

GGE Biplot analysis of genotype \times environment interaction in chickpea genotypes

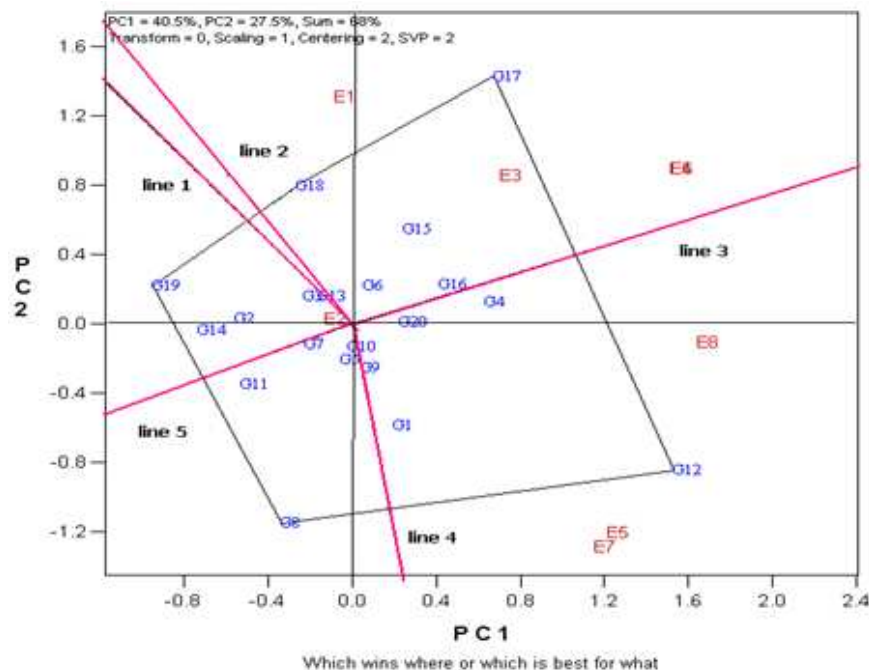
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ABSTRACT

The objective of this study was to explore the effect of genotype (G) and genotype \times environment interaction (GEI) on grain yield of 20 chickpea genotypes under two different rainfed and irrigated environments for 4 consecutive growing seasons (2008-2011). Yield data were analyzed using the GGE biplot method. According to the results of combined analysis of variance, genotype \times environment interaction was highly significant at 1% probability level, where G and GEI captured 68% of total variability. The first two principal components (PC₁ and PC₂) explained 68% of the total GGE variation, with PC₁ and PC₂ explaining 40.5% and 27.5% respectively. The first mega-environment contains environments E1, E3, E4 and E6, with genotype G17 (X96TH41K4) being the winner; the second mega environment contains environments E5, E7 and E8, with genotype G12 (X96TH46) being the winner. The environment of E2 makes up another mega-environment, with G19 (FLIP-82-115) the winner. Mean performance and stability of genotypes indicated that genotypes G4, G16 and G20 were highly stable with high grain yield.



Key words: Chickpea, genotype \times environment interaction, combined analysis of variance, GGE Biplot.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is Iran's most important food legume crop, comprising nearly 64% of the area grown to food legumes in the country [1, 21]. Chickpea is grown on 700,000 ha in Iran and ranks fourth in the world after India, Pakistan and Turkey [2]. The agricultural sector of Iran is attempting to improve high yielding chickpea genotypes with identification and introducing of stable and adaptive cultivars [3, 4]. However, high yield is often associated with decreased yield stability [5]. The terms 'stability' or 'adaptability' refer to consistent high performance of genotypes across diverse sets of environments [6]. In order to identify the most stable and high yielding genotypes, it is important to conduct multi-environment trials [7]. Genotypes tested in different environments often have significant fluctuations in yield due to the response of genotypes to environmental factors [8]. These fluctuations are often referred as genotype \times environment interaction (GEI). The methods used for evaluation of GEI and stability performance can be classified into two groups: graphical (GGE biplot and performance plots) and non-graphical [parametric (univariate and multivariate) and non-parametric].

The yield of each cultivar in each test environment is a mixture of environment main effect (E), genotype main effect (G) and genotype \times environment interaction (GEI). Moreover, G and GE must be considered simultaneously when making cultivar selection decisions. For this reason, instead of trying to separate G and GE, Yan *et al.* [9] combined G and GE and referred to the mixture as GGE. Yield data from regional performance trials, or more generally, multi environment trials (MET), are usually quite large, and it is difficult to understand the general pattern of the data without some kind of graphical presentation. The biplot technique [10] provides a powerful solution to this problem. A biplot that displays the GGE of a MET data, referred to as a GGE Biplot (graphical method), is an ideal tool for MET data analysis [11, 12]. In analyzing Ontario winter wheat performance trial data, Yan and Hunt [13] used a GGE biplot constructed from the first two principal components (PC₁ and PC₂) derived from PC analysis of environment-centered yield data. GGE biplot can be useful in two major aspects. The first is to display the which-won-where pattern of the data that may lead to identify high-yielding and stable cultivars and discriminating the representative test environments [12].

The objectives of this study were (i) to interpret G main effect and GE interaction obtained by combined analysis of yield performances of 20 chickpea genotypes over eight environments (ii) application of the GGE biplot technique to examine the possible existence of the different mega-environments in chickpea-growing regions and (iii) visually assess how to vary yield performances across environments based on the GGE Biplot.

MATERIALS AND METHODS

Plant materials

In order to identify stable and high performance genotypes of chickpea (Table 1) a randomized complete block design (RCBD) with three replications was carried out in two different environments (rainfed and irrigated) for four growing seasons (1387-1390) (8 environments E1 to E8) in the Campus of Agriculture and Natural Resources of Razi University of Kermanshah, Iran (47° 20' N, 34° 20' E and 1351 m above sea level). The maximum and minimum temperatures were 44°C and -27°C and the average rainfall was 478 mm. The soil of experimental field was clay loam with pH7.1.

Each plot consisted of five rows of 1.5 meter length. Row to row and hill-to-hill distances were kept at 30 and 10 cm, respectively. Data on seed yield were taken from the middle three rows of each plot. At harvest seed yield was determined for each genotype at each test environments.

Table 1. The codes and names of chickpea genotypes

Genotype Codes	Genotype names	Genotype Codes	Genotype names
G ₁	X96TH54	G ₁₁	X95TH12
G ₂	FLIP-82-150C	G ₁₂	X96TH46
G ₃	FLIP-00-40C	G ₁₃	FLIP-82-245
G ₄	S96085	G ₁₄	X95TH154
G ₅	Bivanich	G ₁₅	ILC482
G ₆	S925274	G ₁₆	FLIP-99-26C
G ₇	S91181	G ₁₇	X96TH41K4
G ₈	S95349	G ₁₈	X95TH69
G ₉	Hashem	G ₁₉	FLIP-82-115
G ₁₀	ARman	G ₂₀	FLIP-00-6C

Statistical analysis

Analysis of variance was conducted by SAS, software to determine the effect of environment (E), genotype (G) and GE interaction. The first two components resulted from principal components were used to obtain a biplot by GGE biplot software [11]. The basic model for a GGE biplot is :

$$Y_{ij} - \mu - \beta_j = \sum_{i=1}^k \lambda_l \xi_{il} \eta_{lj} + \varepsilon_{ij} \quad (1)$$

Where Y_{ij} = the mean yield of genotype $i(=1,2,\dots,n)$ in environment $j(=1,2,\dots,m)$, μ = the grand mean, β_j = the main effect of environment j , $(\mu + \beta_j)$ being the mean yield of environment j , λ_l = the singular value (SV) of l th principal component (PC), the square of which is the sum of squares explained by $PC_l(=1,2,\dots,k$ with $k \leq \min(m,n)$ and $k=2$ for a two-dimensional biplot), ξ_{il} = the eigenvector of genotype i for PC_l , η_{lj} = the eigenvector of environment j for PC_l , ε_{ij} = the residual associated with genotype i in environment j .

To generate a biplot that can be used in visual analysis of MET data, the SVs have to be partitioned into the genotype and environment eigenvector so that the model (1) can be written in the form of

$$Y_{ij} - \mu - \beta_j = \sum_{i=1}^k g_{il} e_{lj} + \varepsilon_{ij}$$

where g_{il} and e_{lj} are called PC_l scores for genotype i and environment j , respectively. In a biplot, genotype i is displayed as a point defined by all g_{il} values, and environment j is displayed as a point defined by all e_{lj} values ($l=1$ and 2 for a two-dimensional biplot) [14].

RESULTS AND DISCUSSION

According to the results of combined analysis of variance (**Table 2**), genotype \times environment interaction was highly significant for grain yield indicating that we can proceed and calculate phenotypic stability. GGE biplot was constructed using the first two principal components (PC_1 and PC_2) derived from subjecting the environment-centered data to singular-value decomposition [15]. Results of GGE biplot also showed that the first two principal components (PC_1 and PC_2) justified 68% of the sum of squares with $PC_1=40.5\%$ and $PC_2=27.5\%$ of the GGE sum of squares. GGE biplot graphically displays G plus GE of a MET in a way that facilitates visual cultivar evaluation and mega-environment identification [9]. Only two PC (PC_1 and PC_2) 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, PC_1 and PC_2 can be readily displayed in a two dimensional biplot so that the interaction between each genotype and each environment can be visualized [14].

Table 2. Combined analysis of variance over eight environments

S.O.V	Df	Mean square
Environment(E)	7	418712.32**
Error1	16	3889.40
Genotype (G)	19	11986.47**
G \times E	133	3412.82**
Error2	304	2301.64
C.V.	-	29.60

** : significant at the 1% level of probability

Winning Genotype and Mega-environment

Visualization of the “which-won-where” pattern of MET data is important for studying the possible existence of different mega-environments in a region [9, 12] (**Fig. 1**). The polygon view of a biplot is the best way to visualize the interaction patterns between genotypes and environments and to effectively interpret a biplot [16]. The vertex genotypes in this investigation were G8, G12, G17 and G19. The vertex genotype for each sector is the one that gave the highest yield for the environments that fall within that sector. Another important feature of **Fig. 1** is that it indicates environmental groupings, which suggests the possible existence of different mega-environments. Thus, based on biplot analysis of 8 environments of data, three mega-environments are suggested in **Fig. 1**. The first mega-environment contains environments E1, E3, E4 and E6, with genotype G17 (X96TH41K4) being the winner; the second mega environment contains environments E5, E7 and E8, with genotype G12 (X96TH46) being the winner. The environment of E2 makes up another mega-environment, with G19 (FLIP-82-115) the winner.

Mean Performance and Stability of Genotypes

In (Fig. 2) the average tester coordinate (ATC X-axis) or the performance line passes through the biplot origin with an arrow indicating the positive end of the axis. The ATC Y-axis or the stability axis passes the plot origin with double arrow head and is perpendicular to the ATC X-axis. The average yield of the genotypes is estimated by the projections of their markers to the ATC X-axis [17]. Genotypes 12 and 17 had the highest mean yield and genotype 19 had the poorest mean yield. Mean yields of the genotypes were in the following order: $G_{12} > G_{17} > G_4 > G_{16} > G_{15} > G_{20} > G_6 = G_1$. The performance of genotypes G_{12} and G_{17} were the most variable (least stable), whereas genotypes G_4 , G_{16} and G_{20} were highly stable with high grain yield.

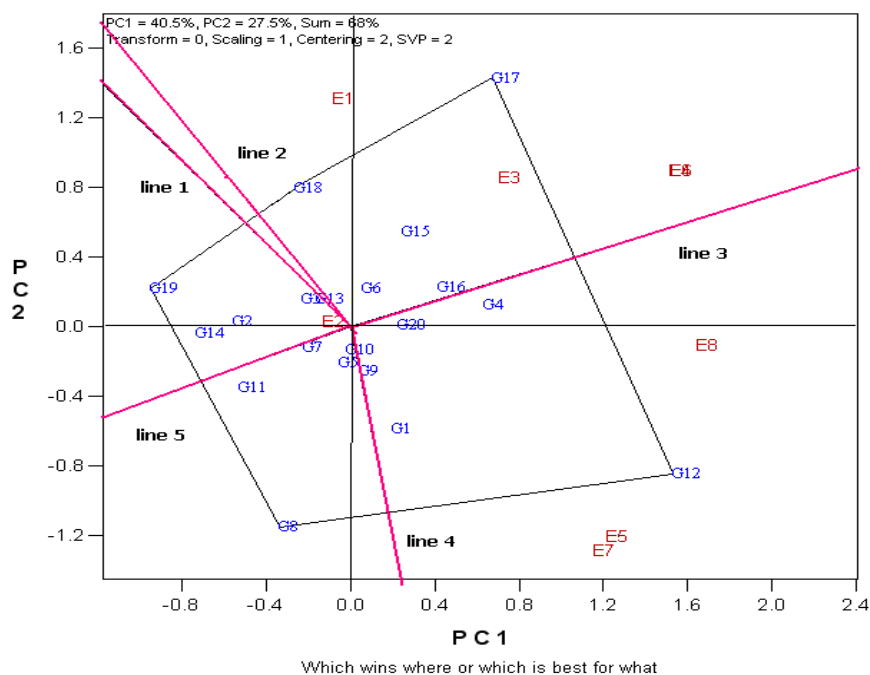


Fig. 1. polygon views of the GGE biplot based on symmetrical scaling for the which-won-where pattern of genotypes and environments

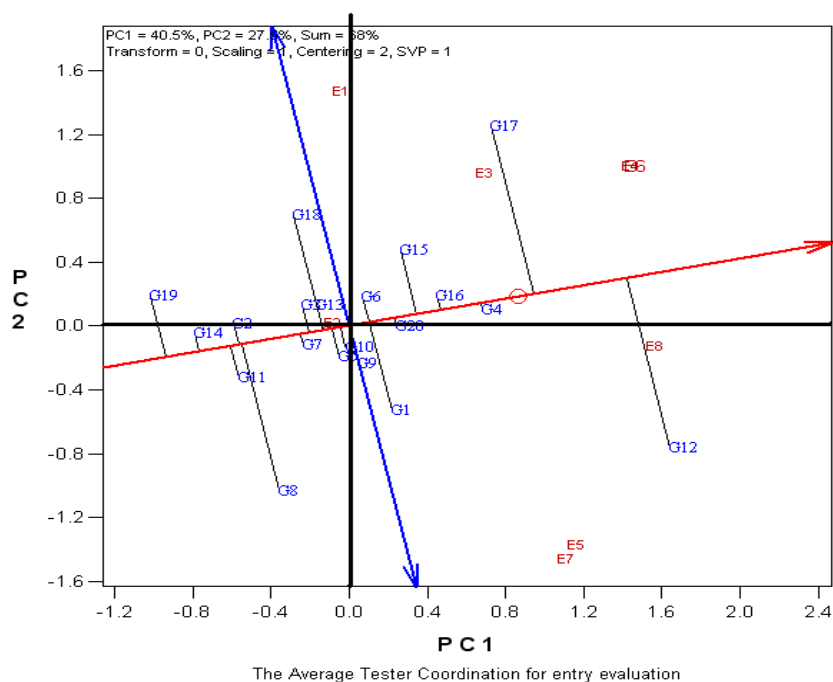


Fig. 2. Average environment coordination (AEC) views of the GGE biplot based on environment- focused scaling for the means performance and stability of genotypes.

Ranking genotypes relative to the ideal genotypes

An ideal genotype is one that has both high mean yield and high stability. The center of the concentric circles (**Fig. 3**) represents the position of an ideal genotype, which is defined by a projection onto the mean-environment axis that equals the longest vector of the genotypes that had above-average mean yield and by a zero projection onto the perpendicular line (zero variability across environments). A genotype is more desirable if it is closer to the ideal genotype. Although such an ideal genotype may not exist in reality, it can be used as a reference for genotype evaluation [18].

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 genotype 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 [19]. Therefore, genotypes G₄ and G₁₂ which fell into the center of concentric circles, were ideal genotypes in terms of higher yield ability and stability, compared with the rest of the genotypes. In addition G₁₅, G₁₆ and G₁₇ located on the next concentric circle, may be regarded as desirable genotypes.

Ranking environment relative to the ideal environment

The GGE biplot way of measuring representativeness is to define an average environment and use it as a reference or benchmark. The average environment is indicated by small circle (**Fig. 4**). The ideal environment, represented by the small circle with an arrow pointing to it, is the most discriminating of genotypes and yet representativeness of the other tests environments.

Therefore, E₈ was the most desirable test environment followed by E₄ and E₆

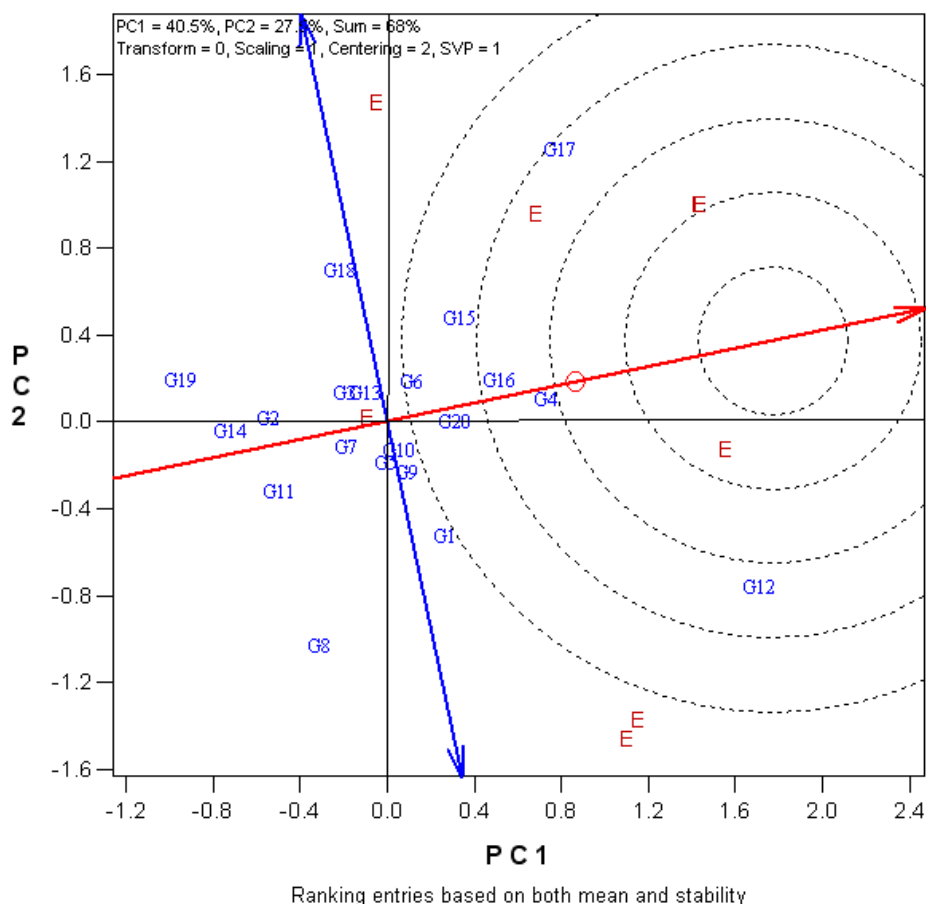


Fig. 3. GGE biplot based on genotype – focused scaling for comparison. The genotypes with the ideal genotype.

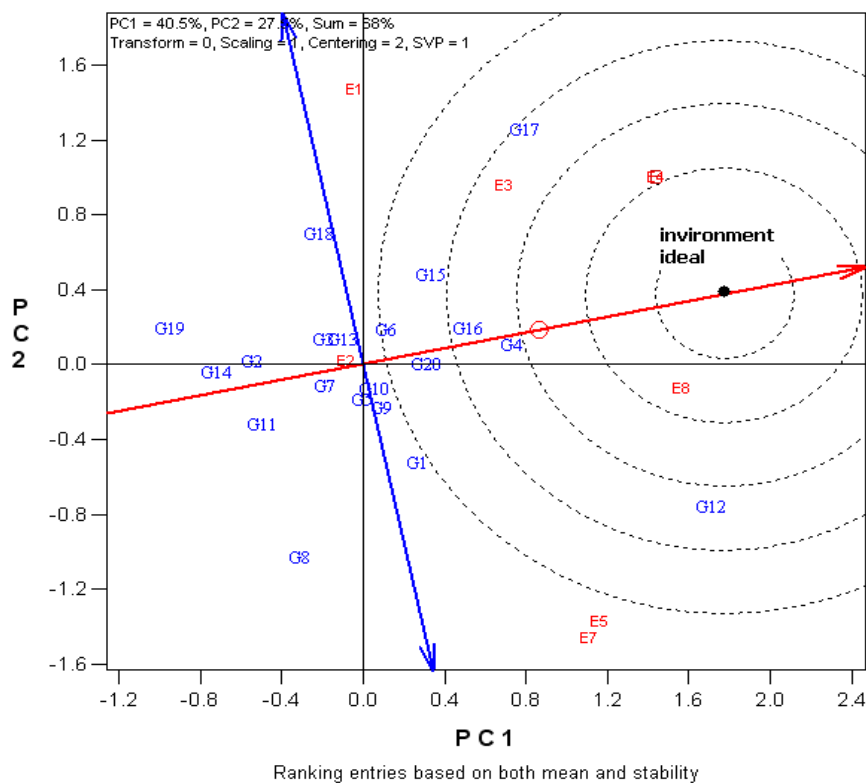


Fig. 4. GGE biplot based on environment-focused scaling for comparison the environments with the ideal environment.

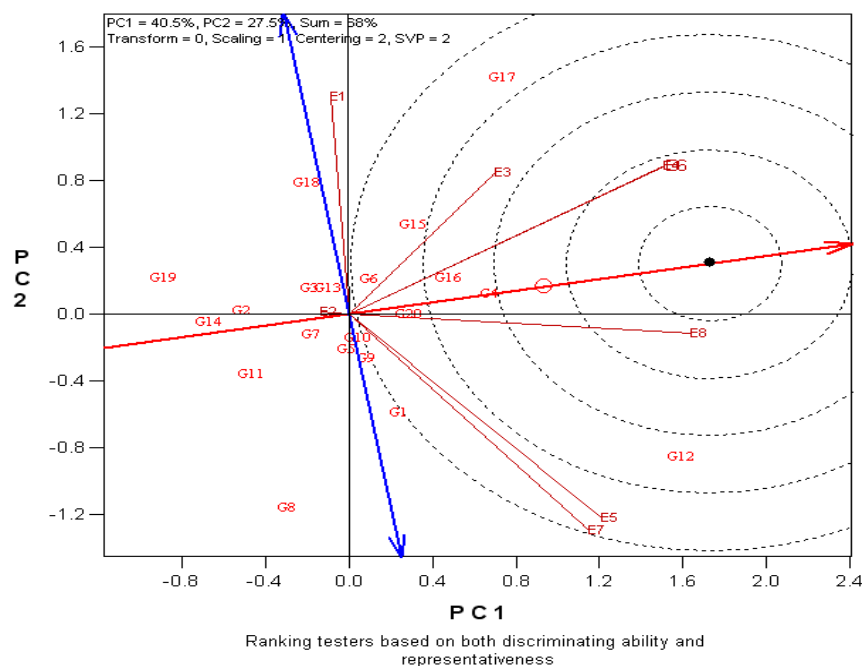


Fig. 5. GGE biplot based on discriminating power and representativeness of the test environment.

Fig.5 is the same GGE biplot as (**Fig.4**) expect that it is based on environment-focused scaling [19]. This type of AEC can be referred to as the "Discriminating power vs. Representativeness" view of the GGE biplot. it can be helpful in evaluating each of the test environments with respect to the following questions: [20].

1. is the test environment capable of discriminating among the genotypes, i.e., does it provide much information about the differences among genotypes?
2. Is it representative of the mega-environment?

3. Does it provide unique information about the genotypes?

Thus E_8 may be regarded as an ideal test environment and E_4 , E_6 , may constitute a next set of test environments if the pattern shown in (Fig.5) is repeatable across years.

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