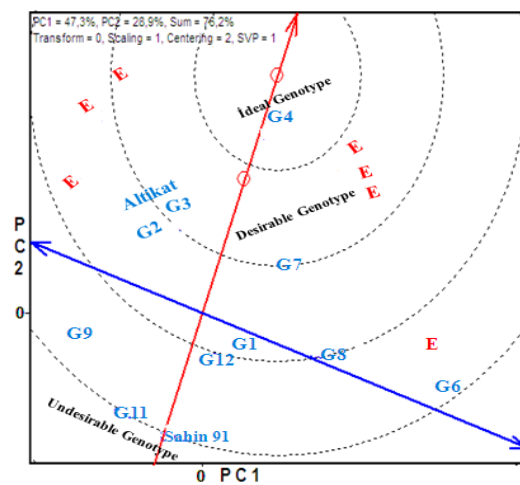


Figure 4. The ranks genotypes based on ideal genotype

The relationship genotype by trait (quality) in seven environments

The relationships between genotype by trait visualize the performance each genotype on traits (Fig. 5).

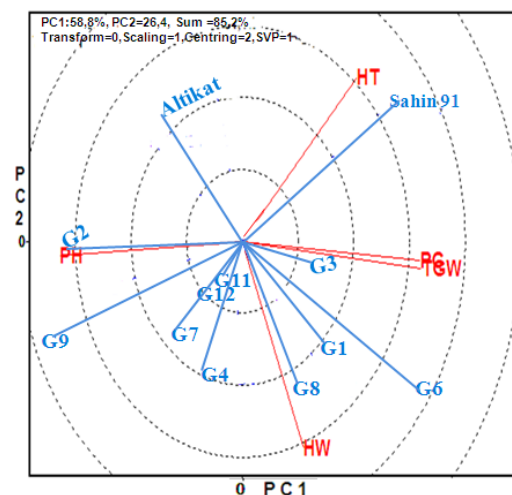


Figure 5. The relationship between genotype by trait

A biplot such a graph to be interpreted bi-directionally has the following comments (Yan et al., 2000; Yan and Tinker, 2006; Kendal and Dogan, 2015). 1) The cosine of the angle between the vectors of the two properties approaches the Pearson correlation between them. Therefore, an angle of less than 90° shows a positive correlation, an angle greater than 90° shows a negative correlation and an angle of 90° shows zero correlation. 2) If the vector of a trait is longer than other vectors, the variation of this trait on genotypes is higher than the other traits, if the vector length of any trait is very short than other traits vector then the variation of this trait is very low. 3) The angle between the vector of any genotype and any trait gives information about the state of the genotypes. If the angle is quite sharp and narrow indicates that the genotype is below of average for that trait if the angle is too large then the genotype is under. 4) The length of the vector of a genotype indicates the strength or weakness of the genotype for all trait profiles. Depend on these principles described in the GT biplot technique, the following observations can be made about Fig. 3. Considering the observations on this figure showed that there was positive correlation (the angel of vectors $<90^\circ$) among protein content (PC), thousand grain weight (TGW) and hectoliter weight (HW), whereas negative correlation (the angel of vectors $>90^\circ$) with plant height (PH) and these three traits. Also, the relationship between genotypes and traits were observed. Therefore, G6 associated with PC, TGW and HW, while G3 with PC and TGW G2 with PH, Şahin 91 with heading time (HT). Because of the genotypes were positioned on these traits. Consequently, the biplot showed excellent discriminating to select special genotypes with special trait and results confirmed that barley parameters were affected by G, GE, and GEI as reported by (Dogan et al., 2016).

The relationship between environments by trait (quality) of four genotypes

The relationship between environment-trait showed in Figure 6 and Table 7. The information and explanations related to the identification of Figure 6 are already given in the upper section (3.5). The biplot showed that there was positive correlation between TGW and HW, between PH and HT, whereas negative correlation among PC and other traits except PH.

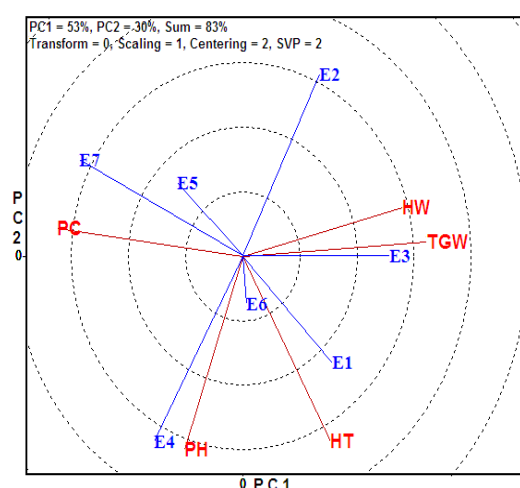


Figure 6. *The relationship between environments by trait*

Also, the relationship between environments and traits were observed. Therefore, E3 associated with TGW, HW, while E1 with HT and E4 with PH and E5, E7 with PC. Because of these environments were positioned on definite traits. Consequently, the biplot showed excellent discriminating to select special environment with special traits and to work environments for recommendation special traits.

Table 7. The traits value of average over environments

Environments	Heading time (date)	Plant Height (cm)	Thousand Grain weight(g)	Hectoliter weight(g/l)	Protein content(%)
E1	105	98	38.1	71.8	12.0
E2	97	60	40.1	70.5	13.4
E3	105	80	38.4	73.1	11.1
E4	109	98	33.6	67.1	15.5
E5	93	85	31.9	69.8	13.8
E6	101	95	35.8	71.1	14.4
E7	92	85	30.6	69.4	18.3
Mean	100	86	35.5	70.4	14.1

Discussion

The methodology of AMMI biplot approach have been reported to be a comprehensive and effective method since it classifies genotypes according to their levels in combination with target environments and graphically rank the genotypes with their strengths and weaknesses in different environments (Yan and Tinker, 2006). On the other, GGE biplot method allows breeders to establish an relations between genotype by traits or environment by traits (Dehghani et al., 2006; Stanisavlievic et al., 2013; Karami et al., 2018; Oral, 2018). The selection genotype by AMMI and GGE biplot method helps breeders to evaluate genotype on grain yield, and to seen the relations between genotype by traits or environment by traits (Sayar and Han, 2015; Dogan et al., 2016).

The AMMI analysis showed that the main effects of genotype (G), environment (E) and GE interaction are very important (*Fig. 1* and *Table 4*). The results of AMMI showed that a large variation explained by environments (80.6%), while a little variation by genotype effect (5.4%). Therefore, the effect of the environment on the fluctuation and variation of the grain yield was found to be higher than the genotype effect and interaction. Many researchers have reported that they have achieved similar results in their AMMI studies (Bantayehu, 2013; Shukla et al., 2015; Kendal and Tekdal, 2016). According to Stanisavlievic et al (2013), majority percent of treatment variation explained by environment, while genotype and interaction effect is very low. On the other hand, the majority percent of multiplicative variance of the sum of the squares based interaction influenced by the first two PCA scores. Vaezi et al. (2017) reported that in the AMMI model in different parameters, because of stability analysis was performed using multiple IPCA numbers, and so it is better than stability analysis using the first IPCA score. Hense, the study showed that G4 is looking as high yielding genotype, but moderate stable, while G8 is looking as stable, but this genotype is looking low yield potential than G4 genotype. According to these explanations, it is possible to determine the best registration candidate for the Southeastern Anatolia Region of Turkey with AMMI method and this study can be used successfully for other regions, countries in different plants as well as.

GGE biplot analysis establishes a framework for classifying target test environments that differ between genotypes which are stable and yielding (Fig. 2). The study showed that G4 is stable for all environment, while G6 is unstable for majority environments. If the effect of genotype in the variation (G) is quite large (47.3%), PC1 scores will be highly correlated with G and PC2 (28.9%) is controlled by GE interaction (Yan and Tinker, 2005; Kendal and Aktas, 2016; Kendal et al., 2016; Vaezi et al., 2017; Oral et al., 2018). GGE biplot gives an idea to evaluate the relationships between all circles (Fig. 3). The GGE biplot defines the relationships between all circles based on the general model of MET data, whereas the simple correlation coefficients define only the relations between the two environments (Farshadfar et al., 2013). In the study, there was positive and significant correlation among E1, E2, E3 and also E4, E5, E7 in which-won-where graphical pattern. In fact, the GGE biplot polygon image is the best method used to determine the best genotype in every mega environment (Elakhdar et al., 2017). The study indicated that G4 is the best genotype for two mega-environment (Fig. 3), while G6 only for mega 1. The genotypes which are favorable discriminating and representative of across environments (Dehghani et al., 2006; Jalata, 2011; Kendal and Sayar, 2016). The study indicated that G4 is favorable genotype on discriminating and representative across test environments (Fig. 4). According to these explanations, it is possible to determine the best registration candidate for the Southeastern Anatolia Region of Turkey with GGE biplot method and this study can be used successfully for other regions, countries in different plants as well as. On the other hand, the results of the study showed that it was possible to make environmental-genotype relations, the stability of genotypes in all circles, the most ideal genotypes and mega environment in all circles with the figures formed by GGE biplot method.

Conclusion

The results of the study evaluated with AMMI and GGE biplot; the genotype (G), environmental (E) main effects and the and GE interaction effect was significant for tested advanced barley genotypes warm and warm-half environments of Turkey and other similar countries. The genotype (G4) showed best performance on grain yield among genotypes across environments, therefore this genotype was desirable in terms of high mean yield and stability. On the other hand; specific genotypes were appropriate for specific environments (G2-E5, G7-E2, G9-E6) and E1 was the best yielding. The result of study indicated that G4 is suitable to recommend for release and G7 desirable origin for yield stability and G6 valuable source for quality to use in barley breeding program. These three lines were obtained from ARUPO /K8755/MORA/3/CERISE/SHYRI/ALELI/4/CAN ELA/5/HART-BAR hybrid. Depend on the results G4 was released as **HEVSEL** in 2017. On the other hand; G7 and G6 protected as genetic material to use as parent in breeding program for improve grain yield and quality, respectively. The multiple environment data can be evaluated by AMMI and GGE biplot analysis, because these two analysis methods allow a meaningful and useful summary of genotype performance across test environments.

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APPENDIX



Picture 1. The locations of research was presented in Southeast Anatolia of Turkey



Picture 2. A photo of the genotypes in the trials



Picture 3. A photo of before and after maturity time of genotypes in the trials