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Evaluation of phenotypic stability in chickpea genotypes using GGE-Biplot

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ABSTRACT

The objective of this study was to explore the effect of genotype (G) and genotype × environment interaction (GE) on grain yield of 17 chickpea genotypes (Cicer arietinum L.) in five different research stations of Iran. Yield data were analyzed using the GGE biplot method. E (environment) explained 86.44% of the total (G + E + GE) variation, whereas G and GEI captured 2.48% and 11.08%, respectively. The first 2 principal components (PC1 and PC2) were used to create a 2-dimensional GGE biplot and explained 56% and 24% of GGE sum of squares (SS), respectively. Collective analysis of the biplots suggests three chickpea mega-environments in Iran. The first mega-environment contained locations: Kermanshah and Gorgan with genotypes G4 and G17. Genotypes G13 and G14 gave the high performance in location Ilam and genotypes G15 gave the high performance in locations Lorestsn and Gachsaran. Genotypes G4, G7, G15 and G17 had the highest mean yield and genotypes G8 and G9 had the poorest mean yield. Also genotypes G1, G4, G7, G10 and G17 were highly stable. On the other hand, Gorgan was the best representative of the overall locations and the most powerful to discriminate genotypes.

Key words: Chickpea, genotype × environment interaction, GGE biplot analysis.

INTRODUCTION

Chickpea is the most important legume in Iran and occupies nearly 64% of the food legume areas of Iran, and 5.1% of the world's area and 2.75% of the world's chickpea production [10]. Chickpea (*Cicer arietinum* L.) is planted on 700,000 hectares in Iran and ranks fourth in the world after India, Turkey and Pakistan. Chickpea productivity in Iran is less than half of the world average yield [9, 10].

Performance trials have to be conducted in multiple environments because of the presence of GE. For the same reason, the analysis of genotype by environment data must start with the examination of the magnitude and nature of GE [20]. Plots which show both the genotypes and the environments simultaneously can be of great assistance in this respect, and these plots, called biplots [5].

Biplot analysis has evolved into an important statistical tool in plant breeding and agricultural research. It can be performed using many statistical packages either as a specialized feature or through customized programming or macros [15, 18].

The first application of biplots to agricultural data analysis was by Bradu and Gabriel [1], who used data from a cotton performance trial to illustrate the diagnostic role of biplots for model selection. More recently, the term "GGE biplot" was proposed and various biplot visualization methods developed to address specific questions relative to genotype by environment data [14]. The term "GGE" emphasizes the understanding that G and GE are the two sources of variation that are relevant to genotype evaluation and must be considered simultaneously for appropriate genotype and test environment evaluation. GGE biplot analysis has evolved into a comprehensive analysis system whereby most questions that may be asked of a genotype by environment table can be graphically addressed [14, 15, 18, 19]. The "GGE" refers to the genotype main effect (G) plus the GE interaction, which are the two sources of variation of the site regression (SREG) model [2].

The GGE biplot has been used to identify high yielding and adapted cultivars by many researchers such as: Fan et al. [7] and Setimela et al. [12] in maize, Morris et al. [8] in wheat, Samonte et al. [11] in rice, Dehghani et al. [3] and Yan and Tinker [19] in barley and Ebadi Segherloo et al. [4] in chickpea.

The objectives of the present investigation were to (1) interpret G main effect and GE interaction obtained by SREG analysis of yield performances of 17 chickpea genotypes over five locations; (2) application of the GGE biplot technique to examine the possible existence of different mega-environments in chickpea-growing regions in Iran; (3) visual assessment of yield variation across environments based on the GGE biplot, and (4) application of this method to determine discriminating ability and representativeness of the environments.

MATERIALS AND METHODS

Plant materials

This study was carried during 2004 and 2005 in five different research stations in Iran. The locations consist of Ghachsaran, Gorgan, Ilam, Kermanshah and Lorestan. These genotypes were developed at different research institutes/ stations of Iran and that of the international Center for Agricultural Research in the Dray Areas (ICARDA), Syria. The names, origin and genotypic codes of these genotypes are given in Table 1. Experimental layout was a randomized complete block design with four replications in each environment. Each plot consisted of four rows of 4 meter length. Row to row and hill-to-hill distances was kept at 30 and 10 cm, respectively. Data on seed yield were taken from the middle two rows of each plot. At harvest seed yield was determined for each genotype at each test environments.

Table 1. Genotype code, name and origin of 17 chickpea genotypes.

Genotype code	Name	Origin
G1	FLIP 97-211	ICARDA
G2	FLIP 97-113	ICARDA
G3	FLIP 97-85	ICARDA
G4	FLIP 97-78	ICARDA
G5	FLIP 97-41	ICARDA
G6	FLIP 97-30	ICARDA
G7	FLIP 97-102	ICARDA
G8	FLIP 97-79	ICARDA
G9	X95TH1	ICARDA
G10	X95TH154	ICARDA
G11	FLIP 97-43	ICARDA
G12	FLIP 97-95	ICARDA
G13	FLIP 97-114	ICARDA
G14	X94TH45K10	ICARDA
G15	X95TH5K10	ICARDA
G16	X45TH150K10	ICARDA
G17	Arman	ICARDA

Statistical analysis

Analysis of variance was conducted by GenStat software, to determine the effect of location (L), genotype (G) and GE interaction among these factors, on grain yield. Correlation coefficients between pairs of locations were computed via Statistica 0.6 software. In addition, principal component axes (PCAs) were extracted and statistically tested by Gollob's [6] F-test procedure [13]. The first two components were used to obtain a biplot by GGE biplot software [15], which is a windows application that fully automates biplot analysis. The E and G×E interaction biplot analysis for windows application version 4.1 [15] was used to generate the E and G×E interaction biplot used to analyze the multi-environment trial (MET) data. The model used for the E and G × E interaction biplot analysis was the no-scaling and tester-centered model.

RESULTS AND DISCUSSION

Analysis variance

In this probe, partitioning and interpretation of the genotype main effect (G) and genotype × environment (GE) interaction were based on SREG models. Yan et al. [14] proposed a standard biplot of G + GE based on a SREG model referred to GGE biplot. It was constructed using the first two principal components (PC1 and PC2) derived from subjecting the environment-centered data to singular-value decomposition.

The site regression analysis of variance of grain yield (Table 2) showed a significant effect of location. Location explained 86.44% of the total (G + E + GE) variation, whereas genotype (G) and interaction G × E captured 2.48 and 11.08%, respectively. The first 2 principal components (PC1 and PC2) which were used to create a 2-dimensional GGE biplot, explained 56 and 24% of GGE sum of squares (SS), respectively. GGE stands for genotype main effect (G) plus genotype by environment interaction (GE), and the GGE concept is based on the understanding that genotype main effect (G) and genotype by environment interaction (GE) are the two sources of variation that are relevant to genotype evaluation and that they must be considered simultaneously, not alone or separately, for appropriate genotype evaluation [16].

Table 2. Site regression (SREG) analysis of variance for grain yield (kg ha^{-1}) of the 17 genotypes tested across 5 locations

Source	Df	Sum of squares	SS%	Mean of squares
Model	84	281559856		3351903**
Location (L)	4	243380341	86.44	60845085**
Genotype (G)	16	6971526	2.48	435720**
G × L	64	31207989	11.08	487625**
IPC1	19	17476474	56	919814**
IPC2	17	7489917	24	440583**
IPC3	15	3744959	12	249664^{ns}
Residuals	13	2496639	8	192049

*ns and**, non-significant and significant at the 0.01 probability level, respectively.*

The GGE biplot graphically displays G plus GE of a MET in a way that facilitates visual cultivar evaluation and mega environment identification [14]. Only two PC (PC1 and PC2) are retained in the model because such a model tends to be the best model for extracting patterns and rejecting noise from the data. In addition, PC1 and PC2 can be readily displayed in a two-dimensional biplot so that the interaction between each genotype and each environment can be visualized [17].

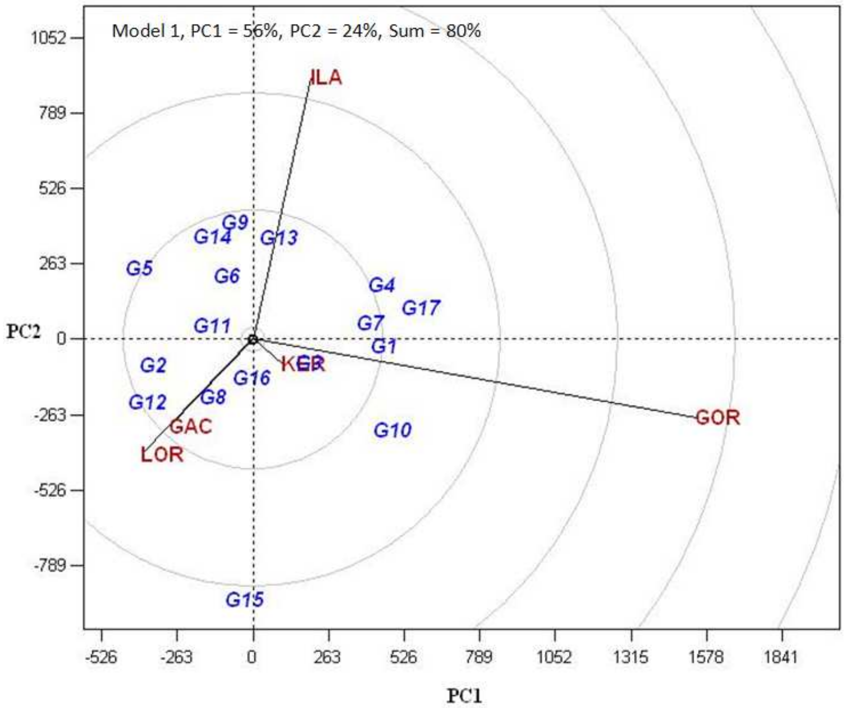

Fig. 1. GGE biplot based on relationships among test environments

Relationships among test environments

GGE biplot, which was based on environment focused scaling, was portrayed to estimate the pattern of environments (Fig. 1). The correlation coefficients among the five test locations are presented in Table 3. The vector view of the GGE biplot (Fig. 1) provides a summary of the interrelationships among the locations. The lines that connect the test environments to the biplot origin are called environment vectors. The cosine of the angle between the vectors of two environments approximates the correlation between them. For example, Lorestan and Gachsaran were positively correlated (an acute angle), Ilam and Lorestan or Gachsaran were negatively correlated (an obtuse angle), and Gorgan and Ilam were not correlated (a right angle).

The distance between two environments measures their dissimilarity in discriminating the genotypes. Thus, the four locations fell into three apparent groups: Kermanshah and Gorgan formed one group, Ilam formed two group and Lorestan and Gachsaran formed three groups.

The presence of close associations among test locations suggests that the same information about the genotypes could be obtained from fewer test locations, and hence the potential to reduce testing cost. If two test locations are closely correlated consistently across years, one of them can be dropped without loss of much information about the genotypes.

Table 3. Correlation coefficients among test locations

Location	Kermanshah	Lorestan	Ilam	Gachsaran
Lorestan	0.21			
Ilam	-0.03	-0.38		
Gachsaran	0.23	0.74**	-0.07	
Gorgan	0.41	-0.39	0.08	-0.21

*** Significant at the 0.01 probability level.*

Which genotype won where and mega-environments with GGE biplot

One of the most attractive features of a GGE biplot is its ability to show the which-won-where pattern of a genotype by environment dataset (Fig. 2). Many researchers find this use of a biplot intriguing, as it graphically addresses important concepts such as crossover GE, mega environment differentiation, specific adaptation, etc [20]. The polygon is formed by connecting the markers of the genotypes that are further away from the biplot origin such that all other genotypes are contained in the polygon. Genotypes located on the vertices of the polygon performed either the best or the poorest in one or more locations since they had the longest distance from the origin of biplot. The perpendicular lines are equality lines between adjacent genotypes on the polygon, which facilitate visual comparison of them. The for example, line 1 is perpendicular to side G13-G4; line 2 is perpendicular to the side that connects genotypes G4 and G17 (the G4-G17 side); line 3 is perpendicular to side G17-G10; similarly, line 4 is perpendicular to side G10-G15, line 5 to side G15-G12, line 6 to side G12-G5, and line 7 to side G5-G9. These 7 lines divide the biplot into 7 sectors, and the environments fall into 4 of them (Fig. 2). An interesting feature of this view of a GGE biplot is that the vertex genotype(s) for each sector has higher (some times the highest) yield than the others in all environments that fall in the sector [16]. Thus, Gorgan, fell into sector 2 delineated by lines 2 and 3, and the vertex genotypes for this sector were G18 and G20, suggesting that lower-yielding genotypes for these 4 environments were G4 and G17. Similarly, Kermanshah, fell into sector 3 delineated by lines 3 and 4, and the vertex genotype for this sector was G10, suggesting that the higher-yielding genotype for Kermanshah was G15. Lorestan and Gachsaran, fell into sector 5 delineated by lines 4 and 5. The vertex genotype for this sector was G15. Ilam, fell into sector 7 delineated by lines 1 and 7, and the vertex genotypes for this sector were G13 and G14.

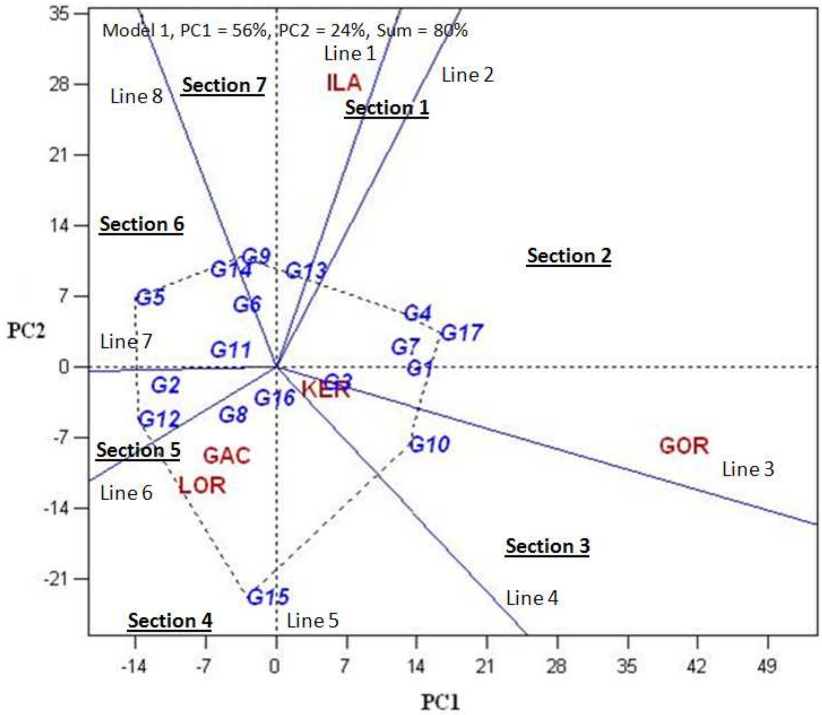

Fig. 2. Polygon views of the GGE biplot based on symmetrical scaling for the which-won-where pattern of genotypes and environments.

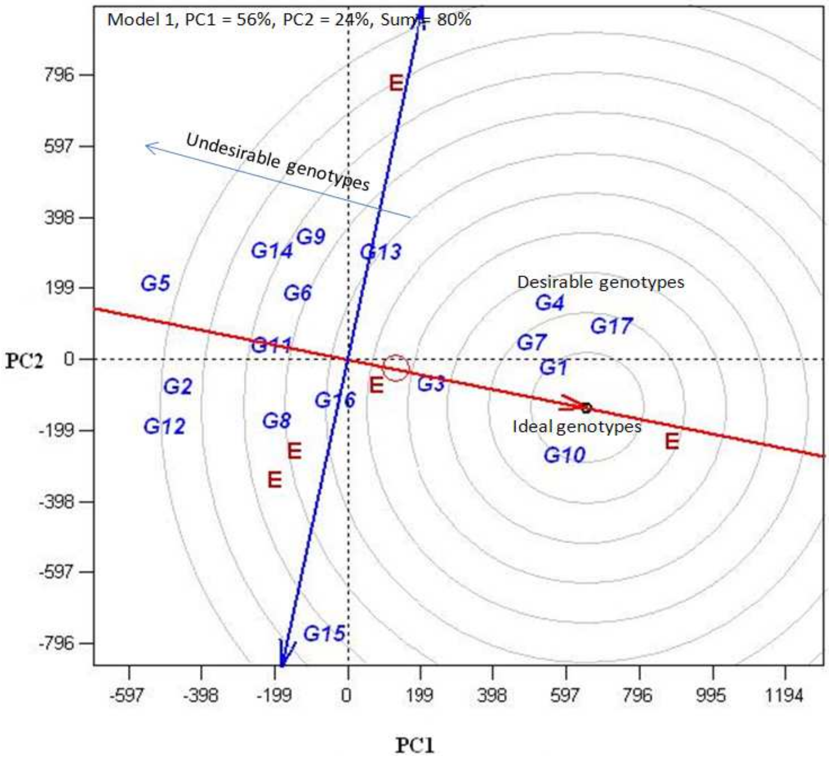

Fig. 3. GGE biplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype.

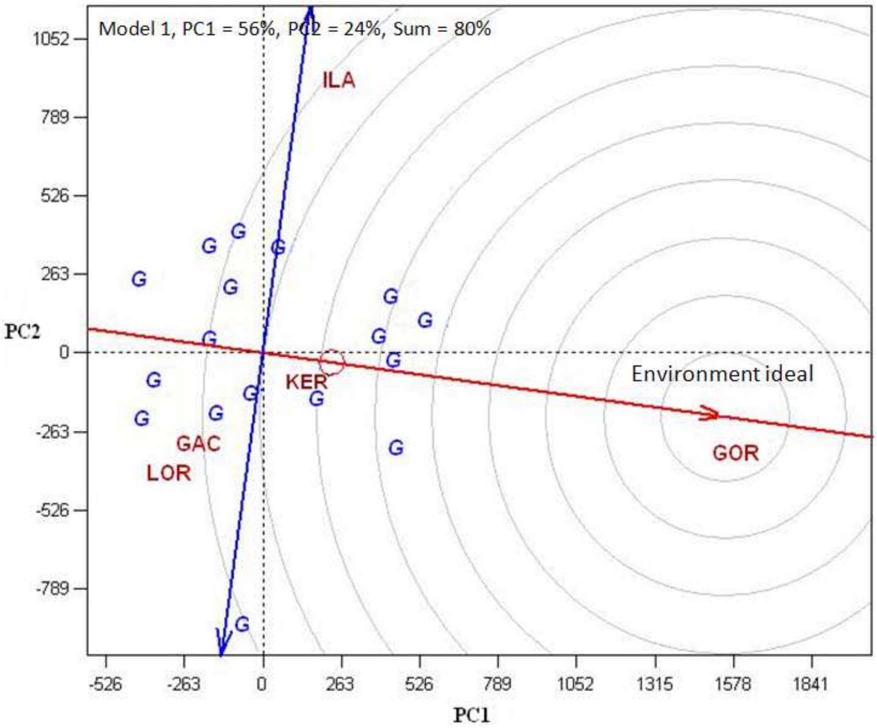

Fig. 4. GGE biplot based on environment-focused scaling for comparison the environments with the ideal environment.

Ranking genotypes relative to the ideal genotype

An ideal genotype should have the highest mean performance and be absolutely stable (i.e. perform the best in all environments). Such an ideal genotype is defined by having the greatest vector length of the high yielding genotypes and with zero GEI, as represented by an arrow pointing to it (Fig. 3). Although such an ideal genotype may not exist in reality, it can be used as a reference for genotype evaluation [20]. A genotype is more desirable if it is located closer to the ideal genotype. Thus, using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype. Because the units of both PC1 and PC2 for the genotypes are the original unit of yield in the genotype-focused scaling (Fig. 3), the units of the AEC abscissa (mean yield) and ordinate (stability) should also be the original unit of yield. The unit of the distance between genotypes and the ideal genotype, in turn, is the original unit of yield as well. Therefore, the ranking based on the genotype-focused scaling assumes that stability and mean yield are equally important [16]. Fig. 3 revealed that G1 and G10, which fell into the center of concentric circles, were ideal genotypes in terms of higher yielding ability and stability, compared with the rest of the genotypes. In addition, G7, G17 and G4, located on the next concentric circle, may be regarded as desirable genotypes.

Ranking locations relative to the ideal location

The ideal environment is represented by an arrow pointing to it (Fig. 4). Although such an ideal environment may not exist in reality, it can be used as a reference for genotype selection in the MEYTs. An environment is more desirable if it is located closer to the ideal environment. Thus, using the ideal environment as the center, concentric circles were drawn to help visualize the distance between each environment and the ideal environment [14]. The ideal location, represented by the small circle with an arrow pointing to it, is the most discriminating of genotypes and yet representiveness of the other tests locations. Therefore Gorgan was desirable test locations, whereas Lorestan, Gachsaran and Ilam were undesirable test locations.

Mean performance and stability of the genotypes

Yield performance and stability of genotypes were evaluated by an average environment coordination (AEC) method [15, 16, 17]. Within a single mega-environment, genotypes should be evaluated on both mean performance and stability across environments. Fig. 5 is the average-environment coordination (AEC) view of the GGE biplot. The single-arrowed line is the AEC abscissa, it points to higher mean yield across environments. Thus, G1, G4, G7, G10 and G17 had the highest mean yield. The double-arrowed line is the AEC ordinate; it points to greater variability (poorer stability) in either direction. Thus, G15 was highly unstable whereas G1 was highly stable, followed by G7, G17, G4 and G10.

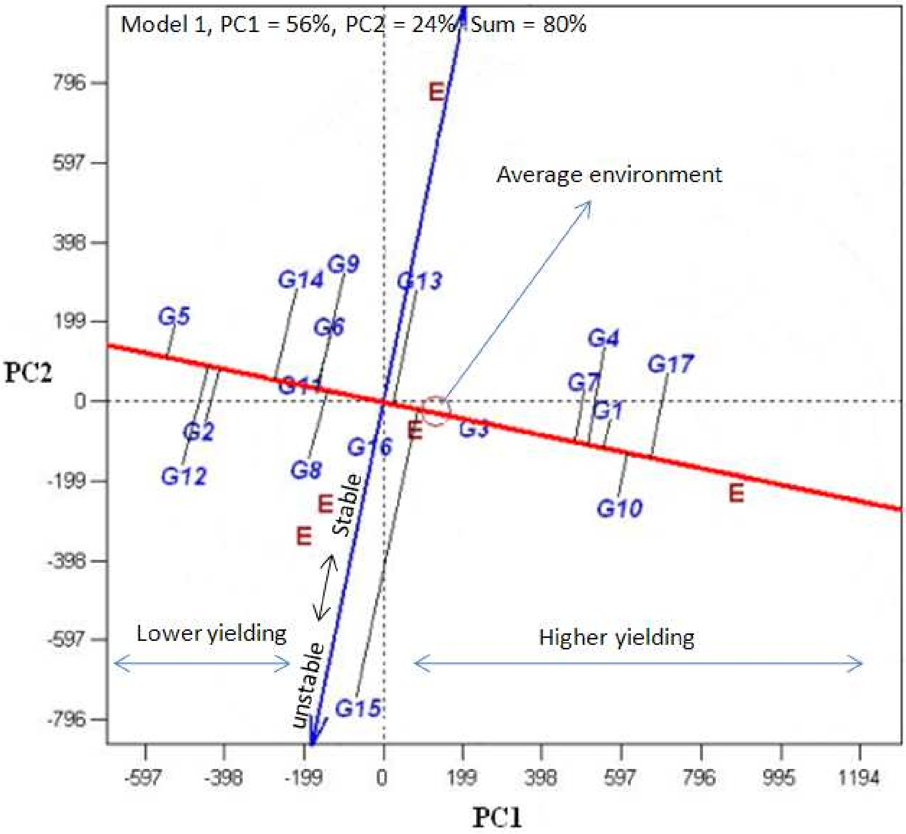

Fig. 5. Average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling for the means performance and stability of genotypes.

Ranking genotypes based on performance in one location (Lorestan)

To rank the genotypes based on their performance in a Location, a line is drawn that passes through the biplot origin and the Location. This line is called the axis for this Location, and along it is the ranking of the genotypes. Fig. 6 ranks the genotypes based on performance in Lorestan. This figure, genotypes G15, G12 and G2 had the highest yield at Lorestan and genotypes G17 and G4 showed the poorest yield.

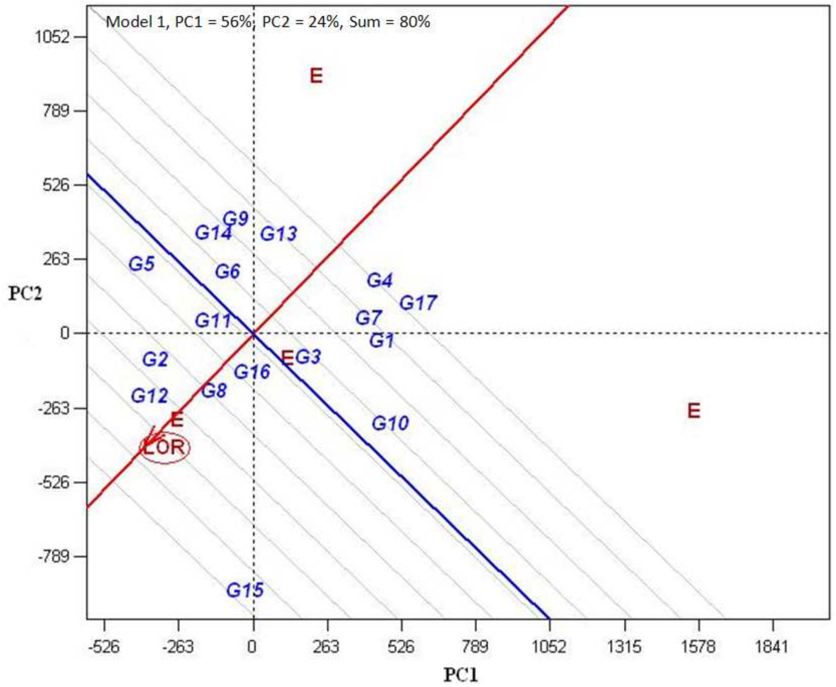

Fig. 6. GGE biplot based on ranking genotypes based on performance in Lorestan

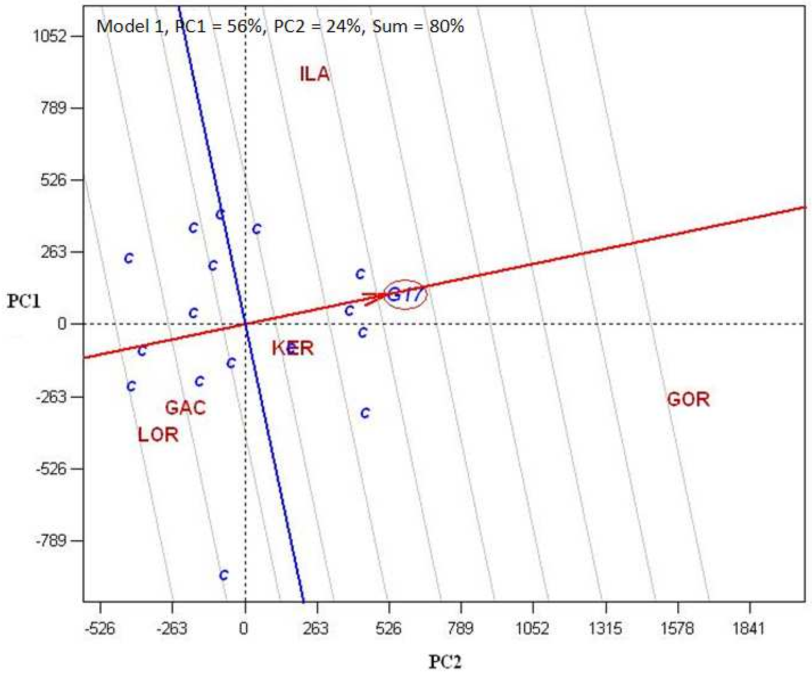

Fig. 7. GGE biplot based on ranking locations based on the performance of genotype Arman

Ranking environments based on the performance of a genotype (Arman)

To study the specific adaptation of a genotype, i.e., to rank the test locations on the relative performance of a genotype, a line is drawn that passes through the biplot origin and the genotype. This line is called the axis for this genotype, and along it is the ranking of the locations. For example, Fig. 7 ranks the test locations based on the relative performance of G17.

It shows that G17 had lower than average yield in Lorestan and higher than average yield in Gorgan.

CONCLUSION

Biplot analysis has evolved into an important technique in crop improvement and agricultural research. GGE biplot analysis provides an easy and comprehensive solution to genotype by environment data analysis, which has been a challenge to plant breeders, geneticists, and agronomists. It not only allows effective evaluation of the genotypes but also allows a comprehensive understanding of the target environment and the test environments. Specifically, biplot analysis can help one understand the target environment as a whole, i.e., whether it consists of a single or multiple mega-environments, which determines whether GE can be exploited or avoided. Within a single mega-environment, biplot analysis can help one understand the test environments: whether they are informative, representative, and unique in terms of genotype discrimination. At the same time, biplot analysis can help one evaluate genotypes in terms of both mean performance and stability across environments.

In this study, we tried to examine different applications of GGE biplot for selecting high yielding, stable genotypes. In brief, we suggest use of the GGE biplot analysis for identification of favorable genotypes and mega-environments in chickpea.

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