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Interpretation of Genotype-by-Environment Interaction for Late Maize Hybrids' Grain Yield Using a Biplot Method

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Abstract: The stability of grain yield of 11 late maize hybrids with a check cultivar were studied in a randomized complete block design with 4 replications for 2 years at 11 sites in multi-environment trials in Iran. The obtained data were analyzed with a GGE [genotype + (genotype × environment interaction)] biplot method. The first 2 principal components (PC1 and PC2) were used to create a 2-dimensional GGEbiplot and explained 44% and 27% of GGE sum of squares (SS), respectively. Ranking of the genotypes based on the ideal genotype revealed that grain yields of G2, G3, and G12 were higher together with being more stable. Ranking of environments for the ideal environment showed that site Rasht (RAS) was the most discriminating, whereas site Hamedan (HAM) was the most representative. There were 5 winning genotypes and 3 mega-environments in our study. The GGE biplot suggests 3 late maize mega-environments in Iran: a minor mega-environment (northern Iran consisting of Rasht and Ghaemshahr), an average one (southern and central Iran consisting of Shiraz (SHI) and Esfahan (ESF)), and a major one (western and central Iran consisting of Arak (ARA), HAM, Karaj (KAR), Kermanshah (KER), Khoramabad (KHO), Varamin (VAR), and Sanandaj (SAN)). As a result, the findings from our study are as follows: (1) genotype G2 was the most stable and is thus recommended for commercial release in Iran; (2) the GGEbiplot method can be used to identify superior genotypes for target sites in Iran and sites in other parts of the world.

Key Words: Multi-environmental trials, GGEbiplot, maize (*Zea mays* L.)

Abbreviations: GGE, G+GE; GE, Genotype × Environment; MET, Multi-Environment Trials; PC, Principal Component.

Introduction

Newly improved cultivars generally need to be tested at many sites and for several years before being recommended for a given site. The main environmental effects (E) and genotype environment interaction (GE) have been reported as the most important sources of variation for the measured yield of crops (Lee et al., 2002; Dehghani et al., 2006; Yan et al., 2007; Sabaghnia et al., 2008). For this reason, multi-environmental trials (METs) are conducted throughout the world for major crops every year (Ma et al., 2004).

Although the measured yield is a combined result of the effects of the genotype (G), E and GE interaction, only G and GE are relevant to cultivar evaluation and mega-environment identification. Typically, E explains most (80% or higher) of the total yield variation, while G and GE are usually small (Yan and Kang, 2003). However, effective interpretation and utilization of MET data in making selection decisions remain a major challenge to researchers. Some important concepts such as mega-environment, specific adaptation, and stability all originate from the GE interaction. A significant GE interaction for grain yield can reduce the usefulness of

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subsequent analysis and limit the feasibility of selecting superior cultivars (Flores et al., 1998).

Numerous methods have been used in trying to understand the causes of the GE interaction (Yan and Hunt, 2001; Crossa et al., 2002). These methods can be categorized into 3 major strategies (Flores et al., 1998). The first strategy involves univariate methods such as environmental variance analysis (Becker, 1981). The second strategy is associated with the use of multivariate analysis such as the Additive Main Effects and Multiplicative Interaction model (AMMI) suggested by Zobel et al. (1988). These methods are parametric and use parametric statistics for stability, while the third strategy uses nonparametric statistics, which are unaffected by data distribution and based on ranks. Several nonparametric methods have been developed such as rank-sum (Kang, 1988).

Although these strategies may differ in overall appropriateness, different methods usually lead to the same or similar conclusions for a given dataset. Using a site regression model (SREG), Yan et al. (2000) combined G and GE, and repartitioned this into a non-crossover GE and a crossover GE interaction and proposed a graphical technique (the so-called GGEbiplot) to summarize the G and GE and to address the issue of cultivar recommendation in MET. Dehghani et al. (2006) in barley (*Hordeum vulgare* L.), Mohammadi et al. (2007) in wheat (*Triticum aestivum* L.), and Sabaghnia et al. (2008) in lentil (*Lens culinaris* Medik) previously exploited the GGEbiplot methodology in GE interaction evaluation and mega-environment investigation in Iran. Dehghani et al. (2006) in visualization of the "which-won-where" pattern of barley MET data and mega-environments identification released 3 different mega-environments for barley producing areas of Iran. Mohammadi et al. (2007) in collective analysis of the yearly biplots for 20 winter wheat genotypes currently grown in the 6 sites suggested 4 winter wheat mega-environments in Iran. In addition, Sabaghnia et al. (2008) suggested that there exist 3 possible lentil mega-environments in Iran. However, they mentioned that this mega-environment pattern needs verification through other METs for this target region.

The objectives of our study were (1) to interpret G, E, and GE interaction effects for grain yield of 12 late maize hybrids in 11 Iranian sites using the GGEbiplot method, and (2) to make a "first" environmental classification of the maize growing environments in Iran based on crossover interactions according to GGE methodology.

Materials and Methods

Data from 2 years' maize late (*Zea mays* L.) hybrid performance trials were used in this study. Eleven genotypes with a check cultivar (G12) were tested in 11 field crop stations: Arak (ARA), Esfahan (ESF), Ghaemshahr (GHA), Hamedan (HAM), Kermanshah (KER), Karaj (KAR), Khoramabad (KHO), Rasht (RAS), Sanandaj (SAN), Shiraz (SHI), and Varamin (VAR) at different ecological sites in Iran, during the 1993-1994 and 1994-1995 growing seasons. The climatic characteristics of the experimental environments are given in Table 1. In each environment, a randomized complete block design with 4 replications was used. The experiments were set up with a planting density of about 50,000 plants ha⁻¹. All management operations were performed as and when necessary to obtain optimum crop growth. Appropriate pesticides were used to control insects, weeds, and diseases, and appropriate fertilizers were applied at the recommended rates as usual in the environment. The plot size was 20.16 m² and each plot consisted of 4 rows with a row spacing of 0.75 m and length of 6.72 m. Grain yield was obtained from a sample of 17.28 m² in the center of the plot from each genotype at each combination of year and site. Upon harvest grain yield was determined for each genotype in each test environment; the average yield was computed in accordance with the experimental design. The Bartlett test for variance homogeneity was significant and therefore square root transformation was applied to the primary data. The results showed that these data had homogeneous variances and all the analyses were performed on the transformed data.

For computing the combined analysis, the effects of year and site were assumed random but the genotype effect was assumed fixed. Thus, the main effects of Y and S were tested against Y × S interaction and the Y × S interaction was tested against the replication within the environment (R/Y × S) term. The G × Y and G × S interactions were tested against the G × S × Y interaction, and the G × S × Y interaction was tested against the residual. The genotype's main effect was tested against (G + G × S × Y) / (G × Y + G × S).

The GGEbiplot method was used to interpret G, E, and GE interaction effects for grain yield of 12 late maize hybrids in 11 Iranian sites and to make a "first" environmental classification of the maize growing environments in Iran based on crossover interactions

Table 1. Climatic characteristics of testing sites.

Sites	Geographic position		Altitude (m)	Rainfall (mm)	
	Latitude	Longitude		93-94	94-95
Arak (ARA)	34°06' N	49°46' E	1708	400.9	429.5
Esfahan (ESF)	32°37' N	51°40' E	1590	198.9	212.3
Ghaemshahr (GHA)	36°27' N	52°53' E	14.7	673.9	845.3
Hamedan (HAM)	35°12' N	48°41' E	1679.7	327.4	662.4
Kermanshah (KER)	34°19' N	47°07' E	1322	587.9	702.6
Karaj (KAR)	35°56' N	50°58' E	1312.5	251.1	339.1
Khoramabad (KHO)	33°29' N	48°22' E	1125	771	706.1
Rasht (RAS)	37°15' N	49°36' E	-6.9	1895.3	1446.4
Sanandaj (SAN)	35°20' N	47°00' E	1373.4	524.9	645.2
Shiraz (SHI)	29°33' N	52°36' E	14.91	341.5	371
Varamin (VAR)	35°28' N	51°44' E	1180	165.1	213

according to GGE methodology. For further details on the theory and application of GGEbiplots, see Yan and Kang (2003). All the statistical analyses were carried out using SAS version 6.12 (SAS Institute, 1996) and GGEbiplot software (Yan, 2001).

Results

The actual mean yield of the maize genotypes is given in Table 2 and the maximum yield values at each environment are underlined. Analysis of variance was conducted to determine the effects of year (Y), site (S),

Table 2. Mean yield data (kg ha⁻¹) of 12 late maize genotypes tested in 11 sites of Iran.

Genotypes	Sites											
	KAR	GHA	SHI	VAR	HAM	KHO	SAN	RAS	ESF	ARA	KER	MEAN
G1	<u>14,044</u>	10,171	<u>11,495</u>	7147	10,733	14,429	8804	9433	<u>9669</u>	9973	8050	10,359
G2	12,880	11,811	8868	6904	10,300	13,924	9366	10,442	8019	11,886	7966	10,215
G3	13,691	10,056	9078	8552	11,065	13,694	9827	8608	7956	<u>12,601</u>	7887	10,274
G4	12,053	10,088	8348	5998	9614	13,043	8918	9783	9159	9009	7954	9451
G5	12,486	10,786	8124	7900	9717	11,868	8977	9451	8038	10,075	6391	9438
G6	13,033	9407	10,934	8919	10,952	13,391	8751	6094	8476	10,339	7441	9794
G7	12,782	9832	8421	8109	9564	13,719	9107	9693	8571	11,748	8230	9980
G8	13,114	10,118	8061	8637	9605	13,178	9502	8457	7898	11,135	8549	9841
G9	12,769	10,653	7442	8391	9675	13,829	9382	10,212	8183	10,932	8731	10,018
G10	13,315	12,113	8105	8649	10,207	12,634	9853	11,715	8290	10,970	8121	10,361
G11	13,231	11,478	7813	<u>9178</u>	9831	<u>15,687</u>	<u>10,103</u>	11,424	7554	12,137	7772	10,564
G12	13,254	<u>12,633</u>	7925	8526	<u>11,431</u>	14,370	9766	<u>12,069</u>	8414	11,146	<u>8772</u>	<u>10,755</u>
Mean	13,054	10,762	8718	8076	10,224	<u>13,647</u>	9363	9782	8352	10,996	7989	10088

^aUnderlined digits are the maximum yield values at each site.

and genotype (G), and all possible interactions among these factors. The results of combined analysis of grain yield across sites and years are given in Table 3. The interaction effects of $Y \times S$, $G \times S$, and $G \times Y \times S$ were significant at the $P < 0.01$ level for grain yield, while the main effect of genotype (G) was significant at the $P < 0.05$ level. The main effects of year, site, and $Y \times G$ interaction were not significant. The variance components for the site, genotype, and genotype \times site based on the yearly data are presented in Table 4 giving an overall picture of the relative magnitudes of the genotype (G), site (S), and genotype \times site interaction (GS) variance terms. S was always the most important source of yield variation, accounting for 79.16% to 84.14% of the total variance ($G + S + GS$) in the 2 years (Table 4). When

fitting the GGE model, the first 2 PCs explained 71% of total variance (44% and 27% by PC1 and PC2, respectively).

The performance of different genotypes in a given site: In this study site KAR (the Headquarters of Iran's Agricultural Research Stations) was selected as a check tester. Figure 1a illustrates a graphic comparison of the relative performance of all the genotypes at KAR (i.e. all genotypes were ranked in the direction of the tester axis). It was done by drawing a straight line passing through the plot origin and the marker of KAR. A perpendicular line (also passing through the plot origin) was drawn to this line that separates the genotypes with grain yields below and above the average in this selected tester site. The parallel lines help visualize the ranking of the cultivars.

Table 3. Combined analysis of variance for grain yield of 12 late maize hybrids tested in 11 sites over the 1993-94 and 1994-95 growing seasons in Iran.

Source	df	Type III SS	MS	F	% of total
Year (Y)	1	14,001.9	14,001.9	3.37 ^{ns}	8.4
Site (S)	10	59,176.3	5917.6	1.41 ^{ns}	35.8
$Y \times S$	10	41,479	4147.9	33.34 ^{**}	25.1
Rep / ($Y \times S$)	66	8213.7	124.4		
Genotype (G)	11	3184.1	289.4	2.124*	1.9
$Y \times G$	11	640	58.2	0.95 ^{ns}	0.3
$S \times G$	110	11,736.9	106.6	1.75 ^{**}	7.1
$Y \times S \times G$	110	6680.5	60.7	2.19 ^{**}	4
Pooled Error	726	20,099.9	27.6		
Total	1055	165,212.3			

*, ** Significant at 0.05 and 0.01 level of probability, respectively.

^{ns} Non-significant.

Table 4. Genotype (G), site (S) and genotype by site (GS) variance terms for grain yield of 12 late maize hybrids multi-site trials at individual years.

Source	d.f	SS †	% of S + G + GS
1993-94			
Site (S)	10	56,980.05	84.14
Genotype (G)	11	1675.341	2.47
GS	110	9067.169	13.13
1994-95			
Site (S)	10	43,675.23	79.16
Genotype (G)	11	2149.11	3.89
GS	110	9350.348	16.94

† SS is sum of squares.

Therefore, genotype G3 had the highest yield at KAR, followed by G12, G2, G6, G1, and G11, but G4 and G5 had the poorest yield at KAR, followed by G7, G8, G9, and G10. G1, G8, G9, and G10 were relatively near the perpendicular line, meaning that the performance of these genotypes was close to the average.

The relative adaptation of a given cultivar in different environments: In this research, G12 was selected as the check entry; therefore, the relative adaptation of this check cultivar was compared in different sites (Figure 1b). Drawing a straight line passing

through the plot origin and the marker of G12, and then drawing a perpendicular line to this line from the site marker achieved this. Thus, the relative adaptation and yield performance of G12 in all sites were: RAS > GHA > HAM > SAN = ARA = VAR > KHO > KAR > KER > SHI > ESF. The perpendicular line to the G12 axis separates the sites in which G12 yielded below the average (ESF and SHI) from the sites in which G12 yielded above the mean (all the other sites except ESF and SHI). However, sites SHI and KER were relatively near the perpendicular line, meaning that G12 yielded near the mean in these sites.

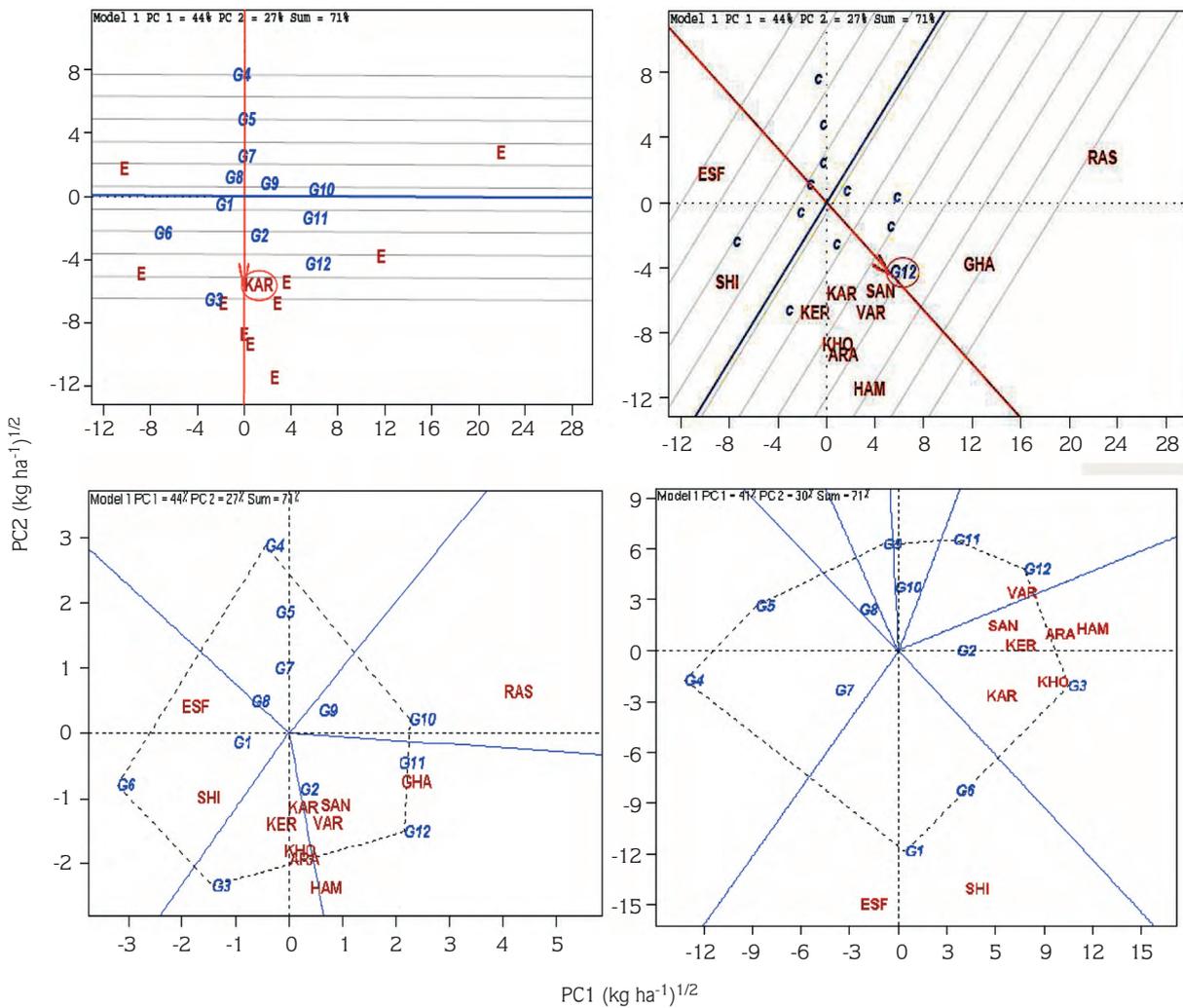


Figure 1. (a) Performance of different genotypes in site KAR, (b) Relative performance of genotype G12 in different sites, (c) Polygon view of the GGEbiplot for the genotype by environment 2-way data, showing which genotypes yielded most in each of the sites and (d) GGEbiplot polygon after sites GHA and RAS were removed. PC1 and PC2 are first and second principal components, respectively; the sites are Arak = ARA, Esfahan = ESF, Ghaemshahr = GHA, Hamedan = HAM, Kermanshah = KER, Karaj = KAR, Khoramabad = KHO, Rasht = RAS, Sanandaj = SAN, Shiraz = SHI and Varamin = VAR.

Who-won-where pattern for the genotypes: The polygon view of a biplot provides the best way for visualizing the interaction patterns between the genotypes and sites and to effectively interpret a biplot. For this purpose, the genotypes were connected with straight lines so that a polygon was formed with all the other genotypes contained within the polygon (Figure 1c). The vertex genotypes in this study were G3, G4, G6, G10, and G12. These genotypes were the best or the poorest genotypes in some or all of the sites since they had the longest distance from the origin of the biplot. For each side of the polygon, a perpendicular line was drawn, starting from the origin of the biplot, so that the biplot was divided into sectors and sites fell into the same or different sectors.

There are 5 sectors in Figure 1c. The vertex genotype for each sector is the one that gives the highest yield for the sites that fall within that sector. Therefore, G3 showed the highest performance in the sites ARA, HAM, KAR, KER, and KHO, while G4 was the poorest genotype in the study (never had the highest yield at any of the test sites). Similarly, G6 performed best at sites ESF and SHI, whereas G12 was the best at sites GHA, SAN, and VAR. On the other hand, the last vertex genotype, G10, was well adapted to site RAS.

Lines perpendicular to the polygon sides connecting the genotypes facilitate the comparison among the vertex genotypes. The comparison between G3, G10, and G12 with G6 and G4 showed that the first 3 yielded higher than the last 2 in all the sites except ESH and SHI, because all the other sites were on the side of the first 3. The

perpendicular line cutting the polygon side that connects G3 with G6 showed that G3 yielded higher than G6 in the 5 sites that fall into the G3 sector. G12 yielded higher than G6 in the 3 sites that fall into the G12 sector as well.

Likewise, the line perpendicular to the polygon side that connects G3 and G12 facilitates the comparison between G3 and G12. Genotype G3 yielded higher than G12 in the 5 sites that fall into the G3 sector, but yield performance of G3 and G12 in the sites HAM and KAR was very similar.

Mega-environment classification: Another use of Figure 1c is that the sites are grouped based on the best genotypes. Accordingly, we have 4 groups of sites: ESF and SHI as the first group; ARA, HAM, KAR, KER, and KHO as the second group; and GHA, HAM, KAR, VAR, and SAN as the third group. Site RAS was the only site within the fourth group. These groups suggest 4 mega-environments. It is worth noting that HAM and KAR sites are in both the second and third groups.

A subset of the data can be analyzed by removing some of the genotypes or sites. Since climate conditions in the RAS and GHA sites (high rainfall and different edaphic conditions) are different from the others, we removed them and then grouped the rest by polygon view (Figure 1d). RAS and GHA sites are different from the rest and are each other similar in some degree, which could lead one to suggest that site GHA can be added to the site RAS to form a distinct group made up by 2 sites. It is also confirmed by the highly significant correlation coefficient ($r = 0.79, P < 0.01$) between these 2 sites in Table 5.

Table 5. Correlation coefficient among test sites.

Sites	ARA	ESF	GHA	HAM	KAR	KER	KHO	RAS	SAN	SHI
ESF	- 0.17									
GHA	0.21	- 0.60*								
HAM	0.46	- 0.25	0.42							
KAR	0.46	0.18	0.29	0.41						
KER	0.44	- 0.10	- 0.10	0.33	0.39					
KHO	0.61*	- 0.01	- 0.12	0.62*	0.65*	0.56				
RAS	- 0.11	- 0.55	0.79**	0.03	0.02	- 0.32	-0.06			
SAN	0.55	- 0.22	0.46	0.31	0.50	0.32	0.76**	0.33		
SHI	0.16	0.72**	- 0.38	0.22	0.53	0.14	0.43	- 0.53	0.01	
VAR	0.41	- 0.34	- .033	0.40	0.71**	.044	0.45	0.09	0.40	- 0.06

*, ** Significant at 0.05 and 0.01 level of probability, respectively.

Moreover, Figure 1c shows similarities between groups 2 and 3, which could be considered as 1 large mega-environment. Actually, the removal of these 2 sites (RAS and GHA) (Figure 1d) serves as a confirmation that they could be thought of as a different mega-environment for maize in Iran, and that groups 2 and 3 in Figure 1c form 1 mega-environment. Then, after a joint observation of these 2 biplots (Figures 1c and 1d) it seems that there are 3 mega-environments for maize in Iran: [i] mega-environment 1 (MG1) consists of sites ESF and SHI, [ii] MG2 consists of sites ARA, HAM, KAR, KER, KHO, VAR, and SAN, and [iii] MG3 consists of sites RAS and GHA. The first and second champion genotypes per mega-environment based on SREG analysis of variance for grain yield of 12 late maize hybrids in 3 mega-environments are given in Table 6.

Ideal environment and genotype: An ideal genotype, which is located at the center of the concentric circles in Figure 2a, is one that has both high mean yield and high stability. Ideal genotype projection on the average tester coordinate (ATC) x-axis is designed to be equal to the longest vector of all the genotypes. The ideal genotype is stable because its projection on the ATC y-axis is zero. Genotypes are ranked based on the average yield and stability of the ideal genotype. A genotype is more favorable if it is closer to the ideal genotype. Therefore, G2 was more reliable (a reliable genotype is characterized

by consistently high yield and stability across the environments (Annicchiarico, 2002)) than all the other genotypes, followed by G3 and G12 as a group. Ranking of other genotypes based on the ideal genotype was $G11 > G1 > G9 > G8 > G10 > G7 > G6 > G5 > G4$. In other words, the lower yielding genotypes of G4, G5, G6, G7, G10, G7, and G9 are unfavorable because they are far away from the ideal genotype. The relative contributions of stability and grain yield to the identification of desirable genotype found in this study by the ideal genotype procedure of the GGEbiplot are similar to those found in other crop stability studies (i.e. maize (Fan et al., 2007), barley (Dehghani et al., 2006), wheat (Kaya et al., 2006), and rice (Samonte et al., 2005)).

Although MET data are used for genotype evaluation, they can also be used in site evaluations. An ideal site should be highly differentiating of the genotypes and at the same time representative of the target site. In Figure 2b, the sites are ranked based on both discriminating ability and representativeness. The center of the concentric circles is where an ideal environment should be; its projection on the ATC x-axis was designed to be equal to the longest vector of all environments; therefore, it is the most discriminating; its projection on the ATC y-axis was obviously zero, meaning that it is absolutely representative of the average environment (Yan, 2001). Therefore, the closer a site is to this virtual site, the better it is as a test site. Thus, HAM was a relatively favorable test site, followed by ARA and KHO as a group; VAR as a group; KAR, KER, and SAN as a group; and SHI as a group, whereas ESF and RAS were the poorest test sites. The KAR projection on ATC y-axis in this study was zero, representing an average site.

Correlation among the sites: In Figure 2c, a vector is drawn from the biplot origin to each marker of the sites to facilitate visualization of the relationship among the sites. The correlation coefficient between any 2 sites is approximated by the cosine of the angle between the vectors. Therefore, the most prominent relations according to Figure 2c are: i) strong negative association between sites RAS with ESF and SHI; between ESF and GHA as indicated by the large obtuse angles between their vectors ($r = \cos 180 = -1$), and ii) near zero correlation between RAS with ARA, HAM, KAR, KER, SAN, VAR, and KHO; between GHA and KER; between ESF with ARA, HAM, KAR, KER, and KHO; and between SHI with SAN, VAR, and KAR as indicated by the near perpendicular vectors ($r = \cos 90 = 0$).

Table 6. The first and second winning genotypes based on SREG analysis of variance for grain yield of 12 late maize hybrids in 3 mega-environments.

Mega-environments	Location	A†	B‡
MG1	ESF	G1	G6
	SHI		
MG2	ARA	G3	G12
	HAM		
	KAR		
	KER		
	KHO		
	VAR		
	SAN		
MG3	RAS	G10	G12
	GHA		

† The first winning genotype

‡ The second winning genotype

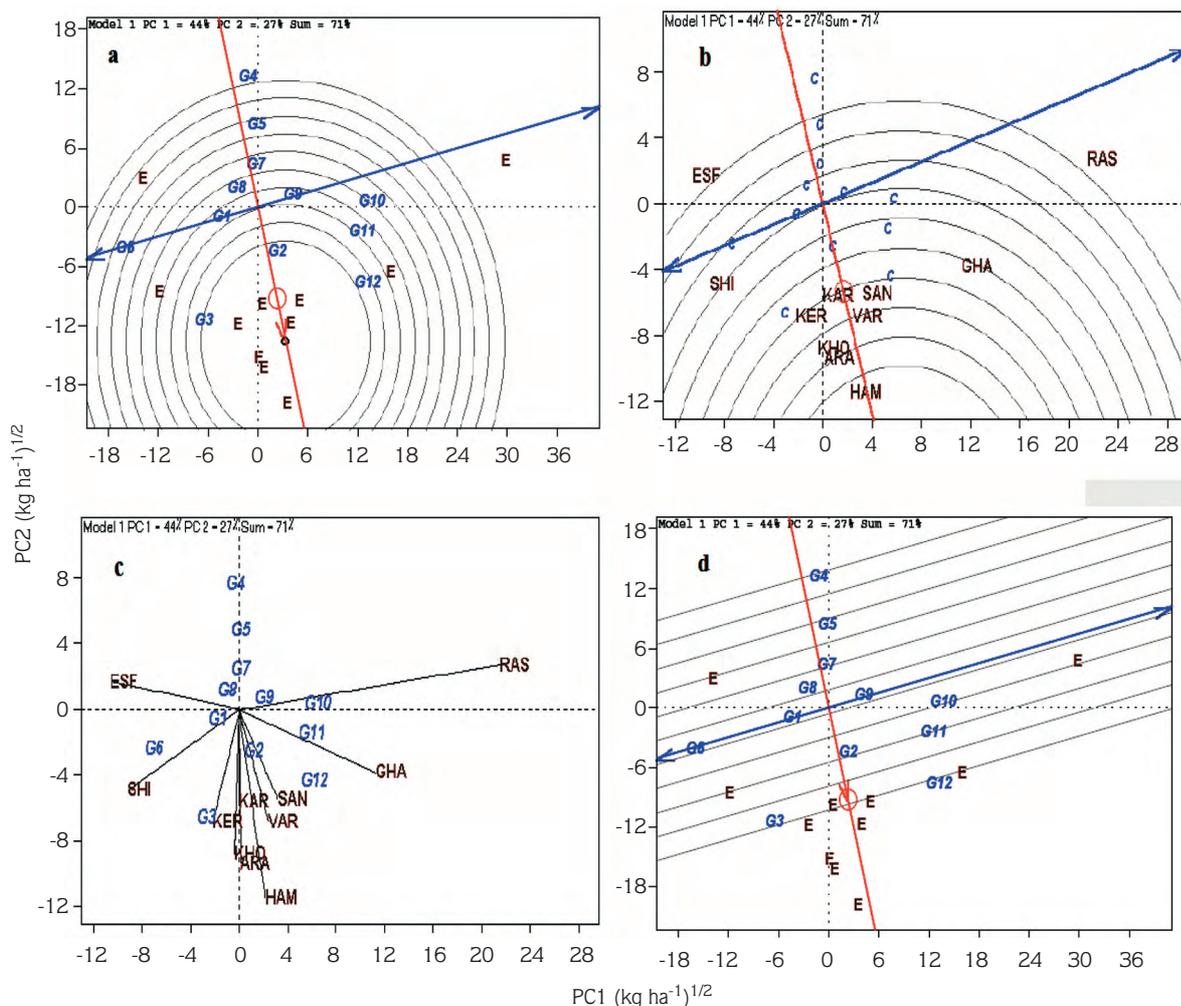


Figure 2. (a) Comparison of the genotypes with the ideal genotype, (b) comparison of the sites with the ideal sites, (c) relationships between sites and (d) mean yield and stability of the genotypes. PC1 and PC2 are first and second principal components, respectively; the sites are Arak = ARA, Esfahan = ESF, Ghaemshahr = GHA, Hamedan = HAM, Kermanshah = KER, Karaj = KAR, Khoramabad = KHO, Rasht = RAS, Sanandaj = SAN, Shiraz = SHI and Varamin = VAR.

Indirect selection can be done in the case where the same character is measured on the same genotype in different sites. Where there are no correlations of error effects among the sites, the phenotypic correlation between the sites may be used to study indirect response to selection (Cooper and DeLacy, 1994). There was a positive association between ESF and SHI and between RAS and GHA and among ARA, HAM, KAR, KHO, KAR, KER, and SAN as indicated by acute angles. The correlation coefficients among the sites indicate that the biplot currently shows a relationship among the sites that had relatively large loading on both PC1 and PC2 (Table

5). Such significant correlation coefficients among test sites suggest that indirect selection for grain yield can be practical across the test sites. For instance, the genotypes adaptable or higher yielding in ESF may also show similar responses to SHI as well. However, indirect selection from one site to another may not be sufficiently successful, considering that for 8 out of 55 sites pair-wise correlations were significant (Table 5).

Visualizing the mean yield and stability of the genotypes: The average yield and stability effects of the genotypes were examined by defining an ATC. The x-axis passes through the biplot origin and the marker of the

virtual site. An average tester (site) is defined as a virtual site whose PC1 and PC2 scores are equal to the average PC1 and PC2 scores, respectively, across all the sites. On the other hand, this virtual site is indicated by a circle and shows the positive end of the ATC x-axis (Figure 2d). The average yield of the genotypes is approximated by the projections of their markers on the ATC x-axis. Thus, the mean yield of the studied genotypes was in the following order: G12 > G3 > G11 > G2 > G10 > G6 = G1 = G9 > G8 > G7 > G5 > G4. This order is highly consistent with the actual mean yield of the genotypes (Table 2).

Since the 2 axes of the mean site coordinate of the GGE-biplot are orthogonal, projection of the genotypes on the perpendicular axis must approximate the GE associated with the genotypes. The longer projection of a genotype regardless of direction, the greater GE associated with the genotype, which is a measure of instability of the genotype across sites. Thus, the performance of G3 and G12 was highly unstable, whereas G2 was highly stable. Although these genotypes (G2, G3, and G12) were in the same group according to the ideal genotype (Figure 2a), G3 and G12 had high yield in comparison to G2, while the stability of G2 was greater in comparison to G3 and G12.

Discussion

Successful cultivars of maize need to be adapted to a broad range of environmental conditions in Iran in order to ensure their yield stability and economic profitability. Farmers are more interested in cultivars that produce consistent yields under their growing conditions and breeders also want to fulfill these needs. Hence, the information on GE interaction and stability is of paramount importance for maize breeders and farmers.

It is clear that the GGEbiplot software is an excellent tool for visual MET data analysis. Compared with conventional methods of the MET data analysis, the GGEbiplot approach has some advantages (Yan and Hunt, 2001; Yan et al., 2007). The first advantage of the biplot is its graphical presentation of the MET data, which greatly enhances our ability to understand the patterns of the data. The second is that it is more interpretative. It facilitates pair-wise genotype comparisons. The third advantage of this method is that it facilitates identification of possible mega-environments.

A potential constraint of the biplot method is that it may fail to explain most of the variation and therefore fail to display all patterns of the data. This is most likely to occur with large datasets, small genotype main effects (G), and complex genotype \times environment interactions (GE). Even when this is the case, it can be ensured that the biplot of PC1 versus PC2 still displays the most important linear patterns of the data (Yan and Hunt, 2001). Nevertheless, other biplots, such as one consisting of PC3 versus PC4, may be needed to fully understand the data. Such options are available in the GGEbiplot software (Yan, 2001). The method of Gauch and Zobel (1996) for estimating patterns versus noise of the data may be adopted to determine if such biplots are needed. The pattern is estimated by the total SS of the environment-centered data minus the noise, which is estimated by the total treatment degrees of freedom, multiplied by the error mean square and can be estimated from replicated data. A biplot of PC3 versus PC4 is needed only when the pattern SS is considerably greater than that explained by the biplot of PC1 versus PC2 (Yan and Hunt, 2001).

Analysis by the GGEbiplot approach in the present research revealed 3 late maize hybrid mega-environments in Iran (Figure 1c and 1d). This has several implications for future breeding and genotype evaluations of maize in Iran. First, different hybrids should be deployed for the 3 mega-environments to achieve optimum adaptation. Second, the fact that 3 mega-environments were identified implies that specific adaptation could be positively exploited. For instance, according to Table 6, winning genotypes at each of the mega-environments (MG1, MG2, and MG3) are different, which means specific adaptation of a genotype to a mega-environment and positive exploitation of the GE interaction. In the case of mega-environments including several locations (as in our case MG2), the low cross-over interactions among sites may lead one to think that recommendation and breeding of late maize hybrids wide adapted to this specific mega-environment are feasible. The finding that some testing sites may be better than others for genotype evaluation suggests that the genotypes may be evaluated at fewer but more representative sites while still achieving the same or even better evaluation. According to results of this analysis, there are 1 key location for MG1, 2 or 3 key locations for MG2, and 1 key location for MG3. This is an important output from our research with some implications for future maize breeding programs in Iran.

Dividing the target locations into different mega-environments and deploying different genotypes in different mega-environments is the best way to utilize the GE interaction. The southern Iran mega-environment (MG1) constitutes only a medium portion of the total Iran maize growing area. The western and center Iran mega-environment (MG2) constitutes the main body of the Iran maize-growing region. The northern Iran mega-environment (MG3) constitutes only a small portion of the total Iran maize-growing area.

In conclusion, G3 and G12 are ideal candidates in this regard as they had the desirable characteristics of high stability with high grain yield for all test locations except for locations RAS, ESF, and SHI. Both yield and stability

of performance should be considered simultaneously to exploit the useful effect of the GE interaction and to make selection of the genotypes more precise and refined. For the locations ESF and SHI, G1 is an ideal candidate, and, for the location RAS, G10 is an ideal candidate in this investigation as they had both desirable specific stability and relatively high grain yield.

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