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Genotypes performance in relation to drought tolerance in barley using multi-environment trials

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Abstract. The selection of stable and superior genotypes, with the aim of improving grain yield in breeding programs, requires the evaluation of genotypes under different environments. In this study, the yields of 10 barley genotypes were evaluated in eight different environments using a graphical method (GGE biplot). These experiments were conducted from 2011 to 2015. There were irrigated and rain-fed conditions, as a randomized complete block design (RCBD) with three replications. Results indicated that the two components of PC1 and PC2 explained 62.9% and 14.9% of the total variation observed in the yield, respectively. Genotypes with a positive value for PC1 (i.e., $PC1 > 0$) had the adaptable and the highest performance, whereas genotypes with a negative value for the first component (i.e., $PC1 < 0$) were non-adaptable and had the lowest performance. Likewise, among the genotypes, some had their second component scores near zero, and they exhibited the greatest stability compared to other genotypes. Specifically, genotype 3 had the highest grain yield and stability, while genotypes 2 and 8 showed relatively high yields.

Key words: Hordeum vulgare, drought intensity, drought tolerance index, genotype × environment interaction index.

INTRODUCTION

Barley is a cereal crop with good adaptation to drought stress, and it can be considered as a genetic model plant to evaluate drought resistance mechanisms (Ceccarelli, 1987; Baum et al., 2007). However, most of these investigations are applied under simulated drought stress conditions to enhance experimental accuracy, but its relevance to real drought stress conditions is unreliable and questionable (Lakew et al., 2011). Among all environmental stresses, drought is responsible for the greatest amounts of damage to plant products on a global scale (Pennisi, 2008; Ceccarelli, 2010). A rise in the frequency of drought stress can be expected because of climate change (Ceccarelli, 2010).

The selection of drought tolerant genotypes by means of long-term breeding programs is a way to reduce the effect of drought stress on crop production. Tolerance to drought stress is influenced by poly-genetic heritability and the high level of environmental diversity. Tolerance may also depend on drought stress intensity and duration, along with its interaction with other environmental factors, which make breeding programs a valuable approach to the improvement of drought tolerance (Lakew et al., 2011). Environmental factors refer to a set of external conditions that affect plant growth and development. Soil texture, pH, soil depth, organic matter, fertility, diseases and insects can influence the environment (Roozeboom et al., 2008). The interaction of genotype and environment generate the type of response to a variety of environmental changes (Crossa et al., 1991). This interaction is a fundamental issue in plant breeding studies, and these can contribute to the improvement of genetic efficiency in plants. This is a continuous concern for plant breeders, especially when there are strong interactions or when the selection of varieties is a difficult task to perform (Roozeboom et al., 2008). The evaluation of adaptability and yield stability of varieties in different environmental conditions are subjects of frequent research in plant breeding programs. When considering the process of selection, it is better to estimate the environmental adaptability of plants, in addition to their grain yield stability, rather than to consider grain yield alone (Mohammadi & Amri, 2009).

When the interaction between genotype and environment is weak, there are two ways to develop varieties. First, there is the process of dividing an area under study into smaller and homogeneous areas where varieties with special adaptability are cultivated. Secondly, there is the possibility of creating cultivars with a wide range of adaptability which can be cultivated in different areas; Ideal varieties are those with high grain yield and proper adaptability to a wide range of environmental conditions (Yan et al., 2007; Yan, 2014). The evaluation of varieties in different environments is often performed to select the best varieties for an environment. This can be accompanied by determining the mega-environments if they are available (Yan et al., 2000). Evaluation of genotypes can involve the interaction between the genotype and environment, and then the selection of superior genotypes can occur when the final selection step is expected. This is essential under multiple environments (Kaya et al., 2006; Mitrović et al., 2012). One important point in the evaluation of genotypes in different environments is that in most cases the effect of environment is great but hard to document. Only the effect of genotype and the interaction between genotype and environment are important in selection of stable genotypes. Both genotype effect and the interaction of genotype and environment must be examined simultaneously (Yan & Kang, 2002).

The GGE biplot (genotype (G) main effect plus genotype by environment interaction (G × E) method makes possible the study of genotype effect and the interaction between genotype and environment simultaneously, which can acquire a graphical form (Yan & Kang, 2002). The biplot technique is a very useful tool for visual assessment and interpretation of varieties, environments and their interaction responses. It is a graphical display and representation of simultaneous behavior of two variables which was proposed for the first time by Gabriel in 1971. The graphical method has been introduced by other authors as a suitable technique for analysis of a large number of observations (Crossa et al., 1991; Gauch, 2006). This technique was developed using spatial regression methods (SREG) by combining the main effect of genotype and interaction of genotype effect versus the environment (Jalata, 2011). The biplot method is also used in order to interpret results of regression. In the process of this method, data pertaining to regional trials are obtained. The factors calculate by the graphical GGE biplot method, in which both genotypes and environments are shown visually (Yan et al., 2000; Yan, 2001). Using the GGE biplot method, a second order matrix can be displayed by using a biplot (Choukan, 2011). This method is superior to other methods because plant breeders can visualize the relationship between genotypes and environments and then determine which variety in any given environment or subgroup has a higher potential, based on the drawn graphical plot (Yan et al., 2000).

Mohammadi et al. (2012) recognized that the GGE biplot model is more accurate and efficient than other models (e.g. regression coefficient, sum of squared deviations from regression, stability variance and additive main effects and multiplicative interaction (AMMI). Farshadfar et al. (2012) used the GGE biplot model to evaluate the stability of 25 wheat genotypes. They introduced the most stable genotype suiting a given environment. Mortazavian et al. (2014) used the GGE biplot method to group environments with barley genotypes. Choukan (2011) studied the genotype, environment and interaction between genotype and environmental effects in 14 corn lines using the GGE biplot, leading to the recognition of stable genotypes. Ahmadi et al. (2012) evaluated the performance of 18 barley genotypes under rain-fed conditions in several stations. The results of the GGE biplot graphical analysis revealed two large environments and the superior genotypes. The GGE biplot model is generally a suitable method for multi-environmental data analysis, the evaluation of big environments and the determination of stable genotypes (XU et al., 2014; Luo et al., 2015; Yan, 2015).

In this research, we have evaluated different barley genotypes by considering the interaction between genotype and environments. The objective of this study was to determine the general and specific adaptability of selected genotypes by using the GGE biplot method, and to compare the performance of different genotypes.

MATERIALS AND METHODS

Plant material

In this study, 10 different genotypes of barley (Table 1) in four agricultural research stations were studied in (RCBD) with three replications, by rain-fed and irrigated conditions for a period of four years (Table 2 and Fig. 1). Planting was done by hand in early November.

Filed experiment

Each experimental plot consisted of six rows, each was two meters in length, having a distance of 25 cm in between the rows, and a planting density of 200 seeds per square meter. Planting was done under rain-fed conditions without irrigation and only relied on natural rainfall. For irrigating, 500 liters of water were applied to each experimental plot for irrigation. During the growing season, weed control was performed manually. The precipitation (i.e., amount and distribution of rainfall) during the experimental period was variable (Table 2). Irrigation occurred during tilling, elongation, flowering, and grain filling stages. After adjusting for margins at harvest, sampling was done from the middle of experimental units in order to measure grain yield of each variety using a digital scale. Then, the yield (kilograms per unit) was converted to tons per hectare.

Table 1. Description of the 10 genotypes of barley used in this study

Code	Cultivar	Spike type	Origin	Year of release	Classification by climate	Drought tolerant /susceptible	Reference
G1	Gorgan	2	Sweden	-	Moderate	Susceptible	(Arshadi et al., 2016)
G2	Rihane	6	ICARDA	1993	Moderate	Moderate	(Nazari & Pakniyat, 2010; Arshadi et al., 2016)
G3	Kavir	6	USA	1979	Moderate	Tolerant	(Nazari & Pakniyat, 2010; Arshadi et al., 2016)
G4	Nosrat	6	Iran	2008	Moderate	Tolerant	(Saeidi et al., 2013; Sadeghi-Shoae et al., 2014)
G5	Nimruz	2	CIMMYT	1997	Warm	Susceptible	(Zare, 2012)
G6	Valfajr	6	Egypt	1985	Moderate	Susceptible	(Nazari & Pakniyat, 2010)
G7	Makuyi	6	Italy	1990	Cold	Susceptible	(Nazari & Pakniyat, 2010)
G8	Zarjo	6	Iran	1949	Cold	Tolerant	(Sadeghi-Shoae et al., 2014)
G9	Gorgan 4	2	Sweden	1962	Moderate	Moderate	(Saeidi et al., 2013; Arshadi et al., 2016)
G10	Strin	2	-	-	-	Susceptible	(Arshadi et al., 2016)

ICARDA: International Center for Agricultural Research in the Dry Areas;
CIMMYT: International Maize and Wheat Improvement Center.

Table 2. Trial sites of the diverse barley for harvest during 2011–2015

Code	Year of cultivation	Site	Location	Latitude	Longitude	Altitude (m)	Precipitation (mm)
E1	2011–2012	Rain-fed	Shiraz	37°29'N	32°52'E	1,540	296
E2	2011–2012	Irrigated	Shiraz	37°29'N	32°52'E	1,540	296
E3	2012–2013	Rain-fed	Firoozabad	35°28'N	40°52'E	1,327	381
E4	2012–2013	Irrigated	Firoozabad	35°28'N	40°52'E	1,327	381
E5	2013–2014	Rain-fed	Sanandaj	35°16'N	47°1'E	1,380	254
E6	2013–2014	Irrigated	Sanandaj	35°16'N	47°1'E	1,380	254
E7	2014–2015	Rain-fed	Ghamloo	35°23'N	46°41'E	1,850	118
E8	2014–2015	Irrigated	Ghamloo	35°23'N	46°41'E	1,850	118

m: meter; mm: millimeter.

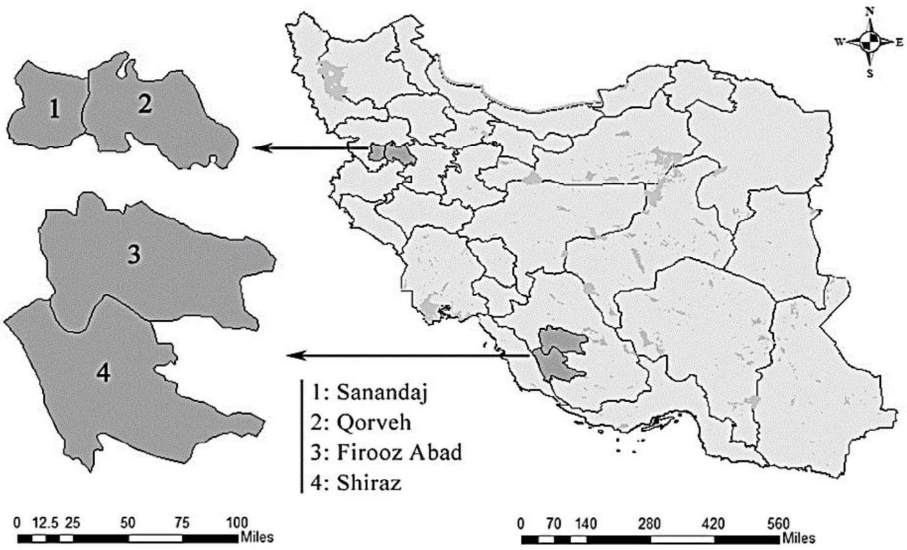

Figure 1. Location of experimental sites on the Iran's map.

Statistical analysis

The Normality Test was done using the SAS statistical software (v9.4). Eight conditions were evaluated, i.e. considering the two conditions of irrigated and rain-fed plants multiplied by the four years (2011–2015). Graphical studies on the interaction between genotype and environmental effects were done using the GGE biplot 6.3 software (Yan, 2001; Yan & Kang, 2002) according to the method proposed by Yan & Hunt (2001). In this study, the genotypes were evaluated according to grain yield in 8 different environments (Table 2). Drought sensitivity index (DSI) was calculated according to the suggested equation by Fischer & Maurer (1978):

$$\mathrm{DSI} = \frac{1 - \frac{\mathrm{YD}}{\mathrm{YP}}}{\mathrm{DII}} \qquad (1)$$

where YD is the average grain yield under stress conditions and YP is the average grain yield under a normal condition. DII (%) is the Drought intensity index which is calculated by the following equation:

$$\mathrm{DII} = 1 - \left(\frac{\overline{\mathrm{YD}}}{\overline{\mathrm{YP}}}\right) \qquad (2)$$

The value of this intensity in this study was calculated as 0.50% (2011–2012), 0.51% (2012–2013), 0.46% (2013–2014) and 0.50% (2014–2015). Genotypes with the least DSI value were then considered as tolerant to drought stress.

RESULTS

The results of combined analysis of variance for yield are shown in Table 3. According to this analysis, grain yield showed a significant difference across environments and genotypes, and also their interaction was highly significant ($p \leq 0.01$). The significance of the interaction between genotype and environmental effects showed that the environments can be arranged in groups according to the effects of interaction.

Table 3. Combined analysis of variance for yield data of 10 barley genotypes evaluated across eight environments

Source of variation	df	SS	MS	F	P
Replication	2	0.224	0.112	0.15	0.865
Environment	7	1317.30	188.19	244.53	0.0001
Error 1	14	10.77	0.769	-	-
Genotype	9	398.644	44.29	103.71	0.0001
G × E	63	306.565	4.866	11.39	0.0001
Error 2	144	61.50	0.43	-	-
CV%	-	-	10.29	-	-

G × E: genotype by environment interaction.

The grain yields of genotypes were significantly different among the various environments. Genotype 3 had the highest yield in environments 1, 3, 4, 5, and 6, whereas genotypes 4, 9, and 8 had the highest yields in environments 2, 7, and 8, respectively. Generally, genotype 3 had the highest yield in all environments and genotype 10 had the lowest grain yield (Table 4). Among the tested environments, the highest average grain yield was obtained in environment 6.

In order to study and interpret the performance of the genotypes, environmental variations and their interaction effects, a graphical analysis was generated and used (Figs 2–6). These charts represent 77.80% of the total data variance (i.e., 62.90% and 14.90% of total variance for PC1 (principal component) and PC2, respectively). Also, the factors PC1 and PC2 indicate the effects of genotype and the interaction of genotype with the environment, respectively. According to the GGE biplot, genotypes with PC1 scores above zero are considered as efficient genotypes (with high grain yield) and genotypes with PC1 scores below zero are known as low yielding genotypes (with low grain yield). The factors PC1 and PC2 divide genotypes into two groups of stable and unstable genotypes based on their scores. Group 1 included stable genotypes of G3, G2 and G8 which had the highest grain yield and the least value of the second factor PC2 (close to zero). The second group included unstable genotypes, such as G4 which had the highest amount of grain yield and scores for PC2. In Fig. 2 the vector length of a tester represents its discriminating ability. The angle between a tester and the AEC abscissa (average environment coordination) axis represents the representativeness of the tester: the larger the angle, the less representative the tester. In this figure, four environments (E2, E3, E6, and E8) were highly correlated in their ranking of the genotypes, indicating that these environments produced similar information about the genotypes (Fig. 2). Correlation analysis of the 8 environments is given in Table 5. Most environments showed a positive correlation with each other except environments 1 and 7 ($r = -0.007$) (Table 5).

Table 4. Mean grain yield (t ha^{-1}) of 10 barley genotypes tested across eight environments

	2011–2012			2012–2013			2013–2014			2014–2015			
	E1	E2		E3	E4		E5	E6		E7	E8		mean yield
Genotype	Stress	Non-stress	DSI	Stress	Non-stress	DSI	Stress	Non-stress	DSI	Stress	Non-stress	DSI	(t ha^{-1})
G1	3.93	5.94	0.68	4.30	6.54	0.67	5.60	5.89	0.11	2.60	3.13	0.34	4.74 (9)
G2	3.83	8.09	1.06	5.47	10.50	0.93	6.38	11.10	0.92	4.31	7.57	0.86	7.16 (4)
G3	4.73	9.48	1.01	7.57	12.29	0.75	7.22	14.83	1.11	4.13	9.34	1.11	8.70 (1)
G4	3.31	9.90	1.34	5.34	12.06	1.08	4.94	11.47	1.23	3.84	7.98	1.03	7.36 (3)
G5	3.09	7.36	1.17	3.45	10.39	1.30	4.94	9.37	1.02	1.96	4.61	1.14	5.65 (8)
G6	3.25	7.18	1.10	4.08	8.52	1.01	3.93	12.70	1.49	3.12	7.03	1.11	6.23 (5)
G7	4.44	6.21	0.58	3.49	8.49	1.14	4.40	8.41	1.03	1.91	8.11	1.52	5.68 (7)
G8	3.95	8.43	1.07	5.39	10.32	0.93	6.49	11.53	0.94	3.83	10.54	1.27	7.56 (2)
G9	3.34	6.00	0.89	4.43	9.48	1.04	5.28	8.89	0.88	5.75	5.89	0.05	6.13 (6)
G10	3.42	5.35	0.73	3.08	7.42	1.14	3.91	4.60	0.32	2.41	3.86	0.75	4.26 (10)
Mean yield	3.73	7.39	-	4.66	9.60	-	5.31	9.88	-	3.39	6.81	-	6.35
LSD 0.05	1.005	0.816	-	0.518	1.261	-	1.345	1.702	-	0.697	1.15	-	-

E: environments; DSI: Drought sensitivity index.

Table 5. Correlation coefficients among tested environments

Year	Environment		E1	E2	E3	E4	E5	E6	E7	E8
2011–2012	E1	Stress	1.00							
	E2	Non-stress	0.197	1.00						
2012–2013	E3	Stress	0.551	0.788**	1.00					
	E4	Non–stress	0.135	0.901**	0.724*	1.00				
2013–2014	E5	Stress	0.582	0.567	0.856**	0.551	1.00			
	E6	Non-stress	0.258	0.828**	0.764*	0.793**	0.514	1.00		
2015–2016	E7	Stress	-0.007	0.322	0.580	0.454	0.498	0.424	1.00	
	E8	Non-stress	0.484	0.705*	0.650*	0.676*	0.498	0.783**	0.363	1.00

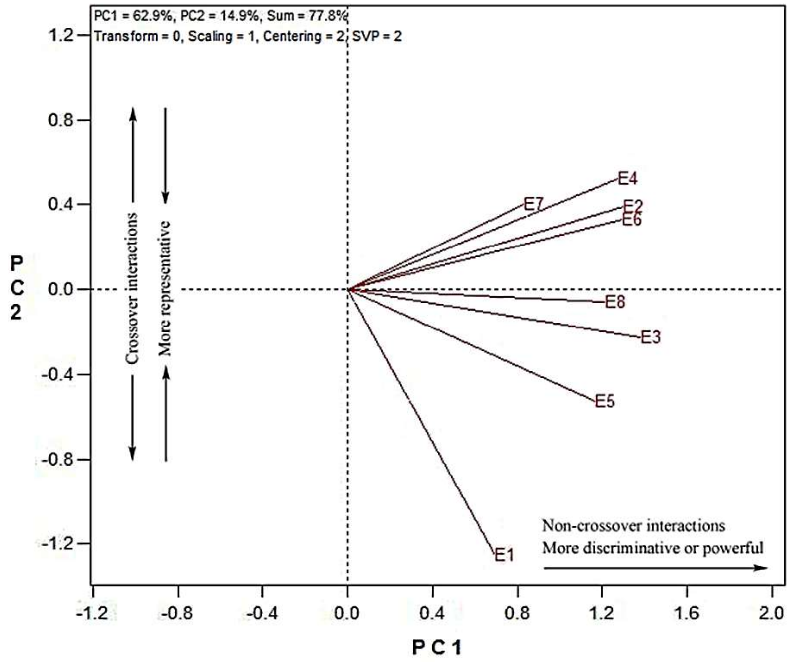

Figure 2. GGE biplot based on environment-focused scaling. PC and E stand for principal component and environment, respectively.

A multi-dimensional diagram is used in order to determine the best genotype for each location (Fig. 3). In this diagram, the varieties which are placed in a special section or environment can prove to have a good performance. Genotypes 2, 3 and 8 had the highest yield in all environments. Moreover, genotype 4 showed the highest yield in environments 2 and 4. The best genotype in each section is a genotype that is placed at the head of the multi-dimensional diagram. Therefore, genotype 3 was the best genotype in the most environments, with respect to its yield. According to the Fig. 4, the origin of the plot is connected to the average of the environments by a direct line (the point of the total average of environments has been determined by a small circle). Genotypes with higher positive values on this axis had the highest yield. Accordingly, genotypes were divided into two groups: group (1) consisting of the genotypes with high grain yield (G3, G8, G2 and G4) and group (2) consisting of genotypes with low grain yield (G9, G6, G7, G5, G1 and G10). An ideal genotype would have the highest performance and stability, which would set a benchmark for other genotypes to be compared and evaluated accordingly. In this study, the ranking of genotypes was shown based on the comparison with the ideal genotype (Fig. 5). For this purpose, the origin is connected to the average point of genotypes by a direct line and continues from two ends. The best genotype is a genotype that is inclined to the positive end of this axis and its vertical distance is shortest from this line. Genotypes with the shortest distance from the center are better. It is demonstrated that genotype 3 is located in the central circle and therefore possesses a high stability and performance. Accordingly, it was considered as the most ideal genotype. Also, genotypes 8 and 2, followed by genotype 4, were placed in the second and third circles, respectively, and were considered as genotypes with acceptable performance.

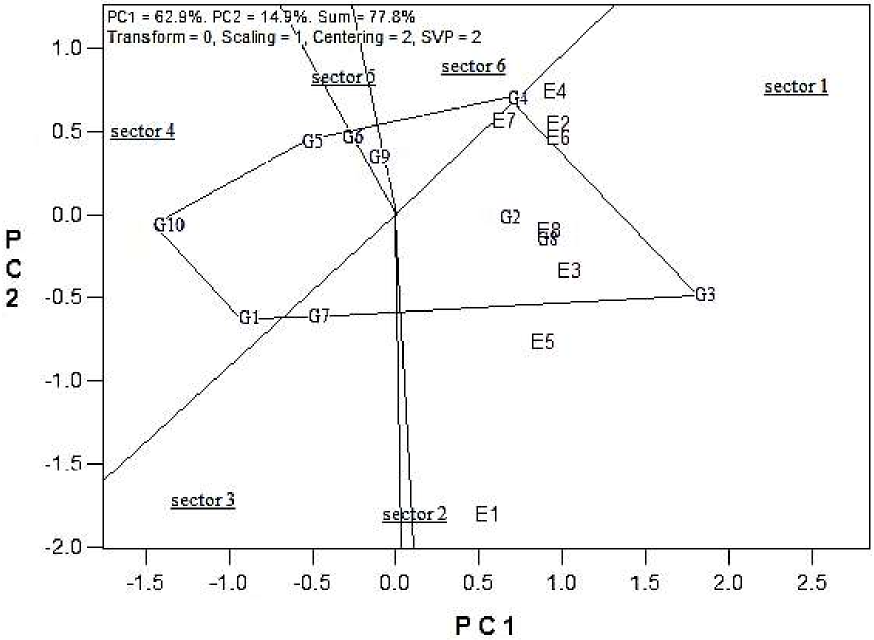

Figure 3. Polygon views of the GGE biplot based on symmetrical scaling for the which-won-where pattern for genotypes and environments. PC, G and E stand for principal component, genotype and environments, respectively.

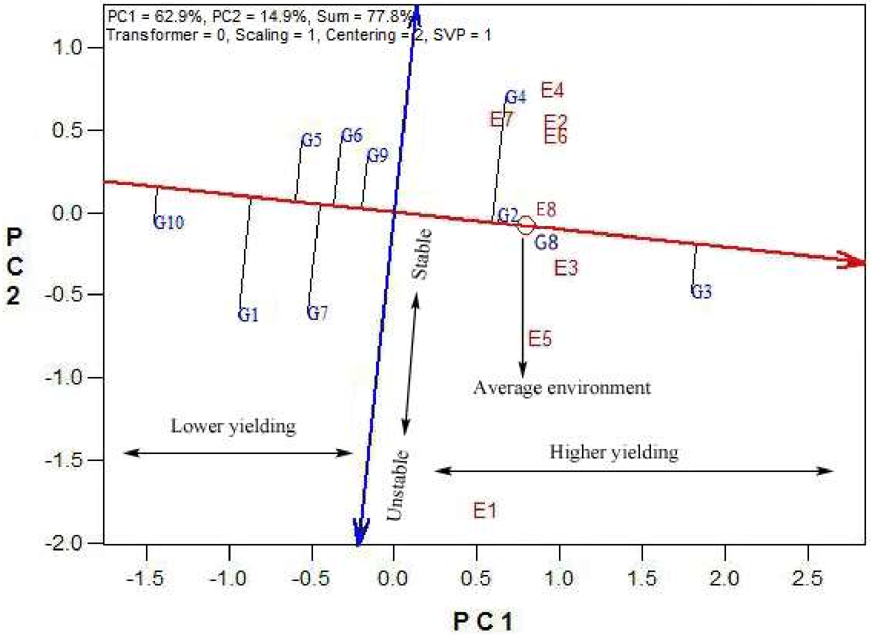

Figure 4. Average environment coordination (AEC) views of the GGE biplot based on environment-focused scaling for the means performance and stability of genotypes. PC, G and E stand for principal component, genotype and environments, respectively.

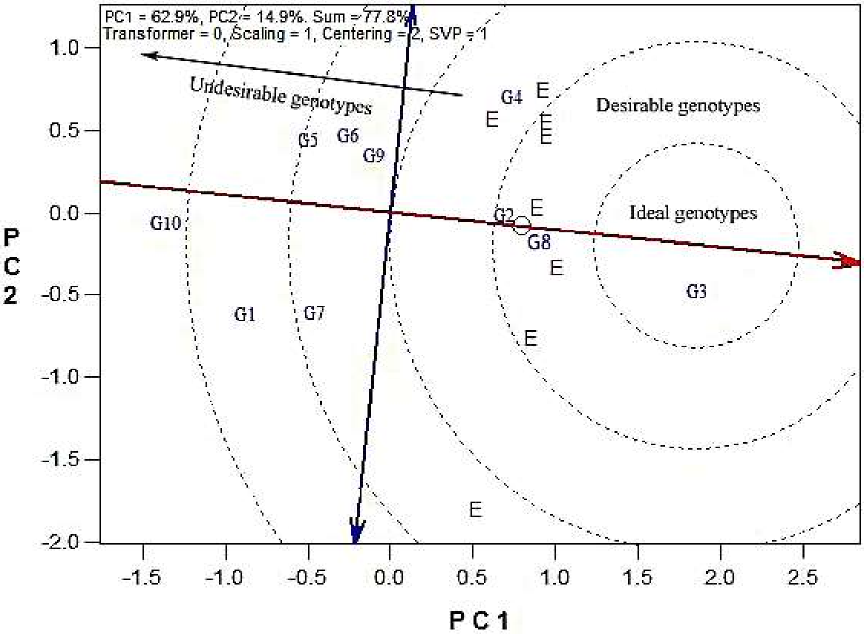

Figure 5. GGE biplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype. PC, G and E stand for principal component, genotype and environments, respectively.

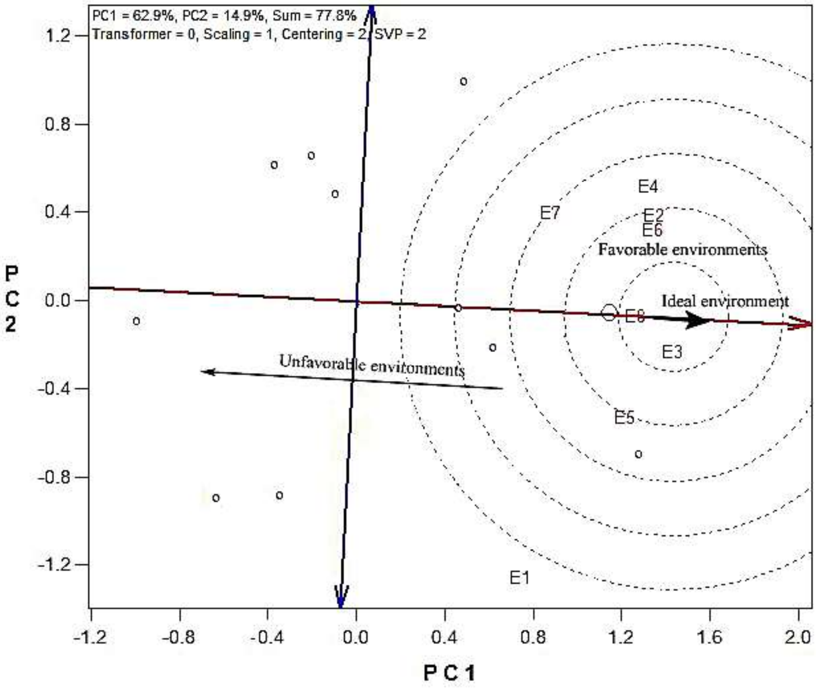

Figure 6. GGE biplot based on environment-focused scaling for comparison the environments with the ideal environment. PC, G and E stand for principal component, genotype and environments, respectively.

The ideal environment had the highest amount of first component (PC1) score and the lowest amount of second component (PC2) score. Fig. 6 shows the ranking of environments based on the ideal environment. The environment that is inclined towards the positive end of the axis and has the shortest vertical distance from it is considered as the best environment. According to Fig. 6, the best point is the center of concentric circles. Other environments are then grouped according to this point. The environments closest to the center are better. As a result, environments 3 and 8 were more ideal environments followed by environments 6, 2, 5, 4, 7 and 10, respectively (Fig. 6).

The drought sensitivity index (DSI) was calculated by assessment of the average yield under normal conditions (YP) and under drought stress conditions (YD) (Eq. (1)). According to Eq. (2), the stress intensity value was calculated in the first season (0.50%), second season (0.51%), third season (0.46%) and fourth season (0.50%). The range of the DSI index in this experiment varied from 0.05 (for genotype 9 in the fourth season) to 1.52 (for genotype 7 in the fourth season) (Table 4). Genotypes with the least drought sensitivity index were most tolerant to drought stress. Generally, this index indicates the type of behaviors exhibited by genotypes under the rain-fed condition. According to this index, genotype 1 had the lowest value of the DSI index, and it did not show a substantial reaction to drought stress. This genotype was more drought tolerant compared to other genotypes under rain-fed conditions and, consequently, showed less yield reduction. Nonetheless, it was not recognized as a desirable genotype because of its low yield potential. In contrast, genotypes 2 and 9 had the highest yield potential, but also had DSI values that were less when compared to other genotypes. Therefore, these genotypes were considered as suitable genotypes under drought stress conditions. Furthermore, genotypes 3 and 2 exhibited the highest stability and yield. On the other hand, genotypes 4, 5 and 6 exhibited DSI values more than one, compared to the other tested genotypes, implying their yields decreased most substantially under rain-fed conditions, and therefore were less tolerant to drought stress.

DISCUSSION

Combined analysis of variance (Table 3) indicated that the effects of environment and genotype versus the environment interaction were significant ($P \leq 0.01$). Also, there was a significant difference among genotypes ($P \leq 0.01$). The interaction effect between genotype and the environment was significant, and genotype performance was different across the environments.

The results indicated that the first and second main components, representing 77.8% of the total variation, related to genotype. The interaction between genotype and environment validated the graph of the biplot in order to explain G and G × E variations in this study. According to Yang et al. (2009), if this diagram can represent at least 60 percent of the total data variance, it can be used to extract positions of mega-environments. In a biplot diagram, the horizontal axis (PC1) represents the main effect of genotype, while the vertical axis (PC2) indicates the interaction between the genotype and the environment. Accordingly, these are considered as a measure of a genotype's instability (Yan, 2002).

When conducting experiments, similar environments can be detected and removed which could reduce the research costs. This can be done by determining the correlation between the environments, during the stability and compatibility tests of varieties which are performed in several years and several places (Yan & Kang, 2002; Yan & Rajcan, 2002). Based on Fig. 2, a test environment may be classified into one of three types. Type 1 environments have short vectors and provide little or no information about the genotypes and, therefore, should not be used as test environments. Type 2 environments have long vectors and small angles with the AEC abscissa and are ideal for selecting superior genotypes. If budgetary constraints allow only a few test environments, Type 2 test environments are the first choice (Yan et al., 2007). Type 3 environments have long vectors and large angles with the AEC abscissa (e.g., E1); they cannot be used in selecting superior genotypes, but are useful in culling unstable genotypes. This AEC view is based on genotype-focused singular value partitioning (SVP), that is, the singular values are entirely partitioned into the genotype scores (GGE biplot option 'SVP = 2') (Yan, 2002). Gauch & Zobel (1997) reported that large environments have two characteristics: first, different superior genotypes are available in different large environments and, second, the variance among large environments is significantly more than the variance within each large environment.

Badu-Apraku et al. (2011) identified four mega environments by evaluating early maturing cultivars of corn in West Africa based on the GGE biplot analysis. A positive significant correlation among the environments indicates that a direct selection for grain yield can be practical among the tested environments that correlate with each other. For example, genotypes with a high and stable performance in environment 2 can also show a similar performance in environments 3, 4, 6 and 7. However, a direct selection in an environment may not be reliable in other environments.

A multi-dimensional diagram is very suitable to determine which variety performs best in the environments (Yan et al., 2000). In this study, genotypes 2, 3, 4 and 8 were placed in sector 1 (Fig. 3). Also, genotype 3 was located at the peak of the multi-dimensional diagram and showed a greater yield and stability among the other genotypes. Furthermore, genotypes that were located near to the origin do not interact much with environmental variations, and environments near the origin do not react to genotype variations. Therefore, genotypes 2, 7 and 8 showed more stability. In order to conduct a simultaneous investigation on a genotype's yield and stability, an average environment coordinate graph was used (Yan & Kang, 2002). This graph was also called the average biplot against stability (Yan et al., 2007). Generally, genotypes near the origin have more stability and do not interact considerably with environmental variation (Abay & Bjørnstad, 2009). An ideal genotype must have a high yield and it must have greater stability. In other words, it must be near the positive end of the average environments axis, and its distance from the axis must be a minimum. Accordingly, genotypes 3 and 8 are the best genotypes (Fig. 4). These genotypes can be used as criteria for the evaluation of other cultivars. On the environment coordinate graph, the closer a genotype is located to the ideal genotype, the more successful and superior it would be in general terms. The ranking of genotypes by this method has been reported by other researchers on several crops (Yan & Kang, 2002; Fan et al., 2007; Baxevanos et al., 2008; Hamayoon et al., 2011; Al-Ubaidi et al., 2013; Roostaei et al., 2014). Yan (2001) stated that a genotype can generate a unique image on the average environment coordinate axis (AEC), giving a proper estimation of the genotype's yield. It was also reported that when considering 33 different wheat genotypes in 8 environments, the correlation between the real yield and the relevant estimations by the biplot method equaled 0.98. The efficiency of genotype image on the average environment coordinate axis has been confirmed in tomato (Kaya et al., 2006) bread wheat (Gedif & Yigzaw, 2014) and barley (Sarkar et al., 2014).

An ideal genotype is a hypothetical genotype which has the highest yield and stability and is located in the center of concentric circles of the biplot. This genotype can further be used to assess other genotypes (Yan, 2001; Mitrović et al., 2012; Mustapha et al., 2014). According to the results of this research, genotype 3 was recognized as an ideal genotype. Other tested genotypes were compared with the ideal genotype. It was indicated that genotypes 2 and 8 are the most similar to the ideal genotype (Fig. 5). Sharma et al. (2010) studied bread wheat genotypes during 5 years and then introduced superior genotypes with qualities close to the ideal genotype. In the current research, there was a sequence in the yield of genotypes in the average environment coordinate biplot (Fig. 4). According to Yan & Kang (2002), this will occur when the amplitude of the first component (PC1) is much more than the second component (PC2). The ideal environment is a hypothetical environment that has a maximum distinction capacity and is located in the middle of the concentric biplot circles (Yan & Kang, 2002). In this research, environments 3 and 8 were known as ideal environments because they were located in the middle of the concentric biplot circles. Since the desirability value of each environment is measured based on its distance from an ideal environment, the environments 6 and 2 were designated as desirable environments because of their closeness to the ideal environment and their environmental vector length (Fig. 6). Previous studies have confirmed that stressful environments create more heterozygosity in populations, when compared to normal conditions (Ceccarelli et al., 2007). This is probably due to the variability in frequency, duration and severity of climatic stresses, particularly when there are differences between the years (not only with respect to the quantity of precipitation, but also regarding rainfall distribution and the interaction between rainfall and temperature). Therefore, this would lead to difficulties in the progress of selecting grain yield within a single location that receives low and variable amounts of rainfall (Lakew et al., 2011).

There are a few advantages in the biplot method: (1) the graphical scheme increases the researchers' understanding and awareness about data (2) it facilitates the interpretation of comparisons between genotypes (3) and is a useful method for the visual discovery of superior genotypes, traits and grouping of genotypes compared to other complex statistical methods (Sabaghnia et al., 2011; Dehghani et al., 2012). Other researchers have also used this method on soybean (Yan & Rajcan, 2002), wheat (Ma et al., 2004), rapeseed (Dehghani et al., 2008), sunflower (Darvishzadeh et al., 2010), bread wheat (Dehghani et al., 2012; Mohamed, 2013; Temesgen et al., 2015) and barley (Solonechnyi et al., 2015; Kendal, 2016; Meng et al., 2016). Furthermore, it has been illustrated that there is a high efficiency in using the GGE biplot method for the evaluation and selection of superior genotypes and environments (Yan et al. (2007), Ding et al. (2007), Yan & Holland (2010) and Yan (2015). In our study, based on the GGE biplot analysis, genotypes 3, 2 and 8 are recognized as superior genotypes with respect to the tested environments. Therefore, these genotypes can be used in future breeding programs. However, these genotypes were also selected as suitable genotypes by Arshadi et al. (2016) when using other methods.

CONCLUSION

The results revealed that the performance of barley genotypes was influenced by different environments. In the current study, genotype 3 showed the best performance in the different environments, and can be suggested as an ideal genotype compared to other tested genotypes. Regarding the GGE biplot analysis, genotype 2 and 8 were recognized as relatively stable and high yielding genotypes because they were (1) close to the ideal genotype, (2) possessed a first component (PC1) value above zero and (3) possessed a second component (PC2) value close to zero. The results indicated that the GGE biplot analysis is a suitable model in order to evaluate the stability of barley genotypes in different environments, and to identify genotypes with respect to proper environments.

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