SELECTION THE BEST BARLEY GENOTYPES TO MULTI AND SPECIAL ENVIRONMENTS BY AMMI AND GGE BIPLOT MODELS

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ABSTRACT

The stability of genotypes is significant to selection and improves new varieties. The effect of genotype x environment interaction is revealed by different analysis methods. Nowadays, majority of researchers have been used the AMMI (Additive main effects and multiplicative interaction) and GGE biplot analysis in multi-environment trials. Therefore, ten barley advanced line and cultivars were used in the study. The experiments were performed according to a complete randomized block design with four replications at six environments in 2010-2011 seasons. The stability and superiority of genotypes for yield was determined using AMMI and GGE biplot analysis. Factors (G, GE, and GEI) were found to be highly significant ($P < 0.01$) for grain yield. AMMI analysis indicated that the major contributions to treatment sum of squares were environments (89.77%), genotypes (7.25%) and GE (2.96%), respectively, suggesting that grain yield of genotypes were effected environmental conditions. The GGE biplot indicated that PCA 1 axes (Principal component) was significant as $P<0.01$ and supplied to 75.33% of complete GxE interaction. The AMMI indicated that G6 was stable, while G10 and G9 were high yielding for grain yield in multi-environment. Moreover, E1 and E4 were high yielding, while E2, E5 and E6 low yielding as forecast. On the other hand, GGE biplot indicated that three group were occurred among environments, first group (E1, E2 and E6), second group (E3, and E4), third group (only E5). Moreover: the study showed that G6 and G9 were the best genotypes for first group, G10 for second and G1 for third of environments, while other genotypes didn't show any relation with environments. The results of AMMI and GGE biplot models indicated that G6 was stable in all environments. Therefore this genotype can be recommend for release to all environments, while G9 for first group and G10 for second group.

KEYWORDS:
Barley, AMMI, GGE biplot, Grain yield, Stability.

INTRODUCTION

Considering of the Food and Agriculture Organization of the United Nations (FAO), the World harvested area of barley (*Hordeum vulgare* L.) was nearly 49.5 million hectares, and the yield of barley was 2923 kg/ha in 2014 [1], while, the Turkey harvested area of barley nearly was 6.5 million hectares, the yield of barley was 2840 kg/ha in 2015 [2]. The results of statistic showed that the yield per hectare of barley in Turkey seems to be under to the world average. For this reason, it is very important to develop new and efficient varieties to raise the average yield per hectare in barley.

Barley (*Hordeum vulgare* L.) is the second important cereal crop of Turkey and accounts for about 25% of the total cereal production (SAP 2010). In South-Eastern Anatolia, barley has been cultivated for many years and has a significant role. It is also grown mainly on rainfall conditions, but genotype × environment interaction (GEI) restricts the progress in yield improvement under rainfed and unpredictable climatic conditions. Therefore, experimental research needs to be carried out over multiple environment trials in order to identify and analyses the major factors that are responsible for genotype adaptation and final selection [15, 16].

The yield of each variety in any environment is a sum of environment (E) main effect, genotype (G) main effect and genotype by environment interaction (GE or GEI) [5]. Yield is a complex quantitative trait that is often controlled by several genes and influenced by environmental conditions. The importance of genotypes by environment interaction (GEI) in national cultivar evaluation and breeding programs has been demonstrated in almost all major crops [4, 11, 12]. Farmers need varieties that show high performance in terms of yield and other essential agronomic traits. Modern barley breeding is largely directed towards the development of genotypes characterized with increased yield potential, wide adaptation and high responses to agronomic inputs [21].

The stability of promising lines is important for testing to estimate of theirs performance under across environments [8]. Therefore, the AMMI (analysis additive main effects and multiplicative interaction) is widely used for GEI investigation among the multivariate methods. This model combines ANOVA for the genotype and environment main effects with principal components analysis to analyze the residual multiplicative interaction between genotypes and environments to determine the sum of squares of the G × E interaction, with a minimum number of degrees of freedom [7]. This method enables better understanding of genotypes performance over several environments, and selection of stable and high yielding genotypes [17]. The degree of complexity of AMMI estimation model is more depend on range of environmental conditions [19, 11]. Therefore, it is most useful for breeders and identifies the best genotypes to release decisions, and also it is very important to identify genotypes for specific sub-region [13].

This study aimed to estimate the adaptability and yield stability of barley genotypes using AMMI and GGE analysis to identification and introduction of genotype that have both high performance and high stability to reach the exact potential under changeable and unstable conditions.

MATERIALS AND METHODS

Plant genetic materials. The experimental material comprising ten genotypes (Table 1) were evaluated in 2010-2011 growing season (Table 2).

TABLE 1
The information's about genotypes.

Genotype	Spike type	Growing type
G1	2 rows	Spring
G2	6 rows	Spring
G3	2 rows	Spring
G4	2 rows	Spring
G5	2 rows	Spring
G6	6 rows	Spring
G7	2 rows	Spring
G8	2 rows	Spring
G9	6 rows	Spring
G10	6 rows	Spring

The experiment was conducted in a randomized block design with four replications at 2010-11 growing seasons. The seeding rate was used 450 seeds m^{-2}. Plot size was 7.2 m^{-2} (1.2 × 6 m) consisting of 6 rows spaced 20 cm apart. Sowing was done by winter stagier drill. The fertilization rates for all plots were used 60 kg N ha^{-1} and 60 kg P ha^{-1} with sowing time and 60 kg N ha^{-1} was applied to plots at the early stem elongation. Harvest was done using Hege 140 harvester up on 6 m^{2}. The general information about locations is given in Table 2.

Statistical analysis. The data grain yields of ten (10) genotypes in 2010-11 growing seasons was evaluated by AMMI analysis [7]. The AMMI and GGE biplot were used to identify the mega- environments and superior genotypes for grain yield and other traits. All statistical analyses were performed using GenStat Release 14.1 (Copyright 2011, VSN Int. Ltd.) and GGE biplot software programs.

The data were graphically analyzed for interpreting GE interaction using the GGE biplot software [31]. GGE biplot methodology is composed of the biplot concept [6] and GGE concept [32]. The graphs generated based on (1) The AMMI 1 model showing genotype x environment means,(2) Mega environments "which-won-where" pattern to identify the best genotypes in each season, (3) GGE biplot showing the performance of each cultivar at each environment, (4)The biplot showing the group of environments and performance of each cultivar at each environments, (5) Ranking genotypes based on traits by mean and stability, (6) The GGE Ranking model shows the stable and high yield genotypes on six environment, The GGE Comparison model compare the desirable genotypes to ideal center.

RESULTS AND DISCUSION

Combined analysis variance of ten genotypes under six environment revealed significant ($p \leq 0.01$) effects of genotypes, environments and interaction (Table 3). The effect interaction of PCA (1, 2 and 3) was also significant, while PCA4 was not significant. The analysis showed that the effect of environment was very high (89.8%) than genotype effect (7.3%) and interaction effect (3.0).

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

Year	Sites	Code of Sites	Altitude(m)	Latitude	Longitude	Annual Rainfall(mm)
2010-2011	Diyarbakır	E1	611	37° 55' N	40°14' E	470
	Hani	E2	995	38° 24' N	40° 24' E	892
	Siverek	E3	800	37° 45' N	39° 19' E	670
	Mardin	E4	495	37° 25′ N	41° 01' E	350
	Kızıltepe	E5*	484	37° 19' N	400 58' E	230
	Adıyaman	E6	685	37° 46' N	400 56' E	592

*(E5) was irrigated in two times (for germination and before heading time (150 mm))

TABLE 3
The variance of AMMI analysis on grain yield of barley

Source	Df	SS	MS	F	Explained SS (%)
Total	239	559148185	2339532		
Treatments	59	465164813	7884149	15.95	
Genotypes	9	46877818	5208646	10.53**	7.3
Environments	5	322349980	64469996	83.58**	89.8
Block	18	13884109	771339	1.56	
Interactions	45	95937016	2131934	4.31**	3.0
IPCA1	13	64139135	4933780	9.98**	60.7
IPCA2	11	17820383	1620035	3.28**	19.9
IPCA3	9	9463204	1051467	2.13*	12.9
IPCA4	7	3658723	522675	1.06ns	6.4
Residuals	5	855571	171114	0.35	
Error	162	80099263	494440		

Df; degrees of freedom; ns: not significant, **: p<0.01; , **: p<0.05.

TABLE 4
The grain yield and IPCA scores of ten genotypes in six environment.

Gen. No	Grain yield (kg ha^{-1})						Mean	IPCAg [1]	IPCAg [2]	IPCAg [3]	IPCAg [4]	**IPCAg (1+2+3+4)***
	E1	E2	E3	E4	E5	E6						
1	5362	2110	3458	3792	3033	1194	**3795**	-38.2311	6.46936	-14.6425	-15.3862	**-61.7904**
2	6613	2093	4067	1971	3925	2135	**3968**	12.47478	17.37798	9.2118	-1.10725	**37.95731**
3	5655	2349	3538	3340	3504	2063	**3951**	-17.5591	1.61898	-2.74515	3.10002	**-15.5852**
4	5330	2377	3408	2356	3063	2183	**3695**	-11.2078	-11.74532	8.82528	-1.08189	**-15.2098**
5	5245	2403	3608	2188	3553	2192	**3773**	-9.00804	-0.29703	17.40825	6.07466	**14.17784**
6	7226	2829	4142	1835	4245	3238	**4661**	14.21454	2.39513	5.31835	4.1401	**26.06812**
7	6954	2238	2710	1748	2679	3200	**3895**	18.23325	-31.45165	-18.1128	3.03128	**-28.2999**
8	5622	2831	3721	2387	3473	2640	**4085**	-9.0951	-12.20352	12.90255	2.84533	**-5.55074**
9	8497	3003	4102	1333	4520	3263	**4793**	35.05002	7.02931	-0.06747	-18.6268	**23.38507**
10	7725	2105	4308	2850	4558	2988	**4964**	5.12849	20.80676	-18.0983	17.01072	**24.84763**
Mean	**6423**	**2434**	**3706**	**2380**	**3655**	**2510**						

*(IPCAg 1+2+3+4)>0 = stable and high yielding genotype, (IPCAg 1+2+3+4)<0 = unstable and low yielding genotype

The grain yield and IPCA scores ten genotypes in six environment showed in Table 4. The grain yield of genotype were ranged from 3695 kg/ha^{-1} (G4) to 4964 kg/ha^{-1}(G10). On the other hand, the grain yield of environment were ranged from 2510 kg/ha^{-1} (E6) to 6423 kg/ha^{-1}(E1). The grain yield of genotypes were changed depend on the genetic characteristics of the genotypes, while the yield of environments were changed depend on the climate, soil, altitude and other characteristics of the locations. The genotypes which have high positive IPCA (1+2+3+4) scores, it means that these genotypes are yielding, while low IPCA scores mean low yielding. Some environmental factors, such as soil type and management practices are predictable, i.e. they are not different from year to year. On the other hand, the year-dependent factors, such as precipitation, temperature and disease attack, cause a high year-to-year variability. These random factors are highly variable and have a strong influence on the G × E interaction.

The degree of complexity of AMMI estimation model was more depend on range of environmental conditions. The results of AMMI analysis was supported by results of [4] and [30], reported that the environment effect had the highest effect than other factors on barley and soybean grain yield respectively. The results of Environment, Genotype and G x E effects obtained from this study illustrated similar results of the studies described above and the effect of environment > genotypes > GEI. The existence interaction of grain yield displayed by GGE biplot, especially when the interaction portioned between two-interaction principal component axes (PCA) (Table 3).

This status of GGE biplot made it establish and the biplot calculate effects of genotype and environment. The results of mean square of the interaction axis PCA 1 was significant (p<0.01), while PCA 2 was not significant [14, 25]. Results of GGE biplot analysis also indicated that the PCA 1 axis accounted 50.87%, PCA2 accounted for 24.46% (Fig. 2). GGE biplot showed existence interactions of G x E, so it was portioned between first and second IPCA (Interaction Principal Component Axes). The barley grain yield variation is more depending on environment factors as shown Table 3 and Fig 2. [7], AMMI stability parameter

(ASV) is also one of parameters that are used to estimate genotypes stability. ASV in fact is distance of a special genotype from the origin coordinates of IPCA1 against IPCA2 two -dimensional scatter plot. Lower amount of ASV value shows greater stability of genotypes [22]. On the other hand, [13] suggested that the AMMI model is the most accurate a model because it can predict using the first two IPCAs.

The AMMI model showing genotype x environment means of grain yield. In the AMMI model, x-axis represents the genotypes and environment main effect and y axis represents the effects of interaction (Fig. 1). According to AMMI, G9, G10 and G6 showed good performance, because of they took place above on axis (mean yield). On the other hand, G4 and G5 and other genotypes demonstrated low performance, due to they located under on axis (mean yield). The environment E1, E4 located above mean axis. Moreover, E2, E5 and E6 had low yield potential environment. G9 and G10 lines had high yield potential, but unstable, while G6 was stable, and yield potential. E1 and E4 could be recommended to tested genotypes with high potential and IPCA values, while other environments are not to be recommended to tested genotypes because of low yield potential. Similar outputs were recorded by [18], in barley. According to [17], the genotypes have small IPCA1 values are more stable, [11], the AMMI analysis supply more useful information for acquiring certain results and the identity of mega-environments and wining genotypes are inevitable.

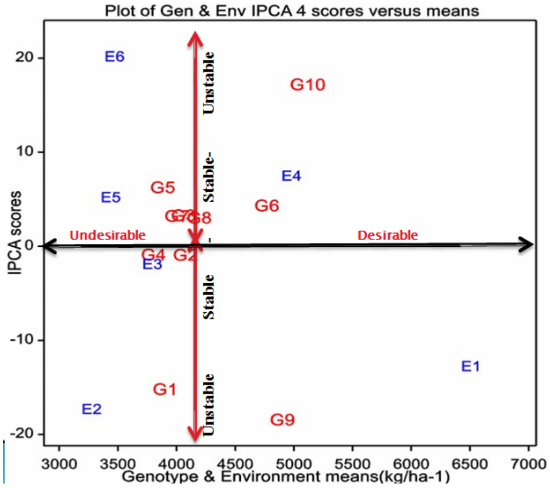

FIGURE 1
The AMMI 1 model showing grain yield (kg/ha-1) of genotypes(G) in 6 environments (E).

Mega environments "which-won-where" pattern to identify the best genotypes in each environment. Discriminating the target environment into meaningful mega-environments and deploying different cultivars for different mega-environments is the only way to utilize positive GE and avoid negative GE and the sole purpose for genotype by environment interaction analysis [31]. A mega-environment is defined as a group of environments that consistently share the same best cultivar(s) [30] This definition explain the following biplot based on the multi-environment trials (MET) data of barley yield illustrates two points: 1) A mega-environment may have more than one winning genotypes (sector 2), and 2) even if there exists a universal winner (G9, G10), it is still possible, and beneficial, to divide the target environments into meaningful mega-environments (Fig. 2 and Fig. 4).

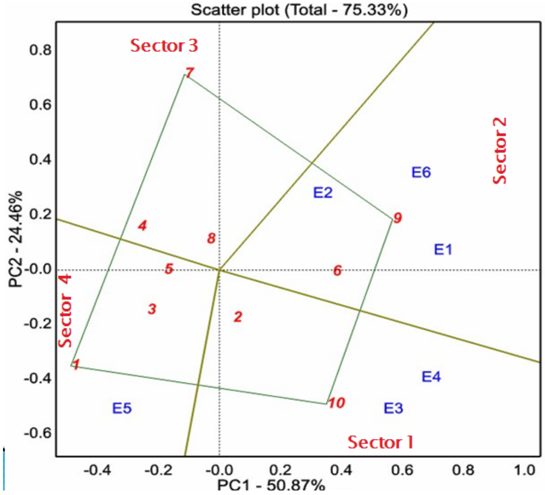

FIGURE 2
The which-won-where view of the GGE biplot.

Mainly, the four lines of biplot graph divide the biplot into four sectors (Fig. 2). The environments located in three separate sectors; this means that the environments had different ecological conditions. On the other hand, first sector consists of G10, and it was high yielding and represented of vertex the E3 and E4 with G2. The second sector consists of E1, E2 and E6 with G9 and G6 and the G9 took places of vertex of this sector. The third sector just consists of some genotypes (G7, G4 and G7), which are not related with study environments. The fourth sector was consisting of G1, G3 and G5 with E5 and the G1 represented of vertex of this sector. Consequently, G9 had high yielding for E1, E6 and E2, G10 for E3 and E4, G1 for only E5; while G4, G7 and G8 did not related with any environments. The result of this study showed that G9, G10 and G1 are suitable to recommend to high potential for special environments. [26], reported that there is a strong correlation between environments, which located in same sector. [23], the large variation due to environment indicated strong influence of environments and existence of mega-environment among trial conducting locations; this suggests the usefulness of GGE biplot technique for identifying mega- environments among barley

TABLE 5
The first four AMMI selections per environment

Environments	Mean	Score	1	2	3	4
E1	6423	33.42	G9	G10	G6	G7
E2	3189	-9.01	G9	G8	G6	G4
E3	3706	-6.79	G10	G6	G9	G2
E4	4893	7.23	G10	G9	G6	G2
E5	3352	-47.06	G1	G10	G3	G8
E6	3385	22.22	G7	G9	G6	G10

growing locations. [19], reported that the GGE biplot graphic analysis defining mega-environments and the cultivars that optimize performance in such mega-environments. Although the crop yield is a result of E, G and G × E interaction effects, only G and G × E are relevant for cultivar and mega-environment identification [29], GGE biplot is a data visualization tool that allows the visual interpretation of the G × E interaction, including environmental evaluation. According to [28], due to the discriminative ability and representativeness of GGE view, the biplot was an effective tool for environments evaluation.

The recommendation of environment: The average grain yield of six environments ranged from 3189 kg/ha to 6423 kg/ha of spring barley genotypes (Table 5). The AMMI analysis indicated that the E1 was the best yielding among test environments, followed E4, since the positive IPCA scores. On the other hand, E2 was the lowest yielding for among test environments, because of the very low IPCA scores. Therefore, the first four AMMI selection genotypes for per environment showed that firstly; G9, G10 and G6 should have been select for E1-E4, while G1 for E5, G7 for E6, because of recommendation of AMMI. [13], reported that it is important to select the genotypes for environment on first four AMMI recommendation.

The GGE Biplot Analysis of genotypes by environments. In this analysis, the results of genotype and environments interaction were examined by GGE Biplot analysis using figure. The biplot of the principal component analysis illustrates relationships between the studied barley genotypes at six environments (Figure 3). The GGE biplot graphically allows PC1 and PC2 to be readily displayed in a two-dimensional biplot so that each genotype × environment interaction is visualized [11]. The first two principal components (PC1 and PC2) were obtained by partitioning the G and G × E interaction trough the GGE biplot analysis. PC1 accounted to 50.87%, while PC2 amounted to 24.46 of the G and G × E interaction. Together, they accounted to 75.33% of the G and G × E interaction sum of squares.

According to Ding et al (2008), GGE biplot is an effective tool for: 1) analysis of mega-environments and specific genotypes can be recommended to specific mega-environments, 2) evaluation of genotype, and 3) evaluation of environment (the power to discriminate among genotypes in target environments). On a GGE biplot, both the genotypic and environmental vectors are shown in Figure 2, illustrating the specific interactions of each genotype with each environment (i.e., the performance of each genotype in each environments).

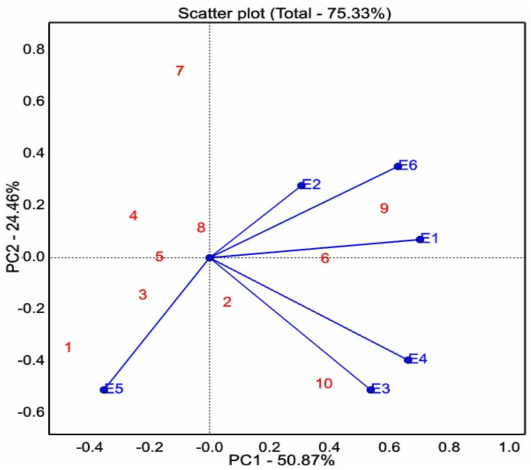

FIGURE 3
GGE biplot showing the performance of each cultivar at each environment

Figure 3 is useful for ranking the genotypes based on their performance in any environment and ranking environments in terms of the relative performance of any genotype. If the angle between environments and genotypes are obtuse, environments and genotypes are negatively correlated. If angle is acute, environments and genotypes are positively correlated, while environments and genotypes are not associated when the angle is 90º [13, 8]. Since, the angle of E5 with other environment is looking negative, while the angle is looking positive between E3 and E4, among E1, E2 and E6. So we can say that there were three groups among test environments (Fig. 4). Close associations between testing environments, suggest that same information about cultivar characteristics could be available from fewer testing environments, reducing the test cost [27]. The presence of an obtuse angle among environments is an indicator of a strong crossover of the G × E interaction [32]. According to [20] the variation in barley grain yield was mostly under control of the growing season and the genotype ×

year interaction. Similarly, [21] reported that in yield trials the effect of the environment affected 80-90% of the treatment variation, and the variation due the G × E interaction was higher than the genotypic variation. Mortazavian et al. [19] also reported that the environment constitutes the highest percent of the total yield variation, while the influence of the G and G × E interaction is usually smaller. On the other hand, there is a relation among genotypes and environment, depend on places of genotype on figure. The G10 with G2 were highly correlated with E3 and E4, the G9 and G6 correlated with E1, E2 and E6, the G1 and G3 correlated with E5, while other genotypes (G4, G5, G7 and G8) which are not related with study environments. The results showed that there is high variation among genotypes; because the genotype located different part of figure. Genotypes located near the center of the biplot contributed less to G and/or GE, whereas genotypes are far of the biplot showed the greatest contribution of G and/or GE [25]. Thus, G9 and G10, which is far from the center of biplot, contributed most to positive outcomes, whereas others, such as genotype G8, is near the center of biplot and contributed less. Thus, these genotypes aligned with specific environments. Although G made major contributions to grain yield, because some of these have opposite directions in the biplot, the genetic contributions may be very different [9].

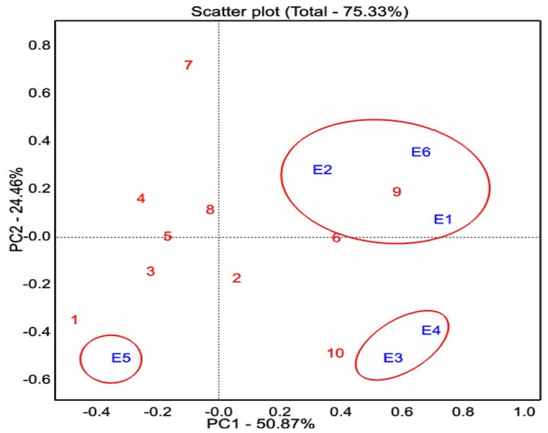

FIGURE 4
The biplot showing the group of environments and performance of each cultivar at each environment.

Ranking genotypes based on mean grain Yield and in stability: The genotype has both high traits mean and high stability is called a favorable genotype. It should have both high mean performance and high stability for all traits (Fig. 5). The center of the concentric circles (ideal) is a point on the AEA ("absolutely stable") 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"). Therefore, genotypes located closer to the stabile line and has high mean values of traits are meaning that it is more favorable than others [31, 5]. The G6 is located center of AEA ("absolutely stable"), but; G2, G9 and G10 took place of near center of AEA and high mean of grain yield. So, these genotypes are favorable than others. According to Fig.6, the G9, and G10 are low stable and more favorable, while G6 are "stable" and favorable, because this genotype has high mean grain yield in all environments. From this example, we can recommend G6 to study for more environments. On the other hand, some genotypes (G1, G3, G4, G5, G7, G8) were unfavorable, because these genotypes had low mean grain yield in study environments.

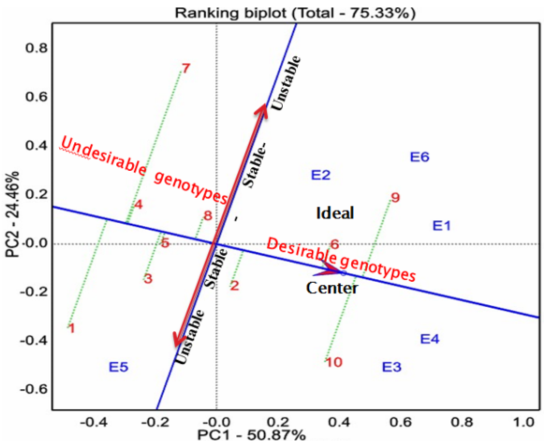

FIGURE 5
The GGE ranking model shows the stable and high yield genotypes on six environments

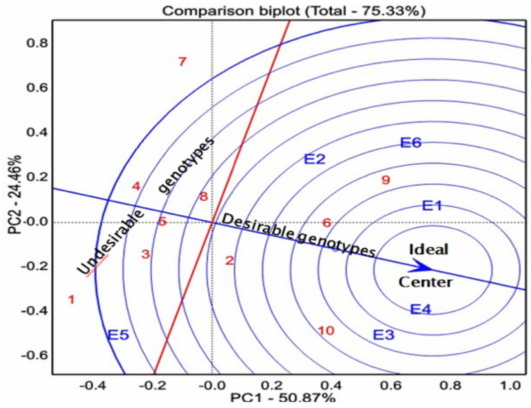

FIGURE 6
The GGE Comparison model compare the desirable genotypes to ideal center

Comparison of genotypes based on grain yield by ideal genotype: The genotype has both high grain yield and high stability is called an ideal genotype (Fig. 6). 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 genotypes on the positive side of AEA ("highest mean performance"). So, genotypes located closer to the ideal circle

TABLE 6
The plant height and heading time of ten genotypes in six environment.

Gen. No	Plant Haigh (cm)						Mean	Heading time (date)						Mean
	E1	E2	E3	E4	E5	E6		E1	E2	E3	E4	E5	E6	
1	125	95	100	120	100	-	108	128	130	126	106	114	118	120
2	105	95	90	115	90	-	99	112	116	112	93	102	110	108
3	115	95	85	120	95	-	102	121	123	122	109	110	115	117
4	90	65	70	90	70	-	77	122	122	127	103	108	116	116
5	90	60	75	100	70	-	79	121	123	126	104	104	116	116
6	110	95	80	115	75	-	95	113	110	112	98	102	110	108
7	105	90	75	100	75	-	89	107	107	106	90	102	105	103
8	90	85	75	95	70	-	83	121	118	126	108	110	114	116
9	110	85	85	120	80	-	96	117	116	113	97	101	111	109
10	117	75	85	110	95	-	96	116	116	113	106	105	112	111
Mean	106	84	82	109	82			118	118	118	101	106	118	

are meaning that it is ideal genotype than others [31, 11]. In the study, any genotype was not located center of AEA ("absolutely stable"), but; G6, G9 and G10 took place of near center of AEA. So these genotypes are ideal than other genotypes. Consequently, G6, G9 and G10 are close to ideal and desirable genotype, so, these genotypes can be recommended for release in terms of grain yield. On the other hand, more genotypes located far from ideal genotype and, these (G1, G3, G4, G5, G7, G8) are undesirable genotypes to study and release. The researchers reported that the biplot show excellent discriminating to select genotypes for all traits and to recommendation for release [20, 24, 11].

The plant height of genotypes were changed from 77(G4) to 108(G1) cm, while the plant height of environment were changed from 82(E5) to 109(E1) cm (Table 6). On the other hand; the heading time of genotypes were ranged from 103 to 120 dates, while the heading time of environments were changed from 101 to 118 dates. The plant height and heading time of genotypes are depend on genetic variability and some environmental factors, such as soil type and management practices are predictable, i.e. they are not different from location to location. On the other hand, the location-dependent factors, such as precipitation, temperature and disease attack, cause a high location-to-location variability. These random factors are highly variable and have a strong influence on the G × E interaction [11], reported that the environmental factors and genetic variability is effect the genotypes and environment plant height and heading time.

CONCLUSION

The results of study indicated that yield performance of barley genotypes were highly influenced by environments. The AMMI indicated that G6 was stable, while G10 and G9 were high yielding for grain yield in multi-environment. Moreover, GGE biplot indicated that three group were occurred among environments, first group (E1, E2 and E6), second group (E3, and E4), and third group (only E5). E1 and E4 were high yielding, while E2, E5 and E6 low yielding as forecast. Moreover: the study showed that G6 and G9 were the best genotypes for first group, G10 for second and G1 for third of environments, while other genotypes didn't show any relation with environments. The results of AMMI and GGE biplot models indicated that G6 was stable in all environments. Therefore this genotype can be recommend for release to all environments, while G9 for first group and G10 for second group.

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